402.4	2953.0	3818.0	3763.5	3380.6	3358.0	4069.9	3034.0	1571.1	1760.4	2045.0
523.2	2139.0	3705.2	2391.7	2145.3	2443.1	2202.5	2414.8	1686.3	1447.0	2672.4
559.4	2107.9	3998.1	1976.7	1046.3	1800.6	1205.2	1637.0	1600.6	1838.9	1782.1
577.3	3909.0	3939.0	3417.7	4322.9	3594.6	4366.3	3868.6	4288.0	2415.2	3512.2
168.1	382.2	379.8	431.3	219.5	306.9	135.8	270.1	278.2	123.9	110.6
383.2	2256.8	2794.9	2892.5	2731.1	2531.6	2792.4	2867.6	1680.1	889.3	2143.0
1830.5	3537.8	4203.5	3464.1	2776.5	3551.3	3007.9	3419.0	3176.3	5074.5	3631.5
1125.6	4535.8	5955.8	5349.1	4212.2	4834.1	5161.0	4543.6	3631.8	3316.3	4978.1
142.2	2321.8	2673.4	2754.6	1891.5	2028.7	3109.2	2796.2	1610.5	424.9	1642.1
168.1	3678.0	3892.4	3541.5	3755.8	4585.4	3812.2	4027.9	2825.6	1627.4	4731.6
187.5	1154.8	1142.7	1183.6	1613.9	843.5	1110.9	2206.4	542.9	305.4	664.2
5616.9	3169.4	3199.5	3480.8	3220.4	3351.8	4821.4	3116.0	2861.9	2109.9	3253.9
293.0	1966.8	2121.1	1875.6	1747.8	1859.6	1568.7	2398.6	2288.0	1700.2	1516.0
5462.0	4427.5	4267.2	4892.8	5335.3	4047.6	4904.6	3844.0	6519.7	4575.2	6314.7
4289.0	3141.8	3153.3	2843.4	3675.8	3069.9	3595.2	3243.7	1721.2	2070.7	1811.9
45.4	79.0	181.6	94.9	97.6	88.4	94.1	92.3	40.7	36.1	73.4
1373.6	4421.0	5690.7	5719.3	6703.3	5789.9	6670.2	5406.0	4844.5	4709.7	3819.3
27.0	33.0	68.8	80.0	97.3	34.1	34.4	182.5	46.2	16.4	55.7
37.6	34.5	77.4	64.6	34.3	27.4	32.0	43.1	26.6	13.2	59.4
50.7	819.2	676.3	564.8	757.3	446.6	490.7	518.5	430.8	163.2	287.2
172.1	3424.6	3075.3	2278.6	1591.8	2599.2	1586.5	2199.0	3593.5	3394.4	2495.3
486.4	2404.2	3019.8	3575.7	2666.6	2594.7	4305.1	2943.6	1892.5	786.3	2664.2
229.1	1105.2	1325.0	1079.5	1143.3	1209.1	1541.4	857.1	1763.8	755.2	2310.6
444.5	2807.1	2717.4	3093.7	3253.4	2505.5	2830.2	3433.9	2643.3	1417.5	2035.6
162.3	1865.2	1754.9	1576.0	1807.2	1433.5	1796.1	1187.9	1022.0	630.8	813.2
1129.7	1484.1	1820.6	2141.1	1340.2	1336.9	1006.1	1090.5	926.3	310.2	1624.8
304.5	624.1	878.3	1298.9	1079.3	612.5	960.2	605.6	247.6	285.6	428.5
3515.7	5300.4	4872.2	4721.5	4776.0	4860.7	4830.7	4435.4	5530.6	5537.0	4880.2
5997.8	1197.7	1850.0	1567.0	1162.1	1325.4	1938.9	1342.5	1256.9	538.4	2094.7
75.0	2434.9	3379.1	2124.3	1769.9	2247.1	1762.5	2317.9	1724.8	1091.3	1809.9
9110.9	3750.1	4419.1	4023.5	3830.4	3684.8	4099.7	3596.8	3698.1	3224.3	4079.1
553.0	2815.8	3308.3	3053.5	1802.4	2473.6	2367.7	2401.2	3324.9	3312.9	3376.8
45.8	18.1	19.2	25.0	39.5	28.8	31.0	16.8	28.1	26.3	29.2
3034.7	2749.8	3242.4	3744.9	2936.9	2835.8	3002.1	2695.8	3045.4	1542.8	3585.3
7602.1	2200.7	2568.7	2419.9	2129.8	1132.4	2230.4	2505.2	2724.1	2424.5	3198.6
286.3	977.4	2096.5	1641.3	932.3	1039.7	1115.6	664.4	1014.6	811.0	972.6
37.1	270.4	400.1	551.0	366.4	299.1	307.0	558.2	105.8	50.6	161.6
202.5	2050.3	3670.8	2870.5	1178.1	1986.3	2025.8	2226.1	1333.4	751.2	2457.0
322.9	1118.9	1766.0	1696.9	1023.1	1253.1	1268.4	1242.7	344.0	520.8	656.8
137.3	817.2	1346.9	1844.0	504.2	672.5	532.6	1085.5	190.5	648.6	721.5
122.9	1130.3	1407.9	1646.6	1037.4	1258.7	1084.4	1303.9	1327.1	92.8	615.8

3019.2	3530.0	5373.6
1800.0	2357.1	3377.9
1450.6	2322.1	1433.2
3669.5	3589.4	4190.6
361.9	337.2	575.7
2551.4	2909.5	3625.1
2756.2	4285.8	4148.6
5123.9	5489.0	5759.2
2788.1	2597.8	3944.5
3942.8	3586.1	5310.7
1382.7	1441.3	2579.8
3465.7	3870.7	4937.6
1754.1	1810.2	2670.8
4570.0	4239.3	4356.6
4058.5	2954.8	3944.6
94.6	174.0	190.5
5861.7	5917.2	6473.6
42.0	54.5	58.7
56.3	66.3	59.9
511.7	829.1	890.4
2108.7	2513.4	3604.2
3117.6	3541.4	4620.0
813.8	1280.7	934.4
2926.5	2999.8	3815.3
1909.2	2149.2	2136.6
1737.6	2197.0	3318.4
650.4	1085.2	1893.6
4695.3	4696.7	6667.7
1403.1	1605.7	1941.9
2184.0	2698.3	3422.6
3339.2	4405.0	4554.0
2773.8	3074.9	3647.4
25.6	26.8	29.1
2569.7	2914.0	4292.1
1861.4	3854.3	2212.0
1155.3	1617.3	1455.7
472.7	622.5	355.2
2494.9	2864.3	3669.6
1217.1	1909.1	3938.1
1428.6	1936.7	1328.8
957.5	1559.3	1506.8

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DQ071530.1 gg_id:233711 microbial cecum captive and free-living capercaillies (Tetrao urogallus) clone TuCw7 DQ071
EU470080.1 gg_id:289802 trancaspain urial feces clone TU1_aaa03f09 EU470
AM697405.1 gg_id:221429 sequencing libraries indoor dust clone BF0001D020 AM697
AY916159.1 gg_id:113797 human transverse colon biopsy clone M490 AY916
AB089039.1 gg_id:77833 termite gut homogenate clone Rs-K92 bacterium AB089
FJ371922.1 gg_id:366885 feces adult twins and mothers; TS8 clone TS8_a03g03 FJ3719
DQ797006.1 gg_id:187006 human fecal clone RL386_aao85f09 DQ797
EU622658.1 gg_id:278098 -feed administered sub-therapeutic chlorotetracycline alters structure and but not a EU622
EU766883.1 gg_id:347024 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU766
DQ803678.1 gg_id:198988 human fecal clone RL200_aai57a11 DQ803
EU887971.1 gg_id:323501 Microbial structure hydrolytic stage two-stage anaerobic digestion grass silage leach EU887
EU506802.1 gg_id:260776 cecal contents Mus musculus strain C57BL/6J; MD20 clone MD20_aap56f01 EU506
EF603362.1 gg_id:232918 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6033
EU452114.1 gg_id:332037 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83 EU452
DQ815954.1 gg_id:167276 mouse cecum clone aab24g06 DQ815
EF603499.1 gg_id:232260 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6034
FJ679323.1 gg_id:517248 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6793
EU471941.1 gg_id:296850 Asiatic elephant feces clone AE3_aaa04e06 EU471
DQ793811.1 gg_id:178684 human fecal clone RL176_aah43f06 DQ793
EU469735.1 gg_id:291917 flying fox feces clone FF_h04_1 EU469
DQ795793.1 gg_id:194778 human fecal clone RL245_aai82e04 DQ795
GQ897459.1 gg_id:540055 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do GQ897
FJ368429.1 gg_id:366722 feces adult twins and mothers; TS3 clone TS3_a04c03 FJ3684
EU509946.1 gg_id:262944 cecal contents Mus musculus strain C57BL/6J; WD11 clone WD11_aak24b08 EU509
DQ905341.1 gg_id:173282 human fecal clone 013B-F5 DQ905
FJ879345.1 gg_id:394512 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8793
EU452674.1 gg_id:332282 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU452
AY916207.1 gg_id:112958 human cecum biopsy clone LF02 AY916
EU455446.1 gg_id:355041 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H74 EU455
AJ488078.1 gg_id:66186 chlorobenzene-degrading consortium clone IB-18 AJ488
FJ879403.1 gg_id:392407 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8794
EU451140.1 gg_id:329458 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU451
AY570589.1 gg_id:108465 -temperature biodegraded Canadian oil reservoir clone PL-38B12 AY570
AY487928.1 gg_id:100412 Acetanaerobacterium elongatum str. Z7 AY487
EF402779.1 gg_id:207624 human fecal clone SJTU_B_12_36 EF4027
EU845152.1 gg_id:347819 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU845
EU775744.1 gg_id:339121 Horse feces clone horsem_aai94d08 EU775
FJ269107.1 gg_id:338187 dissimilatory ferric iron reducers arsenic contaminated Hunan south China paddy soil FJ2691
FJ367099.1 gg_id:358674 feces adult twins and mothers; TS28 clone TS28_a03e06 FJ3670
EF604611.1 gg_id:231168 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6046
GQ502524.1 gg_id:590995 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf4- GQ502

62.0	231.3	454.1	304.7	218.2	331.9	41.1	303.9	140.3	329.7	130.8
1739.8	6787.2	7461.7	7646.2	7271.8	6608.6	8658.2	6487.4	6095.5	5373.7	8412.9
38.2	170.6	248.0	264.2	98.6	224.1	179.8	175.5	74.5	25.0	95.4
817.4	1218.5	1385.5	1724.1	1308.3	1049.2	1214.8	1266.7	591.3	372.8	960.1
1459.7	4695.0	5707.4	5207.1	5592.1	5341.3	4664.2	5895.1	5582.1	7360.6	4146.4
6607.4	3183.9	3904.0	3510.6	3515.1	3134.8	4001.7	3227.5	4110.9	3443.8	2773.6
1533.0	3485.9	3249.6	3615.9	3011.1	3368.0	3431.0	3825.0	4286.1	3277.1	3076.0
76.3	229.5	313.5	195.6	102.1	128.1	124.9	149.2	54.6	52.5	44.1
41.3	44.0	83.3	93.0	58.4	50.3	42.0	165.0	100.7	28.2	66.1
2501.6	2605.0	2541.1	2651.3	2357.0	2600.4	2631.3	3017.3	1569.4	491.4	2505.1
607.1	4113.3	5138.6	5185.4	4312.1	4111.2	5210.8	4498.1	4157.1	2334.4	3381.8
1021.6	1518.3	1733.4	2131.1	1242.3	1300.4	1398.7	1404.0	1893.4	1021.6	1296.5
12603.6	4407.0	3887.4	4011.2	3665.0	3590.1	4025.6	4381.3	3537.4	2867.7	5098.6
579.4	4224.9	3758.3	2946.6	2936.0	2677.9	3140.4	3453.2	2370.7	725.3	4939.5
55.4	1280.2	2339.1	1770.5	977.0	1724.2	1416.1	1564.3	769.5	1413.4	1080.6
11862.2	8998.7	6756.5	7169.6	7358.7	6422.4	7670.1	7137.5	9954.3	5790.0	9477.7
3461.9	3572.1	4272.9	4494.6	5460.5	4176.3	5512.9	4437.9	3323.2	4724.8	3494.2
2391.3	4763.1	6170.8	6424.4	7255.2	5182.6	7850.1	5143.2	5155.4	2962.1	6550.0
2585.7	2113.6	2433.8	2357.0	1938.4	2268.8	2469.5	2306.8	1812.6	1502.8	2933.2
6798.9	6808.6	6839.9	7020.2	6689.2	6479.9	6881.0	7410.4	7910.2	5825.3	9243.6
3425.1	5655.6	6679.4	7154.3	7593.0	6187.3	7545.2	6095.6	6875.0	9268.0	7738.8
1211.5	4591.6	5363.6	5680.5	3266.0	4366.0	4513.8	4492.2	3266.8	4259.0	4976.6
2961.7	2384.0	3064.7	2557.7	1395.7	2871.5	2141.0	2565.0	1864.1	2065.2	1815.3
60.7	595.0	2666.2	731.4	208.2	819.6	232.1	435.0	401.2	45.3	472.7
1099.3	4557.0	3821.5	4734.3	3475.4	3797.4	4190.9	3791.1	4391.9	4342.9	3432.3
2548.1	3259.5	3823.0	4715.0	3584.9	3484.5	4108.9	3762.2	2466.9	1441.6	3494.0
2517.1	3367.5	2349.0	2533.9	2421.6	2335.8	2900.6	2699.3	4031.8	2758.7	3496.9
249.9	2296.1	2501.0	2980.8	1870.6	2847.8	3268.2	2872.6	1938.4	585.5	2157.0
1670.9	2709.8	3462.5	2795.7	2524.9	2511.5	2524.7	2928.1	2168.7	2411.5	2425.6
53.0	136.0	531.7	420.3	65.0	218.2	138.1	381.4	142.5	41.4	102.7
59.0	102.2	240.1	233.1	60.6	99.7	120.9	260.2	57.2	285.0	55.8
1885.4	5075.4	5612.2	5556.9	6091.8	4934.2	6475.7	5335.0	3762.6	5153.5	5124.0
74.3	254.1	324.4	266.7	358.0	218.2	371.5	209.9	99.2	106.4	237.6
44.5	66.1	102.0	159.8	37.5	50.4	59.8	40.1	27.8	24.7	32.3
46.7	24.1	32.5	30.2	32.5	22.1	30.1	24.1	22.0	18.5	25.8
1301.3	2428.4	2888.7	2872.6	2370.7	2629.0	2421.5	2962.0	1538.5	1583.5	1816.6
230.4	1066.4	1744.8	1840.3	802.4	946.4	1721.2	1500.3	583.5	293.2	977.7
20623.3	4947.9	4653.7	4823.6	4337.2	4066.1	5333.7	4059.9	6221.0	4934.7	6669.3
430.2	1614.0	2515.1	2380.4	2178.7	1910.0	1925.3	2054.1	827.8	1417.4	1156.0
5300.8	2564.5	2253.6	1718.8	1427.1	1787.2	1992.3	1606.9	3501.2	2659.5	3243.4
1603.8	3995.9	4571.6	4423.6	3545.3	3821.7	4464.5	3836.0	3492.7	2190.2	4132.6

319.3	487.5	840.0
7009.5	6682.5	8176.2
190.9	343.6	637.6
1494.6	2026.6	2073.7
4580.5	5570.0	5783.6
2917.9	4854.2	4704.7
2805.9	3341.3	4484.7
199.3	174.7	340.2
74.1	148.1	67.9
2493.3	2789.1	2919.5
4735.9	4806.7	7425.7
1516.9	2619.0	2946.8
3913.9	4984.1	6606.4
2396.2	3579.2	3893.3
1858.2	1871.0	3007.3
6212.7	7270.3	9271.8
4243.1	4684.7	6467.9
4659.8	6467.1	7053.3
1511.7	3014.5	1971.9
5861.0	7255.6	6374.1
6345.4	7126.7	7762.5
4103.2	4601.2	7054.1
2594.6	2639.1	2958.8
1041.5	945.5	1009.3
3472.6	4670.9	5015.7
3147.8	4797.4	4461.7
1979.2	3799.4	2722.0
2897.1	2513.5	4855.0
2924.1	3715.0	5166.0
370.9	199.9	451.7
331.9	184.7	481.6
5176.2	6027.9	7109.4
232.6	420.9	713.6
81.4	115.1	131.6
31.2	28.2	219.0
3329.2	3068.4	4909.2
1389.1	1445.4	3595.7
4236.2	5777.2	4221.0
2350.8	2242.3	3422.9
1656.6	2525.0	1647.6
4052.5	5105.4	5995.4

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EU462611.1 gg_id:294242 Sumatran orangutan feces clone orang2_aai66a12 EU462
EU506329.1 gg_id:260859 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aap63d05 EU506
EU506188.1 gg_id:268806 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aaa02g02 EU506
DQ805002.1 gg_id:187524 human fecal clone RL385_aao83h09 DQ805
DQ796382.1 gg_id:189994 human fecal clone RL179_aah26e06 DQ796
EU463788.1 gg_id:291111 domesticated horse feces clone horsej_aai92h01 EU463
DQ904661.1 gg_id:168845 human fecal clone 001-c11 DQ904
AY622268.1 gg_id:100124 subsurface soil clone S-F26 AY622
EU452362.1 gg_id:312979 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75 EU452
DQ905623.1 gg_id:170271 human fecal clone 014B-H9 DQ905
DQ807121.1 gg_id:179301 human fecal clone RL244_aaj46e08 DQ807
EU469245.1 gg_id:289125 Speke's gazelle feces clone SP3_g02_1 EU469
FJ825458.1 gg_id:550485 Microbial during start-up mesophilic biogas plant clone 135_BE5_6 FJ8254
AB270141.1 gg_id:172165 Influence temperature and humidity on heifers rumen contents Holstein heifer (Bos AB270
AY984523.1 gg_id:123415 human stool clone B450 AY984
EU506576.1 gg_id:272283 cecal contents Mus musculus strain C57BL/6J; MD19 clone MD19_aaa04f01 EU506
EU765144.1 gg_id:314884 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B EU765
GQ867487.1 gg_id:579293 and prevalence blaTEM genes Arctic seals colon content clone CSG58 GQ867
EU531982.1 gg_id:276231 Predominant role host genetics controlling gut microbiota FMF remission stool clone EU531
DQ800460.1 gg_id:174827 human fecal clone RL183_aah24h03 DQ800
EU472119.1 gg_id:296626 francois langur feces clone FL_1aaa02g05 EU472
EU456056.1 gg_id:315580 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80 EU456
EF071169.1 gg_id:195415 library survey and quantitative measurement major mucosa- IBD human colonic muc EF0711
EU462752.1 gg_id:302382 Sumatran orangutan feces clone orang2_aai68e04 EU462
AB234479.1 gg_id:148075 termite gut homogenate clone MgMjR-012 AB234
GU303965.1 gg_id:538145 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU303
DQ015351.1 gg_id:131324 mouse cecum clone M3_a07 DQ015
EU461068.1 gg_id:289969 red kangaroo feces clone KO1_aai43e06 EU461
GQ448715.1 gg_id:532859 Microbiome neonatal calves: shedding microorganisms fecal clone calf784_10wks_ GQ448
DQ817325.1 gg_id:173276 mouse cecum clone aaa73d09 DQ817
AJ576369.1 gg_id:103744 hindgut homogenate Pachnoda ephippiata larva clone PeH56 AJ5763
EU771106.1 gg_id:333205 Asiatic elephant feces clone AE3_aaa02b02 EU771
EU506196.1 gg_id:261365 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aaa03c05 EU506
GQ047291.1 gg_id:423254 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1011a GQ047
EF603339.1 gg_id:234992 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6033
DQ800226.1 gg_id:181527 human fecal clone RL303_aal69h06 DQ800
EU506587.1 gg_id:263968 cecal contents Mus musculus strain C57BL/6J; MD19 clone MD19_aaa04g10 EU506
EU794136.1 gg_id:307564 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_AE37 EU794
FJ368767.1 gg_id:362041 feces adult twins and mothers; TS49 clone TS49_a04c07 FJ3687
EU455609.1 gg_id:345861 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H80 EU455
EU454483.1 gg_id:310557 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77 EU454

10107.4	5805.1	5907.7	5089.5	4663.6	5193.0	5127.3	4551.0	6855.8	5868.4	5519.3
98.8	2194.2	2509.4	2503.8	3028.0	2179.4	2765.4	2179.9	1787.2	1771.4	1671.3
204.8	3018.2	4263.5	3632.0	2299.1	2983.6	3121.5	3422.7	1790.7	1366.2	2881.1
3972.6	4727.9	5973.3	5597.9	3795.3	4908.5	5160.6	5820.8	4622.0	3320.9	5593.6
8866.5	4455.2	5361.7	6085.1	5470.1	4863.4	7935.0	4334.4	3664.5	5739.3	5342.7
264.3	1895.4	2762.5	2615.4	2972.9	2177.6	2768.8	2483.6	1503.2	745.5	2154.3
562.1	5618.8	4701.1	4087.8	3203.9	4248.9	3712.0	3457.2	5977.9	6170.6	6005.9
32.7	503.6	1012.2	918.3	433.4	553.9	888.9	719.6	196.6	126.1	320.5
78.5	1213.6	1476.0	1034.4	484.0	948.2	486.6	843.6	1090.4	1241.6	565.8
308.3	3480.1	4336.5	3382.9	3952.3	3403.5	4435.8	3355.1	3852.9	2182.8	3221.4
1025.5	2081.8	2641.1	2889.1	2131.1	2044.2	2541.1	2713.1	2330.1	826.0	1903.7
239.8	1658.1	2236.2	2470.7	1903.1	1786.6	1386.0	2627.5	596.9	994.5	1344.2
273.4	2154.2	2339.3	2244.9	3093.6	2341.1	3194.9	2194.8	1909.5	649.5	1353.5
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594.8	3914.4	2556.1	2685.5	2597.8	2516.5	2709.2	2548.7	4397.5	1963.2	2784.0
700.9	366.1	628.0	610.6	512.6	365.7	293.8	389.4	752.9	232.4	346.3
41.8	473.6	649.7	580.2	321.5	387.9	532.6	509.8	222.8	189.4	214.6
24953.5	8130.3	6210.4	7687.8	6948.9	6822.0	7280.2	6985.2	10020.3	7648.9	10472.9
5635.8	6436.0	6022.3	6388.8	6542.6	6023.2	6443.6	6417.2	5195.2	3613.8	7825.1
696.1	810.9	1504.6	1888.4	1318.1	931.6	1432.4	1137.2	407.7	249.9	613.2
935.1	921.3	1686.0	1471.3	933.6	922.3	996.7	1723.1	833.9	263.8	1197.0
44.4	263.8	417.0	448.8	146.2	269.4	291.9	373.8	205.6	163.7	175.8
38.8	73.0	70.9	58.3	27.4	26.9	30.8	22.4	26.5	22.9	29.8
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246.0	1491.4	2463.9	1630.6	1660.3	1900.1	1826.3	2165.3	1424.5	1760.4	1403.0
324.6	2200.0	2130.4	1886.3	1826.9	1982.3	2012.5	2586.1	1014.0	842.4	2158.4
65.5	853.7	1056.6	548.1	278.2	569.9	398.0	660.6	592.1	388.2	365.9
4287.2	1592.2	2183.1	1810.6	1725.9	1680.9	1572.0	1260.0	1167.1	752.8	1231.1
130.1	87.2	131.3	144.1	83.4	76.7	95.0	74.6	76.9	88.2	104.3
81.7	658.4	762.5	843.6	639.1	724.1	872.9	817.0	386.9	197.8	385.9
2415.7	2884.1	2560.7	2004.9	1998.5	2918.1	2111.1	2575.2	2043.2	1230.6	2720.6
222.3	2866.2	3493.4	3394.5	2695.1	3232.0	2294.4	3507.1	3848.2	1911.1	3768.9
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2331.1	2833.0	4008.2
3476.2	3173.3	4674.2
5481.6	6175.9	6509.3
4700.5	7308.8	4861.7
2490.0	2785.6	3695.7
3877.1	3445.4	4459.5
875.7	713.9	1246.3
874.7	980.2	1756.0
4437.5	3445.5	5786.7
2372.4	2609.2	2836.9
1572.9	1811.2	3685.3
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2481.2	3543.0	4233.2
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1227.6	1950.7	1947.3
446.6	703.6	342.6
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25.1	23.9	544.5
1687.1	2425.6	5205.0
1551.7	1595.9	1356.5
615.5	786.4	948.6
1767.2	1622.5	2961.6
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FJ879335.1 gg_id:420816 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8793
EU467284.1 gg_id:291196 hamadryas baboon feces clone BAZ_a12 EU467
EU453205.1 gg_id:350575 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU453
FJ368179.1 gg_id:365529 feces adult twins and mothers; TS3 clone TS3_a01b08 FJ3681
EU767264.1 gg_id:335138 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C2 EU767
DQ455846.1 gg_id:157888 pre-adolescent turkey cecum clone CFT19C4 DQ455
EF603241.1 gg_id:232048 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6032
AY854324.1 gg_id:109841 herbivore gastrointestinal tract clone Thompsons37 AY8543
EU472376.1 gg_id:297774 Angola colobus feces clone EAC_1aaa04b03 EU4723
EU766492.1 gg_id:328236 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU7664
EU772256.1 gg_id:333948 Argali sheep feces clone AS2_aao34b08 EU772
FJ368800.1 gg_id:362922 feces adult twins and mothers; TS49 clone TS49_a04g02 FJ3688
EF604823.1 gg_id:228391 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6048
EF603352.1 gg_id:232042 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6033
DQ809978.1 gg_id:189758 human fecal clone RL184_aao66f03 DQ809
EU871402.1 gg_id:305146 Genetic Bovine (Bos taurus) Rumen Thailand clone CF342 EU8714
GQ175456.1 gg_id:535444 Chicken intestinal microbiota modulations various feed supplementations DGGE and GQ175
EU510091.1 gg_id:261325 cecal contents Mus musculus strain C57BL/6J; WD3 clone WD3_aak01c01 EU5100
EU506686.1 gg_id:258926 cecal contents Mus musculus strain C57BL/6J; MD20 clone MD20_aap54e03 EU5066
EU505553.1 gg_id:272277 cecal contents Mus musculus strain C57BL/6J; myd5 clone myd5_aaa02e12 EU5055
GQ451212.1 gg_id:575559 Fecal Yunnan snub-nosed monkey feces clone J66 GQ451
DQ015035.1 gg_id:131182 mouse cecum clone M2_c06 DQ015
GQ491889.1 gg_id:560663 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
EU451586.1 gg_id:349538 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU4515
EU507209.1 gg_id:271754 cecal contents Mus musculus strain C57BL/6J; MD22 clone MD22_aaa03e10 EU5072
DQ815929.1 gg_id:167166 mouse cecum clone aab24d05 DQ815
EU509948.1 gg_id:264695 cecal contents Mus musculus strain C57BL/6J; WD11 clone WD11_aak24b10 EU5099
AF371759.1 gg_id:30067 swine intestine clone p-2506-18B5 AF3717
EU509855.1 gg_id:258260 cecal contents Mus musculus strain C57BL/6J; WD11 clone WD11_aak22e08 EU5098
EU773500.1 gg_id:325524 Bonobo feces clone BNO_aaa04e04 EU7735
EU778735.1 gg_id:322931 Springbok feces clone SBSD_aaa04b06_1 EU7787
EU767072.1 gg_id:307566 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU7670
EU259422.1 gg_id:253559 Rumen yak (Bos grunniens) sequences rumen fluid clone YRC46 EU2594
FJ672969.1 gg_id:530829 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6729
EU358715.1 gg_id:351451 structure archaeal denaturing gel electrophoresis and sequencing mesophilic biogas EU3587
EU468521.1 gg_id:287988 okapi feces clone OK1_h03_1 EU4685
DQ796435.1 gg_id:198029 human fecal clone RL179_aah28d02 DQ796
EU764739.1 gg_id:347893 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2 EU7647
EU474451.1 gg_id:291314 bighorn sheep feces clone BHSD_aaa02b12 EU4744
FJ364955.1 gg_id:360031 feces adult twins and mothers; TS1 clone TS1_a01b10 FJ3649
EU461035.1 gg_id:291117 red kangaroo feces clone KO1_aai42g02 EU4610

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138.0	1346.3	1675.1	1703.2	2147.4	1729.4	1676.9	1635.7	1308.1	161.8	990.6
3963.5	2657.1	3785.8	3876.3	2395.5	2396.1	2568.8	2823.0	3427.8	729.6	3327.7
2264.3	2200.1	2462.3	3009.7	1675.4	1912.0	2069.1	2510.2	2032.2	1747.5	1703.8
5782.1	2711.0	4247.6	3900.5	3760.5	3691.5	3414.3	3980.5	2752.5	4880.2	3371.8
30.7	64.5	121.0	77.5	125.0	95.5	131.7	83.4	51.6	25.2	35.2
23585.2	7612.3	6664.7	7477.2	6636.5	6956.4	7441.3	6672.4	12173.1	10303.4	10819.0
39.8	301.1	185.0	123.3	177.4	245.1	147.4	341.0	415.5	91.5	122.1
4059.5	2674.4	2355.0	2533.5	2337.7	2457.3	3290.7	2222.5	3351.7	3039.4	2585.1
37.2	986.1	1680.6	1381.7	749.3	365.6	824.6	1552.3	546.1	166.2	1082.7
690.5	6991.4	5294.9	5667.7	5292.1	4556.0	5271.7	7574.3	5565.0	6788.9	6049.7
2764.5	2418.6	3082.7	3041.5	3774.1	2654.9	3614.7	3272.5	2607.1	1512.8	3017.7
16101.0	9010.8	8526.5	8466.3	7176.1	8152.8	8279.6	7235.0	11570.8	9578.5	11630.8
1362.6	1863.0	1387.0	1240.8	1091.5	1150.4	1414.3	1184.9	1332.3	1221.8	2301.3
4290.2	2255.9	2778.0	2420.0	2365.7	2353.6	2145.6	2094.7	3589.0	3353.5	3178.4
868.4	2683.7	3808.1	3556.6	1956.1	3066.9	2769.9	4188.9	1492.1	2210.6	2742.5
42.2	570.1	553.2	791.6	221.9	343.9	333.8	762.9	112.3	32.5	184.2
1876.2	2792.7	3353.3	3474.9	2356.0	2738.2	2736.2	2801.9	1521.7	2286.2	2397.5
265.5	2346.8	2842.5	2909.9	2295.1	2408.3	2556.1	2942.9	1437.8	3058.6	1806.3
5396.6	3375.6	3331.2	4587.9	3203.3	3495.1	4013.0	3234.4	5268.4	2978.0	4138.1
118.1	828.0	1402.6	1469.4	1540.3	1096.4	1179.3	952.8	424.5	472.0	483.4
41.3	55.7	79.2	81.2	76.4	60.9	70.6	82.9	34.0	32.2	60.9
143.8	353.5	591.3	489.6	318.5	376.2	450.5	533.2	432.3	403.9	428.2
1405.9	3262.7	3708.3	3457.8	4055.7	3180.1	3773.6	3485.2	3068.4	1571.0	2760.4
10011.3	5220.0	5545.5	5946.7	5833.9	5096.0	6436.9	5490.1	5663.6	3314.3	6067.1
16321.3	4919.4	4670.5	5062.2	4047.4	4227.7	4630.1	4375.0	6384.2	5075.0	6642.9
349.3	4662.8	4274.2	4719.5	5042.4	3752.8	5072.6	4327.5	3198.9	2552.9	4554.1
116.5	598.3	596.2	506.1	631.4	364.9	519.0	488.2	438.3	209.8	276.8
10341.7	1642.9	1823.0	1842.1	1762.7	1639.4	1975.5	2020.5	1663.7	1530.3	1783.8
45.0	678.5	1294.3	837.5	473.2	675.9	620.9	753.0	406.4	94.7	656.8
167.9	1253.3	1393.9	1492.2	1371.6	1046.7	1456.2	1229.0	1035.5	737.6	621.7
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4396.8	5377.0	6320.8	6724.3	6392.7	5333.2	7680.2	5753.4	4846.4	5017.7	5811.5
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132.7	277.1	416.1	393.6	242.0	180.6	306.1	316.2	249.1	252.5	152.9
2581.5	2358.2	2761.7	2626.6	2680.0	2204.3	2356.8	2288.7	2692.0	1436.4	3330.3
7473.6	4637.0	3971.3	4438.9	4060.2	4025.2	4039.3	3729.6	5532.8	3455.9	5192.5
1490.0	1849.0	2114.5	2048.6	2014.6	1701.7	2124.7	2410.3	2452.3	1948.8	1630.4
322.2	3364.5	4773.6	4176.9	3076.4	3795.5	3366.2	3989.4	1579.2	2058.6	4175.1

1282.9	1681.0	2308.9
1158.4	1855.9	2236.5
2453.4	3656.6	3041.4
2297.9	2617.5	3898.3
4155.0	3814.0	4700.4
128.5	117.0	98.0
6899.2	8169.7	8424.7
127.0	217.3	103.6
2172.1	3612.6	2785.2
1107.8	1364.2	2011.1
4723.6	5933.3	6439.1
3230.9	4152.2	3523.5
7261.4	9172.5	9369.1
1004.1	1971.3	1345.2
2303.1	3843.2	3216.7
3139.7	3504.4	5821.5
704.1	467.7	2458.5
3342.0	3268.1	3303.0
3409.9	3383.2	5366.0
3281.7	3955.3	4022.1
1068.0	1104.7	2334.7
85.7	98.2	72.8
450.8	646.6	1143.2
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3877.0	5467.0	5954.1
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451.3	344.1	533.4
2024.0	2191.3	2047.1
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5976.3	5864.9	7440.6
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6931.2	6469.8	8513.4
297.1	450.8	612.2
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EF603271.1 gg_id:229291 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6032
GQ502529.1 gg_id:589530 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf4- GQ502
EU768072.1 gg_id:314565 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C4 EU768
EU850470.1 gg_id:304165 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF49 EU850
EU510224.1 gg_id:270297 cecal contents Mus musculus strain C57BL/6J; WD3 clone WD3_aak03b09 EU510
EF603286.1 gg_id:234373 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6032
EU763025.1 gg_id:304725 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU763
AY976193.1 gg_id:125597 human ascending colon mucosal biopsy clone LW10 AY976
DQ327508.1 gg_id:145878 Metagenomic gut microbiome healthy human stool clone EA83 DQ327
DQ325649.1 gg_id:146048 Metagenomic gut microbiome healthy human stool clone B215 DQ325
EF603298.1 gg_id:232031 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6032
FJ365192.1 gg_id:368412 feces adult twins and mothers; TS1 clone TS1_a04a02 FJ3651
EF099963.1 gg_id:195689 mouse cecum clone SWPT5_aaa02h03 EF0999
DQ800544.1 gg_id:195667 human fecal clone RL183_aah29d10 DQ800
EU455299.1 gg_id:333969 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N EU455
EU506732.1 gg_id:276761 cecal contents Mus musculus strain C57BL/6J; MD20 clone MD20_aap55c08 EU506
GQ896776.1 gg_id:590125 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do GQ896
EU768021.1 gg_id:328363 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C4 EU768
AF371766.1 gg_id:107272 swine intestine clone p-4546-4Wb3 AF371
EU774361.1 gg_id:353322 Chimpanzee feces clone CHIMP1_aaj37f02 EU774
DQ793759.1 gg_id:177903 human fecal clone RL246_aai76h04 DQ793
EF559116.1 gg_id:220174 mesophilic anaerobic digester clone C35_D7_H_B_C05 EF5591
DQ116011.1 gg_id:130793 bovine teat canal clone D-74 DQ116
FJ366095.1 gg_id:367681 feces adult twins and mothers; TS25 clone TS25_a02f06 FJ3660
EU772286.1 gg_id:340066 Argali sheep feces clone AS2_aao36e12 EU772
GQ448532.1 gg_id:510233 Microbiome neonatal calves: shedding microorganisms fecal clone calf784_6wks_gr GQ448
EU158190.1 gg_id:235474 Clostridium sp. str. SW512 EU158
AM277638.2 gg_id:233253 fecal microbiota irritable bowel syndrome patients significantly that healthy subject AM277
EF603366.1 gg_id:229110 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6033
EU778786.1 gg_id:349884 Springbok feces clone SBSD_aaa02e08_1 EU778
DQ800873.1 gg_id:185826 human fecal clone RL183_aao04f02 DQ800
FJ363634.1 gg_id:363716 feces adult twins and mothers; TS14 clone TS14_a01e11 FJ3636
DQ794088.1 gg_id:187393 human fecal clone RL176_aan57h02 DQ794
EF603784.1 gg_id:244484 Salmonella enterica serovar typhimurium exploits inflammation compete intestinal n EF6037
EU454869.1 gg_id:311725 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU4548
FJ366738.1 gg_id:361920 feces adult twins and mothers; TS27 clone TS27_a03c09 FJ3667
FJ440066.1 gg_id:546958 Megamonas hypermegale colonization correlates Campylobacter jejuni exclusion pou FJ4400
FJ680947.1 gg_id:531238 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6809
FJ366104.1 gg_id:361201 feces adult twins and mothers; TS25 clone TS25_a02g04 FJ3661
EU779323.1 gg_id:342446 Visayam Warty Pig feces clone VWP_aaa02g01 EU779
EU511636.1 gg_id:271303 cecal contents Mus musculus strain C57BL/6J; WD9 clone WD9_aak08a08 EU511

730.1	2199.2	3075.8	3150.0	3393.7	1455.2	3346.3	2530.0	1688.3	977.2	2330.6
416.5	2713.8	3144.2	3522.2	3332.3	3000.9	3578.0	3689.9	2070.7	2916.5	2042.8
314.6	93.6	395.8	311.0	314.8	250.1	101.2	323.6	195.4	164.2	328.0
4146.5	7780.7	7734.9	7643.6	8236.9	6761.8	7232.7	7879.5	7890.9	6661.4	8647.1
35.2	229.0	264.7	284.7	233.0	152.1	287.6	174.0	67.6	51.3	65.6
4956.1	2324.3	2596.8	2216.7	1710.5	2310.5	2036.0	2561.2	3052.1	2569.7	3063.8
7894.8	3639.3	4422.6	3470.0	1542.4	3403.5	3589.9	3523.7	4261.4	3647.1	4475.4
145.1	1845.8	2146.2	1624.7	301.1	1405.7	1026.0	1792.1	1859.1	2901.2	1955.5
6522.2	2017.8	2311.4	2710.1	1983.9	2015.3	803.5	2582.9	2007.4	1306.6	2003.7
69.8	70.7	82.7	73.5	52.9	45.4	39.3	69.5	40.0	27.4	41.5
8047.0	3395.4	3720.0	4626.4	4005.1	3280.4	4712.4	2646.4	4966.7	3251.6	4680.3
61.3	1143.6	1566.7	2273.3	477.0	779.5	541.0	1279.2	247.5	555.0	565.0
5950.9	2689.4	3937.1	3315.0	3056.5	3381.9	2137.2	3268.0	2232.6	2693.1	2193.3
1101.3	3108.1	4419.1	4975.1	3949.1	3490.5	3621.8	3887.0	3113.2	5379.6	3713.9
9814.6	5675.1	6120.8	5602.0	4980.6	5541.4	6163.8	4809.4	7552.0	6331.8	8719.3
4350.2	1585.1	2019.4	1833.9	1801.5	1796.3	1875.4	2056.8	2121.4	1362.1	1402.2
2550.8	2745.3	3288.9	2750.6	2236.0	2619.4	3073.2	3028.6	1819.2	3082.1	2263.3
42.2	1053.9	1244.7	1096.6	530.4	675.8	627.3	662.2	343.8	264.7	524.5
48.7	111.1	211.2	171.5	121.6	101.0	176.4	106.0	80.5	47.3	65.1
44.4	1369.5	2245.0	1936.3	1482.5	1431.7	1390.3	1575.6	937.3	329.2	1049.3
948.4	950.7	1042.0	1311.2	990.6	857.1	955.0	786.1	796.1	758.0	1145.0
35.1	114.0	191.7	217.4	41.2	39.0	49.1	122.0	44.0	33.7	66.8
139.1	1300.1	2530.7	2057.6	1930.7	1954.0	2654.3	2066.4	539.5	274.9	1555.2
2746.4	2973.3	3479.9	3901.7	3271.7	3321.6	3968.4	2738.3	4854.4	3374.8	3439.1
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80.9	223.7	828.8	845.4	315.3	94.6	384.3	524.1	416.3	120.9	215.2
82.9	1198.9	1510.4	1404.8	985.5	1110.3	1399.0	1373.5	746.8	354.2	1049.8
30.5	43.5	62.7	37.9	41.5	81.9	28.7	123.5	16.9	26.5	342.3
45.8	393.1	935.2	677.8	161.2	620.8	451.9	521.3	285.4	142.4	286.3
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107.5	1728.1	1876.4	1856.6	896.3	1050.6	846.8	1273.7	2229.3	1380.6	673.1
59.5	923.3	1237.8	1078.9	571.5	1518.9	885.5	1104.6	228.4	92.4	666.6
984.6	3996.0	4137.7	3786.7	4726.6	4393.2	4826.6	3801.6	2532.6	3088.4	4676.6
7173.5	5691.7	4383.8	2866.2	4077.0	4043.2	4167.3	4317.9	5214.5	2756.9	6875.6
206.2	2364.6	2425.7	2305.4	1829.5	1970.9	1937.1	2071.6	2416.4	1933.2	1480.8
214.3	2809.4	4488.5	3871.4	3826.5	4019.7	4878.8	3615.1	2042.4	5497.5	3469.0
619.7	4287.3	4950.9	5395.0	5641.9	4706.6	6391.0	5365.0	5336.3	3664.6	4437.2
73.8	920.6	1147.8	1201.0	1071.3	780.5	1103.2	1069.4	420.4	332.4	464.8
36.6	78.3	135.8	169.0	87.4	127.6	133.9	207.4	47.8	31.8	58.5
934.2	3780.1	2885.6	3225.8	3984.0	3345.2	3966.3	1399.3	2679.1	1889.0	2139.2

2651.1	2855.4	3371.3
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253.8	404.0	213.4
6873.1	6777.4	7712.1
219.4	306.2	790.6
2140.0	3186.0	3319.3
1825.9	3627.1	3716.5
1452.0	2295.7	1767.2
2581.0	3055.6	3573.3
58.1	89.2	114.8
2997.4	4461.5	4816.0
1903.3	1838.5	2372.0
3281.1	3655.0	5350.9
3571.3	4466.8	5547.3
5307.2	6867.0	5516.2
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2731.1	3328.8	3220.1
925.5	856.6	1712.9
91.4	171.2	326.3
1808.7	1338.4	2440.0
904.9	959.7	907.9
132.7	154.1	79.9
1544.8	1868.5	2790.8
2868.3	4363.4	4900.3
5095.9	6153.7	4780.3
452.0	658.8	744.3
1518.4	1385.6	1523.9
27.0	57.8	31.8
491.3	635.5	986.2
7844.4	7919.5	8052.7
2540.8	2931.7	3013.7
1562.8	1926.7	2459.4
690.0	685.1	1184.0
3612.3	4507.9	5454.5
4147.9	4734.9	4499.1
2450.5	2700.7	3221.0
4030.4	4566.0	5873.3
4669.2	4442.4	6677.4
764.8	1373.4	2068.3
151.7	202.7	556.9
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EU509971.1 gg_id:273737 cecal contents Mus musculus strain C57BL/6J; WD11 clone WD11_aak24f03 EU509
GQ491419.1 gg_id:558068 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
GQ491157.1 gg_id:581278 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
EU842952.1 gg_id:303785 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU842
EU748046.1 gg_id:355404 neotropical folivorous flying bird adult hoatzin crop clone hoa2_43g04 EU748
EU465638.1 gg_id:301382 argali sheep feces clone AS1_aao40e01.Contig1 EU465
EU844075.1 gg_id:328379 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
FJ374214.1 gg_id:369525 Inter- and intraspecific humivorous scarab beetle larvae (Pachnoda spp.) larval hindgu FJ3742
FN436123.1 gg_id:539296 Molekularbiologische Charakterisierung der bakteriellen Populationsdynamik eines t FN436
FJ363880.1 gg_id:361066 feces adult twins and mothers; TS14 clone TS14_a04d11 FJ3638
EU506986.1 gg_id:274921 cecal contents Mus musculus strain C57BL/6J; MD21 clone MD21_aar09d08 EU506
EF603494.1 gg_id:234342 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6034
FJ881322.1 gg_id:459119 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8813
EU006198.1 gg_id:256016 Salmonella enterica serovar typhimurium exploits inflammation compete intestinal r EU006
AJ608244.1 gg_id:149660 human biopsies ulcerative colitis biopsy clone UC7-69 AJ6082
DQ802767.1 gg_id:199696 human fecal clone RL188_aan96c12 DQ802
EU764801.1 gg_id:331168 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2 EU7648
GQ451266.1 gg_id:565404 Fecal Yunnan snub-nosed monkey feces clone J245 GQ451
FJ368624.1 gg_id:361341 feces adult twins and mothers; TS49 clone TS49_a02e05 FJ3686
EU474535.1 gg_id:289015 bighorn sheep feces clone BHSD_aaa04h11 EU474
DQ456247.1 gg_id:158456 pre-adolescent turkey cecum clone CFT211A12 DQ456
EF686627.1 gg_id:257352 Sequences Manifest Rumen Yunnan Yel Cattle (Bos Taurus) rumen fluid clone YNRC1 EF6866
EF445160.1 gg_id:215193 rabbit cecum clone NED3A12 EF4451
FJ365131.1 gg_id:370011 feces adult twins and mothers; TS1 clone TS1_a03c05 FJ3651
EF603330.1 gg_id:230238 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6033
EU453550.1 gg_id:341015 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77 EU453
EU507924.1 gg_id:268722 cecal contents Mus musculus strain C57BL/6J; MD24 clone MD24_aaa03e09 EU507
DQ904669.1 gg_id:164541 human fecal clone 001-c7 DQ904
AB288879.1 gg_id:200879 termite gut homogenate clone BOf1-09 AB288
EU507998.1 gg_id:276229 cecal contents Mus musculus strain C57BL/6J; MD25 clone MD25_aaa01e10 EU507
AY916333.1 gg_id:114325 human stool clone C342 AY9163
GQ451236.1 gg_id:578147 Fecal Yunnan snub-nosed monkey feces clone J158 GQ451
FJ371419.1 gg_id:358780 feces adult twins and mothers; TS6 clone TS6_a04g03 FJ3714
EU508713.1 gg_id:269238 cecal contents Mus musculus strain C57BL/6J; MD4 clone MD4_aap49g09 EU508
DQ796608.1 gg_id:192022 human fecal clone RL179aan75g07 DQ796
DQ325941.1 gg_id:147410 Metagenomic gut microbiome healthy human stool clone B814 DQ325
FJ363232.1 gg_id:362622 feces adult twins and mothers; TS148 clone TS148_a04g08 FJ3632
DQ793709.1 gg_id:176372 human fecal clone RL246_aai76a06 DQ793
EU772408.1 gg_id:315393 Hamadryas Baboon feces clone BAZ_aah91d12 EU772
DQ815688.1 gg_id:173264 mouse cecum clone aab21a03 DQ815
EF603333.1 gg_id:228320 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6033

207.7	4526.7	4164.7	4218.2	4083.5	3599.1	4982.1	5387.9	2743.0	2078.4	3853.8
38.3	66.5	82.1	108.8	47.5	51.9	59.0	32.4	27.8	33.1	27.2
1128.1	2596.5	3804.6	2956.2	1806.9	2298.1	1873.9	2358.3	2022.3	1241.4	1617.5
334.1	2388.7	3099.2	3185.5	2383.6	2882.5	3129.8	3529.5	1273.3	2485.9	2109.0
6833.7	4434.5	5467.9	6044.0	5829.2	5327.3	6907.1	4365.6	4808.5	4627.0	5006.6
728.4	3032.7	3214.1	3252.4	2447.0	2411.8	2917.4	2691.3	2135.7	2623.2	1996.7
56.2	585.0	1066.7	769.2	420.9	641.3	570.5	1118.7	196.3	251.1	344.2
2679.0	1172.2	1681.0	1687.3	1101.2	1072.5	1910.8	1434.7	708.8	255.1	952.5
192.3	1987.7	2172.0	2708.3	1933.2	1740.0	1638.6	1547.5	1030.2	349.0	991.5
2519.8	4737.6	4320.6	3710.5	3142.5	4026.5	2774.1	3846.8	6449.4	5211.5	6563.8
37.4	18.1	21.7	36.3	23.3	15.1	20.5	14.9	27.8	12.4	22.9
1907.9	2398.9	2092.6	2742.7	2566.7	1810.2	2323.0	2340.7	411.6	587.9	1875.6
402.4	2117.2	2109.2	1468.1	1262.2	1639.8	1019.3	1285.1	2248.9	3455.9	1768.4
236.0	1698.3	2071.5	2092.5	1992.7	1200.0	2108.5	1713.2	1889.6	491.4	1548.2
93.6	505.5	698.5	966.2	800.6	657.2	882.7	942.3	366.3	218.3	574.5
6550.9	1365.2	1471.9	1742.4	1434.5	1031.1	1176.9	1344.0	602.7	430.2	1398.8
4634.0	3636.2	3939.9	4497.6	3383.2	3282.0	3931.1	3375.1	3158.6	3509.4	4225.6
1081.2	3224.9	4304.7	4517.1	2556.1	3416.0	2517.8	3926.9	1878.2	1288.9	2847.1
7283.9	3881.0	3877.0	3698.3	3520.0	3646.3	4114.6	3207.0	5838.8	3592.6	5042.8
65.8	1482.1	1737.6	1858.6	999.7	1451.1	1940.6	1518.7	451.4	331.3	918.3
51.5	154.8	230.9	263.5	142.8	155.5	204.9	154.6	104.9	63.4	94.7
3681.3	4284.7	6000.6	5961.3	3315.1	4715.1	4742.3	4844.8	3673.3	2199.2	4900.6
58.3	39.4	32.5	37.6	21.7	19.8	23.2	19.0	14.6	20.0	27.0
228.1	1031.6	1315.1	1681.9	1463.8	1287.9	1844.3	1710.7	2055.0	1107.3	1090.3
1785.6	5808.8	5586.2	5526.1	6613.1	5495.6	6305.4	6101.5	5973.0	7024.0	7474.4
5771.0	1824.1	1829.8	1676.0	1563.8	1539.8	2154.1	1282.9	2671.8	2441.8	3406.0
3661.2	3360.3	4073.8	3578.5	3518.2	2946.3	3572.3	3420.5	2515.8	3227.4	4046.9
5023.8	5548.5	6164.2	5590.0	6563.0	5468.5	6535.8	4550.2	5760.9	6231.4	7700.6
73.8	53.5	75.3	72.0	89.8	55.3	101.2	55.9	31.4	27.1	74.5
163.0	967.7	1433.8	1376.2	1276.5	1025.3	1568.2	1096.9	1490.5	560.6	901.5
2865.5	6054.8	7023.4	6020.9	5600.1	6030.3	5900.0	6112.7	5389.2	6148.8	6092.8
7346.4	2550.9	3213.9	3056.8	2936.7	2597.1	2691.0	2788.5	3075.5	2600.5	3506.0
40.9	1727.7	2133.0	1707.5	1276.5	1182.0	1369.4	1319.2	585.9	307.1	748.5
2977.4	1480.0	2018.5	1927.7	1186.4	1584.9	1711.0	1107.1	1824.3	658.2	2202.8
214.5	3002.4	2653.2	1419.1	1382.6	2154.6	1197.0	1972.9	2553.3	2827.0	1586.7
58.2	83.1	161.1	203.2	90.9	90.1	149.2	689.6	59.4	39.6	453.8
2287.0	4615.2	3667.8	2532.2	1894.5	3286.3	2327.4	2119.4	4298.9	2657.0	1910.3
58.7	1883.4	1865.3	1664.7	1565.8	1619.4	1526.6	1685.1	2038.7	1017.7	1537.5
1456.7	7201.5	9359.2	7964.5	8659.6	8066.6	8266.4	8286.1	7506.4	4667.4	8319.5
784.8	4373.6	5907.6	6148.4	3780.4	4108.6	4710.0	4900.3	3926.6	2469.8	3551.8
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2866.1	3100.5	4241.6
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4427.9	4183.4	3721.2
15.8	24.8	20.0
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1642.7	1742.5	1266.2
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651.5	860.6	962.2
1472.9	927.8	2750.3
3266.0	4744.0	4691.4
3647.2	4263.3	7654.5
2675.1	4511.7	3893.1
1239.1	1436.6	3474.1
135.3	132.4	192.9
4810.4	4798.1	8296.1
19.8	34.6	29.9
1187.2	1707.9	1936.0
4734.6	6288.0	7530.7
1395.2	2167.1	1311.5
3170.2	4528.6	4145.4
4852.4	5760.7	5964.3
92.9	78.0	124.4
1672.6	1451.9	1811.7
5619.9	6412.3	7284.1
2950.7	3251.8	4135.7
1183.9	1289.3	2554.3
1848.7	2979.4	1601.7
1769.0	2063.2	2858.6
76.5	143.2	243.2
2121.9	2531.4	3368.4
1357.6	1553.8	2505.5
8695.0	6413.8	8240.9
4122.3	5003.7	7181.7
3247.2	3862.0	4806.5

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EF686600.1 gg_id:247858 Sequences Manifest Rumen Yunnan Yel Cattle (Bos Taurus) rumen fluid clone YNRC8 EF6866
EU469255.1 gg_id:297622 Speke's gazelle feces clone SP3_h06_1 EU469
EU453520.1 gg_id:343276 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83 EU453
EU170433.1 gg_id:240700 Clostridium sp. str. W72 EU170
FJ365004.1 gg_id:366702 feces adult twins and mothers; TS1 clone TS1_a01g01 FJ3650
DQ793719.1 gg_id:185168 human fecal clone RL246_aai76b08 DQ793
EU463106.1 gg_id:294065 naked mole-rat feces clone molerat_aai70a01 EU463
AB307643.1 gg_id:268556 clay wall used Japanese traditional buildings clone B42 AB307
DQ800879.1 gg_id:198184 human fecal clone RL183_aao04f08 DQ800
EU457334.1 gg_id:331013 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80 EU457
EF400652.1 gg_id:210777 human fecal clone SJTU_E_16_56 EF4006
DQ015580.1 gg_id:131378 mouse cecum clone M3_g06_2 DQ015
DQ394651.1 gg_id:155932 on -Arctic peninsula Svalbard Norway determined genes and rumen isolates reindee DQ394
DQ808780.1 gg_id:190703 human fecal clone RL243_aai85b07 DQ808
FJ366863.1 gg_id:357503 feces adult twins and mothers; TS27 clone TS27_a04g03 FJ3668
EU843786.1 gg_id:343476 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
EU509268.1 gg_id:263766 cecal contents Mus musculus strain C57BL/6J; MD8 clone MD8_aap46h08 EU509
AM693109.2 gg_id:525997 Microbial level alterations overall gastrointestinal microbiota diarrhoea-predominar AM693
EF404038.1 gg_id:213124 human fecal clone SJTU_C_03_83 EF404
EF603287.1 gg_id:231021 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6032
GQ449055.1 gg_id:561879 Microbiome neonatal calves: shedding microorganisms fecal clone calf783_10wks_ GQ449
EF409954.1 gg_id:211472 Isolation equol-producing fecal clone QE4 EF4099
EU470456.1 gg_id:297964 Grevy's zebra feces clone GZ_aaa02h03 EU470
AY916351.1 gg_id:113822 human stool clone D036 AY9163
FJ364575.1 gg_id:361644 feces adult twins and mothers; TS15 clone TS15_a04e11 FJ3645
AF376224.1 gg_id:50072 ckncm320-B3-25 clone AF3762
EU775897.1 gg_id:330061 Horse feces clone horsem_aai93d07 EU7758
DQ800561.1 gg_id:178571 human fecal clone RL183_aah29g05 DQ800
DQ905474.1 gg_id:170185 human fecal clone 014-b10 DQ905
DQ803929.1 gg_id:189820 human fecal clone RL200_aai60a09 DQ803
EU764469.1 gg_id:311864 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B EU7644
EU469193.1 gg_id:291668 Speke's gazelle feces clone SP3_h03_1 EU469
EU468601.1 gg_id:302588 okapi feces clone OK1_g10_1 EU468
FJ673780.1 gg_id:527976 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6737
GQ175446.1 gg_id:566899 Chicken intestinal microbiota modulations various feed supplementations DGGE an GQ175
AY854329.1 gg_id:110824 herbivore gastrointestinal tract clone Thompsons41 AY8543
EU461148.1 gg_id:294246 hamadryas baboon feces clone BAZ_aah89b06 EU461
EU508360.1 gg_id:271519 cecal contents Mus musculus strain C57BL/6J; MD27 clone MD27_aaa03g03 EU508
DQ237939.1 gg_id:143881 influence fumarate disodium on ruminal metabolism goats goat rumen clone M2 DQ237
FJ368475.1 gg_id:362854 feces adult twins and mothers; TS3 clone TS3_a04g11 FJ3684
EU761698.1 gg_id:338035 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU761

50.5	1258.3	1534.2	1741.2	1224.7	1112.9	1434.4	1597.4	786.2	268.5	846.6
12449.7	3743.5	3479.0	2720.3	3360.9	3834.9	4263.2	3556.1	5005.5	4541.3	5757.0
518.7	2087.2	2063.4	2009.9	2229.3	1825.9	2269.2	2380.1	2907.7	2422.0	2001.7
20236.8	9374.0	8990.0	10049.6	7419.8	8931.5	10143.8	8946.2	10786.9	11594.8	13583.1
7654.5	5276.8	5021.1	5002.2	3837.9	2842.4	3930.0	4497.1	5255.3	3166.9	4428.0
65.9	329.0	469.8	436.8	210.5	155.5	245.5	295.7	135.7	321.7	329.6
3986.7	2852.3	2956.9	2843.4	3285.5	3052.9	4730.7	2997.1	2858.5	2768.4	2615.4
111.4	781.2	983.8	1216.0	764.1	965.2	1064.9	807.5	809.7	505.6	810.9
50.6	411.1	450.2	986.1	192.5	140.3	134.4	164.2	68.2	58.9	159.1
97.5	2658.0	2208.7	1564.4	1166.8	1996.5	1303.8	2035.4	2147.4	2301.1	1400.2
154.3	1673.3	1461.9	1839.6	1210.9	1107.2	1283.6	1451.5	2196.4	1961.8	909.6
9670.3	4070.4	4174.4	3184.3	4163.2	3988.0	3607.1	3828.1	3749.1	3372.9	4572.9
37.8	431.1	1105.0	607.2	123.0	452.2	489.9	469.6	241.9	77.3	177.9
140.6	1806.1	1966.4	2069.0	2087.9	1580.8	2290.2	2289.0	726.5	1480.2	1870.7
292.3	327.9	299.9	359.3	221.8	262.6	290.4	321.9	282.7	318.8	240.1
333.6	1561.9	1823.8	1612.0	1564.5	1234.8	1200.2	1908.0	554.7	857.9	1732.2
5775.0	1588.1	1885.2	1847.6	1580.6	1637.8	1736.3	1715.2	2569.5	1709.5	2249.2
61.3	297.1	378.0	463.3	449.2	321.2	597.3	353.2	98.0	107.0	169.9
38.7	20.4	32.4	36.4	38.0	38.4	23.7	23.8	23.2	16.8	20.4
3878.0	5155.5	5584.6	4716.9	3574.9	4882.2	5498.6	4715.1	5394.0	3023.1	4348.4
2527.9	4169.3	4796.8	4773.2	4427.9	4183.9	4625.0	4031.5	4273.1	2181.7	4269.9
187.8	78.0	109.8	107.8	73.6	83.7	82.4	209.9	60.0	44.3	84.3
54.7	1070.4	2067.8	1501.2	836.2	801.5	1052.0	1227.7	659.9	237.3	817.7
11691.7	5331.2	4981.2	6854.2	6226.3	5701.2	6380.7	5096.9	6059.1	4454.7	7362.8
5154.6	2124.0	3538.4	3433.3	2202.8	2260.6	2827.4	3189.9	1092.7	1594.5	1560.4
50.7	17.1	21.7	32.3	18.5	14.8	23.8	19.7	24.4	22.4	16.1
1808.7	2867.3	3649.3	3165.8	2218.1	2745.2	2479.4	3292.2	2426.0	1566.2	3441.1
55.7	342.3	540.2	317.7	560.2	299.5	512.0	377.8	230.7	135.1	184.9
400.4	2258.5	2365.7	2352.8	730.9	1381.5	1130.7	1103.7	1482.0	649.4	674.1
40.1	43.9	97.9	65.5	30.4	29.9	54.6	99.2	22.4	15.5	34.7
3089.0	3174.4	3597.1	4035.5	2878.1	3196.1	2946.2	4704.8	3421.7	1020.3	3414.2
1898.9	3736.6	4321.7	5165.7	4099.6	4097.4	4970.3	4260.5	4188.1	5567.6	3890.8
152.8	3454.1	3582.0	2827.6	2181.3	2753.8	2974.2	2946.7	3596.3	2957.0	2719.5
12002.6	5975.2	7155.3	7412.4	5236.9	6227.0	6143.4	7072.5	4491.3	6394.0	6672.4
36.8	63.9	89.6	93.2	88.1	54.5	123.2	141.3	65.9	35.1	66.6
71.0	39.0	44.7	41.0	35.5	22.9	23.3	23.9	25.8	24.1	27.9
3473.5	2345.0	1720.4	2051.4	1956.1	1891.4	1978.7	1806.9	1976.7	1348.6	2759.2
18084.4	7766.3	7185.5	8248.3	7921.6	7697.3	8010.2	8546.3	9486.1	7934.8	9954.4
47.7	196.0	476.4	269.5	212.5	226.4	217.4	296.2	102.0	161.1	130.6
1108.5	2446.2	3185.3	3056.0	1489.6	3058.5	3017.7	2687.1	1988.7	1873.8	2415.2
403.8	3904.8	4961.5	4105.1	3434.2	4152.5	5049.8	5916.0	2483.6	1268.2	4946.1

1699.4	1715.1	2601.2
3353.8	4886.0	3577.0
2498.2	2097.0	3035.2
8530.4	9492.9	9720.5
4855.8	5389.0	4672.0
290.9	419.5	360.3
2353.1	4410.2	3275.3
819.8	984.2	1330.9
389.5	335.1	296.2
1617.8	2112.6	2187.2
1559.0	1707.9	2355.9
3193.2	4393.7	3446.0
334.4	728.7	955.9
1316.3	2858.6	2484.0
256.1	401.2	104.0
1537.3	1812.9	2565.4
2064.1	2506.6	2248.3
273.6	208.7	800.3
26.6	65.2	132.7
4156.3	5045.9	6987.2
3813.9	4440.9	6568.0
106.0	53.6	98.2
1104.1	951.1	1724.5
4969.1	5782.8	5772.2
3015.7	2266.9	5459.5
18.9	20.7	18.3
3013.6	2509.2	3077.4
405.8	514.9	576.8
1413.0	1877.0	3120.5
76.6	77.6	295.7
3986.0	4485.2	4863.2
3973.3	4804.3	5545.9
2733.7	3064.6	3728.3
6289.8	7071.4	9826.8
98.4	142.3	218.2
36.0	37.8	48.2
1973.7	1683.2	2856.7
7502.0	9361.6	8898.2
289.9	520.5	1402.2
2641.6	3433.9	3287.9
4033.6	5039.2	4923.7

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DQ800732.1 gg_id:176290 human fecal clone RL183_aao02g01 DQ800
EF434360.1 gg_id:208911 human infant gastrointestinal tract microbiota stool mother babies 13 and 14 7 mont EF4343
AB234454.1 gg_id:146455 termite gut homogenate clone MgMjD-029 AB2344
DQ673514.1 gg_id:161997 rumen fluid clone GRC49 DQ673
EU842855.1 gg_id:352007 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU8428
EU381669.1 gg_id:263881 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid ; EU3816
AY980635.1 gg_id:122955 human rectum mucosal biopsy clone LL09 AY9806
DQ809631.1 gg_id:196782 human fecal clone RL184_aan81g10 DQ809
EU472112.1 gg_id:287351 francois langur feces clone FL_1aaa04a01 EU4721
EF402506.1 gg_id:210552 human fecal clone SJTU_B_08_85 EF4025
FJ366734.1 gg_id:367775 feces adult twins and mothers; TS27 clone TS27_a03c04 FJ3667
GU304571.1 gg_id:548654 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU304
EU468515.1 gg_id:292708 okapi feces clone OK1_f10 EU4685
EF603304.1 gg_id:230751 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6033
GQ502533.1 gg_id:574604 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf4- GQ502
EU506537.1 gg_id:266214 cecal contents Mus musculus strain C57BL/6J; MD19 clone MD19_aaa03f04 EU5065
EU794307.1 gg_id:346705 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_L25 EU7943
EU794105.1 gg_id:345871 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_W46 EU7941
DQ014883.1 gg_id:130110 mouse cecum clone M1_h02_3 DQ014
GU174108.1 gg_id:592004 Microbial Bactrian camel estimated rumen clone XJC79 GU174
EU842993.1 gg_id:308786 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8429
AB234478.1 gg_id:146871 termite gut homogenate clone MgMjW-23 AB2344
FJ366107.1 gg_id:364527 feces adult twins and mothers; TS25 clone TS25_a02g07 FJ3661
DQ815960.1 gg_id:169219 mouse cecum clone aab24h04 DQ815
EU504849.1 gg_id:270413 cecal contents Mus musculus strain C57BL/6J; myd2 clone myd2_aaa03c03 EU5048
EU511174.1 gg_id:270030 cecal contents Mus musculus strain C57BL/6J; WD7 clone WD7_aal03h04 EU5111
DQ793285.1 gg_id:189122 human fecal clone RL199_aaj41g04 DQ793
EU887972.1 gg_id:323591 Microbial structure hydrolytic stage two-stage anaerobic digestion grass silage leach EU8879
DQ804871.1 gg_id:187847 human fecal clone RL385_aao81h01 DQ804
FJ371344.1 gg_id:370052 feces adult twins and mothers; TS6 clone TS6_a03h02 FJ3713
EU006164.1 gg_id:236225 Salmonella enterica serovar typhimurium exploits inflammation compete intestinal r EU0061
DQ798670.1 gg_id:199475 human fecal clone RL181_aan99g11 DQ798
EF603268.1 gg_id:232658 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6032
DQ809981.1 gg_id:175170 human fecal clone RL184_aao66f07 DQ809
DQ795049.1 gg_id:178859 human fecal clone RL310_aam39e10 DQ795
FJ367663.1 gg_id:369320 feces adult twins and mothers; TS2 clone TS2_a02b03 FJ3676
EU453675.1 gg_id:313431 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N EU4536
AY986321.1 gg_id:121129 human stool clone D715 AY9863
GQ897679.1 gg_id:559659 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ897
EU774417.1 gg_id:309482 mammals their gut microbes Eastern Black and White Colobus feces clone COL_aai14 EU7744
EU463401.1 gg_id:299759 domesticated horse feces clone horsem_aai93c02 EU4634

2304.5	2401.5	2434.4	3257.8	2653.3	2388.2	2504.5	2807.0	1857.8	1064.1	2399.5
44.4	51.8	45.4	45.3	38.0	48.1	32.4	60.5	37.3	28.6	44.3
53.7	1472.7	2553.3	2028.8	1217.5	1779.4	1607.3	2181.8	1049.5	652.7	1874.9
62.1	105.4	116.4	146.9	154.6	64.3	266.8	117.5	52.8	48.5	86.1
68.3	1599.0	1139.8	534.8	225.3	996.6	152.7	617.2	957.0	715.3	325.8
76.4	1825.7	2533.3	2064.6	2271.6	1694.5	2356.0	2121.4	1012.0	609.4	1798.8
45.6	125.2	156.1	196.5	217.6	138.6	255.7	177.2	66.8	45.2	97.7
235.7	2335.6	2454.1	3352.7	1645.0	1593.0	2175.6	1982.3	1672.2	1990.4	1496.1
369.3	1656.3	2155.6	2423.3	1124.2	1197.9	1246.4	1481.5	509.1	166.5	1054.0
48.7	2338.5	2891.8	3283.2	1994.9	2266.6	2500.6	3091.8	2728.3	523.3	2400.2
12739.3	5032.8	5390.6	5383.3	3763.0	4473.5	4648.4	4233.9	7499.5	4799.4	6777.4
40.7	1182.4	1331.7	921.8	440.3	833.9	423.3	973.4	507.1	201.5	544.7
16668.0	8634.7	7850.2	9273.2	8904.8	8098.6	9469.2	8006.6	8771.1	9237.8	10336.0
11141.1	8042.9	7913.1	9388.5	7860.0	7771.1	11806.9	8143.3	10770.7	8687.3	10655.5
4388.8	5740.8	6253.7	6803.2	5524.7	6002.9	6408.0	5846.7	5867.4	2157.4	7030.5
40.6	134.8	249.4	268.7	87.0	96.4	146.1	116.5	82.4	199.5	71.8
620.2	4454.0	6423.9	6479.8	3664.9	4755.8	5192.9	7180.4	4691.6	2280.7	3933.7
841.9	2935.9	4693.5	4334.5	2887.7	2747.6	3566.7	3372.5	2295.7	2347.7	2972.9
2243.2	2234.8	2274.8	2881.7	2302.0	2391.6	2550.7	2241.2	1262.3	1663.9	3214.3
3332.0	1711.3	1824.1	1444.6	1270.1	1769.5	1359.9	1703.2	506.5	618.9	696.3
285.8	2020.4	1920.9	2108.6	2016.9	2179.9	1861.0	2671.7	2167.6	983.4	1189.2
42.7	159.2	282.9	368.4	190.4	147.9	204.3	165.3	81.9	37.4	112.5
416.5	3263.1	3751.0	4335.0	3066.0	2954.8	3682.4	3421.4	1961.9	2993.5	2258.5
6235.6	3180.8	3633.5	3266.3	3125.2	3524.5	2885.4	3093.0	2675.2	3223.7	3876.4
13964.7	4786.7	6607.4	6607.7	4645.9	4790.8	5244.8	5150.2	8108.6	6134.0	5262.3
81.1	1585.9	1925.1	2161.2	1312.8	1471.4	2056.0	2207.0	678.5	462.9	1087.8
2279.7	3229.2	3802.6	3654.1	3374.3	2993.0	3346.2	3199.4	2855.0	2708.9	3807.1
83.9	1675.8	2604.8	2145.7	1556.9	1772.9	2059.1	1942.8	1086.0	451.3	1792.3
737.5	1270.4	1911.6	1829.3	514.4	830.1	1705.1	1474.5	878.2	184.3	1188.9
2424.6	2097.5	2251.1	2362.8	2034.8	1944.2	2335.0	2175.8	1904.1	1331.4	1787.0
9333.3	5920.6	4762.2	4127.3	5988.8	5482.6	5798.3	4771.1	6835.3	5978.9	8088.0
1130.2	1137.3	1887.9	1480.2	804.7	955.2	761.4	797.1	915.0	386.4	1412.6
1067.4	1026.5	1299.7	1576.9	1060.0	1057.4	1227.7	887.1	1266.1	1092.7	1403.9
270.0	474.9	789.4	909.7	568.4	575.1	702.4	1073.7	233.2	781.0	304.2
1862.7	1522.2	1719.0	1779.5	1517.6	1416.5	1544.0	1555.8	901.4	1278.2	1095.2
1744.6	3139.0	4598.3	4536.7	3353.8	3643.4	3940.1	3968.0	2577.9	3861.0	4326.0
3297.5	4209.5	5442.6	5762.7	4612.4	4897.7	5415.8	5713.7	5780.9	7043.8	4870.9
213.4	3798.1	4036.4	3508.7	2689.1	3557.0	3752.8	4186.5	3090.7	2793.7	2711.4
53.9	43.3	201.3	198.2	52.2	53.5	144.5	110.6	54.5	20.7	75.8
4524.1	3775.7	4190.5	4155.9	3688.7	3574.2	4636.0	3398.9	3873.5	3220.0	3559.8
73.8	1001.1	1018.7	1457.5	834.6	559.0	803.1	928.9	394.5	143.1	512.8

2071.0	2861.7	5397.8
36.2	53.0	64.2
1725.1	1597.5	1882.9
103.5	75.2	485.4
760.4	968.4	1108.1
1909.4	2416.5	2412.6
163.6	176.5	258.6
2716.7	2257.8	4340.3
1493.1	1495.0	2321.8
1821.8	2584.5	4489.1
4453.2	5961.9	6150.3
952.3	880.9	2631.0
8041.8	8714.3	10379.9
6145.9	8055.8	8455.5
5746.3	6496.7	7253.6
159.3	489.7	242.9
4888.2	5345.7	6520.8
3302.0	5058.1	5065.6
1443.8	2988.8	2562.0
1594.1	1646.9	2756.8
3595.4	2789.4	3218.9
166.7	331.6	1561.1
3820.6	4013.4	6732.2
3169.4	4276.9	3155.8
4818.4	6447.3	5408.4
1718.5	1638.7	4342.6
3009.8	3876.5	3685.2
1756.7	1933.3	2864.8
1346.2	1149.2	1346.7
2103.7	2995.8	3098.5
4982.5	5963.7	5058.4
782.3	1086.7	2059.3
1015.8	1571.2	1089.2
1208.3	594.8	1537.0
1718.5	1662.9	2340.7
4098.0	3851.4	5426.3
5553.2	6133.1	8239.2
3868.3	4406.6	6349.2
48.9	83.5	153.1
2998.1	4880.0	5613.0
811.0	1077.5	2299.2

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EU773222.1 gg_id:349444 BigHorn sheep feces clone BH1_aao25h06 EU773
DQ796716.1 gg_id:184287 human fecal clone RL179_aao53e11 DQ796
EF445157.1 gg_id:216557 rabbit cecum clone NED1A10 EF4451
GU304029.1 gg_id:590712 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU304
DQ673580.1 gg_id:171848 rumen fluid clone GRC115 DQ673
EU465584.1 gg_id:296437 argali sheep feces clone AS1_aao38f10.Contig1 EU465
FJ880813.1 gg_id:437273 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8808
EU461017.1 gg_id:302744 red kangaroo feces clone KO1_aai42d09 EU461
EU470386.1 gg_id:293477 Grevy's zebra feces clone GZ_aaa02e11 EU470
EU382005.1 gg_id:272899 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU382
GU303495.1 gg_id:582952 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU303
EU470037.1 gg_id:303164 trancaspain urial feces clone TU1_aaa03b09 EU470
DQ801064.1 gg_id:193895 human fecal clone RL387_aao91f04 DQ801
EU250958.1 gg_id:363509 degraded cellulose lindane NSC-7 NFC-7 grown 50 degrees Celsius compost compose EU250
DQ793756.1 gg_id:188225 human fecal clone RL246_aai76g11 DQ793
AB185540.1 gg_id:104439 rumen clone F23-D09 AB185
EU464078.1 gg_id:303244 reticulated giraffe feces clone gir_aah93b06 EU464
EU469077.1 gg_id:296415 Speke's gazelle feces clone SP3_a12 EU469
EU462596.1 gg_id:295615 Sumatran orangutan feces clone orang2_aai65h01 EU462
EU506620.1 gg_id:258946 cecal contents Mus musculus strain C57BL/6J; MD20 clone MD20_aap53e02 EU506
EF096988.1 gg_id:198512 mouse cecum clone SWPT13_aaa03g08 EF0969
EU842961.1 gg_id:315150 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU842
EU466444.1 gg_id:287377 bighorn sheep feces clone BH2_aao23g10 EU466
FJ681223.1 gg_id:528725 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6812
EU842439.1 gg_id:340770 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
EU794257.1 gg_id:344025 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_J17 EU794
AB198524.1 gg_id:135518 termite gut wall fraction clone RsW02-034 AB198
EF454875.2 gg_id:221978 termite hindgut clone 290cost002-P3L-568 EF4548
EU465567.1 gg_id:299012 argali sheep feces clone AS1_aao37h07.Contig1 EU465
AY858483.2 gg_id:109604 gastrointestinal tract eland clone ELAND_3 AY8584
EU794310.1 gg_id:307291 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_P3 EU7943
AB185579.1 gg_id:103145 rumen clone F24-A06 AB185
EU794264.1 gg_id:354632 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_L34 EU794
AF050582.1 gg_id:16073 contaminated aquifer clone WCHB1-54 AF050
EU794192.1 gg_id:323910 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_E02 EU794
AM183003.1 gg_id:251289 and its spatial composts compost clone SMA17 AM183
EU844610.1 gg_id:311446 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
AB009176.1 gg_id:16063 rumen clone RFN17 bacterium AB009
EU775199.1 gg_id:329360 Reticulated giraffe feces clone gir_aah94d12 EU775
DQ801076.1 gg_id:176718 human fecal clone RL387_aao91g09 DQ801
EU794129.1 gg_id:356245 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_AE6 EU794

4478.6	1763.8	2672.8	2487.6	1656.3	1570.4	1967.0	2025.3	1766.2	1821.7	1732.5
851.4	106.6	152.3	196.5	186.5	143.1	296.6	150.3	121.6	61.9	105.9
55.7	101.2	127.3	206.9	158.8	93.5	127.1	112.0	59.0	38.0	60.1
6206.0	3804.9	4764.0	4395.4	2869.0	3516.5	4941.3	3565.8	3080.4	2909.0	5193.6
1063.5	1374.7	1715.8	1748.7	1368.8	1115.9	1539.7	1039.2	1447.8	537.2	1709.6
9600.2	7645.2	8604.9	9441.0	8014.1	7758.7	8860.4	8931.9	7280.7	5369.8	8680.7
395.7	5473.4	6083.4	4349.8	5246.5	4764.0	4393.1	4251.9	5162.2	3945.4	4544.1
3567.4	7906.3	8852.1	10456.7	7381.0	7675.0	8559.8	7798.9	7994.0	6500.0	8242.2
87.1	1490.3	2364.5	2389.7	2198.0	2050.3	2019.7	2384.3	1591.0	1040.3	1325.9
1426.8	2747.0	4133.3	2936.9	1665.0	2950.7	2954.5	4402.4	2162.5	1243.8	2784.9
1944.8	4091.3	4897.1	5561.8	3695.7	4409.3	4118.2	4556.7	5784.5	3177.9	6859.9
3691.7	1936.8	3045.1	2671.5	1896.2	2384.1	2548.9	2409.4	1694.0	1349.4	2268.9
32.3	208.7	293.9	187.8	92.0	203.6	632.2	155.9	72.5	86.7	104.2
359.6	752.6	1256.9	1306.4	471.3	663.6	739.4	993.9	372.0	225.8	518.3
42.0	25.3	19.2	51.3	14.6	21.1	14.6	20.3	29.1	15.3	17.4
47.1	297.5	392.2	688.9	257.2	259.2	366.0	740.4	137.4	58.7	181.0
11240.4	8478.6	8877.4	10084.4	11070.8	7960.5	10369.9	8676.9	10769.8	8303.8	9992.2
147.6	2596.1	4537.3	3230.2	3031.0	2939.3	4220.0	3408.5	1897.9	1684.9	2535.9
775.3	4973.1	6761.5	6867.8	4106.2	4922.0	5019.5	5402.2	3503.8	1731.8	4387.8
5890.3	3005.7	3064.5	3721.5	2938.2	3109.2	3076.1	3358.6	3256.1	4117.3	3144.5
1159.0	923.7	1962.3	1226.2	1249.1	1251.8	1646.1	1754.1	2469.1	3564.4	1343.1
157.8	1500.6	1752.1	2116.0	2279.1	1640.1	2768.6	1844.7	1960.1	966.2	1180.5
115.5	3362.6	4508.9	4533.5	2811.1	3331.4	3431.8	4007.6	2360.8	766.7	2767.6
936.8	2946.3	3542.3	3913.5	3306.4	3005.6	4052.5	3205.7	2338.4	2416.8	2672.7
1534.4	3288.8	3610.1	3999.9	4689.8	3480.2	4701.5	3518.6	3697.1	2833.9	2382.1
49.9	484.0	982.1	606.9	442.2	799.2	437.5	745.5	241.8	340.5	355.2
43.6	114.8	87.8	87.1	69.8	76.4	87.2	84.0	102.4	47.0	42.7
42.3	594.9	1033.1	741.2	376.1	741.6	507.7	629.4	278.6	109.1	323.1
43.6	177.6	266.7	258.2	29.5	101.8	136.3	81.6	59.3	34.6	49.7
40.0	407.8	863.8	600.2	890.6	664.7	388.1	716.6	463.1	71.5	309.7
4248.2	6204.6	8596.2	8253.3	5386.6	6579.0	7162.8	6926.8	6298.0	5099.0	6702.5
31.2	69.7	96.0	94.3	93.3	99.6	97.3	107.1	47.8	35.6	86.8
2466.5	4097.0	5420.7	5022.3	3238.2	4252.1	4782.3	4581.7	3327.6	2156.4	4105.5
1392.0	3853.1	4207.2	4150.6	3560.8	3678.9	3708.0	4474.5	4309.8	3415.8	3500.8
194.6	1904.3	2394.9	2864.5	2063.3	1954.0	2289.1	1893.5	1390.6	1008.5	736.5
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3703.8	4290.7	4974.9	5274.6	2645.4	4335.7	3497.4	5605.1	3643.1	5245.7	4952.0
39.7	2040.2	2179.0	2688.8	1634.8	1612.8	1751.9	1905.9	967.0	981.0	1030.8
115.6	958.4	1200.8	1371.3	1087.6	1026.1	1424.0	1176.3	549.0	250.6	650.4
10530.9	6058.9	5350.6	6374.6	6140.8	6549.6	7657.0	5454.2	7031.5	5123.4	7017.1
4456.2	894.0	958.7	1317.6	994.4	986.7	1800.2	1104.4	716.4	1326.2	686.9

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90.3	176.7	343.1
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8310.1	8015.5	9643.8
3938.4	4071.6	5601.9
7673.5	9256.3	10359.0
2315.8	2377.0	2911.1
2225.4	2483.9	3884.3
3494.9	4176.2	3663.3
2098.6	3084.5	3407.8
287.7	201.9	222.0
981.7	1233.6	2481.9
40.0	39.6	44.1
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9040.1	10684.3	11226.4
3292.5	3564.5	4824.1
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1875.8	1688.8	2945.1
3183.9	3888.7	3222.4
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EU474824.1 gg_id:300854 takin feces clone TAK_aaa02g06 EU474
EU774438.1 gg_id:342510 mammals their gut microbes Eastern Black and White Colobus feces clone COL_aai1 EU774
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EU794087.1 gg_id:312992 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_U43 EU794
EU773732.1 gg_id:346413 Cheetah feces clone CE3_aai05h11 EU773
DQ394632.1 gg_id:151144 -Arctic peninsula Svalbard Norway determined genes and rumen isolates reindeer o DQ394
DQ394634.1 gg_id:151267 -Arctic peninsula Svalbard Norway determined genes and rumen isolates reindeer o DQ394
EU794085.1 gg_id:314757 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_Z35 EU794
EU471995.1 gg_id:298553 francois langur feces clone FL_1aaa03c03 EU471
AB233996.1 gg_id:156549 anaerobic reactor clone B-3 AB233
GQ451308.1 gg_id:592857 Fecal Yunnan snub-nosed monkey feces clone J325 GQ451
EU453210.1 gg_id:349798 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77 EU453
EU844645.1 gg_id:339252 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
EU794156.1 gg_id:349201 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_L42 EU794
AB198484.1 gg_id:135720 termite gut wall fraction clone RsW01-056 AB198
EU466282.1 gg_id:289200 bighorn sheep feces clone BH2_aao21c11 EU466
GU454868.1 gg_id:518493 Understanding short-chain fatty acids accumulation enhanced alkaline digestion: kir GU454
EU461091.1 gg_id:301917 red kangaroo feces clone KO1_aai44a02 EU461
EU468985.1 gg_id:301716 Speke's gazelle feces clone SP2_d07_1 EU468
GU174133.1 gg_id:551562 Microbial Bactrian camel estimated rumen clone XJC124 GU174
EU844169.1 gg_id:326767 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
EU461512.1 gg_id:303394 black rhinoceros feces clone RH_aaj91c12 EU461
EU462243.1 gg_id:299441 chimpanzee feces clone CHIMP1_aaj38c11 EU462
AB185776.1 gg_id:105514 rumen clone U29-D05 AB185
EU762139.1 gg_id:307647 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU762
EU468725.1 gg_id:290201 okapi feces clone OK2_g04_1 EU468
EU794278.1 gg_id:325883 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_H46 EU794
EU509875.1 gg_id:270519 cecal contents Mus musculus strain C57BL/6J; WD11 clone WD11_aak22h11 EU509
DQ797051.1 gg_id:199149 human fecal clone RL386_aao86c11 DQ797
EU850568.1 gg_id:303584 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF379 EU850
EU381809.1 gg_id:273552 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU381
FJ681730.1 gg_id:522625 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6817
FJ681667.1 gg_id:517931 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6816
EU773299.1 gg_id:329112 BigHorn sheep feces clone BHSD_aaa04e12 EU773
EU464400.1 gg_id:295056 hamadryas baboon feces clone AFBAB_aai04d05 EU464
DQ808758.1 gg_id:177437 human fecal clone RL239_aaj12h05 DQ808
EU469314.1 gg_id:293987 Speke's gazelle feces clone SP3_h03_3 EU469
FJ681337.1 gg_id:518060 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6813
DQ456148.1 gg_id:157036 pre-adolescent turkey cecum clone CFT29A2 DQ456
EU776470.1 gg_id:340210 Red Kangaroo feces clone KO2_aai17e12 EU776

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1126.4	744.2	1300.6	1020.4	776.3	548.4	598.3	561.5	668.8	578.8	520.5
857.7	2555.8	3342.6	3493.6	2572.6	2763.2	2522.3	3938.7	2230.0	1657.2	2205.0
637.4	1943.1	2627.5	2621.9	1552.0	1984.9	1867.6	1654.7	889.6	469.5	1054.2
874.5	4149.0	5857.9	4835.6	3209.0	4092.0	5166.4	4457.3	3971.2	3037.2	4674.3
55.2	116.6	165.1	251.8	64.6	87.4	71.7	64.2	51.3	53.1	68.0
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181.3	1296.7	1900.6	2559.8	1392.4	1361.5	1764.2	1450.9	1424.0	754.6	1010.1
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89.4	444.1	723.6	908.0	444.6	442.0	448.7	360.5	168.1	147.5	197.6
257.0	1672.8	2140.8	2089.7	2080.8	2072.2	2261.8	1689.3	1595.6	1469.3	934.2
1019.8	3669.5	5096.8	5850.6	2865.1	4061.6	3611.8	4269.5	2659.9	1542.3	4370.2
198.5	1426.6	2062.7	2069.7	1969.0	1524.0	1794.2	1657.2	584.7	400.7	947.1
45.0	55.3	120.2	133.1	51.0	47.8	76.8	61.4	54.4	28.7	39.1
656.6	6062.5	8741.8	8657.6	5049.3	6608.0	6969.5	7678.6	3103.7	1449.6	6112.1
3185.3	3111.7	3915.5	4121.4	3287.8	3294.4	3298.2	3354.6	4155.3	2058.2	3453.0
885.3	5883.9	5836.4	5996.1	5693.6	5115.1	6613.1	5572.3	5835.4	7615.3	5061.1
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33636.7	8509.3	8447.2	8908.5	7785.5	8261.1	8524.4	8952.8	10673.7	9862.1	11599.7
2785.1	3866.6	4488.7	3871.4	4651.4	4219.6	4649.9	3564.2	2940.3	3078.5	4041.0
4269.2	5379.4	6831.0	6779.7	7806.1	6285.2	9964.9	6526.6	5414.5	4342.0	5871.2
27.9	16.7	24.6	23.8	19.2	16.2	15.4	17.1	16.1	9.4	20.2
5646.0	5017.2	5907.9	5512.7	4920.0	5077.6	5828.4	5265.8	5461.3	5432.1	6309.0
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49.0	84.8	123.2	167.9	124.3	74.6	108.8	92.1	43.8	40.9	46.7
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FJ366012.1 gg_id:366309 feces adult twins and mothers; TS25 clone TS25_a01f12 FJ3660
GQ449144.1 gg_id:511242 Microbiome neonatal calves: shedding microorganisms fecal clone calf784_6wks_gr GQ449
EU773276.1 gg_id:349695 BigHorn sheep feces clone BH2_aao22h09 EU773
EU771349.1 gg_id:321127 Asiatic elephant feces clone AE2_aaa02h02 EU771
EU776451.1 gg_id:354054 Red Kangaroo feces clone KO2_aai17g04 EU776
EU844199.1 gg_id:304015 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
EU472419.1 gg_id:293879 Angola colobus feces clone EAC_1aaa03d10 EU472
DQ801138.1 gg_id:181671 human fecal clone RL387_aao92g09 DQ801
EU776342.1 gg_id:320831 Red Kangaroo feces clone KO1_aai42g11 EU776
EF686635.1 gg_id:237134 Sequences Manifest Rumen Yunnan Yel Cattle (Bos Taurus) rumen fluid clone YNRC1 EF6866
EU465539.1 gg_id:289774 argali sheep feces clone AS1_aao37c02.Contig1 EU465
EU464112.1 gg_id:296798 reticulated giraffe feces clone gir_aah93h11 EU464
AF050581.1 gg_id:16062 contaminated aquifer clone WCHB1-49 AF050
EU470437.1 gg_id:289438 Grevy's zebra feces clone GZ_aaa03g08 EU470
EU843153.1 gg_id:353179 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
EU463648.1 gg_id:288212 domesticated horse feces clone horsej_aai90d05 EU463
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EU470173.1 gg_id:292016 trancaspain urial feces clone TU2_aaa03h02 EU470
EU794179.1 gg_id:331046 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_A15 EU794
EU470148.1 gg_id:300089 trancaspain urial feces clone TU2_aaa02b09 EU470
EU470366.1 gg_id:287724 Grevy's zebra feces clone GZ_aaa01d12 EU470
GQ502523.1 gg_id:583328 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf4- GQ502
DQ805504.1 gg_id:187508 human fecal clone RL203_aai63e04 DQ805
EU458486.1 gg_id:291270 spotted hyena feces clone HY2_h02 EU458
EU772024.1 gg_id:335757 Argali sheep feces clone AS2_aao36e09 EU772
GQ451202.1 gg_id:578310 Fecal Yunnan snub-nosed monkey feces clone J52 GQ451
GQ448531.1 gg_id:594107 Microbiome neonatal calves: shedding microorganisms fecal clone calf784_6wks_gr GQ448
EU779127.1 gg_id:328671 Trancaspian Urial feces clone TU2_aaa02e08 EU779
DQ801040.1 gg_id:196502 human fecal clone RL387_aao91c07 DQ801
AB192042.1 gg_id:142583 termite gut homogenate clone M1NP1-42 AB192
AB198499.1 gg_id:135452 termite gut wall fraction clone RsW01-073 AB198
EF686609.1 gg_id:239644 Sequences Manifest Rumen Yunnan Yel Cattle (Bos Taurus) rumen fluid clone YNRC9 EF6866
EU468734.1 gg_id:297952 okapi feces clone OK3_b09 EU468
FJ366638.1 gg_id:362693 feces adult twins and mothers; TS27 clone TS27_a02a10 FJ3666
GQ448437.1 gg_id:547348 Microbiome neonatal calves: shedding microorganisms fecal clone calf783_10wks_g GQ448
FJ684375.1 gg_id:528722 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6843
EU772128.1 gg_id:337202 Argali sheep feces clone AS2_aao36f02 EU772
EU779349.1 gg_id:344615 Somali Wild Ass feces clone WA_aaa04g06 EU779
FJ680570.1 gg_id:522248 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6805
EU844036.1 gg_id:344137 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844

118.1	2138.9	2522.5	2504.8	2087.0	2095.8	2097.6	2521.0	1213.9	772.6	1641.5
119.5	3452.7	4145.7	3841.5	2707.3	3869.5	2949.3	3310.7	2611.2	3440.4	2316.3
241.5	1835.1	1806.6	2143.3	1587.1	1970.2	1654.0	1698.2	1642.1	817.6	1807.5
241.2	3861.0	5506.7	5091.8	3272.3	3649.3	4888.2	4298.2	4075.2	1552.7	3590.0
774.3	4936.4	6973.8	4854.3	3556.4	4550.1	4559.0	5014.9	4995.1	2497.9	5524.2
63.4	1114.9	1911.0	1769.4	1071.6	1049.3	1203.0	1047.3	410.2	498.3	601.9
572.8	2066.1	2389.6	2075.6	1938.8	2115.6	2428.7	2111.4	2421.3	1536.5	2617.2
96.4	1665.7	2268.8	2018.5	1527.2	1742.0	1292.5	1659.9	546.6	391.8	1013.8
3365.0	3867.4	3426.2	2982.8	1757.2	3529.1	2674.6	2921.1	4185.0	2970.4	2946.8
3696.1	4425.0	4982.4	5128.9	4987.5	4578.5	5668.5	4572.3	3854.1	3624.9	4402.5
5520.1	5131.2	6296.6	6397.5	5879.9	6056.4	6647.4	5007.8	5912.4	4868.9	6103.3
191.4	5034.4	6886.9	6513.4	3450.7	5096.0	5402.1	5640.6	2585.4	1807.6	4632.4
778.0	4653.4	5478.0	5419.2	5356.9	4762.7	6634.7	5129.2	3850.9	2429.2	3643.2
44.9	188.8	234.2	282.8	121.7	188.6	151.3	156.8	84.8	331.4	138.6
1132.6	3188.4	3472.7	3186.9	2231.9	3167.4	3291.9	3399.9	1201.0	825.9	3288.2
698.4	3017.7	4797.6	4965.1	2253.5	3585.1	3030.7	3809.9	2671.5	3426.1	4045.3
2746.6	4962.5	4926.4	5473.1	6620.5	5745.3	7185.4	6071.8	7203.9	5649.0	8667.3
580.2	3137.4	5210.4	3214.7	3583.0	3185.3	2758.7	4045.8	3209.8	3234.7	3480.0
8282.8	7801.6	8126.2	8950.3	8239.9	7702.4	8656.3	7691.5	9356.7	9386.6	9010.2
3357.5	5322.1	5761.4	6825.7	6485.6	5220.2	8009.9	5594.8	5778.2	3631.2	6079.6
4303.2	5755.4	6503.4	6635.4	6675.6	5453.0	7935.6	6157.2	4450.9	2467.0	5597.3
2334.3	6320.7	7249.2	7711.8	6582.6	6045.4	7595.0	6058.1	6751.6	3500.9	5731.7
200.7	4399.5	4935.3	4774.5	5252.9	4500.0	5787.4	4566.0	2188.7	1232.0	3753.2
3831.6	2470.6	2215.7	2452.5	2197.8	2421.8	2018.5	2105.7	2477.5	1218.7	3436.4
34.8	203.2	525.9	480.9	254.4	258.8	383.7	275.2	166.5	61.0	139.9
2100.4	4406.4	5412.6	5760.6	4628.4	4439.5	5763.5	5405.7	5198.3	3614.9	4250.3
520.2	2574.3	3298.7	3712.3	3708.6	3527.7	5042.0	4456.1	2600.1	2168.1	3839.6
1377.8	2492.5	2626.1	2828.0	2197.5	2924.0	2604.7	2499.8	4414.3	2689.0	2755.6
304.6	1410.7	1716.1	2035.0	1362.1	1285.5	1759.8	1561.9	575.4	613.4	1124.1
163.8	2878.1	3485.6	3914.0	2864.0	3091.5	3278.6	3262.7	2074.9	1457.1	2799.8
53.1	1386.8	2675.2	1847.6	1658.3	1811.1	1484.8	2371.8	1887.5	1152.8	2364.5
818.9	2553.5	2830.3	3195.1	3442.9	2896.3	3124.1	2752.7	2156.6	1475.0	2632.3
879.1	2417.9	3024.6	2328.6	2593.6	2346.5	2633.2	2530.5	3766.4	1455.0	3614.6
3635.5	7861.1	9254.3	9635.9	6829.9	8111.8	9025.7	8766.4	7790.8	4909.4	8412.4
483.7	2028.8	2259.6	1738.9	1521.7	1594.8	1702.5	1661.9	2357.6	1361.6	2449.6
1236.5	4107.8	4839.4	5235.2	4693.1	4129.4	5582.1	4404.4	3989.3	2433.3	4115.4
1858.4	2404.6	3097.1	3109.3	2124.1	2551.3	2643.4	2355.1	1298.6	1191.9	1930.7
4075.4	2412.1	3285.7	3148.6	2055.8	2748.7	2934.7	3527.4	3070.0	1939.7	2619.7
1262.9	4067.4	6043.6	5980.3	4024.3	3920.7	5827.9	5543.2	4591.0	2031.1	4787.0
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2908.9	3370.5	5261.6
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3985.9	4659.0	5398.2
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1678.1	2667.7	2893.7
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8103.7	9026.0	9956.9
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3777.9	4820.6	6331.5
1734.2	2097.5	2012.9
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1227.2	1606.3	2225.5
3045.2	3750.1	4832.2
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1962.1	3228.7	3244.6
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1386.5	1507.0	3372.5
3914.4	4691.1	6892.8
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3818.4	3244.1	4725.5
4629.3	4312.1	5876.1
4872.6	4913.5	5779.4
5641.2	4669.3	6349.1

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FJ680572.1 gg_id:528121 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6805
EU794263.1 gg_id:326926 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_J18 EU7942
EU794233.1 gg_id:346556 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_AF12 EU7942
EU509795.1 gg_id:264941 cecal contents Mus musculus strain C57BL/6J; WD11 clone WD11_aak21b06 EU5097
GQ898040.1 gg_id:552448 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ898
EU466218.1 gg_id:290974 bighorn sheep feces clone BH1_aao28c02 EU4662
EU466103.1 gg_id:296496 bighorn sheep feces clone BH1_aao25h04 EU4661
EU470320.1 gg_id:297021 Grevy's zebra feces clone GZ_aaa04h11 EU4703
EU468812.1 gg_id:291161 okapi feces clone OK3_g06_2 EU4688
EF088287.1 gg_id:190918 Sulfobacillus acidophilus str. 1 EF0882
AY007665.2 gg_id:33263 Sulfobacillus yellowstonensis str. YTF-1 AY0076
EU495236.1 gg_id:275497 Sulfobacillus benefaciens str. MT606 EU4952
EU499919.1 gg_id:279555 Sulfobacillus thermosulfidooxidans str. N19-50-01 EU4999
U75648.1 gg_id:14342 Sulfobacillus thermosulfidooxidans str. BC1 U75648
EF612374.1 gg_id:236874 historic semiarid lead-zinc site mine tailings clone K6-C04 EF6123
EU419196.1 gg_id:264046 Sulfobacillus acidophilus str. DK-I15/45 EU4191
AY079150.1 gg_id:60544 Sulfobacillus sibiricus str. N1 AY0791
EU419151.1 gg_id:270741 Microbial and ecology selected andesitic hydrothermal acidic hydrothermally modifi EU4191
DQ464142.1 gg_id:157528 acid mine drainage clone D3-5 DQ464
EF612378.1 gg_id:244429 historic semiarid lead-zinc site mine tailings clone K6-C81 EF6123
DQ834229.1 gg_id:164112 Geochemical Controls on Microbial and Joseph's Coat Springs Yellowstone National DQ834
AM749742.1 gg_id:246891 Isolation ing candidate division soils New Zealand steam-affected geothermal soil cl AM749
EF612379.1 gg_id:250416 historic semiarid lead-zinc site mine tailings clone K6-C107 EF6123
EU419149.1 gg_id:273033 Microbial and ecology selected andesitic hydrothermal acidic hydrothermally modifi EU4191
EU419137.1 gg_id:275460 Microbial and ecology selected andesitic hydrothermal acidic hydrothermally modifi EU4191
DQ464143.1 gg_id:157541 acid mine drainage clone D3-28 DQ464
AY805540.1 gg_id:108883 thermophilic bioleaching clone JTC05 AY8055
EU419152.1 gg_id:266474 Microbial and ecology selected andesitic hydrothermal acidic hydrothermally modifi EU4191
NR_028814.1 gg_id:583050 Thermaerobacter subterraneus str. C21; ATCC BAA-137 NR_028
AB061441.1 gg_id:50462 Thermaerobacter nagasakiensis str. JCM 11223 AB0614
AB454087.1 gg_id:323069 Thermaerobacter sp. str. Ni80 AB4540
EU214629.1 gg_id:331773 Thermaerobacter subterraneus ir-12 EU2146
AY936496.1 gg_id:114490 Thermaerobacter riparius str. KW1 AY9364
AB011495.1 gg_id:13721 Thermaerobacter marianensis AB0114
AB254790.1 gg_id:160816 Biogenic Fe-oxyhydroxides nodules (takashikozo) encrusted iron-oxide reducing sedi AB2547
DQ234653.1 gg_id:143589 subsurface water clone DR546BH1103001SAD85 DQ234
AF465653.1 gg_id:25424 G+C Gram-positive clone YNPRH70A AF4656
EF612375.1 gg_id:255886 historic semiarid lead-zinc site mine tailings clone K6-C05 EF6123
AF391988.1 gg_id:27433 thermal soil clone YNPFFP9 AF3919
EU419144.1 gg_id:275922 Microbial and ecology selected andesitic hydrothermal acidic hydrothermally modifi EU4191
AM749765.1 gg_id:240376 Isolation ing candidate division soils New Zealand steam-affected geothermal soil cl AM749

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973.7	3760.4	4613.2	4934.6	3666.0	3639.7	4197.4	4441.4	3906.4	2517.6	3988.4
4385.9	4717.7	5308.1	5575.2	4391.8	4652.8	5450.8	4780.0	4808.8	3685.8	4973.0
6461.1	2467.5	3418.1	2851.0	2726.5	2790.0	2922.8	3421.0	2837.3	2345.7	2961.6
1519.5	3556.2	4358.0	3505.4	3203.9	2931.9	4476.0	3460.5	2977.4	3177.7	3384.3
8593.9	4505.9	4686.5	4341.7	4302.7	4101.7	4724.7	4402.3	5700.6	4003.2	6051.0
46.9	832.7	1316.4	1499.7	614.0	1018.0	1132.1	1213.4	274.5	204.3	602.1
118.5	1373.3	1699.0	1727.5	1042.3	1378.1	1495.7	1673.3	751.2	241.8	857.3
12051.2	5972.3	7837.9	7788.9	5358.0	5734.7	6801.4	6376.4	5325.8	2755.1	6618.9
270.4	644.6	861.2	1000.1	1201.7	810.5	1286.2	1230.0	823.2	146.1	610.5
70.6	159.3	227.1	273.3	363.0	203.2	374.0	366.9	287.6	69.0	138.0
1147.4	2744.0	3133.9	3001.2	3002.8	2691.2	3166.9	3383.8	2497.2	1236.8	2801.8
421.1	2741.0	3250.1	3371.1	3131.7	3146.6	3623.8	3443.5	2055.2	1377.9	2761.8
7520.6	3394.1	3678.0	4026.1	4109.6	4029.7	4928.7	3627.6	6007.3	3376.9	5235.0
5881.0	8937.8	8171.9	7463.7	6359.8	8124.4	10825.2	7736.1	13601.4	4816.1	11370.2
42.1	892.8	1181.1	1322.9	853.8	1073.3	1306.1	1838.0	802.3	270.2	820.2
164.5	3503.6	4380.2	3720.6	3932.7	4393.9	4014.6	3654.0	2987.4	1819.4	3606.5
108.3	1260.5	1488.8	1860.7	1327.6	1533.0	1363.1	2072.4	1118.4	372.7	1067.5
54.9	47.7	49.9	62.1	68.8	61.4	59.1	62.3	46.0	55.5	55.6
1186.6	4672.1	5427.8	4798.8	5611.2	4845.9	7632.2	5196.2	3301.5	2545.2	5991.0
78.3	301.1	447.0	416.3	687.9	516.8	473.9	307.4	263.0	1084.4	250.4
787.5	4152.6	2876.5	4286.5	2811.5	3779.6	5856.3	4014.1	1900.2	2093.6	3710.4
591.0	2929.1	2884.4	2957.7	3042.5	2664.8	3195.4	2905.2	2554.8	2184.6	2667.2
8680.1	4694.6	4560.2	4335.7	3649.9	4319.9	5246.7	4883.4	5878.2	3351.3	6090.6
4411.3	4332.5	4513.6	4812.6	4935.4	4332.0	5716.8	4006.0	7272.9	3902.3	3905.5
36.1	170.6	208.2	149.7	138.9	99.8	152.0	116.5	83.2	28.6	65.3
35.4	54.2	88.5	97.5	60.3	29.7	79.6	76.2	37.1	36.1	61.3
50.6	75.3	125.5	102.2	116.6	73.4	96.5	190.1	56.1	45.4	97.5
322.4	2120.0	2296.8	2601.9	3412.7	2454.5	3660.3	2495.2	1394.6	1438.3	2251.7
617.7	3001.3	2950.9	3507.0	4544.1	3224.0	4695.0	3532.3	2367.8	2318.4	2981.5
1020.3	3820.5	4063.4	4430.2	5192.0	4196.2	5194.5	4683.3	2728.2	2729.3	4210.1
313.5	2988.8	2809.1	2958.0	3289.4	3262.5	4446.4	4146.3	1760.9	883.1	3090.1
388.5	2242.5	2167.7	2603.1	3503.7	2414.3	3265.0	2428.9	1174.5	1809.6	1803.5
524.6	3244.1	3053.1	3757.8	5130.4	3369.8	4828.1	3517.8	2616.0	2057.2	3282.9
132.1	381.1	523.8	466.3	497.5	451.8	377.7	460.3	286.8	330.8	523.8
698.8	5420.8	5027.6	5720.9	5713.9	5025.3	5966.9	6926.8	3805.8	4011.1	6710.0
926.5	3540.1	3594.5	3722.2	4155.5	3532.3	4261.9	3502.0	3254.8	1362.1	2943.3
704.0	4978.6	5119.8	7132.3	4540.0	5092.1	7104.9	4951.2	5991.4	3902.0	4252.8
2115.1	6111.6	5726.5	5307.7	4899.3	5567.5	5629.1	5336.3	5897.0	5023.0	5259.7
92.1	789.7	1102.8	1006.3	1032.9	986.0	1088.4	1537.2	291.9	528.1	1242.4
738.4	3601.2	4183.9	3953.4	5065.2	4162.7	5500.0	3956.4	2695.2	2146.6	3002.0

3083.9	3944.9	3597.4
3959.5	4884.7	7022.0
4888.8	5594.2	7311.4
3699.6	4251.5	3858.4
2886.4	3733.5	6053.5
4012.1	5798.1	5140.5
946.5	1303.3	2161.6
1118.0	1965.6	3350.1
6237.7	6100.1	7932.9
884.5	1288.6	1282.3
216.1	414.1	329.7
2804.9	3240.2	4071.1
2691.1	3345.9	4406.2
3395.2	5310.7	4213.1
5186.9	7674.1	6781.1
1000.8	2007.8	1920.4
3566.3	3770.5	4039.5
1565.6	1849.7	2342.3
51.4	99.8	50.1
3952.0	5009.4	7919.2
443.0	707.5	651.2
2576.6	3305.9	5132.1
1676.1	2811.4	3288.1
2910.0	5471.7	3824.9
3785.0	4212.2	5025.0
97.9	160.2	194.9
34.2	59.9	87.5
202.6	116.9	80.1
2169.0	2715.9	3679.3
3140.5	3666.3	4965.5
4044.9	4790.6	5530.6
3231.9	4232.3	4762.9
2343.0	2569.8	3700.4
3273.7	3879.3	4681.8
383.3	690.6	871.9
4486.6	6302.7	6504.1
3049.3	3560.5	5390.5
4520.5	4881.9	6587.5
4411.4	6525.4	8290.8
933.1	1389.6	1680.4
3168.7	4793.3	7873.9

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AP006840.1 gg_id:129187 Symbiobacterium thermophilum IAM 14863 str. IAM14863 AP006
AB361629.1 gg_id:243859 Symbiobacterium sp. str. KY38 AB361
AB455238.1 gg_id:322976 Symbiobacterium sp. str. KY46 AB455
AB455239.1 gg_id:344098 Symbiobacterium sp. str. KA13 AB455
DQ112187.1 gg_id:132753 Syntrophomonas sporosyntrophas str. Y4-1 DQ112
FJ799130.1 gg_id:559105 Microbial Responsible Intermediates Degradation Anaerobic Digestion System Deterr FJ7991
AF050586.1 gg_id:13690 contaminated aquifer clone WCHB1-82 AF050
AF482445.1 gg_id:77471 granular sludge clone R5p27 AF482
DQ984666.1 gg_id:257916 Anaerobic degradation unsaturated or saturated long chain fatty acids (LCFA) prese DQ984
AY290767.1 gg_id:87293 Syntrophomonas curvata str. GB8-1 AY290
AB252683.1 gg_id:172658 and activities propionate-oxidizing that affected propionate concentration anaerobic AB252
AB186861.1 gg_id:103994 polychlorinated dioxin dechlorinating microcosm clone TSBW01 AB186
AB248633.1 gg_id:146259 mesophilic anaerobic butyrate-degrading reactor clone BHB04 AB248
EF559161.1 gg_id:217350 mesophilic anaerobic digester clone G35_D8_L_B_A02 EF5591
AM947547.1 gg_id:259682 Minor changes detected microbial structure and after three week thermophilic dige AM947
CR933176.1 gg_id:110152 Evry municipal wastewater treatment plant clone 008H01_B_SD_P15 CR933
AB248623.1 gg_id:149149 mesophilic anaerobic butyrate-degrading reactor clone BLB01 AB248
FJ799160.1 gg_id:511304 Microbial Responsible Intermediates Degradation Anaerobic Digestion System Deterr FJ7991
AB234271.1 gg_id:150183 Biotransformation Polychlorinated Dioxins Microbial Dynamics Sediment Microcosm AB234
X99980.1 gg_id:13689 Thermosyntropha lipolytica str. JW265 X99980
DQ339710.1 gg_id:208155 assessment complex microbial degrading long chain fatty acids (LCFA) methanogeni DQ339
DQ080135.1 gg_id:137138 reductive dechlorination 2345-tetrachlorobiphenyl three s: evidence involvement D DQ080
AB192059.1 gg_id:141089 termite gut homogenate clone M1PL1-18 AB192
AB248632.1 gg_id:145683 mesophilic anaerobic butyrate-degrading reactor clone BHB03 AB248
AB234008.1 gg_id:154827 anaerobic reactor clone B-15 AB234
NR_028910.1 gg_id:552212 Pelospora glutarica str. WoGl3; DSM 6652 NR_02
EF515712.1 gg_id:222308 Electricigen Enrichment MFC full-scale anaerobic bioreactor sludge treating brewery EF5157
FJ799131.1 gg_id:510041 Microbial Responsible Intermediates Degradation Anaerobic Digestion System Deterr FJ7991
AB274497.1 gg_id:203894 packed-bed reactor clone CFB-8 AB274
AB021305.1 gg_id:13691 Syntrophothermus lipocalidus str. TGB-C1 AB021
AB539943.1 gg_id:567072 Evidence syntrophic acetate oxidation coupled hydrogenotrophic methanogenesis -t AB539
X76743.1 gg_id:13762 Clostridium thermoamylolyticum str. DSM2335 X76743
AY350594.2 gg_id:221143 Thermoanaerobacterium aciditolerans str. 761-119 AY350
EU999016.1 gg_id:322435 Predominance Methanolobus and Methanoculleus spp. Archaeal Saline Gas Field Fo EU999
FJ268955.1 gg_id:356922 Thermoanaerobacterium saccharolyticum str. B6A FJ2689
EU563363.1 gg_id:272616 Thermoanaerobacterium saccharolyticum str. D22 EU563
FM999998.1 gg_id:532726 Thermoanaerobacterium sp. PO-2009 FM999
L09172.1 gg_id:13755 Thermoanaerobacterium xylanolyticum str. LXIIT L09172
AY140670.1 gg_id:59208 Thermoanaerobacterium bryantii str. mel9 AY140
AY331143.1 gg_id:106330 Mahella australiensis str. 50-1-BON AY331
AF247003.1 gg_id:27592 Thermoanaerobacterium thermosaccharolyticum str. D120-70 AF247

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1004.0	4500.1	5459.0	6689.0	8038.6	5779.4	8319.4	5493.7	4375.8	5883.1	5453.0
3600.4	6529.4	5481.0	5435.2	5059.3	4787.2	5915.2	5167.5	3808.7	2565.2	5794.0
527.1	1078.1	1187.5	1985.8	1295.0	1459.3	1339.6	848.7	1179.6	344.1	1148.5
41.3	269.5	621.9	446.0	414.0	342.2	401.8	409.1	214.8	242.3	257.7
34.8	376.7	320.4	348.7	424.2	359.3	491.3	411.2	676.9	103.2	234.4
3709.5	7076.0	7885.5	8480.5	9362.5	7252.1	8274.8	7505.4	7648.9	5745.3	7239.0
52.5	620.9	683.9	870.7	622.6	684.3	1110.6	968.6	392.7	501.2	352.5
33.2	16.7	31.2	22.8	20.5	19.0	20.6	20.2	17.0	14.3	25.9
32.6	374.0	506.8	567.7	1974.6	704.3	1309.8	344.0	257.5	59.2	159.0
1914.2	4434.7	5083.2	4725.0	4483.5	4377.4	6154.7	3697.6	3815.7	3625.8	3931.6
18756.7	6375.3	6703.3	6729.3	7259.5	6094.7	7901.5	6116.7	7495.7	5722.8	8281.5
228.0	1612.0	2418.3	2208.7	2605.8	1604.2	2682.6	2195.4	1372.2	3095.4	1292.8
48.7	83.7	145.6	141.2	221.4	98.9	290.5	126.6	69.4	36.3	78.7
197.3	3451.5	4528.7	4020.6	4650.4	3491.8	4604.8	4510.4	2003.5	2983.9	2874.7
33.1	62.8	86.5	90.5	37.1	58.7	59.9	47.2	29.7	22.8	57.5
50.5	1972.7	2433.4	2237.6	982.0	1192.0	3065.0	1414.3	179.5	122.5	841.4
80.9	916.3	982.1	934.3	1398.9	936.9	2084.5	833.3	365.4	801.7	491.2
44.6	87.1	144.5	29.5	23.6	54.0	23.1	27.2	24.5	14.2	24.7
347.4	2097.5	3000.9	2989.7	1967.6	1622.3	2069.4	2337.5	1297.0	581.7	2661.4
36.9	192.3	270.3	139.5	171.7	205.3	372.1	280.1	111.1	57.0	102.6
1787.8	2982.9	3057.2	3174.4	4139.8	2916.5	4115.1	2992.9	4633.1	3669.2	3195.7
37.8	18.9	22.9	24.2	25.8	19.2	27.3	21.3	15.2	11.2	18.9
38.7	263.3	463.4	371.8	552.0	363.6	514.9	244.8	153.8	51.0	20.9
5344.5	5635.3	5673.7	5751.9	6578.1	6019.3	7422.0	6203.3	4187.3	3415.8	5995.7
1309.6	1387.8	1902.9	1685.9	1604.8	1631.7	1688.6	1564.9	1903.3	1343.6	1213.1
600.9	4027.4	4004.9	4749.3	4713.0	5117.8	4865.1	4549.5	2615.8	7396.0	3036.9
11736.6	6275.1	6186.5	6282.7	5952.7	4812.0	6059.9	5451.6	7662.1	4668.6	6478.4
5750.8	8437.9	8091.5	9415.9	10081.1	9994.3	9566.3	8625.8	6411.8	4302.2	7915.2
35.1	20.6	26.3	29.4	32.8	24.2	25.9	20.0	16.3	7.9	16.7
1964.1	5783.5	7119.1	7140.0	7306.0	6662.7	7995.1	5937.2	5900.2	6480.7	6307.8
67.5	1655.1	2185.2	1710.2	1743.6	1873.7	2078.3	2371.1	853.1	1087.1	1593.5
609.1	3839.2	4276.9	3669.7	3109.6	3604.3	3455.8	3834.5	2355.6	2738.6	3275.5
2981.5	9572.7	9419.2	10480.2	8910.4	9165.8	9365.8	7755.9	11338.8	8445.3	8512.1
564.5	3719.6	4138.5	3528.3	2971.3	3509.4	3007.1	3990.5	2316.4	2723.4	3234.5
68.5	2922.8	2652.6	2953.2	2997.8	2664.1	3894.0	2649.2	995.7	524.6	1991.4
579.6	4320.0	4455.0	4982.0	4104.5	4300.7	5205.2	4887.8	2288.3	1861.0	3822.7
85.1	4666.4	4222.2	3419.4	3442.2	3423.4	4648.6	3581.2	2758.2	1333.7	2757.8
457.0	3101.3	4069.6	3863.2	5184.3	3435.2	5030.9	2976.6	2004.0	1757.4	2580.7
55.6	836.2	943.5	759.3	698.4	708.0	869.7	708.5	400.1	286.8	699.6
54.4	1669.7	2430.9	1717.4	1464.5	1850.7	1460.2	2158.7	691.7	1030.0	1328.9

259.6	385.8	1036.9
5053.8	6296.2	8356.8
4730.3	5033.4	7238.5
1000.8	1132.5	1817.2
390.3	628.4	1225.5
384.4	868.8	4331.8
7861.4	7642.9	10381.9
903.7	979.0	2008.7
14.7	22.7	30.1
345.3	606.4	1039.5
4170.9	5048.1	5896.7
5942.6	7168.4	7298.7
2227.0	2777.8	4812.5
133.5	214.2	593.1
3858.7	5542.8	10531.3
43.9	59.2	862.5
453.2	639.6	3089.8
811.6	1811.7	1697.4
12.1	67.4	252.6
2778.1	2629.2	5410.7
250.1	362.3	972.4
3158.2	3099.8	3602.9
21.4	31.4	37.5
335.8	316.8	1225.6
6307.4	7212.0	9265.8
1657.4	2008.7	2825.2
4774.3	5724.0	5350.7
5391.5	5471.0	6766.0
8067.1	8651.2	11360.2
17.7	26.2	43.2
6883.7	6626.7	9933.0
1805.8	1883.8	3528.8
3677.0	3313.2	6098.9
7975.9	9224.4	9948.4
3574.5	3224.9	6181.9
2203.0	2188.4	4452.1
4211.2	3751.8	6425.5
2830.6	2545.9	5263.8
2990.5	3969.3	5601.3
404.5	915.7	1413.1
1986.6	2052.7	4460.5

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o__Clostridiales	f__Thermoanaerobacterales Family III. Incertae Sedis
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o__Clostridiales	f__Veillonellaceae

g__Thermoanaerobacterium
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g__Anaeroglobus
g__Anaerospora
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g__Anaerospora
g__Desulfosporomusa
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s__unclassified	49893
s__Acidaminococcus fermentans	50245
s__Acidaminococcus fermentans	50272
s__Acidaminococcus fermentans	50535
s__Acidaminococcus intestini	50571
s__unclassified	50834
s__unclassified	50482
s__Anaerospora hongkongensis	50927
s__unclassified	50142
s__unclassified	50647
s__Desulfosporomusa polytropa	50530
s__unclassified	50137
s__unclassified	50211
s__unclassified	50394
s__unclassified	50486
s__unclassified	50672
s__unclassified	50673
s__unclassified	50712
s__Dialister invisus	50107
s__Dialister invisus	50213
s__Dialister invisus	50408
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s__Dialister micraerophilus	50124
s__Dialister pneumosintes	50428
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EF507903.1 gg_id:239939 Caldanaerobium fijiensis str. JW/YJL-F3 EF5079
EF060090.1 gg_id:199473 Acidaminococcus fermentans str. ADV 6092.03 EF0600
EF060091.1 gg_id:176163 Acidaminococcus fermentans str. ADV 1338.05 EF0600
EU728758.1 gg_id:337187 Acidaminococcus sp. str. DJF_RP55 EU7287
EF028685.1 gg_id:199297 Acidaminococcus intestinalis str. LBN 321 EF0286
EU773566.1 gg_id:307454 Goeldi's Marmoset feces clone CAL_b10_1 EU7735
NR_028812.1 gg_id:539819 Anaeroglobus geminatus str. AIP313.00; CIP 106856; CCUG 4477 NR_028
AY372050.1 gg_id:94360 Anaerospora hongkongensis str. HKU15 AY3720
AY728067.1 gg_id:104334 decayed velvetleaf seed clone S1-6-CL2 AY7280
DQ816346.1 gg_id:172987 mouse cecum clone aaa80f06 DQ816
EU981222.1 gg_id:340874 sulfate reducing living bench scale aquifer packed bed clone A7_FB EU9812
AB288880.1 gg_id:201846 termite gut homogenate clone BOf1-11 AB2888
EF454547.2 gg_id:224315 termite hindgut clone 290cost002-P3L-2304 EF4545
FJ542917.1 gg_id:510013 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone A FJ5429
AM158322.1 gg_id:156235 Sporomusa rhizae str. RS AM158
AJ279799.1 gg_id:21147 Sporomusa malonica str. DSM 5090 Type AJ2797
AJ279801.1 gg_id:25868 Sporomusa sphaeroides str. DSM 2875 Type AJ2798
NR_025415.1 gg_id:541895 Sporomusa acidovorans str. DSM 3132 NR_025
GQ047238.1 gg_id:466398 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1010d GQ047
FJ372052.1 gg_id:364054 feces adult twins and mothers; TS9 clone TS9_a01c02 FJ3720
DQ794346.1 gg_id:187487 human fecal clone RL197_aah86a07 DQ794
EU762181.1 gg_id:340520 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A› EU7621
DQ803760.1 gg_id:180927 human fecal clone RL200_aai58a11 DQ803
NZ_ACIM02000001.1 gg_id:470239 Dialister invisus str. DSM 15470 NZ_AC
FJ370202.1 gg_id:369002 feces adult twins and mothers; TS56 clone TS56_a01g01 FJ3702
FJ363905.1 gg_id:358364 feces adult twins and mothers; TS14 clone TS14_a04g03 FJ3639
AF473837.2 gg_id:136415 Dialister micraerophilus str. ADV 04.01 AF4738
U13040.1 gg_id:13826 Dialister pneumosintes str. SC3D U13040
FM872697.1 gg_id:365104 occupant source house floor dust clone FA02F02 FM872
EU461194.1 gg_id:290748 hamadryas baboon feces clone BAZ_aah90c07 EU4611
DQ071524.1 gg_id:229365 microbial cecum captive and free-living capercaillies (Tetrao urogallus) clone TuCc32 DQ071
FJ364585.1 gg_id:363398 feces adult twins and mothers; TS15 clone TS15_a04g01 FJ3645
FJ833261.1 gg_id:512439 Microbial Ecology Crop Folivorous Hoatzin crop contents clone A3Q302_40H05 FJ8332
FJ832358.1 gg_id:593767 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P1Q301_87G11 FJ8323
DQ326331.1 gg_id:145728 Metagenomic gut microbiome healthy human stool clone C320 DQ326
EU464320.1 gg_id:293799 hamadryas baboon feces clone AFBAB_aai02f07 EU4643
FJ834270.1 gg_id:564560 Microbial Ecology Crop Folivorous Hoatzin crop contents clone A2Q401_63G08 FJ8342
AY850119.1 gg_id:109904 Dialister sp. str. ADV 1053.03 AY8501
EU773545.1 gg_id:349811 Goeldi's Marmoset feces clone CAL_e11 EU7735
EU764686.1 gg_id:325573 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1 EU7646
DQ353930.1 gg_id:145968 Fecal Wild Gorilla (Gorilla beringei) wild gorilla feces clone Z83 DQ353

57.6	103.6	497.9	103.3	59.9	108.9	58.7	201.1	93.0	183.2	151.0
421.6	2910.8	2099.2	2133.2	3127.5	2099.0	3051.5	2072.0	1905.2	2370.6	3236.9
756.5	3615.3	3648.0	3488.4	3944.2	3792.0	3795.2	3348.3	3087.2	3041.4	4719.8
2673.0	3701.7	4318.4	3978.8	3833.1	4085.3	3716.0	4460.1	3082.6	4081.9	5021.6
53.8	298.2	537.3	478.0	231.2	448.9	442.3	607.6	312.6	31.9	911.1
1392.8	3174.8	3905.2	3461.7	3266.6	3499.1	3441.4	3804.8	3007.7	3842.6	3450.0
40.2	29.5	33.8	41.4	41.9	27.8	31.1	34.5	24.1	26.0	39.8
7600.9	5483.7	6475.9	5123.2	4564.4	4876.5	5239.6	5248.8	4358.9	2218.7	4996.9
3726.7	2763.3	3746.6	2064.6	1753.5	2242.7	1813.7	2797.1	1767.7	844.4	2074.7
6609.2	6210.8	7001.4	5668.6	5789.6	6012.6	6968.6	6119.9	6123.8	4360.0	6587.5
6883.5	6371.9	6800.1	5824.6	4730.4	5892.1	5512.0	5955.5	5520.5	4028.5	5855.5
3442.1	8502.0	9067.0	9280.2	9403.0	8903.7	9698.4	9766.6	8744.6	10038.6	9564.5
9019.3	6773.7	7437.0	7741.5	7580.7	7590.2	7412.7	6285.2	5675.1	4785.7	5483.6
174.5	3342.0	5031.6	3414.8	2487.4	3171.9	3656.3	3660.1	2786.3	403.5	2490.5
33.1	286.9	1457.8	242.7	188.2	155.4	174.3	451.9	142.9	81.6	233.2
3225.6	3651.6	4814.8	3985.6	3423.7	3541.8	3920.8	3974.4	2213.1	1284.6	2538.7
214.1	1086.7	1835.2	1145.2	1149.5	1123.0	1689.3	1096.7	816.6	275.0	721.1
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3016.3	2034.3	2199.3	1830.5	1973.7	2601.7	1956.6	2489.7	3119.1	1438.0	2887.4
2624.6	3795.9	3715.2	3176.9	3097.1	4850.4	2885.7	3686.1	6156.3	4707.4	2549.8
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408.2	3328.0	4502.6	4045.8	4374.2	3899.6	3850.6	3800.6	4174.0	1410.7	3627.0
103.8	528.0	1074.4	702.6	661.3	714.8	475.5	878.6	298.9	341.3	505.9
56.7	1505.6	2593.7	2122.5	1896.9	2734.5	1609.2	2491.6	2935.8	778.2	1188.2
13547.4	6601.4	5533.8	6277.5	7219.6	5336.5	6784.5	6194.2	7348.3	6600.3	6632.8
8958.0	7519.5	7437.8	7045.4	7725.9	7407.1	7921.4	7928.4	11963.8	7317.8	9751.2
52.2	36.2	25.8	29.8	40.3	31.7	33.3	31.5	30.1	25.3	24.4
38.0	30.4	50.8	45.4	45.0	37.5	33.7	42.6	28.7	27.2	35.7
5826.8	6412.5	7345.5	7642.9	5398.4	6431.5	5829.8	5626.9	8766.7	7318.6	6408.3
14878.5	6270.3	5827.5	6275.2	8835.4	5893.0	6136.1	5696.2	7159.7	6951.3	8116.7
46.3	80.5	193.6	64.2	68.5	75.5	92.8	77.3	49.0	26.8	82.7
1322.5	1173.4	1837.0	1246.1	895.5	1199.8	1351.8	1813.7	904.7	1287.8	1526.4
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1552.4	5246.9	4993.3	4501.9	5350.3	4605.9	5338.5	4943.9	5967.8	1842.7	3736.5
415.1	2859.8	2799.9	2724.4	2698.3	2425.4	2720.1	2508.3	2791.5	2390.8	2707.8
339.6	2967.9	3042.6	2965.7	2740.5	2721.7	2530.7	3492.4	2352.2	2783.6	2429.1
6855.2	6080.2	5517.3	5646.0	5444.1	5473.0	5804.5	4956.2	7132.6	5052.0	7005.1
414.3	1529.0	2359.5	1578.1	1231.0	2045.6	1541.7	1895.1	1058.0	280.2	1054.6
54.3	604.2	730.2	399.7	219.3	351.4	376.0	608.5	208.2	98.0	332.8
594.1	2298.9	2726.7	1891.1	1555.2	1888.3	2002.8	2548.3	2500.6	1648.8	3299.5
52.6	254.1	646.9	519.0	379.3	329.3	425.6	521.3	128.1	237.8	296.8

140.3	432.4	286.7
1832.6	2301.6	2434.1
3052.5	3611.0	3118.8
3941.6	4419.6	3476.8
425.5	378.0	62.5
3719.1	4308.9	3743.1
29.4	40.0	38.0
5387.5	4844.5	6553.3
2787.2	1978.0	2881.4
6024.9	6695.0	6981.0
5649.5	5261.3	7686.9
9513.0	8821.7	12524.5
6747.6	7053.8	6663.3
3291.4	3887.1	6218.8
79.9	140.9	1411.7
3800.4	4611.7	4806.5
949.4	1135.8	1488.3
3340.2	3957.3	6242.8
1768.8	2865.4	2750.2
3503.3	4833.0	3943.5
770.7	1297.8	1241.4
3609.3	3434.7	4930.0
1167.9	945.9	1114.4
1557.3	3047.9	2232.0
5731.2	6795.1	7444.8
5830.6	9255.0	7778.3
23.2	34.1	37.1
40.5	39.6	37.9
5866.9	7384.2	6974.9
5291.7	6423.8	5714.4
53.5	91.0	438.6
1142.7	1624.2	1828.8
2567.1	3014.2	4006.8
4170.7	4893.0	6448.7
2226.0	2354.7	3298.6
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1612.3	2044.5	2267.9
226.4	569.1	1829.8

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DQ796597.1 gg_id:184999 human fecal clone RL179aan75f02 DQ796
EU009830.1 gg_id:240947 intestinal microbiota domestic and wild turkeys turkey cecum clone WTB_M8 EU009
EU464269.1 gg_id:287863 hamadryas baboon feces clone AFBAB_aai01d11 EU464
DQ325965.1 gg_id:148937 Metagenomic gut microbiome healthy human stool clone B855 DQ325
AY958942.1 gg_id:128228 Microbes on human vaginal epithelium clone rRNA169 AY958
DQ809210.1 gg_id:196169 human fecal clone RL308_aal83d11 DQ809
GQ014629.1 gg_id:495037 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw762b GQ014
GQ156497.1 gg_id:590051 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
DQ353912.1 gg_id:146557 Fecal Wild Gorilla (Gorilla beringei) wild gorilla feces clone Z25 DQ353
FJ833651.1 gg_id:563580 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J1Q402_64H08 FJ8336
DQ325967.1 gg_id:146807 Metagenomic gut microbiome healthy human stool clone B859 DQ325
GQ082178.1 gg_id:382947 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw GQ082
DQ325932.1 gg_id:150078 Metagenomic gut microbiome healthy human stool clone B792 DQ325
NR_028862.1 gg_id:585826 Allisonella histaminiformans str. MR2; DSM 15230 NR_02
EU009856.1 gg_id:255834 intestinal microbiota domestic and wild turkeys turkey cecum clone WTB_X48 EU009
FJ832445.1 gg_id:582014 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P3Q101_25A04 FJ8324
EU475193.1 gg_id:295381 bonobo feces clone BNO_aaa01c01 EU475
AY959160.1 gg_id:130495 Microbes on human vaginal epithelium clone rRNA387 AY959
FJ832730.1 gg_id:562702 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J3Q101_38F05 FJ8327
EU775402.1 gg_id:342839 Western lowland gorilla feces clone GOR_aag73e12 EU775
DQ071435.1 gg_id:228821 microbial cecum captive and free-living capercaillies (Tetrao urogallus) clone TuCw4 DQ071
FJ489245.1 gg_id:513909 Megamonas hypermegale str. ABXD_AE27 FJ4892
DQ071446.1 gg_id:228113 microbial cecum captive and free-living capercaillies (Tetrao urogallus) clone TuCw1 DQ071
NR_025514.1 gg_id:552592 Megamonas hypermegale str. DSM 1672 NR_02
EU465518.1 gg_id:287786 lion feces clone LI3_aah78g03 EU465
EU939429.1 gg_id:343257 Fecal wild pygmy loris feces clone WF16S_275 EU939
U95029.1 gg_id:53032 Megasphaera elsdenii str. S3 U9502
AY038996.1 gg_id:24370 Megasphaera elsdenii str. YJ-4 AY038
DQ905695.1 gg_id:170226 human fecal clone 014C-G12 DQ905
DQ904992.1 gg_id:170296 human fecal clone 002-g5 DQ904
DQ278866.1 gg_id:151623 Megasphaera sp. TrE9262 DQ278
DQ904832.1 gg_id:168912 human fecal clone 001C-a6 DQ904
DQ904811.1 gg_id:173152 human fecal clone 001B-g7 DQ904
ABWK02000005.1 gg_id:579171 Mitsuokella multacida str. DSM 20544 ABWK
NZ_ABWK02000010.1 gg_id:470692 Mitsuokella multacida str. DSM 20544 NZ_AB
AY985193.1 gg_id:119553 human stool clone C039 AY985
DQ325931.1 gg_id:148483 Metagenomic gut microbiome healthy human stool clone B785 DQ325
AY982411.1 gg_id:117325 human sigmoid colon mucosal biopsy clone MK92 AY982
AY977807.1 gg_id:123930 human cecum mucosal biopsy clone LE93 AY977
NR_028840.1 gg_id:590732 Mitsuokella jalaludinii str. M9; DSM 13811 NR_02
DQ223731.1 gg_id:140868 Pectinatus haikarae str. VTT E-88329; DSM 16980 DQ223

3644.7	4364.7	4902.9	5738.2	5529.0	4480.2	6156.4	5538.6	4975.5	3817.1	5594.1
49.3	1947.8	1712.7	925.8	1382.9	1164.7	1190.4	1269.2	578.2	576.4	880.2
29434.9	6128.7	5978.8	5979.1	8799.8	5396.5	6197.5	4974.6	8604.7	7519.1	8565.6
1177.3	4336.9	4014.3	3864.7	3530.2	3324.8	3973.6	3771.6	4647.8	2786.7	4799.8
2000.1	4796.3	6096.3	4651.9	3824.8	5031.2	3964.0	4625.8	4276.5	3449.0	4308.9
69.5	226.6	268.2	424.9	166.8	209.1	252.7	193.9	84.5	88.7	116.0
11192.7	7247.3	7775.1	8315.2	6149.4	8217.0	7685.9	7114.8	8734.3	5654.5	8873.4
5973.2	9284.4	11717.4	6965.3	7138.6	10739.4	7741.5	8686.8	11593.0	7940.9	11768.0
37.4	117.7	55.2	624.8	30.9	26.8	32.3	581.5	35.6	18.1	399.4
276.4	3459.8	4542.3	2917.9	2315.9	3584.4	2361.5	3441.2	3578.2	6436.5	2940.2
770.3	4297.3	4493.4	4525.3	4300.8	3708.2	5624.1	3873.3	4455.7	3793.3	4126.4
153.2	3085.5	5086.1	3583.1	2311.9	3453.1	3773.1	4310.0	2220.4	1759.0	2609.6
34.2	581.4	900.4	576.1	254.4	465.0	335.3	434.3	214.4	150.5	225.4
47.9	135.2	166.9	248.2	219.5	141.5	254.7	239.0	63.6	27.5	68.1
602.5	4951.9	5059.9	4241.4	4951.8	5575.8	5112.7	5038.5	3941.7	5262.2	4839.4
462.5	3981.1	4365.8	3576.6	2363.9	3765.1	3063.2	4477.2	3208.1	2906.6	3518.5
1973.8	666.1	485.3	181.1	494.7	497.9	579.2	421.1	688.4	824.4	712.9
18028.4	6876.9	7797.7	7041.8	4866.5	6180.9	5820.4	6796.3	5375.8	6078.6	8229.6
3561.4	4153.3	4873.8	4464.6	3494.0	4056.4	3885.9	4042.6	4984.8	3575.4	4162.7
143.5	596.0	750.9	679.9	744.3	632.0	717.8	728.4	255.5	100.9	505.0
9403.6	7524.2	7521.6	7394.3	7259.9	7432.6	8020.2	8481.1	7474.3	5175.5	9069.5
124.7	998.5	1124.5	1174.6	1042.2	985.3	1206.6	1046.8	795.1	999.3	997.1
141.3	3052.9	2940.4	3082.8	3071.4	3049.3	3499.7	3911.6	2642.8	959.5	2415.8
38.6	16.9	14.5	17.6	27.1	17.0	20.4	17.6	21.5	15.6	20.0
346.0	2199.5	3205.2	2465.4	1697.2	2274.7	2495.3	2976.6	1703.9	2507.2	2283.5
688.8	2535.9	3955.3	3619.7	2416.0	3103.8	3198.0	3729.1	1677.7	982.7	2741.7
36.9	2090.9	3417.0	2554.3	1194.4	2232.9	1686.7	2697.8	1278.2	319.9	2188.4
1958.6	1813.9	2569.9	2290.3	3029.3	1887.9	3108.0	2210.4	1543.6	526.0	1563.5
89.8	2007.3	3462.9	3139.7	2013.3	2898.2	2748.9	2450.0	1342.1	2313.6	2246.3
10932.8	5313.8	5372.9	5672.4	5458.4	5031.1	5627.8	5348.0	5665.8	6045.9	6220.7
58.4	31.8	38.3	35.6	35.4	25.8	41.3	29.8	34.5	30.9	38.1
242.2	2809.6	4117.3	3918.9	3104.9	3931.1	3471.8	3668.3	3626.0	5505.6	2967.0
329.6	2284.8	3101.1	3171.7	1893.2	2481.2	2669.2	3400.3	1490.3	802.6	1701.2
5548.0	3827.8	3493.8	3982.9	4572.2	3353.1	4357.2	4118.7	3468.9	3547.1	2380.3
67.5	1041.8	799.8	1059.1	501.3	865.3	902.6	974.5	846.3	1353.2	506.8
179.0	1295.7	1334.7	1897.9	1183.3	1332.9	1136.3	1765.7	1545.2	956.3	965.9
137.5	2096.0	3534.4	1989.7	1474.5	2783.1	1511.4	2615.2	1566.2	1665.2	1968.5
13001.7	5094.7	4455.3	5439.9	4341.2	5291.2	5056.1	5702.6	7333.7	6404.2	4605.4
146.4	1234.5	1220.6	1645.7	1199.0	1508.2	1238.0	1797.6	1093.8	836.0	747.2
31.7	445.6	771.0	874.1	279.9	555.5	334.4	549.4	97.1	23.7	250.2
30.9	87.9	222.8	124.3	87.3	107.9	235.5	106.1	38.4	58.3	85.8

4605.7	4426.7	6129.3
1272.6	1853.2	1589.4
5207.7	6100.1	5609.5
2230.3	3679.0	4820.3
4727.6	4837.8	6612.1
209.5	272.2	440.5
6484.3	7321.1	8183.2
6530.2	8963.0	7939.3
703.6	54.8	53.1
3352.1	2936.7	5405.6
3466.9	5208.1	4986.1
4196.6	3774.0	4713.7
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3978.4	4677.0	5567.5
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2082.4	1320.8	3049.5
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5997.5	5653.2	6915.4
28.7	31.9	37.4
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3111.1	4219.0	3057.2
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1389.9	2363.3	1125.5
1761.5	3303.1	3661.9
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GQ492364.1 gg_id:556835 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
GQ491916.1 gg_id:591490 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
FJ366265.1 gg_id:370318 feces adult twins and mothers; TS25 clone TS25_a04f05 FJ3662
EF404155.1 gg_id:206419 human fecal clone SJTU_C_05_48 EF4041
GQ493381.1 gg_id:587536 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
FJ368136.1 gg_id:357831 feces adult twins and mothers; TS30 clone TS30_a04f02 FJ3681
DQ805306.1 gg_id:183098 human fecal clone RL249_aaj84h07 DQ805
GQ492054.1 gg_id:594375 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
FJ362702.1 gg_id:367004 feces adult twins and mothers; TS13 clone TS13_a02b03 FJ3627
EU009791.1 gg_id:255530 intestinal microbiota domestic and wild turkeys turkey cecum clone WTB_A48 EU009
EF400225.1 gg_id:212456 human fecal clone SJTU_E_10_50 EF4002
X72867.1 gg_id:13860 Phascolarctobacterium faecium X72867
GQ492591.1 gg_id:575113 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
EU009762.1 gg_id:239970 intestinal microbiota domestic and wild turkeys turkey cecum clone DTB_AC19 EU009
NR_025418.1 gg_id:559721 Propionispora vibrioides str. FKBS1; DSM 13305 NR_02
AY878646.1 gg_id:112413 Selenomonas noxia str. AIP 45-92 AY8786
AY947498.2 gg_id:114498 subgingival plaque clone OH4A AY9474
AY878645.1 gg_id:111934 Selenomonas noxia str. AIP 518-78 AY8786
AF161581.1 gg_id:13799 Selenomonas ruminantium str. K2 AF1615
EU381812.1 gg_id:276744 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU3818
AY685145.1 gg_id:99746 Selenomonas ruminantium L6 AY6851
EU327399.1 gg_id:237808 Selenomonas ruminantium str. LongL1 EU3273
AB198429.1 gg_id:257094 Selenomonas ruminantium str. S36 AB1984
DQ673518.1 gg_id:165042 rumen fluid clone GRC53 DQ673
EF112197.1 gg_id:178224 Selenomonas ruminantium str. 65 EF1121
AB003379.1 gg_id:13812 Selenomonas ruminantium str.JCM6582 AB0033
AF001774.1 gg_id:13813 rumen clone RFP7 AF0017
ACKP02000033.1 gg_id:589013 Selenomonas sputigena str. ATCC 35185 ACKP0
AF373023.1 gg_id:17310 Selenomonas sputigena str. ATCC35185 AF3730
EF195237.1 gg_id:180877 Selenomonas sp. str. MCB2 EF1952
AY685142.1 gg_id:99281 Selenomonas ruminantium M40 AY6851
AY207052.1 gg_id:83279 human mouth clone P2PA_80 AY2070
AF287790.1 gg_id:23591 human subgingival plaque clone DM071 AF2877
NR_028796.1 gg_id:550364 Selenomonas noxia str. ATCC 43541 NR_02
EU669564.1 gg_id:292356 Profiles Root Caries Elderly Patients supragingival plaque tooth root surface clone O EU6695
AY349403.1 gg_id:93019 human oral cavity clone FT050 AY3494
DQ673510.1 gg_id:168649 rumen fluid clone GRC45 DQ673
AM419977.1 gg_id:252996 Noma subgingival plaque clone 101H05(oral) AM419
AF538861.1 gg_id:59529 Selenomonas sp. oral clone P4PA_36 P2 AF5388
AY878647.1 gg_id:112215 Selenomonas sp. str. AIP 308-97 AY8786
FM873718.1 gg_id:368850 occupant source house mattress dust clone MA03E01 FM873

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7529.1	3847.0	4304.6	4623.5	3529.2	3634.9	4384.7	3926.9	4229.2	3315.7	3686.0
2727.3	3438.3	3957.9	3551.9	3132.8	3117.3	4100.1	3277.3	3151.4	1768.0	3384.3
1769.5	2347.0	2330.4	2341.4	1975.2	2187.6	2275.8	2174.9	4166.8	1721.1	2932.4
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3590.9	3309.6	3650.8	3952.0	4327.7	3289.8	3873.7	3199.3	2773.9	1886.0	4298.5
3766.1	3423.4	3635.6	3536.6	4017.7	3275.9	4039.6	3411.5	3648.7	3016.6	3570.4
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AY349409.1 gg_id:92349 human oral cavity clone JI021 AY3494
AM420026.1 gg_id:254272 Noma subgingival plaque clone 201F02(oral) AM420
GU302661.1 gg_id:586155 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU302
EU850496.1 gg_id:329400 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF265 EU8504
AY278627.1 gg_id:86707 Selenomonas genomosp. C1 AY2786
AM420028.1 gg_id:252936 Noma subgingival plaque clone 201F04(oral) AM420
AY341820.1 gg_id:92263 Selenomonas genomosp. P5 AY3418
AM419959.1 gg_id:241050 Noma subgingival plaque clone 101C02(oral) AM419
GQ006802.1 gg_id:502861 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu87h08c GQ006
GQ006643.1 gg_id:503020 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu86a02c GQ006
AM420074.1 gg_id:238385 Noma subgingival plaque clone 301F12(oral) AM420
EU669566.1 gg_id:295019 Profiles Root Caries Elderly Patients supragingival plaque tooth root surface clone O(EU6695
AM420113.1 gg_id:240321 Noma subgingival plaque clone 303G10(oral) AM420
DQ394645.1 gg_id:155308 -Arctic peninsula Svalbard Norway determined genes and rumen isolates reindeer o DQ394
DQ145536.1 gg_id:141405 Geosinus fermentans str. R7 DQ145
NZ_AAWL01000001.1 gg_id:192281 Thermosinus carboxydivorans str. Nor1 NZ_AA
AJ009486.1 gg_id:13842 TCB-transforming consortium clone SJA-112 AJ0094
DQ125719.1 gg_id:134207 uranium contaminated soil clone AKAU3815 DQ125
AF275913.1 gg_id:72075 anaerobic digestor clone AA01 AF2759
AB195907.1 gg_id:109195 Anaerobic sludge clone N39 AB1959
AB486682.1 gg_id:559077 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCOR(AB4866
EU864464.1 gg_id:310615 structures under selection pressure levels antibiotics Xiao River receiving treated ox EU8644
AB240309.1 gg_id:141751 microbial structure Phragmites rhizosphere biofilm reed bed reactor laboratory clon AB2403
AB487569.1 gg_id:571451 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNSR0 AB4875
FJ673072.1 gg_id:516219 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6730
AB486151.1 gg_id:586628 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC AB4861
FJ683262.1 gg_id:512213 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6832
EU843176.1 gg_id:304446 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8431
AJ006980.1 gg_id:13862 Succinispira mobilis str. 19gly1 AJ0069
EU344280.1 gg_id:273405 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU3442
FJ683898.1 gg_id:521321 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6838
AF407698.1 gg_id:60600 Great Artesian Basin clone G07 AF4076
FJ880994.1 gg_id:405629 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8809
NR_025298.1 gg_id:575973 Anaeroarcus burkinensis str. DSM 6283 NR_025
FJ676048.1 gg_id:530548 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6760
GQ038559.1 gg_id:383518 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu4 GQ038
AY244964.1 gg_id:84451 cow rumen clone BS10 AY2449
FJ799146.1 gg_id:583522 Microbial Responsible Intermediates Degradation Anaerobic Digestion System Deterr FJ7991
FJ672960.1 gg_id:519106 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6729
DQ801441.1 gg_id:198328 human fecal clone RL388_aao95e11 DQ801

1601.6	2751.7	2777.8	3732.1	1506.6	2280.4	1879.7	2777.5	2376.8	2331.7	2360.3
36.7	2870.4	4479.7	3602.9	2297.5	3184.3	4472.4	3338.9	2763.5	840.1	2186.0
374.2	1662.2	1914.2	2794.6	1763.2	1957.2	1725.7	1978.7	1426.5	1720.2	1543.8
40.0	51.3	70.1	59.1	76.7	59.2	64.8	68.1	36.1	60.5	41.2
70.4	2530.1	2390.3	1849.3	1437.7	1652.2	1456.3	1641.9	2530.8	1720.7	1559.4
33.6	157.6	306.4	137.6	127.6	150.2	132.8	159.4	91.0	44.3	147.8
67.8	2693.6	3873.8	3380.8	3697.0	3595.0	3596.1	3265.0	1721.4	5809.9	2102.7
1297.8	4940.3	5584.5	5433.4	4965.7	4758.3	5439.4	5289.7	4064.6	4421.3	5285.9
640.8	2790.4	3472.3	4010.7	2576.0	2753.4	3020.7	2849.1	1246.0	1208.7	2159.8
38.4	161.3	265.8	287.2	179.4	165.2	380.4	338.8	95.2	36.6	209.7
6186.7	6444.1	5671.6	6399.2	6192.8	5940.1	6719.4	5687.6	8270.8	6014.8	6321.6
484.8	3363.0	3609.1	3455.4	3103.3	2805.7	4272.8	3309.1	2011.6	2313.8	3009.1
45.3	77.2	196.8	72.6	81.1	103.6	60.8	116.7	82.7	24.0	55.2
12177.7	6802.1	6505.9	6560.0	5888.4	6338.8	6306.7	6822.8	7603.8	5782.7	7409.8
27.3	213.2	470.6	372.2	259.8	314.6	337.9	373.4	80.1	41.6	175.5
178.4	6126.7	8438.8	5432.7	3744.5	6316.8	4046.9	5659.6	4553.9	3708.0	6788.2
40.2	182.6	471.4	130.6	108.1	162.6	130.3	154.6	78.8	29.6	163.1
653.5	2790.6	7042.3	2060.4	1975.6	2784.6	1683.4	2342.5	1519.6	1532.4	2366.5
1689.8	3070.6	5472.6	1951.5	3081.2	3067.2	1982.3	3266.4	2641.4	4553.9	2287.8
2201.8	5211.9	7451.2	5068.0	4954.7	6428.6	4520.5	4381.0	3228.4	4029.3	3883.8
124.5	4404.0	6523.7	4258.3	3979.2	4758.5	3699.3	4228.5	2657.4	5795.0	3683.7
147.6	3082.6	5025.0	1984.8	1841.6	2728.6	1945.0	2174.2	1558.4	533.0	2150.5
62.2	1500.5	1765.6	1202.1	689.7	938.5	2494.5	1306.0	547.2	180.0	935.9
1516.3	3959.2	6637.6	3939.2	2717.5	4214.6	3264.3	4759.5	3035.1	4199.2	4829.3
79.5	4849.5	7260.5	4349.4	2752.6	5446.1	3029.1	4608.9	3156.1	946.8	5307.2
10619.5	2771.1	3861.5	3175.7	1964.6	2894.1	2727.3	3084.6	1103.4	2138.7	2818.5
45.8	2536.7	3865.3	1571.7	739.8	2359.9	776.8	2303.3	1157.9	2094.8	1794.0
9162.0	3254.6	4499.1	3968.4	3406.4	3750.8	3903.4	3475.8	3703.1	2772.3	3931.6
87.0	1069.7	1354.3	1218.9	1362.1	1139.0	1399.0	1578.5	667.3	317.0	847.6
119.0	550.8	503.9	708.7	420.6	515.1	580.2	697.4	183.0	92.8	399.4
161.2	2181.5	3206.9	2833.2	2180.1	2355.5	2561.9	2613.9	1475.9	1298.3	2059.2
44.0	222.8	568.7	517.3	406.1	279.4	406.2	384.0	140.6	34.1	327.1
18751.1	6156.9	8151.2	8671.7	5362.9	7864.4	5263.5	6470.1	7486.1	6549.1	6612.3
1050.9	5577.0	5448.6	5321.8	4060.3	4919.7	6575.8	5753.1	5320.6	4610.1	5487.5
945.9	4970.4	5975.8	5346.0	4419.3	6669.1	3742.1	6580.2	3660.9	6815.1	6994.4
83.4	3812.8	4874.8	4270.1	2912.7	3634.3	3891.0	4354.3	3569.3	1429.0	3664.6
78.6	136.3	344.1	401.5	226.6	176.2	234.6	464.6	109.0	67.0	256.6
35.6	1963.4	1654.9	1418.2	1617.2	1899.2	1686.5	1398.4	1448.2	416.2	1012.2
2009.2	4831.7	6870.9	6704.4	5461.1	5769.1	4512.9	5457.4	5039.2	2627.5	8174.4
5915.2	4783.2	5824.2	5745.0	5079.0	5075.0	5214.3	5774.5	5882.6	6027.3	6874.4
1064.2	4611.4	7515.9	8392.3	8249.3	4849.3	10544.1	8447.8	11828.6	1584.6	6044.4

2381.8	3407.5	2923.3
4270.0	4104.6	5517.3
2013.6	2276.2	2357.4
59.5	137.9	100.9
1877.5	2055.5	1854.7
129.5	190.3	203.4
3788.1	3765.7	5573.5
5023.1	5400.8	6779.4
3532.9	3598.5	3505.0
159.1	107.8	177.1
5390.3	5890.0	6995.1
2822.0	3728.8	4851.7
335.6	133.7	108.4
6993.3	7261.7	8335.5
251.0	519.5	747.5
5136.0	4424.4	6444.1
103.5	200.3	251.8
1923.5	2341.3	2994.0
3377.9	3655.6	4610.2
7059.2	5277.7	4941.7
3796.7	3856.3	6461.7
1881.7	2376.5	3375.1
861.0	898.1	1130.2
4414.0	4092.7	5370.6
3488.5	3030.2	4590.1
3179.2	3423.5	4445.1
2159.8	2379.0	3068.2
3730.5	5376.4	6664.1
981.7	1312.7	1791.1
632.8	584.1	708.5
2949.6	2813.5	3505.0
501.4	243.7	427.1
7875.7	6481.1	5636.0
4610.7	4842.0	5818.6
5946.4	5330.9	6144.4
4494.7	4383.8	6228.8
163.6	212.9	153.8
1349.7	1041.4	2130.6
5783.9	4283.5	3892.3
4728.8	6015.6	6232.0
5521.3	6814.5	4503.1

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FJ678610.1 gg_id:522237 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6786
FJ832386.1 gg_id:533799 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P1Q401_22F03 FJ8323
EU775040.1 gg_id:351818 Francois Langur feces clone FL_2aaa04b12 EU775
AB487852.1 gg_id:548067 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNSR AB487
FJ681608.1 gg_id:517653 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6816
FJ386549.1 gg_id:364845 vaccination sludge backf pumping house Xilang municipal wastewater treatment plar FJ3865
FJ834254.1 gg_id:575321 Microbial Ecology Crop Folivorous Hoatzin crop contents clone A2Q401_14F02 FJ8342
EU773455.1 gg_id:328240 Black lemur feces clone BKLE_g09_1 EU773
DQ833299.1 gg_id:170560 Anaerobic Reductive Dechlorination Vinyl Chloride ly Enriched Bachman Aquifer Sed DQ833
FJ684672.1 gg_id:532119 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6846
FJ678209.1 gg_id:528615 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6782
AY684401.2 gg_id:110815 mucosal biopsies human intestine clone HuAC20 AY684
AB486629.1 gg_id:577345 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCOR AB486
EU531895.1 gg_id:263067 Predominant role host genetics controlling gut microbiota FMF remission stool clone EU531
AF071415.1 gg_id:13851 Anaeromusa acidaminophila str. DSM 3853 AF071
EU469036.1 gg_id:303124 Speke's gazelle feces clone SP2_c09_3 EU469
DQ824735.1 gg_id:179447 human fecal clone RL185_aaj72d08 DQ824
FJ683901.1 gg_id:521470 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6839
GU304004.1 gg_id:549795 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU304
FJ673979.1 gg_id:516340 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6739
DQ833301.1 gg_id:164274 Anaerobic Reductive Dechlorination Vinyl Chloride ly Enriched Bachman Aquifer Sed DQ833
FJ682035.1 gg_id:525023 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6820
EU307091.1 gg_id:251142 Changes microbial metabolic and along hydrogeochemically variable profile unsatura EU307
AB034135.1 gg_id:48795 rumen clone 4C28d-2 AB034
DQ904885.1 gg_id:163607 human fecal clone 001C-f2 DQ904
GQ005015.1 gg_id:504647 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu65h1 GQ005
FJ676618.1 gg_id:532032 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6766
FJ678334.1 gg_id:527813 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6783
AB486685.1 gg_id:572648 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCOR AB486
FJ678463.1 gg_id:527603 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6784
EU845665.1 gg_id:336552 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU845
FJ682745.1 gg_id:527983 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6827
FJ684630.1 gg_id:514989 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6846
EU774198.1 gg_id:346793 Chimpanzee feces clone CHIMP1_aaj39c11 EU774
EU307090.1 gg_id:243204 Changes microbial metabolic and along hydrogeochemically variable profile unsatura EU307
EU775009.1 gg_id:316336 Francois Langur feces clone FL_2aaa02b05 EU775
EU747937.1 gg_id:337267 neotropical folivorous flying bird adult hoatzin crop clone hoa13_77E10 EU747
DQ310746.1 gg_id:199797 Recurring seasonal dynamics microbial stream habitats riverine sediment clone WC DQ310
AY995255.1 gg_id:123766 human vagina clone FX8B2-5 AY995
AY667269.1 gg_id:103280 TCE-dechlorinating groundwater clone TANB127 AY667
FJ674118.1 gg_id:518615 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6741

328.7	1364.1	2162.0	1787.4	796.7	1554.4	1466.2	1726.6	918.4	426.5	1084.6
8612.1	4595.3	4570.3	5005.2	4260.8	4609.3	5096.9	4293.5	6481.6	4936.2	6193.6
4852.4	6411.0	6484.1	7337.8	6647.4	6474.0	8974.8	7926.0	8762.1	5167.1	7426.7
626.5	6882.1	6600.9	5375.1	4180.5	5389.1	4774.0	4787.7	3818.3	3966.6	4759.3
921.6	2690.4	3678.6	4101.8	3353.0	3184.2	4304.4	3629.8	2299.9	1058.4	3127.0
1059.6	3821.8	5817.2	4770.8	4844.8	3419.5	4806.3	4878.8	7054.5	6050.9	4775.2
114.3	1942.4	2617.6	1825.3	1208.6	1671.1	1242.9	1868.3	1194.8	2029.6	1040.1
17628.7	4874.1	4824.1	4806.5	4624.0	4458.3	5355.6	5590.0	5388.0	4345.4	6114.1
2204.2	5203.7	6289.0	2712.0	1998.1	3770.1	2781.5	3397.6	3087.4	2488.5	3551.5
781.4	4100.9	5497.6	4719.7	3233.6	4191.3	4536.8	4429.1	3560.6	1836.1	3953.9
290.9	6753.5	8108.8	7181.4	7812.3	6766.1	7868.9	7305.8	6764.7	2944.4	5979.1
53.8	1273.2	2210.3	2530.8	462.2	1272.9	699.5	1906.0	489.6	51.1	3270.5
1171.4	5869.4	8611.6	7384.9	10222.1	7676.9	10160.2	6344.9	8344.0	4229.1	7185.7
2174.2	4715.0	5663.3	5490.2	4699.1	5117.5	5820.1	5485.9	4858.3	6856.3	4370.3
837.5	4935.7	6490.2	5501.4	5108.3	5225.7	5795.5	6135.5	4404.5	7452.7	6806.4
1681.7	4355.5	4523.3	5218.3	4374.7	5070.5	4713.9	5048.7	4577.2	4406.4	6355.8
68.6	472.4	967.1	522.9	369.0	454.0	556.2	651.9	440.4	123.8	456.6
6041.0	4693.3	5720.9	5067.4	3715.6	4522.0	5012.8	5054.0	4754.8	3163.4	4544.8
7529.7	5350.2	5673.5	5553.3	3626.9	5734.3	4691.2	4735.8	6727.9	5803.0	7033.0
7749.1	2865.1	3886.0	3337.9	2393.7	3023.8	2932.1	2887.8	2897.8	3453.5	4113.9
2475.2	6347.6	7963.3	6521.1	6007.0	6760.2	6052.2	7166.7	7363.4	8978.6	8080.1
95.2	4260.7	5174.9	4545.9	2811.4	4214.3	4146.9	4643.7	2634.9	1366.3	3713.1
4410.3	5638.1	6434.9	6169.2	4682.7	5745.2	4558.9	5383.0	3250.5	4322.0	6093.9
33.2	56.7	127.5	73.3	49.1	65.8	34.2	107.9	28.1	14.2	55.3
660.3	3381.3	4253.9	4665.6	3206.3	3719.0	4726.6	4876.6	2116.5	1909.3	3088.3
6386.5	3562.8	4090.4	4105.9	4091.0	3809.2	3460.5	4353.5	3977.4	3987.6	3806.1
4756.9	5191.8	5223.6	5499.5	4191.1	4585.0	5747.4	4863.6	5868.0	2273.2	5588.0
311.2	2043.1	2511.1	2565.7	1958.4	2091.7	2419.6	2337.1	1647.7	761.7	1965.2
3664.2	10061.6	11905.7	10451.3	10997.9	10050.4	11635.6	9201.8	13232.1	9267.9	13501.1
93.4	4405.4	5394.1	5131.2	3930.2	4413.5	5248.2	5001.8	3052.4	1918.3	4565.9
3610.2	5416.3	4574.7	6782.3	6319.6	6451.2	6085.8	6279.1	5568.3	6089.8	6759.0
113.3	3551.2	4915.1	4456.6	3499.5	3989.2	3910.3	4100.4	2570.7	1768.6	4077.7
3803.0	5137.0	5182.4	4892.8	4559.7	4708.1	7184.1	6052.0	4742.8	3138.5	5397.6
6279.2	3989.8	6185.3	6689.4	3964.7	3446.3	4431.7	4750.4	6642.7	3699.9	5292.5
40.3	1792.3	2785.0	2512.0	1124.8	2068.1	1789.4	2001.6	1107.3	1206.9	1755.0
27534.5	8018.7	7246.2	7996.7	7675.8	7307.1	10815.0	7989.8	10559.9	8181.2	12283.5
14589.5	5212.0	4562.1	5217.2	4718.2	3752.5	5585.4	4575.9	5694.2	4722.4	7061.0
182.8	6644.7	7757.3	5491.2	4847.3	6580.8	4736.6	6427.3	5232.3	2921.3	6069.1
51.8	278.7	500.1	272.7	147.1	228.1	378.5	308.7	183.5	49.8	193.3
1936.7	6175.4	7419.4	7137.0	7147.6	6473.3	8357.9	6613.1	5834.8	5406.7	7222.0
6648.2	3676.5	4462.6	4228.5	3212.1	3564.8	3428.7	4014.1	4270.9	2061.3	4660.7

1664.1	1639.8	2614.3
4812.2	5473.7	4076.8
6140.9	7008.2	7364.6
5044.7	4709.2	6549.5
3616.2	3404.8	4999.9
3831.2	6025.8	4364.1
1712.9	2702.8	4282.3
4537.0	5424.7	5982.6
3280.9	2851.5	4160.1
4676.9	4939.4	7520.5
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4930.3	1271.1	4173.2
5631.8	9110.3	10160.2
4968.1	5445.2	6723.2
5782.8	5156.2	6805.1
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556.3	557.7	865.9
5060.7	5165.1	6706.2
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3110.3	4392.3	3625.0
7141.2	7639.3	9965.6
3865.0	4754.6	7770.1
5305.8	6020.9	6934.3
64.7	76.6	149.1
3869.8	4869.1	6195.8
3657.5	3437.6	3781.2
5039.2	6216.7	6013.4
2165.6	2661.7	3513.0
8134.3	10079.6	12734.1
4880.8	4678.6	6466.3
6012.9	6328.5	7912.8
4875.2	4669.1	7045.5
4302.4	4788.8	5908.6
4348.9	4565.0	5283.2
1870.4	2070.9	2151.4
7020.2	8416.5	6820.0
5364.5	6156.7	4887.2
5877.2	4963.8	7918.8
232.9	214.7	815.5
6622.0	7414.0	8212.2
3606.1	4666.0	5018.9

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GQ179679.1 gg_id:455949 Heterogeneity vaginal microbial within individuals vagina clone VE44F01 GQ179
FJ678138.1 gg_id:521053 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6781
FJ678575.1 gg_id:531578 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6785
FJ682764.1 gg_id:518322 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6827
AY672080.2 gg_id:149234 Microbial on patients stomatitis and healthy biofilm denture wearers clone DWE10 AY672
DQ217599.1 gg_id:139963 Zymophilus raffinosivorans str. VTT E-90406; DSM 20765; ATCC 496 DQ217
FJ673355.1 gg_id:525608 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6733
FJ679306.1 gg_id:520520 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6793
FJ372095.1 gg_id:363046 feces adult twins and mothers; TS9 clone TS9_a01f12 FJ3720
AB034141.1 gg_id:28188 rumen clone 3C28d-10 AB034
AY985859.1 gg_id:117810 human stool clone D133 AY985
DQ113674.1 gg_id:132784 dog colon clone C2-26 DQ113
AB185750.1 gg_id:103463 rumen clone U29-B01 AB185
GU303125.1 gg_id:570205 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU303
EU842705.1 gg_id:318812 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
FJ674045.1 gg_id:521328 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6740
AB034079.1 gg_id:51519 rumen clone 3C3d-10 AB034
FJ680777.1 gg_id:510572 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6807
EU747918.1 gg_id:346208 neotropical folivorous flying bird adult hoatzin crop clone hoa12_26B04 EU747
FJ673180.1 gg_id:514372 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6731
AB486409.1 gg_id:546268 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC AB486
AF371705.1 gg_id:45688 swine intestine clone p-286-a3 AF371
AB486202.1 gg_id:575498 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC AB486
FJ684083.1 gg_id:520119 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6840
AJ009494.1 gg_id:13843 anaerobic TCB-transforming consortium clone SJA-143 AJ0094
GQ060518.1 gg_id:462753 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw02g03 GQ060
GQ451274.1 gg_id:514095 Fecal Yunnan snub-nosed monkey feces clone J269 GQ451
AF357557.1 gg_id:72198 mpn-isolate group 9 AF357
AF371701.1 gg_id:34987 swine intestine clone p-2365-55G5 AF371
AB198438.1 gg_id:237356 Selenomonas ruminantium str. S206 AB198
AF473834.1 gg_id:38606 Megasphaera micronuciformis str. AIP 412.00; CIP 107280 AF473
EU382011.1 gg_id:268506 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU382
EU794209.1 gg_id:334383 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_O30 EU794
EU475011.1 gg_id:296159 red river hog feces clone RRH_aaa03c07 EU475
FJ674071.1 gg_id:521929 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6740
FJ372342.1 gg_id:368157 feces adult twins and mothers; TS9 clone TS9_a04e03 FJ3723
EF063619.1 gg_id:193173 Microbial ecology autotrophic denitrifying anaerobic methanogenic UASB reactor clo EF0636
DQ223729.1 gg_id:140753 Megasphaera sueciensis str. VTT E-97791 DQ223
EU779137.1 gg_id:354926 Trancaspian Urial feces clone TU1_aaa03b10 EU779
FN563256.1 gg_id:554464 Impact changing HRT OLR on prokaryotes involved biomethanizitaion and fuzzy logic FN563
EU747978.1 gg_id:349584 neotropical folivorous flying bird adult hoatzin crop clone hoa13_48H06 EU747

2632.2	8048.4	9936.8	6405.6	5128.5	8567.0	5015.6	6948.2	8223.1	12933.0	9359.8
75.5	2647.6	3221.3	2742.6	1811.7	2159.1	2540.7	2652.9	2873.1	1083.5	3144.3
8995.1	4572.8	5288.1	4728.4	3716.5	4228.7	4923.2	4979.6	3873.0	1584.6	4438.1
67.5	2914.5	3361.9	2936.9	2508.0	2657.8	3346.5	2824.4	1386.8	1470.4	2208.8
37.1	44.2	47.7	46.2	48.5	23.6	34.6	25.7	31.4	27.0	30.2
516.1	5719.8	8172.8	8015.1	5033.4	6474.4	5518.3	6589.3	3986.6	4009.5	7108.2
11446.8	6042.0	5769.7	5205.6	5478.9	6143.1	6114.6	5548.5	6246.4	6848.1	5238.9
2880.0	4818.3	6525.2	6057.4	4491.2	5246.2	5485.6	5931.4	4724.6	3461.8	5452.2
175.2	3048.3	3943.6	3624.4	4194.3	3643.5	4482.5	4277.6	1934.7	1490.1	2322.4
63.5	264.9	284.6	308.4	210.0	226.4	445.4	353.5	119.8	77.3	147.4
143.4	323.0	509.8	657.6	33.3	346.3	586.7	406.9	264.1	20.5	236.6
35.7	2029.2	1882.0	1982.8	1718.0	1445.6	2972.2	1797.5	1313.8	909.4	1197.6
24422.8	7869.3	8298.6	8801.6	7630.3	7984.1	8487.6	7256.5	12373.4	15971.5	11162.3
56.6	809.5	1228.6	1119.9	1122.5	918.1	1292.4	1450.8	946.2	398.4	735.6
600.6	3479.2	4417.9	3950.8	3878.7	4360.7	3910.0	4207.5	2927.2	3555.0	3535.3
6090.5	5121.9	5413.4	5961.4	6193.4	5599.7	6426.1	5484.3	4488.7	2437.3	5053.9
833.8	2748.1	3789.1	2961.5	2002.5	2971.5	2399.0	2222.5	3555.0	2416.7	2748.3
112.3	3794.2	4509.5	4597.9	3650.5	3398.6	5009.4	3842.5	2723.6	797.5	3855.1
897.4	2201.1	3170.8	3066.8	2158.5	2443.9	2418.5	2964.0	2113.7	2119.2	2228.3
4004.2	3507.5	4264.8	4603.6	2994.8	3477.2	3745.7	4056.6	3671.4	3499.6	3958.8
56.4	3853.1	6324.9	3590.4	1982.6	4077.6	2123.2	3932.0	2244.0	492.3	4216.9
22932.7	7529.2	6994.2	8187.2	8891.5	6825.1	9217.8	8109.1	7521.3	5233.6	8741.1
159.8	6572.7	7895.8	5587.8	4798.1	6656.8	4864.4	6340.0	5075.2	2894.2	6421.4
131.9	2930.5	3609.1	3664.3	3960.3	3281.5	3977.4	3606.8	1968.6	2203.7	2942.1
53.2	636.6	1092.3	973.9	509.6	707.8	726.7	866.4	222.6	249.7	636.9
741.0	2727.6	4521.0	2547.7	2124.1	2459.8	2775.8	3221.1	1703.3	855.8	2477.9
1548.2	9685.9	11578.5	9218.3	9109.8	9802.4	9181.7	10717.1	9974.6	9417.7	13459.5
62.1	994.9	1509.6	1054.4	301.2	873.9	300.7	876.6	305.3	644.4	556.6
2077.7	2501.4	4109.7	3071.6	3602.2	2394.4	3072.8	3281.1	6014.0	1856.3	2266.0
2692.5	1799.6	3293.8	2595.7	2771.2	1756.4	2806.9	3409.2	5018.5	1307.9	1794.2
142.0	396.6	902.6	489.6	285.5	356.5	353.4	653.8	113.3	132.9	329.6
6549.6	5949.5	8166.3	8520.9	6712.1	5732.3	7021.9	8171.2	6409.3	5834.0	6555.2
3940.8	5628.7	6526.1	6913.1	6825.1	5583.4	7435.9	6089.7	5380.8	4344.3	6130.9
7675.0	8465.8	7330.4	8403.6	7121.0	7296.6	8364.0	8017.7	8167.9	5359.0	8499.1
8630.9	6680.5	6594.5	6750.7	6247.1	6104.0	6921.5	5853.9	8367.7	7066.2	7269.1
222.1	4216.7	4596.7	4360.2	4104.0	3686.9	4672.6	5434.5	2141.9	1892.0	3153.2
21280.2	8642.9	7942.6	9353.6	8271.3	7663.7	9487.8	8171.1	14743.7	8069.9	11561.6
53.7	29.4	33.0	38.4	30.3	23.9	69.8	19.2	21.8	14.6	29.1
421.6	2225.3	3086.8	3363.6	2680.1	2264.0	3411.7	2386.8	1547.2	930.0	2658.7
13822.2	7756.1	9343.0	7661.1	8199.1	7448.8	8571.1	7972.2	8542.6	6933.5	7115.9
15002.2	6156.6	7122.2	8017.1	7124.6	6103.8	8250.5	6690.3	6167.5	3378.1	6487.1

7388.9	6656.5	8866.6
2497.8	2926.1	3558.7
5016.0	5091.0	5486.1
2705.4	2903.0	6411.7
30.8	41.2	33.0
8067.6	6471.0	8967.6
5335.1	7349.4	6286.5
6829.1	5472.5	7793.0
3342.4	4207.5	5163.9
259.4	320.1	214.6
328.9	448.8	606.1
1650.7	1733.6	2197.2
8537.5	8520.6	8289.9
1071.5	1109.7	1656.9
4336.1	4333.6	5187.7
5699.8	6168.5	6803.9
2567.6	3439.6	2190.9
3268.0	3978.2	5352.8
2917.9	2954.6	3005.5
4146.4	4833.3	5125.2
2934.9	2459.7	4608.4
7795.9	8048.8	9471.6
5827.6	4792.4	7666.6
3292.7	3318.1	4579.6
514.6	773.2	1624.4
2569.9	2414.6	3093.8
8759.5	8931.2	13260.3
1228.3	823.7	793.2
2272.5	2995.6	2173.5
2522.5	3182.8	2657.4
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6274.7	6568.2	8358.2
5015.2	4435.2	7204.0
7423.6	8504.6	8066.0
5716.0	7953.5	7098.1
3669.4	4398.6	6320.3
7739.9	9312.0	7712.8
27.1	26.2	28.6
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CU920189.1 gg_id:572427 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU920
AB486952.1 gg_id:541359 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCOR(AB486
AY959093.1 gg_id:131417 Microbes on human vaginal epithelium clone rRNA320 AY959(
FJ675815.1 gg_id:531229 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6758
FJ678660.1 gg_id:519991 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6786
FJ673588.1 gg_id:526829 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6735
FJ673153.1 gg_id:529494 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6731
AB198425.1 gg_id:246110 Selenomonas ruminantium str. S2 AB198
EU850607.1 gg_id:334117 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF440 EU850
AB034134.1 gg_id:42912 rumen clone 4C28d-6 AB034
AB218316.1 gg_id:148501 Fecal microbial (dugong dugon) determined genes Dugong feces clone dgB-66 AB218
AY958931.1 gg_id:153751 Microbes on human vaginal epithelium clone rRNA158 AY958
GQ004077.1 gg_id:505586 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu68d0 GQ004
AB486076.1 gg_id:569899 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC AB486
AB487430.1 gg_id:540748 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNIR0 AB487
FJ682840.1 gg_id:520575 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6828
FJ393127.1 gg_id:362899 Fusing Biology Engineering Improve Power Output Microbial Fuel Cells microbial fuel FJ3931
U81750.2 gg_id:13861 fluidized bed anaerobic digestor fed vinasses (waste wine distillery) clone vadinHB04 U8175
FJ833201.1 gg_id:594131 Microbial Ecology Crop Folivorous Hoatzin crop contents clone A3Q102_39G05 FJ8332
FJ673713.1 gg_id:524216 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6737
GQ006579.1 gg_id:503085 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu85b11c GQ006
FJ386554.1 gg_id:369923 vaccination sludge backf pumping house Xilang municipal wastewater treatment plar FJ3865
FJ673625.1 gg_id:530256 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6736
EF399619.1 gg_id:206942 human fecal clone SJTU_E_01_29 EF3996
EU009839.1 gg_id:254812 intestinal microbiota domestic and wild turkeys turkey cecum clone WTB_Q48 EU009
EU234118.1 gg_id:252011 receiving river and un techniques anaerobic process WWTP treating penicillin G prod EU234
AB198432.1 gg_id:242601 Selenomonas ruminantium str. S109 AB198
DQ295866.1 gg_id:191985 Pelosinus fermentans str. UFO1 DQ295
FJ172883.1 gg_id:352391 Qinghai Yak Ruminal and Fungi China rumen clone RB-2F2 FJ1728
FJ680477.1 gg_id:523055 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6804
FJ682404.1 gg_id:513552 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6824
AB486876.1 gg_id:578241 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCOR(AB486
EU259482.1 gg_id:241086 Rumen yak (Bos grunniens) sequences rumen fluid clone YRC106 EU259
AY981016.1 gg_id:116502 human rectum mucosal biopsy clone V190 AY981(
FJ680012.1 gg_id:515217 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6800
FJ677302.1 gg_id:528220 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6773
DQ795993.1 gg_id:188086 human fecal clone RL202_aai50a03 DQ795
GU214167.1 gg_id:593991 and biota slimes Canadian paper mills slime mill taken wet section around papermal GU214
DQ777892.2 gg_id:166356 rat feces clone R-1170 DQ777
AB034191.1 gg_id:38984 Anaerovibrio lipolyticus str. ATCC 33276 AB034
EU748414.1 gg_id:328699 neotropical folivorous flying bird adult hoatzin crop clone hoa5_08h08 EU748

431.7	2950.3	2207.1	2986.0	2508.9	1836.5	3083.8	2672.8	1617.3	2835.5	1878.7
1047.1	5193.5	7693.5	6320.0	5658.7	5884.0	6148.6	5619.1	7118.4	2683.2	6163.6
11147.4	4826.0	3745.0	4362.8	4999.5	4777.0	5202.0	4478.3	6028.5	4723.8	7341.7
6897.0	3055.2	2535.4	2369.9	2036.7	2276.6	2161.6	2190.9	3515.1	1952.5	2028.7
38.4	2164.9	2922.8	2858.4	2682.3	2021.3	3924.6	3032.7	983.2	908.1	1620.1
3391.0	4344.5	5697.8	5443.3	5466.6	5013.3	5820.5	5146.6	4027.9	1700.7	5170.8
41.2	2665.7	3335.3	3159.7	2895.4	2587.2	2859.6	2771.7	2763.4	736.3	2490.0
3954.2	3379.0	4130.5	3889.7	3557.7	3341.5	4055.0	4322.8	3858.2	3344.6	3760.6
798.8	2437.7	3565.9	3693.1	3377.5	2576.3	3834.4	2884.4	2520.3	839.6	2549.0
869.1	1388.6	1552.5	956.7	793.7	1070.0	1070.3	1154.0	452.6	539.3	672.4
48.8	73.0	93.0	66.0	67.0	90.7	62.6	85.4	50.3	35.6	55.6
339.3	1686.5	1797.0	2513.9	1645.0	1684.3	1676.7	2217.9	1024.5	554.7	1611.6
6545.1	5162.4	6631.3	6342.8	6802.7	5652.9	6268.3	5340.3	4728.1	7696.4	6193.5
43.7	3431.4	5858.5	2177.4	1073.3	3068.3	1200.1	3075.2	1575.9	1540.8	2328.1
233.4	8213.2	10478.2	6991.9	5105.4	8630.0	4911.0	6942.5	7607.1	7198.7	10288.2
265.5	4219.8	4490.5	4041.3	2971.3	3640.0	3161.3	3999.5	3376.5	1722.8	3758.3
625.3	6600.3	8637.8	6205.9	6339.6	6191.7	6125.9	6812.4	4807.7	4520.9	7207.9
475.7	4500.2	4855.0	5074.6	4063.1	3954.8	5819.6	4520.1	3103.9	2578.0	3959.3
773.0	4042.5	4313.9	4551.0	4291.6	4134.4	5077.8	5038.8	2512.4	2001.2	4761.1
18072.2	6811.7	6476.7	6366.7	6082.9	6110.8	6783.9	6241.4	6834.2	7532.4	7105.4
11452.2	5090.2	5798.4	5632.5	7058.3	4598.8	7505.0	5195.5	5022.8	2598.0	5384.5
1192.2	1999.6	4801.0	4815.1	4316.0	2370.8	4112.6	4396.3	10041.1	1372.4	2714.3
11324.4	6105.2	6580.8	6686.4	6925.5	6088.3	6618.5	6001.0	7423.7	5837.9	7855.7
45.9	1134.4	1610.6	1600.0	826.6	965.5	1426.4	391.7	383.6	65.0	1228.2
573.3	3100.6	4132.6	4087.0	2765.9	3539.6	3352.9	3675.0	2729.2	3137.8	2933.9
636.4	1363.2	1851.2	1124.9	1002.5	1248.2	1189.9	1099.6	348.0	241.4	915.5
5984.4	2560.3	4232.7	3612.3	3413.8	2784.2	3400.1	3443.5	7033.8	2527.0	3088.3
79.4	5573.3	8037.8	4519.6	2870.1	5690.7	3126.9	4771.2	3995.6	1948.2	5718.2
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10021.1	7611.8	6970.9	7392.7	7075.7	7293.2	7639.6	6638.7	10276.2	7794.3	8910.3
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5593.6	5952.4	6629.7	7057.3	6440.6	5790.2	9909.8	7647.0	7994.9	4650.0	6520.6
6065.4	7487.3	7578.3	6466.0	6324.8	6443.1	6317.4	6323.1	7571.0	6506.2	8600.9
40.2	21.3	77.6	41.6	25.8	23.5	21.8	23.4	27.0	26.6	30.8
54.6	24.9	21.5	23.5	26.1	21.2	20.4	32.0	24.9	19.4	27.2
183.6	1121.3	1566.4	1220.2	812.2	1345.0	959.6	1633.3	680.9	490.0	1045.6

2295.2	1952.8	2534.3
5600.5	5811.2	8201.9
3861.1	4023.2	5170.5
2038.8	3436.7	2420.7
3512.4	2627.6	3728.9
4835.3	6333.6	6155.0
2634.5	2791.7	2871.7
4262.6	4265.4	5039.2
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985.0	1208.3	1674.8
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1893.8	2725.3	2662.6
6756.7	5494.5	8083.8
2770.6	2757.2	4230.5
6482.2	5281.3	8046.6
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6038.6	5833.5	6988.9
4081.4	4363.1	6232.1
4248.8	4801.4	5587.3
5963.3	7546.2	6944.7
4826.2	5229.6	6976.4
2756.1	4846.2	2800.1
5900.2	7465.9	7172.7
924.0	393.3	729.2
3637.2	3221.1	4487.7
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4119.3	3566.7	5747.0
4743.2	5460.0	6904.0
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AJ229233.1 gg_id:16834 anoxic bulk soil flooded rice microcosm clone BSV90 clone AJ2292
AY244972.1 gg_id:83021 cow rumen clone BS18 AY2449
FJ683141.1 gg_id:528857 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6831
NR_029357.1 gg_id:547456 Propionispira arboris str. 12B4; DSM 2179 NR_02
GQ004964.1 gg_id:504698 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu65d0 GQ004
EU344158.1 gg_id:260291 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU3441
FJ825568.1 gg_id:559706 Microbial during start-up mesophilic biogas plant clone 21_BS5_39 FJ8255
AB198435.1 gg_id:236008 Selenomonas ruminantium str. S150 AB1984
AB486785.1 gg_id:541916 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCOR(AB4867
EU461059.1 gg_id:288601 red kangaroo feces clone KO1_aai43d02 EU461(
DQ168841.1 gg_id:154690 Fermentative biohydrogen production heated anaerobic sludge clone J25 DQ168
EU468247.1 gg_id:290103 domesticated horse feces clone horsej_h07 EU4682
EU463594.1 gg_id:302001 domesticated horse feces clone horsej_aai89d11 EU4635
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EU096495.1 gg_id:253506 Veillonella sp. 18 EU0964
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AY514996.1 gg_id:99976 Veillonella rodentium str. ATCC 17743 AY5149
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GQ010293.1 gg_id:499375 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ010
GQ114701.1 gg_id:381455 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ114
FJ558085.1 gg_id:528199 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5580
EF434331.1 gg_id:210713 gastrointestinal tract microbiota microarray reference pool created pooling products EF4343
GQ091818.1 gg_id:411006 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ091
EF515580.1 gg_id:218801 Electricigen Enrichment MFC full-scale anaerobic bioreactor sludge treating brewery EF5155
GQ338722.1 gg_id:573384 and function human intestinal microbiota ileostomy effluent healthy patient clone A GQ338
EU460862.1 gg_id:301827 short-beaked echidna feces clone ECH_aai39e05 EU4608
GQ101329.1 gg_id:453095 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw493g GQ101
GQ006752.1 gg_id:502912 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu87c06c GQ006
GQ022064.1 gg_id:487605 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu3 GQ022
FJ374768.1 gg_id:585419 Veillonella sp. str. S101 FJ3747
GQ109121.1 gg_id:448078 Topographical and Temporal Human Skin Microbiome skin palm clone nbw608f12c1 GQ109
GQ031217.1 gg_id:422979 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor GQ031
GQ055579.1 gg_id:381881 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1117e1 GQ055
GQ011614.1 gg_id:498054 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw794c08 GQ011
GQ113791.1 gg_id:414090 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw(GQ113
GQ030037.1 gg_id:437122 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw866c0 GQ030
AY995768.1 gg_id:119118 Veillonella atypica str. ATCC 17744 AY9957
GQ030108.1 gg_id:459734 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw867c0(GQ030

47.1	567.9	1020.6	808.3	354.0	709.1	575.5	671.3	389.6	415.8	509.1
86.4	2202.6	2891.8	2789.8	2982.6	3004.2	3377.0	2992.1	1770.7	1598.9	2062.4
59.3	1040.2	2122.0	1489.9	577.4	1058.5	1069.3	1120.7	575.4	209.0	1045.2
2761.0	2558.9	3877.1	3683.4	1550.0	2470.8	2075.5	2236.0	1919.8	678.3	3230.9
384.8	3764.6	5000.8	4256.9	4138.3	3978.1	5776.1	3883.9	2425.7	3765.5	3951.1
3463.4	5875.4	6310.2	6245.2	5454.0	5516.0	5586.9	5772.4	6924.0	5200.4	7481.0
15729.3	5930.4	6430.4	6202.2	5894.1	5640.3	6802.0	5565.4	8113.7	5953.6	7254.2
2098.1	3058.3	3705.8	3641.6	3510.6	3051.3	3265.0	2976.0	5270.2	2529.8	3652.3
3047.1	6901.1	7450.1	6330.6	6555.7	6891.7	6080.7	5829.3	5167.4	3337.1	5342.0
982.8	3315.4	4234.8	3856.2	3826.3	3280.1	5395.7	4125.5	2657.7	1617.6	2931.7
489.3	1573.4	3426.2	3430.0	4943.2	1974.5	3822.3	3326.9	7362.5	2594.3	2449.2
946.8	5231.1	5746.4	5874.0	5637.0	5202.2	7061.9	5603.1	3848.0	4021.1	4772.5
1470.7	5216.3	6826.4	6129.0	5820.1	6021.6	6564.9	5848.5	4542.3	9251.5	6195.3
12390.5	8062.4	8182.7	8100.9	7551.4	8246.0	10009.4	7791.0	12201.8	7815.5	10961.2
1428.8	3991.3	5666.6	5052.0	4161.2	3981.9	5384.1	5276.7	3221.7	1872.4	3314.7
2819.9	6940.0	8479.6	7908.6	7375.7	6887.4	7624.9	7755.3	7648.8	4121.5	7882.8
51.7	502.5	581.6	688.7	409.3	310.7	701.5	297.8	155.2	107.0	414.1
43.8	2850.5	2364.6	1666.1	1554.3	2613.5	1572.2	1653.6	3177.8	1342.2	1412.2
674.7	2238.8	3275.2	2836.3	1995.7	2150.4	2774.1	2466.3	1540.4	1600.8	1709.1
33.9	626.1	1064.0	848.8	591.8	418.7	1263.7	1232.8	201.5	639.8	432.8
225.4	1890.5	3099.1	2446.3	1493.8	2334.4	2295.8	3260.0	1303.1	1988.7	1696.3
229.1	1221.5	1450.6	1890.9	1355.6	1245.7	2231.1	1466.9	2091.1	943.9	1340.3
240.6	1186.9	1863.3	1714.2	1048.0	972.3	2062.7	1421.9	416.7	131.1	683.3
31.8	1152.3	1662.6	1655.0	1044.5	586.8	2796.3	776.5	168.3	129.2	534.3
2479.2	5211.9	5970.2	4785.1	4380.2	4963.0	6025.5	4606.8	5117.2	1889.2	6164.2
5728.5	6860.9	7083.4	7161.0	6293.9	6286.4	6887.5	6420.7	7720.1	3128.1	8568.2
41.3	1126.1	1943.2	1350.4	730.8	988.4	1473.8	2012.2	711.0	844.0	1260.2
3111.6	184.2	218.3	229.9	249.2	174.2	117.5	291.2	118.0	77.4	119.5
2751.9	5095.8	6565.1	6649.2	4892.4	6264.0	6437.6	5609.7	5572.3	1972.6	6120.0
7112.0	3136.2	3778.2	4179.5	3887.6	3038.2	5383.5	3699.0	3360.9	1780.4	2901.2
97.6	1001.3	1596.9	1041.3	686.7	755.5	1177.7	906.3	579.3	342.1	792.2
2379.0	732.3	1601.2	1666.1	1252.9	1099.7	1178.8	1540.8	659.7	773.8	982.5
92.7	491.3	533.5	427.0	319.8	373.8	565.4	850.3	159.5	136.3	303.5
31.2	1434.1	1539.3	951.1	618.3	1074.2	1098.1	798.1	940.1	341.5	571.6
2692.6	5419.6	6547.8	4813.5	3928.1	4579.7	5145.1	4918.4	5489.8	2370.5	7876.5
6307.1	6395.0	5859.1	6323.6	5628.3	5364.0	7495.6	6374.6	7672.2	4062.9	4973.6
16536.7	8243.3	8069.2	8735.8	7587.3	7533.3	7680.2	7869.0	10057.6	7191.5	11883.9
1676.8	2609.2	3381.2	2880.5	2050.4	2134.9	3226.9	2602.4	2389.2	262.5	2922.5
69.4	3917.4	3942.8	2961.8	1828.4	3709.6	2238.2	2773.7	3223.3	1430.7	1845.5
56.1	185.7	324.9	297.3	175.1	181.2	209.1	310.1	108.5	91.4	163.3
239.7	1001.2	1335.4	1301.1	1249.0	1118.8	1474.6	1652.8	1140.0	972.6	542.6

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1215.6	1560.4	2712.7
3003.9	2181.9	1808.9
2947.2	3935.5	6550.8
6119.2	5906.0	5851.4
4889.0	7490.7	5722.9
2718.2	3402.9	2825.9
4584.9	4849.4	7670.6
3543.4	3279.0	4358.2
1992.6	4492.5	2712.5
4718.6	5695.5	7865.1
5398.6	6481.0	9316.8
7550.2	5893.1	7049.0
5546.8	4694.3	6891.2
6757.1	7028.6	8167.5
256.2	192.5	197.4
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2221.9	2116.4	3047.6
725.1	314.2	455.2
3057.8	2788.3	4223.6
708.3	1299.9	1217.5
959.8	645.4	1100.1
302.8	137.0	332.7
2878.4	5001.4	5674.0
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1780.7	1146.0	2396.2
386.9	629.4	253.0
6469.8	5291.5	8196.6
3992.3	3556.8	4160.0
671.0	787.2	1077.1
1730.6	2170.9	2140.4
438.9	495.0	1142.3
499.6	294.7	269.1
2706.5	4444.3	5237.4
5797.4	6252.6	6996.2
7154.0	9011.4	8503.6
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327.8	312.5	256.1
1372.0	1456.1	2573.1

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AY244769.1 gg_id:85594 Veillonella montpellierensis str. 2001-112662 AY2447
GQ005879.1 gg_id:503784 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbu97g GQ005
GQ006870.1 gg_id:502794 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu88g07c GQ006
GQ113854.1 gg_id:375581 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ113
AM697482.1 gg_id:219084 sequencing libraries indoor dust clone BF0001D097 AM697
GQ016366.1 gg_id:493301 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ016
DQ346420.2 gg_id:145149 individual-specific oral microflora during initial colonization enamel human mouth; ir DQ346
GQ073330.1 gg_id:427426 Topographical and Temporal Human Skin Microbiome skin palm clone nbw207g06c1 GQ073
AY995769.1 gg_id:127371 Veillonella parvula str. ATCC 17745 AY9957
GQ022740.1 gg_id:486930 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu3 GQ022
AF186072.1 gg_id:13824 Veillonella criceti str. ATCC17747 AF186
GQ113989.1 gg_id:468332 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor GQ113
GQ088982.1 gg_id:465651 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ088
GQ114846.1 gg_id:374291 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ114
GQ075584.1 gg_id:437044 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ075
GQ073254.1 gg_id:420928 Topographical and Temporal Human Skin Microbiome skin palm clone nbw206h05c GQ073
X84007.1 gg_id:13822 Veillonella atypica str. DSM 20739 X84007
GQ019382.1 gg_id:490287 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu189d GQ019
GQ030048.1 gg_id:430534 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw866d0 GQ030
EU774885.1 gg_id:329844 Short-beaked Echidna feces clone ECH_aai40g10 EU774
GQ101667.1 gg_id:404939 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw497g11 GQ101
GQ071993.1 gg_id:459656 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw190h04 GQ071
GQ005607.1 gg_id:504056 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl GQ005
EU774889.1 gg_id:324786 Short-beaked Echidna feces clone ECH_aai38d06 EU774
GQ006690.1 gg_id:502974 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu86e02c GQ006
GQ114743.1 gg_id:381926 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ114
GQ113658.1 gg_id:405229 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ113
EF185167.1 gg_id:192322 Veillonella dentocariosa str. RBV106 EF1851
AY355140.1 gg_id:95347 Veillonella caviae str. DSM 20738 AY3551
GQ006838.1 gg_id:502826 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu88d03c GQ006
GQ114136.1 gg_id:439586 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ114
GQ101225.1 gg_id:420790 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw49 GQ101
GQ048453.1 gg_id:429982 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbu51 GQ048
GQ031800.1 gg_id:464887 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ031
GQ000861.1 gg_id:469425 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ000
GQ101676.1 gg_id:458976 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw497h10 GQ101
GQ019421.1 gg_id:490247 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu189g GQ019
FJ558100.1 gg_id:517047 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5581
GQ027279.1 gg_id:416279 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ027
GQ073269.1 gg_id:467872 Topographical and Temporal Human Skin Microbiome skin palm clone nbw207a10c1 GQ073

15498.9	6803.2	7075.4	7769.9	6845.0	6381.4	8115.1	6242.2	9027.3	7641.3	9171.8
36.9	124.4	229.6	201.8	136.4	139.2	135.7	233.7	93.2	76.1	123.0
38.9	588.2	718.9	673.7	479.4	429.7	641.7	344.8	208.1	119.3	455.6
5664.4	2656.0	2981.1	2617.9	2297.8	389.5	3604.3	2450.9	4872.9	2410.5	3464.0
2466.9	4313.2	5006.0	4589.0	3251.5	5053.6	4398.2	3973.0	5370.5	2913.0	6429.1
122.5	1693.8	2704.4	2384.9	1171.0	1672.4	2159.4	2557.9	1042.1	1031.7	1179.2
32.3	1001.7	1592.2	1373.5	888.5	632.7	2032.7	1384.9	268.7	733.5	634.4
314.9	3487.2	1981.1	2198.6	3610.6	2851.2	1901.8	1600.2	2071.5	2815.9	833.0
41.0	326.8	517.6	441.2	335.1	268.0	667.6	939.7	186.5	741.9	310.6
28.3	1173.2	1674.5	1595.0	1108.9	646.4	2299.1	1031.9	212.0	201.1	537.8
62.5	299.6	613.8	479.7	366.9	350.2	507.7	585.2	213.3	183.2	288.4
424.8	3311.5	3470.1	3780.5	3220.4	3107.7	3914.4	3463.0	1910.9	1196.1	2339.5
24.1	331.9	402.2	462.2	304.6	210.6	580.9	270.0	61.0	105.8	148.9
1559.6	4977.6	6421.0	6789.1	4483.7	5548.2	4835.8	6105.2	5453.3	6048.9	7877.6
1671.6	2335.6	2773.7	2366.2	1782.4	2004.2	2740.8	2251.3	2131.5	169.5	2963.7
1519.6	5116.5	4452.5	4613.9	3877.5	3905.9	4873.5	4286.4	6611.2	3794.5	4854.6
71.0	534.9	1218.3	608.2	242.0	453.4	549.9	610.2	422.4	83.1	588.0
631.1	1199.7	1625.3	1374.7	1694.9	1155.4	2338.3	1533.7	1246.0	1037.6	1062.9
1894.3	2458.2	3290.9	2567.6	1891.7	2256.1	2746.5	2563.4	2718.6	427.6	2924.0
361.1	3739.7	3525.2	3224.7	4005.1	4022.0	5216.8	3111.7	4645.8	1945.8	2109.3
109.5	3632.1	5110.6	4750.9	3613.3	4043.3	5118.5	5119.6	2890.1	1549.1	3055.3
64.0	1441.3	2038.9	1902.4	1269.7	891.7	2539.7	1635.5	365.5	691.1	1057.5
6763.4	6574.5	7814.6	8562.5	7145.7	5840.9	8442.6	7369.0	5362.1	2135.4	6180.0
2313.0	4336.7	5040.9	4622.5	3270.7	5063.8	4440.7	3986.2	5373.3	2914.7	6438.0
13070.8	8204.8	8725.9	9219.0	8104.9	10155.7	9568.3	7634.1	11463.2	7409.1	12612.6
32.4	607.4	1029.5	830.2	572.9	408.1	1212.6	1212.5	197.8	686.8	437.1
2857.6	2770.9	3510.1	3525.8	3884.2	2639.5	4933.3	3509.4	3037.3	646.3	2106.6
1673.1	2921.0	3728.9	3175.2	2266.4	2434.6	3540.4	2752.4	2337.2	299.7	3321.1
782.9	1285.0	1651.4	1346.9	1703.7	1144.4	2535.4	1664.9	1581.6	1486.2	1152.7
833.6	1763.9	2285.2	2047.3	1647.1	1523.4	1961.4	2154.7	1154.3	1283.3	1406.0
725.5	1857.1	2168.6	2085.9	1476.6	1516.3	1702.4	1894.3	975.9	838.6	1142.8
8907.3	2884.7	3153.9	3161.0	2692.4	2682.2	3510.8	2434.7	4137.0	2969.0	5035.2
1700.1	5956.3	5893.7	5784.4	4328.1	4955.1	6155.3	5870.6	7152.6	2950.9	5161.0
26.4	523.5	729.9	736.2	383.3	312.3	933.2	774.0	124.8	514.8	303.8
48.7	194.7	321.2	240.0	178.9	184.2	383.2	655.2	96.3	538.1	288.3
372.5	2550.5	3412.5	2782.7	1890.1	2004.7	3440.3	3208.3	2395.0	1519.0	2239.5
562.5	3935.4	5513.9	4976.1	5068.5	4082.9	5590.1	5296.4	3269.6	2326.5	3857.1
1788.4	2608.6	3441.5	2703.2	1982.8	2405.0	2893.4	2723.1	2457.5	285.2	2953.2
2584.6	2558.9	2598.8	2703.9	2421.5	2383.3	2996.2	3171.3	2708.0	2316.4	2733.1
1451.8	2219.7	2715.1	2561.0	1884.3	2077.6	2463.0	2875.1	1809.3	2485.6	2480.2
102.5	903.3	1207.2	1116.5	563.6	939.1	1269.7	1763.9	480.3	554.5	1473.2

5887.7	6460.2	6731.4
327.8	181.7	233.4
355.1	255.2	188.5
2000.8	2329.1	2273.6
2778.7	3954.0	4690.9
2550.1	2104.7	2703.3
819.9	362.9	642.8
2991.2	1265.1	1978.1
687.9	327.3	412.1
521.9	306.5	679.3
500.6	686.9	555.6
3287.2	3726.8	4073.9
226.1	101.2	224.1
5890.0	5907.8	7315.3
971.5	1943.6	2541.7
3275.9	3124.9	4289.2
597.7	562.9	1308.1
1425.3	1298.4	1510.7
1216.6	2220.8	3210.3
3683.4	3340.8	4214.4
5496.1	3734.9	6988.0
752.2	426.7	768.6
7326.0	6171.9	7812.6
2770.9	3959.6	4702.3
7912.2	8289.7	9004.8
718.1	311.9	478.1
2696.1	2407.0	3616.3
1445.6	2364.5	4088.7
1789.4	1998.0	1594.9
1829.0	1961.8	3105.8
1485.4	1343.4	1734.3
3124.0	2505.1	2695.1
3928.4	4445.8	5307.2
415.7	267.8	639.9
421.6	173.8	319.2
1901.7	2002.7	1749.8
4689.1	3721.5	5444.0
1395.1	2356.9	3785.9
2711.3	3084.0	3698.5
2812.8	2467.8	3098.9
1262.6	844.2	1419.9

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s__Veillonella dispar	50876
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s__Veillonella montpellierensis	50654
s__Veillonella parvula	49992
s__Veillonella parvula	50131
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s__Veillonella parvula	50185

GQ081299.1 gg_id:452838 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl GQ081
GQ027242.1 gg_id:430526 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw! GQ027
GQ054340.1 gg_id:386212 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw1108 GQ054
GQ113978.1 gg_id:387664 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor GQ113
GQ026752.1 gg_id:424674 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ026
GQ012701.1 gg_id:496965 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw! GQ012
GQ012679.1 gg_id:496988 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw! GQ012
GQ073407.1 gg_id:468068 Topographical and Temporal Human Skin Microbiome skin palm clone nbw208f10c1 GQ073
GQ032582.1 gg_id:375502 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw! GQ032
GQ073344.1 gg_id:393528 Topographical and Temporal Human Skin Microbiome skin palm clone nbw207h08c: GQ073
GQ076880.1 gg_id:400365 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw1154 GQ076
GQ032461.1 gg_id:463442 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw! GQ032
GQ073357.1 gg_id:459514 Topographical and Temporal Human Skin Microbiome skin palm clone nbw208b01c: GQ073
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GQ073343.1 gg_id:395352 Topographical and Temporal Human Skin Microbiome skin palm clone nbw207h07c: GQ073
GQ114938.1 gg_id:377847 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw685c03 GQ114
GQ054349.1 gg_id:409913 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw1108 GQ054
GQ073109.1 gg_id:378037 Topographical and Temporal Human Skin Microbiome skin palm clone nbw205b12c: GQ073
GQ032236.1 gg_id:433236 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw! GQ032
GQ073722.1 gg_id:412083 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ073
GQ012772.1 gg_id:496894 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw! GQ012
GQ076847.1 gg_id:408841 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw1154 GQ076
GQ033104.1 gg_id:434692 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ033
GQ027285.1 gg_id:428376 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw! GQ027
GQ032864.1 gg_id:466022 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ032
GQ032144.1 gg_id:465685 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw! GQ032
GQ032547.1 gg_id:383330 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw! GQ032
GQ032561.1 gg_id:379283 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw! GQ032
GQ032526.1 gg_id:443459 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw! GQ032
GQ027702.1 gg_id:462502 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw! GQ027
GQ009508.1 gg_id:500157 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw77 GQ009
GQ054356.1 gg_id:383423 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw1108 GQ054
GQ016840.1 gg_id:492829 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw826b0 GQ016
GQ076950.1 gg_id:377262 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw1155 GQ076
AF439639.1 gg_id:25275 Veillonella dispar str. ATCC 17748 AF4396
X84006.1 gg_id:13820 Veillonella dispar str. DSM 20735 X84006
AF473836.1 gg_id:26894 Veillonella montpellierensis str. ADV 281.99 AF4738
GQ006633.1 gg_id:503031 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu85g12c GQ006
GQ087817.1 gg_id:375551 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw359b0 GQ087
GQ073137.1 gg_id:388944 Topographical and Temporal Human Skin Microbiome skin palm clone nbw205e07c1 GQ073
GQ086284.1 gg_id:422736 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ086

78.3	603.4	819.0	720.3	523.9	471.3	820.7	904.1	283.3	356.3	437.0
230.6	985.3	1397.7	1113.0	778.2	893.1	1022.7	1566.9	465.5	485.6	956.5
1221.0	2389.9	2318.0	2513.2	1896.6	2094.3	2160.3	3079.6	1649.9	1275.5	1259.9
604.1	1970.4	2862.9	2373.9	1781.1	1807.5	2260.1	2485.0	1623.7	820.1	2153.3
236.8	1146.4	1631.1	1358.6	961.5	957.3	1515.8	2014.3	615.9	851.6	1093.1
340.2	1962.7	2545.5	2702.0	1632.9	1759.4	2740.9	3133.1	2543.1	1482.4	1924.3
712.5	3715.0	4139.4	3473.1	2752.4	3124.9	3473.1	3981.8	3133.7	2520.7	3555.3
201.4	845.7	1296.2	1074.1	753.2	664.3	1218.9	1677.8	506.2	871.1	877.0
57.6	464.4	670.4	556.8	411.1	387.9	600.6	942.8	252.9	742.0	499.5
213.4	748.1	1156.0	947.5	657.4	573.2	980.6	1190.3	466.2	408.7	685.8
237.6	977.3	1381.9	1061.5	758.0	818.7	1124.2	1610.8	508.3	569.6	1016.6
80.1	774.3	1078.2	917.0	643.9	570.9	941.6	1336.0	386.9	785.0	736.6
206.5	978.4	1379.5	1150.6	804.7	805.7	1175.4	1384.4	523.2	395.9	889.1
150.9	880.9	1099.6	920.8	649.1	677.3	1055.3	1526.2	451.2	654.1	943.3
13597.0	6470.6	6180.5	6608.1	6145.8	6296.1	6925.3	6986.2	5881.1	6069.3	9141.5
2448.6	2851.3	3776.3	3600.8	2925.9	2794.4	3593.1	3833.2	1746.7	2880.4	3106.7
14747.2	6701.1	7213.4	7226.0	6400.5	6025.5	7093.7	6351.7	8183.9	6648.2	8549.4
62.1	492.2	541.6	452.8	287.6	360.3	395.8	578.2	219.6	611.4	374.0
1476.6	1766.3	2602.1	2386.6	1966.3	1922.0	2479.4	3394.8	1325.1	1956.4	1926.8
55.3	410.1	657.1	573.4	424.3	331.0	780.9	1076.1	236.5	785.2	432.0
105.1	1481.0	1646.8	1864.9	1272.8	1459.7	1858.2	1890.1	1044.8	922.1	1732.3
1818.2	4907.5	5623.5	6617.9	4826.7	4971.2	5425.8	5757.9	4441.5	3181.1	5845.9
37.4	264.6	441.5	394.9	298.3	202.6	499.0	529.3	163.0	337.9	179.3
630.6	2463.3	3738.1	3592.5	2957.4	2784.1	3704.9	4082.2	3666.2	3171.2	2035.0
233.0	1115.2	1563.1	1310.9	917.6	926.5	1341.2	1581.2	596.5	457.5	957.0
233.8	1101.1	1549.5	1292.5	899.8	913.6	1321.2	1575.6	591.4	456.5	950.4
15558.7	5850.6	6021.8	6490.2	5942.3	5675.5	6596.0	6990.4	6950.0	7939.9	8460.0
89.6	551.6	704.1	625.9	445.0	426.4	533.2	610.2	270.1	188.0	425.9
182.9	1297.3	1579.5	1156.3	985.5	1049.0	1426.6	1838.8	554.8	1114.6	1242.0
199.7	1083.3	1522.1	1375.6	990.8	1027.3	1176.1	2048.1	789.7	1219.6	1289.7
97.4	767.8	1061.6	901.2	641.7	571.5	941.7	1332.5	387.7	728.7	725.9
1295.0	3873.8	3871.4	3813.9	2965.2	3360.7	3816.1	4422.6	3760.0	3329.8	3748.2
862.9	2372.8	2504.4	2434.6	1818.2	1937.5	1922.6	3691.9	1165.2	1497.8	1960.6
4774.1	5294.9	6464.7	5536.8	5723.7	5107.9	5909.3	5605.7	6015.0	6795.5	6333.1
900.3	1419.1	1922.1	1643.6	1363.8	1361.3	1556.4	1796.6	1108.6	766.1	1282.0
232.7	754.7	1084.5	942.8	628.0	740.2	764.6	1166.8	336.5	203.8	571.1
37.6	29.3	34.9	31.8	33.6	31.3	37.1	44.8	26.6	22.9	38.9
2178.9	5343.8	5243.0	4112.8	4771.8	5018.8	5324.6	4226.6	5979.0	3699.9	3697.0
8867.5	6115.1	5476.5	5561.8	4590.7	5492.2	5449.2	5344.9	8953.5	5463.8	6500.5
120.1	3635.7	3383.6	2797.3	2906.6	3793.8	2669.2	3370.1	3403.3	2401.0	2107.5
43.7	331.7	395.4	298.3	257.8	229.3	265.4	501.2	177.2	550.2	265.8

799.0	468.6	824.8
1230.0	951.0	1429.0
2787.6	2018.9	2100.0
2169.3	2206.2	3673.2
1612.8	1031.1	1535.8
2343.4	2445.2	3876.9
3407.6	3136.9	3739.4
1357.9	737.5	977.6
798.1	392.4	367.9
1076.2	621.3	768.8
1240.5	896.9	1502.8
1011.5	619.8	987.8
1193.0	857.0	1355.2
995.5	787.9	1343.0
6844.8	6641.4	8015.3
3168.7	3454.0	4150.3
6222.4	7344.5	7407.7
553.9	476.0	999.4
2768.2	2451.7	3171.4
876.2	382.7	487.8
2110.7	1271.5	2048.6
5063.6	4818.0	5619.7
528.3	232.2	231.2
3195.2	4046.4	4317.6
1356.5	977.3	1559.7
1353.6	961.4	1531.0
5705.5	5845.7	5090.0
590.5	398.5	587.9
1149.4	1147.1	1514.7
1300.9	1485.8	1538.1
1011.1	617.1	918.5
3765.7	2991.7	3974.9
2387.8	2203.0	3094.2
6269.7	5990.6	6265.9
1686.5	1671.9	2227.8
889.8	999.8	1368.4
49.8	38.2	29.9
4346.3	4362.1	4325.7
4116.4	6644.6	4629.4
3703.0	2728.6	3405.2
376.0	379.4	510.2

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
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o__Clostridiales	f__Veillonellaceae
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g__Veillonella
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g__Halothermothrix
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g__unclassified

s__Veillonella parvula	50234
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s__Veillonella parvula	50289
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EU766448.1 gg_id:328607 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU766
GQ047868.1 gg_id:451862 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbu GQ047
AM179906.1 gg_id:148234 Identification microflora (Oncorhynchus mykiss) rainbow trout intestine clone G3-1 AM179
GQ006791.1 gg_id:502872 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu87g04c GQ006
AY947495.2 gg_id:114821 subgingival plaque clone OH1A AY947
AF439641.1 gg_id:35224 Veillonella atypica str. ATCC 17744 AF439
GQ027353.1 gg_id:421354 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ027
EF510493.1 gg_id:217660 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aeru EF5104
GQ032280.1 gg_id:370470 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ032
GQ074330.1 gg_id:430796 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw161f GQ074
GQ084875.1 gg_id:431117 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw26 GQ084
GQ086120.1 gg_id:463770 Topographical and Temporal Human Skin Microbiome skin interdigital web space cl GQ086
GQ114042.1 gg_id:373803 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clo GQ114
GQ086092.1 gg_id:404253 Topographical and Temporal Human Skin Microbiome skin interdigital web space cl GQ086
GQ114025.1 gg_id:385911 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clo GQ114
AF439640.1 gg_id:30716 Veillonella parvula str. CIP 60.1 AF439
EF510428.1 gg_id:218682 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aeru EF5104
GQ027272.1 gg_id:457673 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ027
GQ006604.1 gg_id:503059 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu85e02c GQ006
GQ072552.1 gg_id:374904 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw19 GQ072
FJ557333.1 gg_id:518743 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5573
FJ369852.1 gg_id:361643 feces adult twins and mothers; TS55 clone TS55_a01e08 FJ3698
FJ369825.1 gg_id:357386 feces adult twins and mothers; TS55 clone TS55_a01c04 FJ3698
FJ370053.1 gg_id:358239 feces adult twins and mothers; TS55 clone TS55_a03h07 FJ3700
AB478008.1 gg_id:576201 Microbial aquifer subsurface accretionary prism Japan geothermal groundwater clo AB478
AY538171.1 gg_id:98963 Desulfitobacter alkalitolerans str. Sk.kt5 AY538
FJ638550.1 gg_id:570010 Temperature dependent succession sulfate reducing muddy southwestern Taiwan h FJ6385
DQ230961.1 gg_id:142730 subsurface water clone DR938CH110701SACH36 DQ230
EU639075.1 gg_id:306415 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic EU639
DQ413080.1 gg_id:153409 Microbial -dependent and Approaches Anaerobic/Aerobic SBR Reactor EBPR sludge DQ413
GQ502520.1 gg_id:542395 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf4- GQ502
DQ988278.1 gg_id:192181 Microbial lab-scale A1-A2-O fixed biofilm system coking wastewater treatment with DQ988
EU638492.1 gg_id:319720 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic EU638
AB118592.1 gg_id:93438 Endosymbiont 'TC1' Trimyema compressum clone TC1 AB118
FJ712502.1 gg_id:526485 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) FJ7125
AB439298.1 gg_id:541578 and microbial oils produced Asia petroleum crude oil (Daqing) imported China clone AB439
EU981271.1 gg_id:353812 sulfate reducing living bench scale aquifer column water clone E9_SW EU981
U32594.1 gg_id:14315 Halanaerobium acetethylicum str. EIGI; DSM 3532 U3259
L22016.1 gg_id:14309 Halothermothrix orenii L22016
X89072.1 gg_id:14311 Halocella cellulolsilytica str. DSM 7362 X89072
L22890.1 gg_id:14313 Halanaerobium salsuginis str. VS-752 L22890

817.1	4082.0	4610.1	3754.8	2730.9	4899.8	3440.8	3238.7	5100.8	3063.6	4769.0
1637.1	1652.2	1753.8	1784.1	1444.6	1251.7	2299.2	1639.6	2194.3	485.8	2168.6
243.8	1850.6	1187.0	1570.1	1145.1	2747.0	828.8	1812.0	993.3	3467.3	893.6
608.9	1823.2	2218.1	2390.9	2191.9	1769.4	3346.4	2970.5	2037.6	2697.4	1954.0
77.3	128.2	370.3	213.9	47.9	131.0	59.1	171.1	81.8	40.9	126.0
185.1	1139.1	1591.5	1491.2	1044.2	981.6	1932.0	2134.4	519.5	799.8	915.7
31.5	1038.4	1072.0	719.7	495.8	830.3	725.4	575.2	705.7	236.3	433.3
969.3	5496.0	5999.6	5294.1	4499.6	4424.5	6429.1	5077.5	6731.9	3790.0	5560.6
2227.2	2498.2	2702.0	2112.7	1429.4	3432.9	2215.2	1722.4	3490.0	1859.2	3061.1
1436.5	2193.8	2310.8	2350.8	2241.9	1826.4	2849.8	2684.4	2148.5	1175.7	2272.8
51.0	267.8	294.8	232.3	233.6	182.1	287.7	308.2	144.9	329.5	216.8
404.8	554.8	848.7	685.1	512.4	507.4	515.9	849.8	457.2	969.0	717.4
5672.0	3106.8	3066.5	3522.3	2789.9	2964.6	4409.5	3094.3	3966.4	1584.5	3040.4
45.3	1040.8	1021.7	545.0	384.0	822.0	497.8	616.4	898.9	307.4	408.5
951.3	2885.0	2953.6	2635.7	3026.8	3461.1	3637.6	2493.5	3080.1	5058.9	2019.5
415.1	529.3	944.3	718.1	519.0	493.0	778.8	1059.0	300.7	93.5	393.9
2758.8	3646.9	4396.6	3585.4	2838.2	2883.0	4862.9	3273.6	5568.3	281.3	4618.1
523.0	2951.7	1967.6	1654.9	1303.7	2829.4	1281.9	1862.5	2293.4	1344.5	1067.3
1515.1	2082.8	2509.3	2167.0	1620.6	1636.5	2398.4	2200.1	2397.8	788.8	2543.0
146.4	1496.2	1595.7	1062.0	675.6	1219.0	997.1	1016.8	1254.2	379.0	651.1
439.5	2359.0	2275.1	1838.8	977.8	3139.9	1642.1	1449.1	3147.4	2154.6	2633.8
53.1	2067.2	3255.3	2439.4	888.6	1775.0	1807.4	2889.5	856.9	1383.2	1742.7
59.1	2863.1	4061.6	3636.1	2402.8	2909.8	3528.8	3935.3	1805.7	1227.1	2199.0
7814.0	5589.5	5458.8	6151.9	4799.9	5784.1	5940.7	5624.4	5809.5	6570.9	5502.2
5148.1	10056.6	10591.8	10862.1	11270.4	10005.9	11966.9	9220.9	8062.4	10691.9	9459.5
85.9	1501.8	2150.9	1674.6	1856.9	1592.7	1872.5	1614.4	538.5	520.6	1328.6
240.7	5643.5	5348.3	5968.7	5697.7	4689.7	6577.7	5231.1	5016.6	4495.5	4409.2
42.0	298.8	388.3	296.5	519.8	614.4	336.2	399.7	226.7	167.8	174.6
28.8	83.9	150.0	208.7	145.0	123.8	258.4	205.1	89.6	55.3	90.4
6592.5	7048.6	7692.1	7164.5	7207.2	6646.0	7692.0	6468.9	6546.3	5842.0	8347.6
3051.7	5627.2	5592.1	5681.8	5879.0	5774.3	5960.1	5943.7	4394.9	4007.9	6022.4
2259.6	7790.7	7993.1	8439.0	8761.9	7874.2	9165.2	6954.4	8088.7	6267.5	7957.6
351.4	3316.9	5268.6	4303.7	2893.7	3349.8	4032.5	3920.0	2291.4	990.6	3261.5
14091.7	6463.9	6955.8	7478.0	8055.7	6013.1	8257.6	6344.4	8518.1	6291.1	7243.9
1607.1	8051.9	8342.3	9127.8	8054.8	7701.5	7907.7	7306.5	6065.8	7905.9	8082.8
724.7	2180.9	2800.5	2339.2	2744.0	2519.0	2538.0	2332.8	3024.1	1876.4	2205.6
205.7	1795.8	2285.5	2127.4	1930.3	1721.5	2075.0	2261.1	1571.3	1470.6	1625.2
39.9	78.4	104.2	123.2	79.1	59.3	71.1	147.3	48.1	73.9	75.4
748.4	4306.0	4109.9	4403.9	4288.3	3901.5	4859.5	3973.7	3286.0	1618.4	3725.1
2834.0	2090.3	2106.3	2157.6	2263.2	2251.1	2187.7	2933.8	1680.6	1367.8	1624.7
3017.0	3820.6	4132.7	3835.4	4841.7	3743.3	3281.2	3710.7	4215.5	2995.0	3241.9

3006.4	3824.1	3831.0
306.0	1364.3	1721.3
1503.6	2537.5	1060.3
1808.9	2068.4	3786.5
154.7	307.0	184.6
1510.6	1350.4	1856.7
407.3	208.3	181.8
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1888.4	2505.0	1424.9
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717.5	861.2	864.8
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699.7	778.4	553.6
1321.0	1715.5	1109.6
3034.9	1612.4	2120.9
4527.0	2734.9	5249.4
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9303.9	9675.6	14071.7
1442.8	1891.1	3995.5
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375.8	531.8	1099.0
133.4	162.6	1667.1
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6887.5	7651.6	9499.0
3652.6	3530.1	6224.0
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EF558989.1 gg_id:244525 Microbial functional groups solid waste digestor stable isotope probing thermophilic EF5589
EU869420.1 gg_id:316746 Microbial hypersaline Sidi Ameur water Himalatt Salt Lake Algerian Sahara clone ARD EU8694
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EF106374.1 gg_id:201587 microbial two endoevaporitic salt crusts evaporitic crust Guerrero Negro Baja clone 2 EF1063
EU245738.1 gg_id:255254 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M5-F07 EU2457
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FJ202891.1 gg_id:320426 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2028
AM947558.1 gg_id:264238 Minor changes detected microbial structure and after three week thermophilic dige AM947
X89077.1 gg_id:14308 Acetohalobium arabaticum X89077
NR_028804.1 gg_id:581342 Selenihalanaerobacter shriftii str. DSSE-1; ATCC BAA-73 NR_028
EF459724.1 gg_id:219578 Prokaryotic Hypersaline Inland Turkey Tuz Lake (hypersaline) clone 4-62B EF4597
EU327343.1 gg_id:288770 Halobacteroides sp. str. 6SANG EU3273
X89074.1 gg_id:14301 Halobacteroides halobius str. DSM 5150 X89074
GU452712.1 gg_id:525021 Natroniella sp. str. AHT18 GU452
X89073.1 gg_id:14302 Orenia marismortui str. DSM 5156 X89073
Y18485.1 gg_id:69790 Orenia salinaria str. SG3902 Y18485
EU245188.1 gg_id:242318 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-H3-G09 EU2451
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AM947554.1 gg_id:270282 Minor changes detected microbial structure and after three week thermophilic dige AM947
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EF558957.1 gg_id:238729 Microbial functional groups solid waste digestor stable isotope probing thermophilic EF5589
EF586053.1 gg_id:257232 Methanol-assimilating anaerobic solid waste digester fed methanol clone M55_D21_ EF5860
EU878323.1 gg_id:567033 Investigation factors influencing production large-scale municipal biogas plant therm EU8783
EU639242.1 gg_id:313846 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU6392
FN436027.1 gg_id:539789 Molekularbiologische Charakterisierung der bakteriellen Populationsdynamik eines t FN4360
AM947555.1 gg_id:266221 Minor changes detected microbial structure and after three week thermophilic dige AM947
EF559059.1 gg_id:243394 Microbial functional groups solid waste digestor stable isotope probing thermophilic EF5590
EF586029.1 gg_id:252533 Methanol-assimilating anaerobic solid waste digester fed methanol clone M35_D20_ EF5860
EF559123.1 gg_id:226234 mesophilic anaerobic digester clone C35_D63_H_B_F12 EF5591
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EF586046.1 gg_id:241887 Methanol-assimilating anaerobic solid waste digester fed methanol clone M55_D15_ EF5860
GU455299.1 gg_id:522555 Understanding short-chain fatty acids accumulation enhanced alkaline digestion: kir GU455
EU358734.1 gg_id:312486 structure archaeal denaturing gel electrophoresis and sequencing mesophilic biogas EU3587
EF422412.2 gg_id:224884 Dethiobacter alkaliphilus str. AHT1 EF4224
AF507887.1 gg_id:62675 Mono Lake at depth 35m station 6 July 2000 clone ML635J-4 AF5078
AJ295640.1 gg_id:31598 uranium mill tailing clone KF-Gitt2-16 AJ2956
AJ582199.1 gg_id:93440 soil near uranium mill tailings clone Gitt-GS-113 AJ5821
DQ432150.1 gg_id:156668 prokaryotic alkaline hypersaline lakes Wadi Natrun Egypt Lake Fazda sediment clone DQ432
AF507888.1 gg_id:55772 Mono Lake at depth 35m station 6 July 2000 clone ML635J-65 G+C AF5078

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1914.1	4956.1	5758.2	5266.9	5209.7	5464.1	5826.1	5583.5	4756.8	3506.3	4749.6
1202.1	3081.3	3305.7	3500.4	4067.2	3284.8	4718.0	3670.5	3057.4	2126.7	3423.3
944.5	4415.5	3963.9	4389.4	4099.6	4102.4	4135.5	4044.3	3556.0	3773.9	4818.6
11036.6	7221.7	7593.9	6637.3	6079.4	7128.1	6976.1	6332.3	8787.9	6008.9	7747.0
48.8	26.3	41.3	51.8	24.7	23.3	39.4	45.4	16.0	14.0	30.8
2650.5	4592.4	4577.0	4110.9	4515.9	3915.0	3852.4	4383.0	4431.6	4120.5	4918.8
2896.3	1849.4	1585.5	1724.0	1765.8	1775.7	1687.3	1871.4	1686.8	1369.9	2144.7
37.5	18.9	16.1	20.3	21.1	14.9	22.1	16.2	23.3	33.8	23.0
1555.5	5265.3	5986.2	5790.7	5222.9	5186.6	6063.3	5937.5	5493.8	4546.8	5064.3
78.3	777.0	622.0	293.9	335.3	635.6	526.9	493.7	469.7	279.3	214.2
48.4	85.6	139.3	73.8	78.1	101.8	92.0	165.9	72.9	68.1	82.8
122.3	181.3	268.6	240.1	121.8	169.1	233.6	284.5	79.8	127.2	184.9
1240.7	6446.8	6388.5	7495.2	7140.5	5914.3	7742.0	6559.7	6841.3	4183.7	7900.6
458.5	1794.5	1871.6	2589.7	2131.5	1896.4	2794.9	2714.2	2217.2	933.0	2560.9
2703.3	6131.5	6376.2	6878.9	7579.6	6671.8	6790.7	6852.5	4879.7	2773.9	5760.0
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5695.7	5410.3	4869.2	5759.2	7700.8	4926.4	7057.1	5104.0	4567.1	2721.6	4139.3
403.9	3169.1	3722.9	3468.5	4522.4	3356.7	5275.9	3459.8	2235.2	2753.7	3037.4
533.6	3495.6	3631.1	4414.6	3859.3	4071.2	4276.4	4576.3	4748.9	5329.3	4035.9
4910.2	4579.1	4614.8	4658.2	3514.3	4302.1	4601.9	4520.7	6714.8	6330.0	5460.0
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163.6	541.2	760.5	626.8	593.9	768.1	615.2	870.0	315.7	494.6	383.8
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261.2	1719.8	2445.3	2157.2	1691.8	1788.0	2138.9	2425.6	1770.5	2780.1	1730.6
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174.1	3162.8	3845.8	2620.1	3731.4	2950.5	3276.7	2757.7	1741.7	1538.7	2315.1
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AJ853529.1 gg_id:110524 landfill leachate clone GZKB35 AJ8535
GQ848216.1 gg_id:544950 and Archaeal Xiarinur Soda Lake Water-sediment Interface water-sediment interfac GQ848
EU878335.1 gg_id:554328 Investigation factors influencing production large-scale municipal biogas plant therm EU8783
DQ206412.1 gg_id:139538 microbial mediates arsenate reduction soda lake water clone ML-AsS-10 DQ206
DQ837275.1 gg_id:244602 Archaeal and pristine National Park Spain Donana coastal aquifer clone 56S_1B_61 DQ837
FJ203016.1 gg_id:351673 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c FJ2030
GQ848219.1 gg_id:541684 and Archaeal Xiarinur Soda Lake Water-sediment Interface water-sediment interfac GQ848
EU812988.1 gg_id:341763 Microbial structure thermophilic reactors biogas reactor fed corn silage clone TUM-N EU8129
EU592468.1 gg_id:573525 Seasonal changes Salton Sea hypersaline sediment clone SSS47A EU5924
GU083673.1 gg_id:542800 Microorganism Xiarinur soda lake sediment clone x269 GU083
GQ848204.1 gg_id:588856 and Archaeal Xiarinur Soda Lake Water-sediment Interface water-sediment interfac GQ848
AF454298.1 gg_id:63836 Bacillus sp. clone ML1228J-1 AF4542
NZ_ABKR01000005.1 gg_id:261070 Natranaerobius thermophilus str. JW/NM-WN-LF NZ_AB
AJ271451.1 gg_id:73970 Natronoanaerobium halophilum G-M14CH-4 AJ2714
AJ271450.1 gg_id:23520 Natronoanaerobium salstagnum O-M12SP-2 AJ2714
AJ271452.1 gg_id:72206 Natronoanaerobium aggerbacterium G-M16NWC-4 AJ2714
DQ354747.1 gg_id:155876 subsurface water clone MS149BH1062003_30 DQ354
AB539949.1 gg_id:571087 Evidence syntrophic acetate oxidation coupled hydrogenotrophic methanogenesis -t AB5399
DQ088759.1 gg_id:132063 0.7 1.4 kmbls sctn cntnntl crst cln BE325FW032701CTS_hl1-69 DQ088
EU250948.1 gg_id:358480 degraded cellulose lindane NSC-7 NFC-7 grown 50 degrees Celsius compost compose EU2509
AY330127.1 gg_id:95976 methanogenic landfill leachate bioreactor clone AC039 AY3301
DQ125604.1 gg_id:134479 uranium contaminated soil clone AKAU3609 DQ125
GQ402678.1 gg_id:512997 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
DQ125579.1 gg_id:132342 uranium contaminated soil clone AKAU3574 DQ125
DQ125547.1 gg_id:129508 uranium contaminated soil clone AKAU3523 DQ125
DQ887916.1 gg_id:168335 thermophilic anaerobic solid waste bioreactor clone GHB3B06 DQ887
DQ125708.1 gg_id:133296 uranium contaminated soil clone AKAU3802 DQ125
FJ381977.1 gg_id:583118 Potentially pathogenic and air stem cell transplant winter hospital shower water BMT FJ3819
EF585978.1 gg_id:246509 Methanol-assimilating anaerobic solid waste digester fed methanol clone B55_K_B_A EF5859
AY330129.1 gg_id:95835 methanogenic landfill leachate bioreactor clone AC007 AY3301
DQ887936.1 gg_id:169354 thermophilic anaerobic solid waste bioreactor clone GMB4H09 DQ887
AB274500.1 gg_id:215152 packed-bed reactor clone CFB-11 AB2745
DQ125736.1 gg_id:134788 uranium contaminated soil clone AKAU3845 DQ125
EU887985.1 gg_id:339192 Microbial structure hydrolytic stage two-stage anaerobic digestion grass silage leach EU8879
AM947551.1 gg_id:260695 Minor changes detected microbial structure and after three week thermophilic dige AM947
FJ985789.1 gg_id:451463 depths Colombia South America soil 0-10 m depth former landfill clone -1 FJ9857
FJ985786.1 gg_id:402134 depths Colombia South America soil 5 m depth former landfill clone C5-11 FJ9857
CU919747.1 gg_id:567508 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU919
CU919791.1 gg_id:534056 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU919
AY684074.1 gg_id:133964 methanogenic enrichment 'MRE50' clone MRE50b10 AY6840
CU919182.1 gg_id:566892 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU919

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966.8	6107.5	7688.8	5117.2	6944.3	6965.8	5746.4	7196.9	5059.0	4617.9	6440.6
1031.6	3943.2	4602.6	4475.2	4602.0	3453.8	5721.6	4687.3	3411.2	1968.2	3466.0
96.0	89.4	92.3	17.9	234.3	115.0	196.1	245.6	43.2	20.1	37.8
336.1	3773.5	4810.5	5472.4	4209.2	4511.6	5173.0	4522.4	2525.2	3999.8	3756.6
5036.8	7905.5	7160.3	7299.2	7845.8	7088.1	6782.5	6748.7	7786.4	5014.4	8100.9
11096.3	6706.9	7183.7	8264.3	8605.9	7313.3	8886.0	7376.5	5991.9	6938.3	8928.5
1025.7	7001.3	7336.8	7357.8	7932.7	7220.2	10608.3	8238.8	6650.8	4415.5	8452.2
2477.8	3841.9	5110.8	4749.2	4418.6	3634.2	5290.5	4270.8	2233.8	2343.6	3045.1
7893.7	7284.4	8674.7	7524.5	7932.6	6811.7	9017.9	6900.6	6654.2	5390.8	6528.4
96.6	946.5	1167.0	1402.7	1256.7	1246.8	1482.6	1098.7	447.3	966.4	1142.3
46.4	114.7	159.5	123.9	203.6	116.0	114.1	174.2	65.7	87.7	67.7
519.7	1744.4	2218.1	2384.3	1892.4	2137.0	2862.3	1872.1	1690.1	1464.0	1722.0
463.6	542.4	714.8	518.7	608.5	580.9	506.2	746.2	233.8	145.8	415.4
42.2	392.4	799.6	513.0	254.5	326.0	370.8	390.3	152.5	61.5	249.6
43.8	2116.5	3563.4	2548.4	2019.9	2150.3	2200.4	2039.8	1359.1	502.2	1604.6
263.0	3194.6	4017.4	4377.5	5147.8	3524.0	4306.4	3763.7	3588.1	3770.6	2571.9
1245.3	5648.1	6143.4	7094.3	7949.9	5525.2	7893.5	6000.4	9812.1	5068.5	6292.5
32.0	46.8	68.5	58.7	69.4	111.3	69.6	120.3	24.3	32.5	58.9
95.9	3676.0	4717.2	3279.9	978.5	3687.1	3469.5	3787.7	3186.1	1660.3	3439.0
393.0	1960.5	2514.9	2512.6	1785.2	1925.3	2025.7	2307.7	1538.1	1878.2	2002.9
141.4	1230.4	1758.3	1180.9	760.6	1371.4	724.7	1448.1	560.4	1608.4	1326.3
16375.5	6710.5	6742.5	7159.4	9064.2	6853.4	8709.0	6957.4	6252.2	5847.4	7017.9
3218.3	2767.2	2802.6	2837.0	2288.0	3018.5	2866.9	2913.8	4091.0	2998.6	2880.4
61.4	1880.5	3186.2	1625.5	1430.2	1711.0	1558.9	1780.8	831.2	575.6	1679.4
41.4	1715.3	3029.6	2668.9	1831.5	2062.5	2354.2	2877.7	763.8	356.5	1550.5
1638.8	1952.3	3032.7	2248.9	1772.5	2483.2	1906.5	3530.8	1620.6	913.9	2907.1
3648.6	2639.1	3151.8	3834.4	3628.7	3049.8	3209.0	3872.5	1820.0	1326.0	2240.4
172.1	2900.6	3015.4	3045.0	3472.7	2795.1	3517.7	2977.8	1720.8	480.4	2103.8
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954.2	2194.8	2136.1	2345.9	3487.7	2021.6	2867.4	1958.9	1553.0	659.3	1691.6
1057.2	4581.5	5439.8	5972.2	6488.8	5542.6	5589.9	5376.7	3424.0	3894.0	3952.6
54.9	407.5	745.4	434.6	506.4	487.1	620.7	655.5	199.7	218.4	521.3
1388.9	3382.7	3216.5	3209.9	4307.5	3125.8	4653.2	3198.0	3859.9	2977.4	2590.6
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7791.2	5737.4	6048.4	5833.7	5272.9	5435.1	5805.6	4524.2	6025.4	6537.0	6938.8
10316.5	5252.1	5730.4	5796.1	6743.6	5447.6	6555.1	4994.6	6693.1	5196.7	6646.9
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AY684093.1 gg_id:131483 methanogenic enrichment 'MRE50' clone MRE50b17 AY684
CU927811.1 gg_id:560195 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU927
AY684100.1 gg_id:131930 methanogenic enrichment 'MRE50' clone MRE50b22 AY684
AY684090.1 gg_id:130626 methanogenic enrichment 'MRE50' clone MRE50b08 AY684
CT573824.1 gg_id:150758 Evry municipal wastewater treatment plant clone 013H11_B_SD_P15 CT573
AY526502.1 gg_id:136583 Microbial thermophilic anaerobic sludge methanol-fed lab scale bioreactor clone D3 AY526
CU919826.1 gg_id:551199 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU919
CU919394.1 gg_id:554083 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU919
EU639084.1 gg_id:320495 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU639
EU638947.1 gg_id:342798 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU638
EF559227.1 gg_id:222005 mesophilic anaerobic digester clone A35_D28_H_B_B01 EF559
CU919273.1 gg_id:572645 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU919
CU918907.1 gg_id:539546 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU918
AB434894.1 gg_id:277048 Effect temperature on microbial glucose-degrading methanogenic consortium under AB434
EU878344.1 gg_id:593716 Investigation factors influencing production large-scale municipal biogas plant therm EU878
EF198048.1 gg_id:185617 Microbial structures mesophilic and methanogenic consortia anaerobic thermophilic EF198
EU639113.1 gg_id:306099 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU639
AB374111.1 gg_id:246025 Effect temperature on microbial glucose-degrading methanogenic consortium under AB374
CR933199.1 gg_id:110387 Evry municipal wastewater treatment plant clone 008A06_B_SD_P15 CR933
CU919263.1 gg_id:549429 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU919
CU918937.1 gg_id:549084 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU918
CU921330.1 gg_id:570394 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU921
DQ899892.1 gg_id:257323 structure receiving long-term augmentations chromium contaminated wastes landfi DQ899
DQ018807.1 gg_id:132376 anaerobic swine lagoon clone C-131 DQ018
AB234270.1 gg_id:145732 Biotransformation Polychlorinated Dioxins Microbial Dynamics Sediment Microcosm AB234
DQ018815.1 gg_id:132872 Unq Mcrbl Anrbc Swn Lgns anrbc swn lgn cln C-146 DQ018
EF586045.1 gg_id:245235 Methanol-assimilating anaerobic solid waste digester fed methanol clone M55_D15_ EF586
EF586061.1 gg_id:243276 Methanol-assimilating anaerobic solid waste digester fed methanol clone M55_D21_ EF586
EF559043.1 gg_id:238463 Microbial functional groups solid waste digestor stable isotope probing thermophilic EF559
AB234000.1 gg_id:152360 anaerobic reactor clone B-7 AB234
FN563383.1 gg_id:578169 Impact changing HRT OLR on prokaryotes involved biomethanizitaion and fuzzy logic FN563
NC_012034.1 gg_id:471220 Anaerocellum thermophilum str. DSM 6725 NC_01
CP000679.1 gg_id:224527 Caldicellulosiruptor saccharolyticus str. DSM 8903 CP000
EF100909.1 gg_id:193269 Caldicellulosiruptor kronotskiensis str. 2002 EF100
U80596.1 gg_id:16088 Caldicellulosiruptor owensensis str. OL U8059
L35151.1 gg_id:16089 Caldicellulosiruptor sp. str. Rt8B.4 L35151
EF100907.1 gg_id:181163 Caldicellulosiruptor kristjanssonii str. 117 EF100
AJ004811.1 gg_id:16095 Caldicellulosiruptor kristjanssonii str. I77R1B AJ0048
L09183.1 gg_id:16093 Thermoanaerobacter cellulolyticus str. NA 10B L09183
FJ189575.1 gg_id:351375 digester anaerobic sludge clone EUB_54 FJ1895

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589.9	2247.9	2741.1	3209.5	2058.6	2589.9	2640.1	3437.2	1918.8	1176.7	2996.7
1156.2	4289.2	4589.0	5116.8	7659.0	5261.6	7324.5	5861.0	3211.3	2528.9	4973.3
80.6	2721.8	3131.3	3283.5	5481.6	3053.0	4957.1	3230.2	1448.8	520.1	1706.3
1251.2	4082.6	4735.4	4081.1	5621.2	4638.3	6240.2	4575.5	2621.2	4159.1	4974.7
41.8	2051.7	1342.0	1322.9	992.1	1432.3	1226.3	1342.7	606.0	923.8	1107.3
201.9	3976.8	3931.6	3902.2	3637.0	3870.5	3792.5	4198.3	3208.3	1728.8	2722.7
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308.8	1955.6	2449.3	2794.2	2794.7	2039.2	3126.8	2388.3	1375.3	1270.0	1916.6
1146.2	8354.5	8301.0	8438.1	8002.6	7497.8	8636.2	7219.8	8070.9	5797.0	9900.6
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3086.0	4339.9	4904.3	4890.0	5222.1	4117.7	5705.5	4978.6	5528.6	5088.9	5979.7
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2168.9	5438.5	6374.4	6616.3	6781.2	6036.3	7472.5	6247.2	4222.8	2842.0	5692.8
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1795.3	2349.4	2635.9	2522.9	2861.4	2659.2	3132.9	2567.0	2304.1	1765.6	2072.7
41.3	17.1	20.4	27.9	23.4	24.8	21.6	23.9	20.8	14.4	32.4
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3764.7	4589.1	6585.1
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6623.4	6368.1	7622.4
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2247.7	3234.5	3798.4
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DQ152922.1 gg_id:139369 Caldicellulosiruptor sp. str. YI5 DQ152
CP001785.1 gg_id:521670 Ammonifex degensii str. KC4 CP0017
EF554597.1 gg_id:233108 Fervidomicrobium thiophilum str. SR EF5545
NC_003869.1 gg_id:471376 Thermoanaerobacter tengcongensis MB4 str. MB4T NC_00
AF174484.1 gg_id:39044 Carboxydibrachium pacificum str. JM AF1744
EU109461.1 gg_id:237130 Thermoanaerobacter subterraneus str. S2302 EU1094
AF212925.1 gg_id:26976 Thermoanaerobacter yonseiensis str. KB1 AF2129
EF554599.1 gg_id:234626 Thermoanaerobacter subterraneus str. 2707 EF5545
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FJ189534.1 gg_id:349650 digester anaerobic sludge clone EUB_13 FJ1895
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AY278483.1 gg_id:87364 Thermoanaerobacter keratinophilus str. 2KXI AY2784
DQ115806.1 gg_id:134076 Thermoanaerobacter tengcongensis str. 185y2 DQ115
CP000141.1 gg_id:140847 Carboxydothermus hydrogenoformans str. Z-2901 CP0001
U76363.1 gg_id:13728 Thermoterrabacterium ferrireducens U76363
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EF542810.1 gg_id:218099 Carboxydothermus siderophilus str. 1315 EF5428
AF487538.1 gg_id:82633 Moorella mulderi str. TMS AF4875
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AY684084.1 gg_id:153109 first genome data rice I methanogens combination cultivation and techniques metha AY6840
FJ189582.1 gg_id:324196 digester anaerobic sludge clone EUB_61 FJ1895
EU638454.1 gg_id:309145 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU6384
AB222053.1 gg_id:137796 Clostridium sp. str. EBR-02E-0600 AB2220
AB020336.1 gg_id:13717 Thermacetogenium phaeum str. PB AB0203
EF559057.1 gg_id:243312 Microbial functional groups solid waste digestor stable isotope probing thermophilic EF5590
DQ647145.1 gg_id:257640 Microbial structure -temperature oil-field produced water Troll formations North Se DQ647
EF558950.1 gg_id:246613 Microbial functional groups solid waste digestor stable isotope probing thermophilic EF5589
EU386162.1 gg_id:265020 Thermacetogenium sp. str. Sp3 EU3861
AB332113.1 gg_id:246435 Continuous cultivation and structure thermophilc propionate-degrading microbial co AB3321
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DQ887938.1 gg_id:165206 thermophilic anaerobic solid waste bioreactor clone GMB4F03 DQ887
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AF542521.1 gg_id:59098 Thermoanaerobacter ethanolicus str. X524 AF5425
DQ128182.1 gg_id:138446 Thermoanaerobacter ethanolicus 3 DQ128
AY701757.1 gg_id:106184 Thermoanaerobacter sp. str. AIP 504.99 AY7017
NC_010321.1 gg_id:259585 Thermoanaerobacter pseudethanolicus 33223 str. ATCC 33223; 39E NC_010
EU262599.1 gg_id:240738 Thermoanaerobacter inferii str. AK15 EU2625
L09167.1 gg_id:13780 Thermoanaerobacter thermocopriae str. JT-3T L09167
DQ128177.1 gg_id:137851 Thermoanaerobacter ethanolicus 6 DQ128
DQ128183.1 gg_id:202453 Thermoanaerobacter ethanolicus 2 DQ128

198.7	890.2	909.5	1006.6	1393.7	1105.7	1326.3	1092.9	457.9	569.3	484.5
1433.8	1821.8	1680.5	2153.2	2373.0	1869.3	2415.9	2030.0	1237.1	1470.5	1496.0
884.7	4610.6	4541.0	4844.7	5612.0	4594.6	5849.6	4672.0	4390.1	3612.3	3181.3
189.5	814.2	922.0	966.8	1161.1	962.5	1283.1	935.2	464.2	800.9	634.3
1074.2	6054.8	5406.1	6163.9	6626.3	6230.7	6962.1	5193.0	7239.2	4724.2	5916.4
2309.2	1951.5	1935.6	2067.8	2318.3	1967.4	2295.6	2106.7	1855.4	1774.6	2196.1
57.5	341.9	540.2	465.6	411.2	335.7	433.8	543.2	211.8	100.9	360.6
1239.3	3642.0	4061.3	4092.5	3740.3	3269.7	3707.9	3314.8	4693.6	3086.9	4681.9
2164.4	2979.3	3951.4	3262.8	3108.5	3210.7	3024.4	3439.9	2856.3	3093.6	3123.4
48.9	1268.2	1386.5	1401.6	1354.0	1339.1	1399.7	1497.8	808.1	686.2	1103.2
83.3	604.8	1023.2	1136.6	675.4	534.0	721.0	1164.1	301.8	193.5	1264.8
133.1	978.7	956.7	1079.6	1179.7	963.3	1140.5	1021.6	1064.6	564.4	1058.0
50.3	248.0	401.8	347.1	227.3	215.7	256.3	316.4	118.4	62.8	261.2
16232.1	7263.6	6724.3	6737.0	6282.6	6672.3	7138.0	6276.0	8776.5	7173.8	8961.6
225.9	2185.8	2658.7	2316.9	2571.2	2289.2	3028.7	2751.0	1614.4	593.0	2312.6
12526.6	6040.1	5456.1	6368.3	5201.6	6216.5	6620.5	5470.2	5730.5	5217.5	9586.5
575.1	2857.9	3440.1	3112.3	3370.7	2988.2	3887.7	3613.8	2231.3	873.3	2986.2
8896.9	3622.2	4020.6	4026.9	3893.2	3849.7	4736.0	3580.6	2514.7	3377.6	3997.9
3608.9	5521.1	5269.3	5248.9	5145.7	4601.8	4400.7	5280.1	5722.0	4565.0	6069.5
397.5	2569.4	3069.3	2766.1	3322.6	2735.5	3842.6	2798.4	2566.1	2740.1	2512.6
12665.8	10509.2	9896.3	9662.2	8364.9	8775.1	8730.5	9387.1	10484.3	9674.6	9579.2
11465.7	9186.5	8923.1	9003.4	9910.8	8324.6	9790.2	8283.9	10168.6	9867.1	9481.1
338.6	2733.8	3424.7	3306.4	3900.2	2893.3	4188.0	3234.0	1067.5	869.1	2495.1
801.2	2491.8	2218.5	2270.4	2269.1	1947.1	2660.4	2562.8	1859.7	1247.7	1875.6
689.3	1905.4	1858.3	1852.8	2398.6	2159.8	2392.1	2052.7	1461.0	1877.6	385.8
1598.9	4708.0	5106.5	5467.8	5647.3	4714.2	6039.0	5372.1	3787.0	3349.5	4447.3
3787.8	4141.5	3905.6	4406.1	5577.7	4501.2	4811.4	3680.2	3552.4	3473.5	4392.8
2323.2	5922.4	6344.9	5472.5	5684.5	5734.6	5693.5	6371.2	7114.0	6753.3	6659.5
196.9	2829.9	2959.1	3105.1	3473.8	3498.6	4508.3	3926.0	1743.1	1945.9	3024.7
482.8	5243.5	6030.0	5774.9	6404.2	6246.8	6067.7	6404.1	5364.5	4850.3	5371.2
47.5	412.5	593.3	329.9	308.7	537.7	365.9	522.5	163.8	132.6	240.3
46.1	618.1	624.4	538.2	570.3	720.7	498.7	825.7	528.2	864.7	468.1
42.2	85.4	115.6	120.6	141.8	106.2	166.6	116.4	54.1	33.4	67.1
7812.0	4385.8	5293.3	4336.3	4057.7	4505.3	934.8	4316.6	4503.2	5125.9	4619.1
7050.9	4214.1	3969.5	4661.2	3425.9	5051.0	3561.8	7066.8	4700.3	2345.9	7713.3
47.6	138.5	205.2	180.9	152.6	137.4	182.5	245.4	91.1	61.4	133.1
41.6	411.2	794.8	443.5	238.4	518.4	206.7	1353.4	270.2	557.7	1012.7
282.7	3467.6	4002.8	3940.7	5291.6	4565.8	4409.0	3866.2	2232.2	1163.1	3037.9
38.2	152.6	257.1	179.4	246.2	168.9	320.8	220.9	80.3	38.9	131.3
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11512.3	8343.9	8946.6	8742.3	6349.8	8789.7	6661.8	9152.5	9002.2	7179.3	12219.3

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1933.5	2256.2	2779.9
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884.2	1200.3	1415.0
220.2	423.0	518.8
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2625.9	2563.2	2142.2
7321.6	7896.4	7120.6
3412.5	3396.6	3033.2
4283.0	4017.6	4446.9
4233.0	6174.5	4721.7
2197.1	3481.6	4744.6
9315.6	10059.8	10392.8
8555.6	10303.9	11658.8
2745.2	3954.8	7071.5
2328.8	2697.8	3639.2
1896.8	2352.3	2618.9
4915.3	5798.1	7353.4
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6574.8	8997.2	8277.7
2579.7	4641.6	6715.5
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99.1	138.7	508.3
4411.8	4789.3	6469.0
3572.2	3851.0	5074.1
144.7	220.3	342.1
404.1	623.2	1069.7
3045.8	4132.5	6797.4
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NR_029301.1 gg_id:574119 Thermoanaerobacter wiegelii str. Rt8.B1; DSM 10319 NR_02
DQ128181.1 gg_id:137863 Thermoanaerobacter ethanolicus 4 DQ128
L09160.1 gg_id:13765 Thermoanaerobacter kivui L09160
DQ681066.1 gg_id:163311 Thermoanaerobacter wiegelii str. B5 DQ681
AF234164.1 gg_id:29733 Thermoanaerobacter sulfurigignens str. JW/SL826T AF234
L09164.1 gg_id:13789 Thermoanaerobacter ethanolicus ATCC 33223 str. 39E L09164
EU731003.1 gg_id:338174 single-species ecosystem deep within Earth fracture water borehole MP104 level 10 EU731
FJ712408.1 gg_id:523660 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) k FJ7124
EU730994.1 gg_id:353154 single-species ecosystem deep within Earth fracture water borehole MP104 level 10 EU730
EU419136.1 gg_id:267107 Microbial and ecology selected andesitic hydrothermal acidic hydrothermally modifi EU419
FJ748761.1 gg_id:545194 Thermoanaerobacter sp. str. RH0804 FJ7487
AB062280.1 gg_id:20457 Thermanaeromonas toyohensis str. ToBE AB062
DQ887945.1 gg_id:168959 thermophilic anaerobic solid waste bioreactor clone GMB4H08 DQ887
AY216596.1 gg_id:85134 Thermoanaerobacter subterraneus str. OCA1 AY216
AB374119.1 gg_id:250276 Effect temperature on microbial glucose-degrading methanogenic consortium under AB374
EU638335.1 gg_id:348663 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU638
FJ638536.1 gg_id:572985 Temperature dependent succession sulfate reducing muddy southwestern Taiwan hc FJ6385
AB374120.1 gg_id:243918 Effect temperature on microbial glucose-degrading methanogenic consortium under AB374
AB434897.1 gg_id:271632 Effect temperature on microbial glucose-degrading methanogenic consortium under AB434
AE013109.1 gg_id:66678 Thermoanaerobacter tengcongensis str. MB4 AE013
AB374132.1 gg_id:243488 Effect temperature on microbial glucose-degrading methanogenic consortium under AB374
AB374117.1 gg_id:238691 Effect temperature on microbial glucose-degrading methanogenic consortium under AB374
AB374134.1 gg_id:256314 Effect temperature on microbial glucose-degrading methanogenic consortium under AB374
DQ097675.2 gg_id:134191 oil field clone B5_otu10 DQ097
AY703479.1 gg_id:138789 Thermosediminibacter litoriperuensis str. JW/YJL-1230-2 AY703
EU638920.1 gg_id:316096 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU638
EU639339.1 gg_id:323523 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU639
EF174273.1 gg_id:190840 direct activated sludge compost maturation stage clone H42-814 EF1742
CU920710.1 gg_id:539239 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU920
DQ079649.1 gg_id:137457 deep terrestrial subsurface fluid-filled fracture clone EV818FW062101BH4MD9 DQ079
AB260059.1 gg_id:179484 Microbial black exposed hot ridge flank crustal fluids Black rust formation on boreho AB260
AB300079.1 gg_id:220063 Wide ancient microbial DNAs Quaternary sediments holocene mud sediment clone A AB300
AM777947.1 gg_id:237589 nonsaline . Influence pore-size filters determination structure alkaline groundwater AM777
DQ088764.1 gg_id:133580 subsurface clone BE325FW032701CTS_hole1-27 DQ088
DQ088772.1 gg_id:131486 subsurface clone BE325FW032701CTS_hole1-1 DQ088
AB426224.1 gg_id:275227 -situ identification study benzene-degrading s under methanogenic condition anaerc AB426
EF632928.1 gg_id:246403 Unique microbial contrasting aquatic altitude Andean Altiplano (northern Chile) fresh EF6329
FJ203601.1 gg_id:339359 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h FJ2036
AB539950.1 gg_id:517375 Evidence syntrophic acetate oxidation coupled hydrogenotrophic methanogenesis -t AB539
DQ256302.1 gg_id:142791 subsurface water clone EV818BHEB6102702SAFF42 DQ256

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54.7	903.3	1497.1	1029.5	610.4	977.0	628.3	1708.6	799.2	925.6	1137.5
9788.4	6011.8	5406.7	5414.9	3998.6	6127.8	4751.3	7978.5	7090.2	5368.7	8049.9
10720.5	5867.8	5741.4	5879.5	5719.6	5638.7	5584.8	4733.1	5343.9	4098.7	5553.9
1106.7	3588.0	5030.6	3803.5	3438.2	4106.3	3350.6	3912.6	3104.3	3843.0	3258.3
31.0	153.6	625.7	586.2	566.8	560.5	589.9	1676.9	255.5	182.6	1515.9
12283.5	7225.4	8280.6	7260.1	7305.4	7568.7	7465.8	6766.4	8463.1	8223.4	9720.4
208.7	1745.6	2022.6	1846.5	2227.0	2256.1	2244.6	2567.9	1181.4	510.7	1824.6
53.2	319.9	449.1	424.0	540.1	395.2	555.3	499.7	118.1	55.5	281.7
77.4	141.0	188.4	176.8	95.8	173.9	178.8	186.9	130.0	41.2	98.1
9126.8	10149.6	10330.0	11929.2	11828.1	9903.8	14419.9	10436.9	15592.7	11160.3	10930.6
2180.8	515.1	599.4	540.8	599.1	524.7	503.0	521.7	597.0	407.3	500.1
75.0	46.7	62.6	80.8	119.5	60.6	118.6	62.6	30.0	25.4	37.5
944.6	9199.1	7554.0	8015.8	8160.5	7990.1	7812.5	7073.6	8964.4	8059.9	5890.1
1721.1	2010.8	2315.6	2333.9	2531.9	2189.4	2333.1	2714.2	1450.7	902.3	2127.9
3208.5	6424.6	7353.2	7421.6	8134.6	6554.1	8972.9	6346.4	9532.2	6869.3	7815.4
42.7	45.3	58.1	39.6	33.3	36.8	40.3	27.9	33.3	17.4	38.3
56.8	526.0	662.1	1032.0	538.1	540.1	816.1	604.9	167.4	516.7	235.7
1916.4	4205.1	4905.6	4457.1	4581.2	4420.4	4611.7	4694.7	3534.9	3649.1	4089.1
292.5	2665.8	2860.4	3109.3	2945.6	2435.3	3181.6	3216.9	1153.2	945.8	2795.3
34.1	18.6	24.1	23.1	38.8	17.0	23.0	19.3	17.2	15.6	13.6
1821.2	1659.1	2561.9	1889.8	1425.9	1885.9	1589.1	2301.6	1327.1	1674.7	1988.9
2167.1	2728.8	3492.4	2997.0	2803.0	2963.7	2816.2	3112.1	2577.2	2928.1	3142.4
108.9	529.2	912.3	649.2	641.2	637.1	665.0	764.8	435.4	296.8	358.6
14328.1	7092.8	7552.9	8459.9	7610.8	7448.6	8733.9	7525.6	6120.9	4195.8	7603.0
1220.9	4709.6	5674.9	5834.6	5864.2	6122.5	7673.1	6428.8	4791.8	3311.5	5389.0
1530.4	3404.5	3152.8	3913.6	2918.0	3509.0	3855.4	4239.4	2392.8	2093.3	4588.2
11161.3	3606.7	3834.4	4388.9	1489.0	3701.6	4713.4	3558.2	4999.2	3934.6	5758.1
79.9	2314.9	3035.2	2650.2	3502.1	2202.7	4758.9	1532.4	1141.0	352.2	1202.4
164.5	2239.7	2308.5	2440.8	3009.6	2305.1	3039.2	2310.6	1352.9	1084.8	1257.1
38.4	44.7	60.6	53.7	68.6	53.8	87.7	42.5	23.6	20.5	30.6
91.9	909.8	2700.5	1309.7	944.0	543.8	1227.1	650.7	260.6	159.8	417.7
45.4	189.5	238.6	268.9	220.3	170.4	228.7	160.2	81.7	68.0	121.9
2312.4	7225.0	6914.4	7605.6	8143.7	7212.9	8903.1	7084.3	6409.5	5470.1	10884.3
65.0	35.4	51.0	48.6	32.3	33.3	26.4	43.4	29.0	30.8	29.3
39.2	215.8	213.9	153.2	345.8	278.3	1094.4	164.5	96.9	36.3	80.2
1286.5	6111.4	5080.9	5173.0	5276.9	4860.1	5434.7	5332.8	5471.8	4205.1	3134.4
31.2	395.0	772.6	561.5	445.6	435.5	575.5	730.6	244.0	79.4	322.1
4770.1	3424.4	3646.0	4318.8	4114.3	3271.6	4276.2	3612.7	2537.0	2176.2	2679.1
2728.0	7349.0	7568.8	7264.1	7832.5	6218.0	8662.5	6857.1	7054.0	5470.9	5147.8
44.1	135.7	229.4	155.3	124.4	142.1	159.2	242.9	96.5	130.3	146.9

6641.8	8625.6	7356.1
1001.4	1171.9	2728.6
4738.9	6730.7	5997.8
4928.1	6305.2	5654.8
3728.6	5451.7	6829.2
389.6	526.5	1549.1
5245.4	8489.0	7754.4
1663.5	2118.6	2997.7
404.4	532.8	1382.2
184.2	208.2	208.8
9698.9	10737.7	12971.2
635.9	1547.5	750.6
66.3	151.2	144.1
6207.7	7011.1	9683.9
2327.4	2164.3	3450.1
6846.1	8215.8	10178.9
29.9	58.5	388.8
645.6	725.3	582.8
4990.2	4551.5	6151.6
3161.8	2765.7	3829.8
15.1	20.1	28.0
1943.0	2036.8	3060.1
3271.5	3170.8	4036.1
663.0	1074.5	2643.3
6627.5	7884.5	10018.2
5190.5	6349.8	8340.3
3883.8	4264.1	4835.4
3295.7	3723.6	4034.9
985.0	1588.6	3147.8
2113.5	1955.0	2234.8
43.5	39.6	70.2
534.6	1067.6	2627.8
131.1	242.8	304.5
6219.3	7127.8	7335.6
42.5	44.4	36.4
304.3	220.4	207.6
5501.0	4636.5	6487.9
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7108.4	8663.0	9153.3
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AJ431236.1 gg_id:79101 Cytophaga sp. str. BHI60-57B AJ4312
EF585979.1 gg_id:257911 Methanol-assimilating anaerobic solid waste digester fed methanol clone B55_K_B_/ EF5859
EF559068.1 gg_id:252254 Microbial functional groups solid waste digestor stable isotope probing thermophilic EF5590
AM947532.1 gg_id:265589 Minor changes detected microbial structure and after three week thermophilic dige AM947
AF282252.1 gg_id:17524 Ferribacter thermoautotrophicus str. JW/JH-Fiji-2 AF2822
DQ815026.1 gg_id:169250 zebrafish digestive tract clone aab49a06 DQ815
DQ815290.1 gg_id:171837 zebrafish digestive tract clone aab52g10 DQ815
DQ815286.1 gg_id:171805 zebrafish digestive tract clone aab52g04 DQ815
DQ815110.1 gg_id:173268 zebrafish digestive tract clone aab50b10 DQ815
DQ815013.1 gg_id:161980 zebrafish digestive tract clone aab56g09 DQ815
AM179923.1 gg_id:145422 Identification microflora (Oncorhynchus mykiss) rainbow trout intestine clone G15-: AM179
DQ815269.1 gg_id:172292 zebrafish digestive tract clone aab52e06 DQ815
DQ815170.1 gg_id:168343 zebrafish digestive tract clone aab51a08 DQ815
DQ815292.1 gg_id:170458 zebrafish digestive tract clone aab52h02 DQ815
EU460633.1 gg_id:297393 polar bear feces clone PB2_aai23f09 EU460
EU460497.1 gg_id:293496 polar bear feces clone PB2_aai21g01 EU460
DQ815229.1 gg_id:164983 zebrafish digestive tract clone aab51h04 DQ815
EU460618.1 gg_id:287660 polar bear feces clone PB2_aai23e02 EU460
EU460666.1 gg_id:296915 polar bear feces clone PB2_aai24b06 EU460
X78419.1 gg_id:11302 Cetobacterium ceti X78419
EU460449.1 gg_id:296950 polar bear feces clone PB2_aai21a07 EU460
EU460631.1 gg_id:298501 polar bear feces clone PB2_aai23f07 EU460
EU460679.1 gg_id:297037 polar bear feces clone PB2_aai24c12 EU460
EU460629.1 gg_id:293351 polar bear feces clone PB2_aai23f05 EU460
GU293194.1 gg_id:562985 Microbial contents and mucus yel catfish (Pelteobagrus fulvidraco) stomach content GU293
EU460532.1 gg_id:297473 polar bear feces clone PB2_aai22c03 EU460
EU460361.1 gg_id:297672 polar bear feces clone PB1_aai27c07 EU460
EU460550.1 gg_id:291093 polar bear feces clone PB2_aai22e07 EU460
EU460627.1 gg_id:291261 polar bear feces clone PB2_aai23f02 EU460
EU460489.1 gg_id:294813 polar bear feces clone PB2_aai21f01 EU460
EU460637.1 gg_id:298087 polar bear feces clone PB2_aai23g02 EU460
NR_025679.1 gg_id:554906 Fusobacterium canifelinum str. RMA 12708; CCUG 49735 Q11 NR_02
AJ295750.1 gg_id:34266 Fusobacterium equinum str. horse VPB 4027 AJ2957
X74408.1 gg_id:11309 Fusobacterium necrophorum str. B FnS-40 X74408
X74407.1 gg_id:11305 Fusobacterium necrophorum str. AB FnS-1 X74407
FJ471661.1 gg_id:524898 Fusobacterium nucleatum str. ChDC F319 FJ4716
GQ004485.1 gg_id:505177 Topographical and Temporal Human Skin Microbiome skin nare clone nbu59b02c1 GQ004
EU772809.1 gg_id:306442 Bush dog feces clone bdog1_aai77h07 EU7728
AF543300.1 gg_id:58280 Fusobacterium nucleatum str. ChDC OS50 AF5433
GQ448468.1 gg_id:511044 Microbiome neonatal calves: shedding microorganisms fecal clone calf784_2wks_gr GQ448
AF481217.1 gg_id:68347 Fusobacterium nucleatum str. E9_12 AF4812

289.7	2306.5	2655.5	3119.1	3402.6	2394.6	3782.4	2803.6	1284.0	1086.0	1946.5
45.1	465.5	471.4	519.2	645.2	550.5	387.1	709.8	195.2	68.7	243.2
661.8	2781.3	3362.4	3482.0	2674.4	2838.4	2738.8	2824.2	1981.3	1135.1	2544.3
5143.8	5811.4	6637.0	6197.4	6062.5	5465.7	6309.3	6252.2	8245.0	4093.6	5670.8
48.6	215.1	264.9	286.4	331.5	203.9	333.4	389.1	111.3	79.1	99.9
162.4	445.8	237.4	249.9	147.2	233.8	450.2	297.8	175.2	56.5	185.0
6236.4	5999.0	5645.3	5986.0	3886.1	5599.7	4681.1	5981.9	4338.7	3044.1	7050.0
1202.5	3849.3	2871.5	2505.9	2445.3	3357.8	2994.3	3974.0	1202.4	542.7	2675.9
5322.3	5679.4	5959.7	6905.8	4538.0	5968.8	4710.1	7077.3	4684.1	2036.0	6688.0
5736.3	6114.3	5868.7	6738.9	5489.2	6692.6	5838.8	7208.4	4563.5	2296.6	6299.9
217.9	559.2	107.2	90.8	52.1	211.3	207.5	243.9	148.1	22.6	99.0
2164.6	7612.3	7479.4	9173.2	6837.8	7274.2	7414.2	7811.7	5779.4	2928.3	10175.8
1195.5	5844.0	5721.1	5900.0	3915.2	6129.1	4319.2	6364.9	3160.2	787.4	5609.4
79.7	206.5	239.8	196.9	87.8	147.9	143.6	231.1	70.7	37.7	147.8
9236.4	7382.5	8343.1	8765.8	8842.0	7733.1	6207.0	7971.9	11144.2	6088.0	8207.4
3259.0	4573.5	5746.5	6022.0	4861.2	5369.1	5623.5	4954.8	4952.8	1874.6	4926.9
1019.5	3164.4	3669.8	4254.7	1527.0	3091.5	2124.5	3424.0	1581.6	520.4	3431.9
2274.5	3846.1	5592.2	6265.4	3722.0	4452.1	4297.7	4831.4	3011.5	480.4	4129.3
8442.8	6449.5	7338.7	7781.8	7704.2	7005.0	7146.7	7349.0	9132.9	5123.0	6994.7
56.7	271.4	412.5	410.6	136.9	479.5	457.1	699.0	274.5	60.9	514.0
3044.8	5131.5	6080.5	5938.9	4346.9	5925.5	4815.1	6498.7	4008.0	1843.2	5606.0
1092.7	3561.0	4640.9	5251.5	3050.5	4016.5	3265.1	5339.3	4043.9	931.5	4636.8
1101.0	3628.9	5654.1	6119.4	4098.5	4409.5	4562.7	5263.2	3198.9	1057.9	3598.6
6732.7	5464.8	5811.7	6216.3	5955.1	5999.2	5842.8	6401.4	11219.6	6442.6	6026.0
5886.7	7069.5	6636.2	6223.3	6282.0	7147.1	6729.8	7201.9	5775.1	3476.5	5879.7
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25028.6	8685.2	9244.2	9340.9	8318.5	7688.5	9013.5	7371.2	15791.2	8270.3	11786.2
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3330.6	6123.3	9456.8	9582.5	5773.5	7611.3	6248.2	8388.5	8380.7	4462.7	8499.0
3414.3	5524.6	5596.6	6340.3	4599.5	6479.3	5969.7	6754.2	3422.4	1669.6	6753.8
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382.7	1792.1	2165.8	2540.3	1386.5	2216.1	2080.2	2456.6	1018.4	249.9	1975.1
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4336.4	4241.0	4554.3	5843.7	3287.2	5240.9	4019.1	4655.2	5735.0	3560.2	7161.0
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892.0	4333.6	4962.0	6501.7	2421.6	5179.8	3830.5	5805.1	3000.9	593.6	5476.7
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1525.0	2940.5	3696.1	4119.2	3336.2	3707.8	3532.4	3773.2	2251.6	1719.8	2621.7
3669.0	4310.8	5081.8	6291.3	2819.9	4249.5	3809.1	4662.3	3797.4	1790.7	5457.5

2149.2	3519.2	5141.8
571.9	514.6	2598.8
909.5	2363.6	4238.2
5222.3	5905.0	7971.2
282.3	279.6	416.0
205.7	235.7	141.3
4799.9	3971.5	2289.5
2484.4	3249.9	2166.2
5570.2	4647.7	4036.8
5675.7	5515.5	5117.9
149.7	293.8	121.8
7162.8	5698.6	5128.3
3971.2	3981.3	2027.0
112.4	250.9	158.9
7473.7	8048.3	9324.7
3915.7	5244.0	4550.4
2512.3	2301.7	1558.0
3638.0	3978.7	3738.3
6553.3	7822.1	8368.8
493.4	299.5	47.7
5293.3	4693.0	3557.9
4725.7	3194.5	3390.2
4640.1	3732.4	4767.2
6007.2	6564.7	6546.0
6041.0	6259.6	5662.2
5183.4	6371.7	6572.3
3912.8	4060.3	3364.3
7239.7	9215.3	8051.8
3919.6	5657.3	4853.3
7245.4	7660.3	6986.0
4655.9	5570.4	3011.9
3278.7	2906.2	2250.3
3716.2	4017.5	4616.1
1712.0	1394.7	619.6
2653.2	1924.9	817.8
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FJ959515.1 gg_id:550936 bottlenose dolphin upper respiratory tract blowhole clone D896_106 FJ9595
NZ_ACET01000043.1 gg_id:470433 Fusobacterium gonidiaformans str. ATCC 25563 NZ_AC
FJ471649.1 gg_id:529903 Fusobacterium nucleatum str. ChDC F290 FJ4716
GQ091870.1 gg_id:449592 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ091
GQ113263.1 gg_id:375228 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor GQ113
FJ978721.1 gg_id:408384 feces clone CL_F_417 FJ9787
EU774026.1 gg_id:308389 Cheetah feces clone CE3_aai08d02 EU774
EF089177.1 gg_id:185041 Fusobacterium nucleatum str. Ulm 14 EF0891
FJ978724.1 gg_id:381867 feces clone CL_F_422 FJ9787
FJ978541.1 gg_id:427042 feces clone CL_F_080 FJ9785
FJ471639.2 gg_id:514347 Fusobacterium nucleatum str. ChDC F113 FJ4716
GQ088072.1 gg_id:459200 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ088
FJ471673.1 gg_id:520375 Fusobacterium periodonticum str. ChDC F334 FJ4716
DQ440563.1 gg_id:156573 Fusobacterium nucleatum str. Ulm DQ440
GQ087757.1 gg_id:395408 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ087
GQ014795.1 gg_id:494871 Topographical and Temporal Human Skin Microbiome skin palm clone nbw764c09c1 GQ014
FJ978525.1 gg_id:468118 feces clone CL_F_056 FJ9785
CP001685.1 gg_id:529857 Leptotrichia buccalis C-1013-b str. DSM 1135 CP001
FJ577251.2 gg_id:568972 Leptotrichia hofstadii str. F0254 FJ5772
AF206305.1 gg_id:71541 Leptotrichia trevisanii AF206
AY134896.1 gg_id:59574 oral periodontitis clone EX103 AY1348
AM420035.1 gg_id:241454 Noma subgingival plaque clone 201G10(oral) AM420
CP001685.1 gg_id:529859 Leptotrichia buccalis C-1013-b str. DSM 1135 CP001
GQ129984.1 gg_id:399980 Genetic inventory 'JPL-SAF' during MSL mission spacecraft assembly clean room floc GQ129
AY207053.1 gg_id:83573 human mouth clone P2PB_51 AY207
AF432138.1 gg_id:31235 tongue dorsum scrapings clone FP036 AF432
GQ000682.1 gg_id:469247 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ000
GQ000882.1 gg_id:469447 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ000
AY349385.1 gg_id:92131 human oral cavity clone GT020 AY3493
FJ976353.1 gg_id:578509 Interindividual healthy human oral microbiota mouth clone 12BB57 FJ9763
AM420193.1 gg_id:258023 Noma subgingival plaque clone 502D06(oral) AM420
GQ016176.1 gg_id:493491 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw GQ016
FJ577259.2 gg_id:566658 Leptotrichia goodfellowii str. F0264 FJ5772
AY029803.1 gg_id:70629 Leptotrichia hofstadii str. LB23 AY0298
AF287814.1 gg_id:38061 human subgingival plaque clone F138 AF2878
GQ032449.1 gg_id:403062 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ032
AF385571.1 gg_id:70038 crevicular epithelial cells clone EI013 AF3855
GQ016227.1 gg_id:493440 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw GQ016
EU137409.1 gg_id:267538 Bartonella-positive fleas: and assembly patterns Oropsylla hirsuta (prairie dog flea) C EU1374
NZ_ACVB02000014.1 gg_id:484462 Leptotrichia hofstadii str. F0254 NZ_AC
AM420110.1 gg_id:256867 Noma subgingival plaque clone 303F08(oral) AM420

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713.7	3856.9	5301.3	6531.0	1882.6	4680.0	3367.3	5581.4	3763.1	209.3	6126.9
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906.6	4874.4	5715.2	6928.3	3178.0	5149.7	5062.4	5925.9	3911.1	2498.3	5995.0
702.7	4215.2	5318.0	6985.2	2328.1	5317.9	4336.4	6226.6	3722.0	626.5	6406.0
8496.1	6057.4	6760.0	7916.4	4749.1	6629.3	5837.6	6430.7	7602.5	5525.2	8613.5
166.6	1910.8	1110.0	855.8	876.5	1023.4	1608.0	1269.9	842.4	1578.2	1116.2
408.9	3481.7	3925.4	4153.0	2922.7	3208.9	4101.9	3805.3	3126.8	2201.9	3981.3
881.7	4323.7	4345.2	4004.4	2272.1	4090.7	3655.3	4245.9	3796.2	1531.5	4676.6
288.9	1944.5	2529.9	3241.1	1275.4	2593.9	2121.9	2721.6	1755.4	475.7	2572.5
513.1	5612.2	6073.6	6876.3	4210.0	5040.5	5849.6	6270.9	4540.6	3227.6	6165.6
1854.4	4247.5	4765.4	5453.8	2919.7	4226.5	4812.0	5707.0	3415.0	1631.5	4837.0
3506.3	3798.5	3631.4	4239.9	2773.3	3703.4	3269.7	4023.2	3109.2	2204.3	3941.3
3975.1	4770.2	5151.7	5934.7	3858.0	4729.8	5133.1	5328.5	4157.4	2421.0	5933.1
616.3	3383.7	3747.6	4411.9	3300.7	3568.1	4782.6	3802.4	2810.3	2479.9	3470.3
855.9	3658.2	3897.1	4315.4	3463.5	3577.0	4811.0	4129.0	3531.1	2432.7	5339.9
54.3	54.4	92.0	59.1	52.0	51.9	47.4	51.8	62.7	31.5	41.2
4384.4	3144.1	3382.1	3382.5	3336.2	3196.4	4040.8	3123.0	3369.0	3087.0	3318.2
3880.8	3841.5	4515.7	4627.5	3315.6	4526.1	4262.0	4853.8	2582.3	3819.4	3904.9
3118.3	5937.3	6053.0	6270.8	5656.6	5775.5	6259.5	5962.1	4007.9	5429.8	5654.4
97.4	1049.7	1128.9	1190.4	871.1	942.9	1322.7	1234.7	711.5	561.9	1039.0
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336.3	3675.2	4951.2	4854.1	5095.2	3942.2	5111.2	4369.9	2524.9	1342.3	4535.3
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11922.6	6151.9	4739.9	6179.5	5395.4	5413.0	5151.8	6048.7	5733.5	4298.9	8095.9
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s__Leptotrichia amnionii	71971
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GQ070510.1 gg_id:399174 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw: GQ070
GQ111263.1 gg_id:375876 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ111
GQ032233.1 gg_id:381314 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ032
GQ422731.1 gg_id:555711 Leptotrichia sp. oral taxon 225 str. FEA2 GQ422
GQ000663.1 gg_id:469228 Topographical and Temporal Human Skin Microbiome skin interdigital web space cl GQ000
GU086183.1 gg_id:593385 Leptotrichia shahii str. PW1036 GU086
NR_026243.1 gg_id:557791 Propionigenium maris str. 10succ1; DSM 9537 NR_02
EU236316.1 gg_id:296908 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg1bD2 EU236
X54275.1 gg_id:11301 Propionigenium modestum X54275
AJ877255.1 gg_id:112138 Ilyobacter psychrophilus str. FQ50 AJ8772
AJ307980.1 gg_id:52873 Ilyobacter insuetus str. DSM 6831 T AJ3079
Y16799.1 gg_id:42042 Propionigenium maris str. DSL-1 Y16799
FJ264772.1 gg_id:324952 Manganese and Iron Dependent Anaerobic Oxidation Methane methane seep sedim FJ2647
FJ717186.1 gg_id:510621 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United King FJ7171
FJ717188.1 gg_id:558150 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United King FJ7171
EU052253.1 gg_id:240997 degradation kinetics and current efficiency cells supplied anode microbial fuel cell fe EU052
AY770718.1 gg_id:110394 Fusobacteria sea urchin Paracentrotus lividus clone PlS49 AY770
CP001739.1 gg_id:518403 Sebaldella termitidis str. ATCC 33386 CP001
EF608534.1 gg_id:228694 predatory Poecilus chalcites their response lab rearing and antibiotic treatment diges EF6085
EF218611.1 gg_id:212738 Leptotrichia amnionii str. CCUG 51847 EF2186
AY078425.1 gg_id:29566 Leptotrichia amnionii str. AMN-1 AY0784
AJ344093.1 gg_id:58542 Sneathia sanguinegens str. CCUG 41628T AJ3440
AB330759.1 gg_id:236558 Streptobacillus moniliformis str. KWG2 AB330
GQ072215.1 gg_id:447942 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw193e1 GQ072
GQ850557.1 gg_id:591820 surface water northern Bering Sea clone u114 GQ850
FJ456795.1 gg_id:545014 microbiota two Antarctic notothenioid fish species intestinal flora clone A007_NCI FJ4567
DQ206413.1 gg_id:139839 microbial mediates arsenate reduction soda lake water clone ML-AsS-15 DQ206
EU044321.1 gg_id:256629 uences structure fosters richness subtropical Altamaha Ohopee River Valley inland d EU044
EF019213.1 gg_id:213629 aspen rhizosphere clone Amb_16S_1909 EF0192
DQ490008.1 gg_id:158907 Microbial Great Boiling Spring sediment hot spring; temperature 80 C clone GBS_L1_ DQ490
EU134698.1 gg_id:255244 tallgrass prarie soil clone FFCH14117 EU134
FM873495.1 gg_id:363705 occupant source house floor dust clone FD04E09 FM873
EF018217.1 gg_id:216704 aspen rhizosphere clone Amb_16S_564 EF0182
EF540422.1 gg_id:220442 oil-shale semi-coke solid waste clone MK51 EF5404
GQ113134.1 gg_id:433730 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw675f0 GQ113
EU283562.1 gg_id:278836 Model Early Earth Harbors Deeply Divergent Divisions Anderson Lake clone A1853 EU283
FJ444672.1 gg_id:591271 Cotton Rhizosphere cotton rhizosphere clone 2y-23 FJ4446
AB240260.1 gg_id:142399 microbial structure rhizosphere Phragmites bulk soil reed bed reactor laboratory clo AB240
DQ640655.1 gg_id:234041 full-scale EBPR sludge clone Skagenf3 DQ640
GQ090575.1 gg_id:440096 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw GQ090
AB234279.1 gg_id:146305 Biotransformation Polychlorinated Dioxins Microbial Dynamics Sediment Microcosm AB234

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177.0	2085.4	2696.8	2845.5	2496.6	2713.4	2997.2	2947.4	936.9	738.4	2007.2
675.2	3856.0	4218.1	4666.4	3931.6	4323.8	4616.9	4540.7	3077.8	1313.1	3675.5
4221.8	6347.3	8358.2	6992.2	5802.4	7277.1	6825.9	6478.4	5137.5	6411.1	9520.2
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2872.5	3314.4	3780.9	3973.5	3251.5	3741.1	3411.3	3843.4	2542.7	2947.2	3798.1
1438.8	5952.4	6762.2	7665.9	5186.0	7060.7	5258.8	6350.6	5870.0	4853.0	6443.7
5579.5	5987.0	7749.1	9444.0	4199.2	6781.2	5050.8	6169.4	4802.7	2888.0	7561.8
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2188.3	8458.0	8941.1	10304.5	5868.5	8659.5	7090.7	8837.4	7670.6	3239.5	9983.1
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425.6	2268.5	2392.8	3086.3	1435.2	2693.1	1842.2	2582.0	2592.0	618.2	3462.2
39.8	19.4	28.1	23.8	21.3	16.2	25.2	23.5	21.4	17.4	25.6
96.3	940.2	1574.1	1940.6	235.9	1246.7	573.0	1656.5	700.1	78.4	1504.7
4122.2	4298.0	4367.8	4629.1	4337.9	4777.3	4785.7	4755.1	4524.2	4545.2	5754.4
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2074.7	6450.2	5853.3	6614.8	6699.5	6279.8	9897.7	5656.5	6488.8	5412.4	6462.8
770.0	1270.9	1262.7	1245.7	1389.9	1308.2	1619.6	1415.2	460.3	1049.1	764.5
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8218.2	4906.6	3891.0	4248.9	4407.3	3785.6	5061.8	3649.8	4917.2	4615.1	5676.7
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2761.6	8007.6	8175.2	8555.8	8393.3	7859.6	8760.2	7685.8	7628.8	6538.3	8193.2
150.6	1449.7	2047.7	2246.8	2099.4	1822.1	2134.3	1998.6	1199.9	523.2	1424.6
39.8	88.9	43.1	38.5	76.0	37.9	45.9	28.2	25.9	18.8	99.8
2005.6	1362.8	1005.2	893.1	2690.9	1259.2	2166.3	1401.3	782.0	360.4	801.5
240.5	1139.3	1544.3	1841.7	3248.6	1548.4	2896.0	2112.1	760.0	537.7	1204.7
145.1	2878.0	3495.3	3898.5	5017.8	3291.5	4859.7	3941.5	1335.9	663.7	2148.4
44.3	499.2	264.5	457.9	2635.3	500.3	1340.6	468.6	88.9	34.9	227.1

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2006.4	2372.6	3114.7
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6989.2	7720.2	7876.3
3203.7	4864.9	4174.2
6393.6	5028.0	4213.6
5216.5	3827.9	3262.5
3814.6	4202.2	2603.7
2658.4	3373.5	1976.7
5256.2	4033.4	3456.0
4981.2	5030.4	4929.5
3346.1	2665.2	2411.9
5422.9	6049.7	5324.4
7779.1	6696.3	3916.0
2847.9	3701.7	1961.5
5594.1	4172.3	3394.3
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852.1	932.4	973.3
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3945.3	4064.7	4474.1
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7628.9	8577.6	9294.3
1666.8	2568.0	2870.5
29.8	49.9	50.8
938.3	1292.2	2400.0
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3094.6	3811.3	4329.3
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AF432648.1 gg_id:104785 lodgepole pine rhizosphere soil British Columbia Ministry Forests Long-Term Soil Pro AF4326
EF157193.1 gg_id:243247 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon EF1571
EF018812.1 gg_id:214676 aspen rhizosphere clone Amb_16S_1283 EF0188
FJ478758.1 gg_id:512313 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4787
EF203205.1 gg_id:207957 phylotypes sediments Lake Kastoria Greece sediment clone Kas174B EF2032
AF432635.1 gg_id:99232 lodgepole pine rhizosphere soil British Columbia Ministry Forests Long-Term Soil Prod AF4326
DQ067025.1 gg_id:133200 Lake Washington sediment clone pLW-82 DQ067
FJ536876.1 gg_id:587747 Linking performance microbiology biofilters treating dimethyl sulphide presence and FJ5368
DQ520169.1 gg_id:160270 shal China sequences hypertrophic freshwater lake clone ML-5-110.2 DQ520
EF018312.1 gg_id:207648 aspen rhizosphere clone Amb_16S_675 EF0183
AF545649.1 gg_id:72899 shortgrass steppe soil (Stunner series fine loamy over sandy Ustic Calciargid) under Bc AF5456
AY218696.1 gg_id:81623 penguin droppings sediments clone KD8-87 AY2186
AB426207.1 gg_id:264973 -situ identification study benzene-degrading s under methanogenic condition anaerc AB4262
EU979110.1 gg_id:336425 Effects intercropping Rhizobium inoculation on microbial biomass and rhizosphere b EU9791
DQ906809.1 gg_id:239203 Oman subsurface soil clone 5B-5 DQ906
EF516323.1 gg_id:225306 grassland soil clone FCPT668 EF5163
EF019647.1 gg_id:215970 aspen rhizosphere clone Elev_16S_798 EF0196
DQ067020.1 gg_id:129424 Lake Washington sediment clone pLW-79 DQ067
FJ479207.1 gg_id:588566 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4792
EF019081.1 gg_id:204271 aspen rhizosphere clone Amb_16S_1670 EF0190
FJ152750.1 gg_id:339480 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX5A_ FJ1527
EU044086.1 gg_id:237353 fluences structure fosters richness subtropical Altamaha Ohopee River Valley inland EU0440
EU193066.1 gg_id:360943 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo EU1930
AM934748.1 gg_id:549433 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM934
AY921939.1 gg_id:114406 farm soil clone AKYG583 AY9219
EU881263.1 gg_id:329628 (long-term grazing and burned annual) Karst region serious disturbance field soil clor EU8812
AY922055.1 gg_id:114310 farm soil clone AKYG703 AY9220
AY921712.1 gg_id:112987 farm soil clone AKYG963 AY9217
AY921894.1 gg_id:114101 farm soil clone AKYG1555 AY9218
EF612383.1 gg_id:237047 historic semiarid lead-zinc mine tailings site soil clone OS-C17 EF6123
AY395378.1 gg_id:103904 pasture soil clone EB1059 AY3953
AY192277.1 gg_id:79951 Rocky Mountain alpine soil clone W2a-1F AY1922
GU359099.1 gg_id:518957 rhizosphere soil peanut clone 2G11 GU359
DQ906907.1 gg_id:253096 Oman subsurface soil clone 12B-7 DQ906
EU801865.1 gg_id:314599 It's all ranking aquatic Chesapeake Bay MD clone 3C003242 EU8018
FJ746162.1 gg_id:512463 Microbial oligotrophic marine sediments: South Pacific Gyre ocean sediment 5306 m FJ7461
EF020040.1 gg_id:211950 aspen rhizosphere clone Elev_16S_1437 EF0200
FJ230809.1 gg_id:325203 Microclimate and limits photosynthesis cyanobacteria Northern Australia hypolithic s FJ2308
AB257644.1 gg_id:259192 Microbial few millimeters be surface dolomite rock 'Val Piora' Alps 1965 meters abo AB2576
AY921918.1 gg_id:113407 farm soil clone AKYG1585 AY9219
EU283563.1 gg_id:279650 Model Early Earth Harbors Deeply Divergent Divisions Anderson Lake clone A1336 EU2835

5238.5	2439.8	2499.4	2945.5	3144.0	2533.5	2980.3	2349.9	2276.5	776.2	3632.8
53.2	2014.1	1805.8	2813.9	4510.1	2043.0	3517.5	2434.2	915.5	205.7	1492.8
112.1	205.0	250.0	181.2	486.2	172.0	226.9	214.3	70.2	63.9	192.3
12589.1	4213.6	5197.5	5819.8	6138.8	4445.5	7700.8	5069.9	3154.0	1812.8	5843.6
3316.2	2501.9	2395.8	2760.9	4840.1	2798.6	5707.0	3177.6	1644.7	1373.8	2192.9
2086.6	3063.9	2636.3	3003.7	4753.5	2610.4	4275.5	3024.1	1823.5	1051.9	2452.0
54.0	2736.2	3258.0	3754.0	4039.3	2206.6	4345.0	2292.7	616.9	344.0	1204.9
46.3	216.5	128.4	193.1	426.9	95.5	309.0	204.7	84.9	71.7	89.3
55.3	593.0	552.0	1538.3	2765.8	852.3	2270.2	999.8	392.2	59.3	624.3
5144.4	4140.4	4691.9	4547.6	5217.9	3975.7	5531.8	4221.7	5279.7	3172.7	4775.6
43.3	54.7	57.3	84.9	139.0	40.7	122.5	35.2	33.5	24.9	40.8
48.8	333.7	316.2	764.3	720.3	328.0	468.8	429.1	174.3	54.4	136.7
584.5	3567.7	4053.8	4943.7	5637.7	4112.6	6007.2	4137.2	2493.5	961.9	3005.4
248.9	1642.6	1722.2	2144.5	4368.7	1837.8	5321.2	2019.7	543.2	377.3	826.2
4050.1	2845.6	3187.9	3157.9	2924.9	1347.8	3722.7	2327.0	2140.9	2023.5	3303.3
41.0	682.5	659.1	742.2	1351.9	718.2	1268.5	924.1	224.4	129.1	504.2
11088.8	4561.8	6031.8	4967.5	7511.0	5112.6	8013.2	5047.7	5938.6	4723.3	4912.7
58.1	1262.4	1507.6	3004.2	3138.4	1166.9	4259.1	1512.5	292.8	450.0	255.1
512.9	3044.9	2895.0	3644.2	6193.8	3121.7	4937.8	3085.5	2011.7	1025.4	2038.2
2287.3	795.1	986.6	987.1	1446.6	1098.7	1220.1	1000.0	397.6	182.6	505.0
536.6	853.0	703.3	1135.2	2989.1	837.2	1721.0	894.6	222.9	301.4	375.3
9862.9	4635.8	5117.9	6126.0	6954.0	4819.3	7247.4	5606.7	3861.4	1801.4	4497.5
3338.1	4317.5	4519.7	5846.4	8061.9	4623.1	8550.8	5455.5	2841.6	2428.7	4215.1
3253.7	9080.9	11674.1	9028.9	8621.1	8558.5	9849.5	9351.6	10079.2	7076.3	12724.9
45.9	249.8	349.2	386.8	370.5	304.3	439.4	396.8	101.3	89.5	234.2
43.7	1511.5	1780.5	2597.0	2748.1	1764.8	3395.1	3159.3	994.2	301.6	1520.5
3317.3	3767.8	4305.1	4522.5	5439.3	4093.7	5433.9	4646.7	2464.5	2871.5	2905.7
1199.5	5472.8	6332.8	6168.6	8606.0	5459.8	8275.0	5959.9	4653.5	3442.0	5881.0
36.5	57.2	71.2	60.7	139.7	49.9	99.7	75.6	24.0	19.0	38.9
9844.9	7793.4	8432.0	8381.6	8705.8	7676.6	8367.0	8899.2	6453.2	6038.3	9763.7
8851.0	5358.9	4627.2	6423.8	8100.1	5328.4	7509.3	5914.9	4550.5	3125.8	4870.8
1840.3	4929.1	4349.0	5090.2	7391.0	4748.9	7206.6	4806.8	3842.4	2096.2	4137.5
125.7	4520.5	3655.6	4486.4	5145.9	3763.7	5537.5	4324.8	5537.0	2055.6	3232.7
1122.5	6603.8	4897.3	4405.9	6179.6	5492.2	6127.5	4106.5	5205.0	5134.6	3228.7
77.6	573.2	696.0	834.3	1956.7	576.0	1433.6	450.9	144.6	151.9	220.3
1001.7	3483.7	3679.2	3833.0	5819.8	3889.1	6139.4	3886.3	3212.1	2449.3	2530.8
213.9	1666.8	2556.1	2112.6	3697.0	2160.6	3146.7	2474.4	1047.0	576.6	2968.9
1079.8	3927.0	4827.1	4150.6	6110.9	4644.0	6341.7	5714.6	3365.9	2179.7	4074.6
8600.7	2853.8	2467.8	3248.0	4994.4	2978.4	4828.8	3260.4	1749.4	1314.7	2295.0
77.2	615.6	766.8	1098.7	2046.4	815.7	1524.8	832.8	371.6	424.3	461.1
5096.7	5482.2	5642.4	5248.4	7642.3	5297.0	7323.5	5191.8	4307.9	3914.7	6918.2

2188.0	3059.5	2937.8
2038.4	1479.1	2698.9
115.8	119.7	625.4
4989.5	5001.7	6450.9
2617.2	2810.3	2725.9
2649.4	2693.7	4107.1
1902.4	2358.0	4624.6
111.6	283.7	306.6
939.9	244.8	206.9
3744.2	4509.0	5313.5
34.0	49.4	40.8
377.3	329.2	668.6
2981.4	4654.4	7046.4
1644.3	1379.6	3786.8
2264.0	3188.4	3686.3
549.0	797.3	728.1
5119.7	4652.6	5972.5
1614.3	712.8	4653.9
2700.6	3011.6	4414.5
659.7	1383.6	2288.8
791.4	1112.7	1796.9
4783.6	5919.0	6474.9
5310.7	4941.5	6867.6
7355.9	7674.0	11564.9
294.9	565.5	448.0
2033.1	2074.2	3787.6
3957.5	4505.3	5476.2
4689.5	5793.2	7096.0
59.5	58.8	121.3
7502.9	8135.3	7364.1
5608.6	5958.7	7136.3
5196.1	4869.3	6876.5
3633.7	4168.5	5778.2
3951.6	4266.4	4991.6
441.3	418.4	1876.3
3643.6	3810.4	5083.3
2083.2	1799.4	3061.8
4728.8	4765.9	5463.0
3131.9	2823.8	4234.5
899.6	1156.4	1378.8
4818.6	5916.0	6909.3

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EU134840.1 gg_id:249299 tallgrass prarie soil clone FFCH11609 EU1348
AY913252.1 gg_id:112876 forest soil clone DUNssu032 (+2C) (OTU#201) AY9132
AB257643.1 gg_id:265561 Microbial few millimeters be surface dolomite rock 'Val Piora' Alps 1965 meters abo AB2576
EU652636.1 gg_id:277713 Seasonal variation microbial Yel Sea sediment clone D8S-116 EU6526
EU048610.1 gg_id:254529 Microbial surface marine sediment Xisha Trough South China Sea clone MD2902-B3 EU0486
AY922130.1 gg_id:114403 farm soil clone AKYH466 AY9221
AY673312.1 gg_id:110882 Gemmatimonadetes Ellin7146 AY6733
FJ479068.1 gg_id:560811 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4790
AY922123.1 gg_id:113603 farm soil clone AKYH1517 AY9221
EF020045.1 gg_id:207989 aspen rhizosphere clone Elev_16S_1446 EF0200
AY921994.1 gg_id:112986 farm soil clone AKYG1838 AY9219
GQ396903.1 gg_id:557467 Functional unvegetated perhumid recently-deglaciated soils do not correlate shifts s GQ396
AY921912.1 gg_id:114146 farm soil clone AKYG1614 AY9219
EU676443.1 gg_id:289924 rhizosphere pioneer plants (Bahia xylopoda and Viguiera linearis) growing on metals- EU6764
EF018145.1 gg_id:208048 aspen rhizosphere clone Amb_16S_479 EF0181
GU205280.1 gg_id:516178 unusual Microbial Venezuelan Tepui (Orthoquartzite) Cave: Dominance Chloroflexal GU205
FJ152768.1 gg_id:335807 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX5A_ FJ1527
AY289480.1 gg_id:90194 soil clone ABS-650 AY2894
GQ113661.1 gg_id:384470 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ113
EF516935.1 gg_id:219517 grassland soil clone FCPN548 EF5169
EU193059.1 gg_id:360637 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo EU1930
DQ532275.1 gg_id:168856 Geographical Variation Microbial Burden and Spacecraft Assembly Johnson Space C DQ532
EF688378.1 gg_id:250371 soil clone F6-84 EF6883
AY921776.1 gg_id:113308 farm soil clone AKYG961 AY9217
EU234231.1 gg_id:242383 river and un techniques downstream Wang Yang River receiving penicillin G producti EU2342
EU881123.1 gg_id:308062 Karst region primary forest soil clone KPF200711-086 EU8811
DQ067019.1 gg_id:128235 Lake Washington sediment clone pLW-78 DQ067
EU134880.1 gg_id:249280 tallgrass prarie soil clone FFCH2651 EU1348
DQ833499.1 gg_id:166488 detected analyses depth sediment Guanting Reservoir clone 69-18 DQ833
AY921771.1 gg_id:113042 farm soil clone AKYG666 AY9217
EF492900.1 gg_id:246196 Iron-manganese Nodule and Its Surrounding Soil soil around iron-manganese nodule EF4929
EU134828.1 gg_id:249948 tallgrass prarie soil clone FFCH6230 EU1348
EU861901.1 gg_id:325238 effects chronic fertilization on alpine tundra microbial implications carbon and cyclin EU8619
FJ755752.1 gg_id:565312 vertical archaeal water and Lake Taihu sediment clone LT-SB-B6 FJ7557
AY218678.1 gg_id:82251 penguin droppings sediments clone KD8-105 AY2186
AY921899.1 gg_id:114389 farm soil clone AKYG781 AY9218
DQ906808.1 gg_id:243477 Oman subsurface soil clone 5B-4 DQ906
GQ263232.1 gg_id:590444 Structure Simulated Level Waste Site simulated level waste site clone F3_42X GQ263
FJ444711.1 gg_id:511297 Cotton Rhizosphere cotton rhizosphere clone 3y-46 FJ4447
GQ263030.1 gg_id:576743 Structure Simulated Level Waste Site simulated level waste site clone F2_153X GQ263
EF174264.1 gg_id:197816 direct activated 4th maturation stage sludge clone F37-814 EF1742

239.0	772.3	763.5	903.3	1333.3	1053.2	1507.7	764.0	386.3	189.4	559.9
64.9	113.8	144.8	141.5	237.5	134.3	169.1	190.4	99.0	58.5	124.8
3375.0	6255.4	6345.8	6800.6	7307.7	5850.8	7808.9	5515.1	6980.7	5745.0	6920.0
2338.2	8457.0	9062.8	9400.2	11275.6	7940.1	10199.5	8089.5	7447.6	4262.2	8123.9
4556.7	3705.6	3653.5	4208.6	4395.7	3532.1	5288.3	3212.9	2442.6	2259.2	3378.5
12165.3	6916.2	6479.1	7539.5	9244.1	6850.2	8960.5	6844.5	6901.6	5346.3	6427.8
42.4	217.6	141.5	160.4	332.9	211.8	377.6	130.4	44.8	143.4	61.8
11521.9	5701.6	4891.7	5425.8	5950.1	5247.8	5924.6	5133.5	5801.4	4871.4	6285.8
78.3	1877.9	2109.9	1992.3	3247.4	1913.5	3667.4	2047.3	1133.9	1145.4	1229.0
75.3	1375.6	1008.5	1230.4	1836.5	1312.6	1446.1	847.8	325.6	129.6	427.8
39.3	501.2	546.4	571.5	721.5	486.3	500.8	499.2	128.0	50.7	209.5
65.8	1728.5	2164.3	2554.5	3982.8	1792.8	3276.7	2023.4	672.0	256.2	571.7
66.9	410.4	373.0	353.4	637.7	423.5	673.7	416.7	121.9	115.0	283.2
4855.5	1504.2	1463.9	2203.8	3644.3	1562.7	2848.1	2091.7	1271.9	274.7	824.6
957.1	852.9	1016.1	946.0	1566.1	990.9	1717.1	908.6	1173.2	840.0	567.0
640.2	3973.2	2923.6	4113.0	6406.1	4021.3	6436.7	4094.0	3457.1	2033.4	3248.4
5099.0	1284.8	1354.9	1568.5	3332.2	1458.0	2856.0	1577.0	589.7	1315.9	1028.0
6534.8	3581.4	2630.2	2955.3	4493.2	3105.8	4356.0	3487.9	2824.2	1984.4	2245.1
17020.2	6803.4	6384.0	6851.7	8552.9	6809.3	7860.9	7487.3	6781.7	5932.2	5653.0
34.5	137.9	193.1	234.9	603.1	143.8	690.3	158.3	47.5	29.6	53.4
2996.5	3397.8	3025.0	3629.5	4715.3	3085.6	4834.5	2810.4	4772.7	3333.6	2634.6
8591.7	6495.9	6110.7	6816.9	8008.1	6353.1	7947.4	7150.1	5932.9	4557.4	5075.4
10469.5	4770.7	4872.6	6482.5	7169.8	4939.5	7074.4	5148.2	3141.5	2139.0	3695.9
5668.6	5692.6	3981.4	3364.0	4507.8	4480.8	4656.9	2912.6	6380.6	3853.2	2802.1
620.0	9846.3	11421.4	11424.6	12619.7	9858.4	13159.4	9511.9	8124.3	8130.3	10718.6
3545.9	3888.1	5179.0	4868.9	5090.9	4106.1	5168.4	6100.9	3284.0	1270.0	5820.8
45.8	49.5	45.2	45.5	420.0	38.1	421.1	39.0	35.9	26.0	98.1
4569.6	5695.2	6081.0	6370.6	10375.8	5627.3	8286.8	5041.2	6430.7	4299.3	6256.6
149.7	385.5	351.3	435.7	390.8	358.3	418.5	344.0	184.5	180.8	252.3
811.8	1983.9	1817.3	1902.4	2471.2	1735.3	2900.7	1749.2	1840.4	1198.1	2273.6
4372.2	4294.5	5201.8	5842.1	6310.4	5394.3	8101.6	6508.5	4767.9	3512.0	8597.9
14621.6	6606.9	6447.8	7460.4	8564.6	7138.3	9612.4	7673.0	5200.5	3545.9	6110.8
2100.7	5261.6	6807.4	7091.2	7032.8	6124.4	6932.6	6781.3	5756.5	5010.6	6935.4
37.8	272.3	209.7	196.1	877.5	162.0	1406.7	538.8	81.8	72.3	194.0
1238.6	2932.5	3138.7	3188.9	4042.6	3272.1	3732.1	2727.3	1881.4	2451.7	4904.1
35.3	1426.0	1426.4	1409.3	1823.8	1719.7	1807.8	2045.9	2661.4	1340.0	1135.3
489.9	1657.4	2101.7	2177.8	2989.6	1805.8	3082.7	3439.0	762.2	527.1	2358.2
34483.6	11864.8	11223.8	12508.3	13075.7	11408.8	13396.5	11740.0	15567.8	11167.6	15529.1
5771.3	8017.2	8203.2	9323.2	10296.6	8085.3	11152.0	8109.3	7602.0	5157.2	8410.7
2252.3	6462.8	6599.9	7320.7	8071.4	6936.1	8377.1	6464.4	5344.7	4505.5	6393.3
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6840.0	6675.8	6089.2
293.8	204.8	249.5
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2055.5	1695.0	1321.2
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EU037358.2 gg_id:277360 structure landfill sediments receiving long-term augmentations wastes chromium co EU037
GQ263154.1 gg_id:579054 Structure Simulated Level Waste Site simulated level waste site clone F3_100X GQ263
GQ397033.1 gg_id:586289 Functional unvegetated perhumid recently-deglaciated soils do not correlate shifts s GQ397
GQ262951.1 gg_id:563031 Structure Simulated Level Waste Site simulated level waste site clone F1_87X2 GQ262
EU979063.1 gg_id:344838 Effects intercropping Rhizobium inoculation on microbial biomass and rhizosphere b EU979
EF157266.1 gg_id:248780 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon EF1572
FJ152642.1 gg_id:312327 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX1A_ FJ1526
GQ263158.1 gg_id:553767 Structure Simulated Level Waste Site simulated level waste site clone F3_106X GQ263
AM935432.1 gg_id:550147 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM935
GQ262827.1 gg_id:584041 Structure Simulated Level Waste Site simulated level waste site clone F1_15X2 GQ262
GQ263089.1 gg_id:593457 Structure Simulated Level Waste Site simulated level waste site clone F2_39X GQ263
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GQ262961.1 gg_id:538070 Structure Simulated Level Waste Site simulated level waste site clone F1_92X GQ262
FJ425592.1 gg_id:363208 communnities healthy and diseased colonies Caribbean coral Montastrea faveolata cl FJ4255
DQ300602.1 gg_id:147735 microbial ocean's interior amplicon single fosmid library pool 130m depth HOT static DQ300
GQ346931.1 gg_id:591890 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ346
DQ295242.1 gg_id:148154 Fragments Six Marine Planktonic Antarctic sea water clone Ant4D5 DQ295
AJ567595.1 gg_id:89477 deep-sea sediment clone MBAE42 AJ5675
EU287180.1 gg_id:251953 Pacific arctic surface sediment clone P13-87 EU287
EU374078.1 gg_id:276624 southern Cretan margin (eastern Mediterranean Sea) canyon and slope sediment clc EU374
AM997489.1 gg_id:548429 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A AM997
FJ205357.1 gg_id:512804 Prokaryotic deep-sea hydrothermal region East Lau Spreading Centre deep marine se FJ2053
AM935228.1 gg_id:574770 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM935
EU652634.1 gg_id:277772 Seasonal variation microbial Yel Sea sediment clone A8S-129 EU652
FJ746291.1 gg_id:572935 Microbial oligotrophic marine sediments: South Pacific Gyre ocean sediment 5306 m FJ7462
AY592149.1 gg_id:106730 marine ANAMMOX sediment clone AY592149 AY592
EU287420.1 gg_id:244505 Pacific arctic surface sediment clone S26-120 EU287
AF186415.1 gg_id:11593 sponge symbiont clone PAUC43f AF186
FJ024313.1 gg_id:359471 Prokaryotic and their role biogeochemical cycling marine basalts basalt Juan de Fuca I FJ0243
AB294923.1 gg_id:226129 -dependent & analyses hydrothermal system off Taketomi Island Japan microbial ma AB294
AF286033.1 gg_id:37339 saltmarsh clone LCP-68 AF286
EU979085.1 gg_id:308997 Effects intercropping Rhizobium inoculation on microbial biomass and rhizosphere b EU979
FJ444650.1 gg_id:560438 Cotton Rhizosphere cotton rhizosphere clone 2h-20 FJ4446
EF540395.1 gg_id:225607 oil-shale semi-coke solid waste clone 1_11MK EF5403
EU134894.1 gg_id:248455 tallgrass prarie soil clone FFCH6442 EU1348
EU134893.1 gg_id:239710 tallgrass prarie soil clone FFCH12021 EU1348
EU193063.1 gg_id:369973 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo EU193
AY921663.1 gg_id:113478 farm soil clone AKYH1024 AY9216
AY493976.1 gg_id:136870 Fingerprinting aggregates soil clone 5 AY4939
DQ431899.1 gg_id:208663 microorganisms catalyzing nitrogen removal and organic matter metabolism perme DQ431
EU491861.1 gg_id:270789 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU4918

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2065.9	6923.4	6287.5	5409.5	7003.6	7279.9	7236.1	5248.0	6681.9	5035.1	4713.9
19544.1	10185.6	10671.4	11265.9	11818.4	10437.5	12660.4	10993.8	16754.9	12122.5	13634.8
15276.7	10904.8	11388.0	13233.1	12412.0	10626.4	14512.1	11357.8	14461.1	10634.3	13702.4
3844.3	2899.3	3041.8	3415.6	4021.4	2926.3	3694.6	5432.1	2162.7	955.3	4855.7
1773.7	5754.7	4998.1	5700.9	6784.5	4940.3	7488.3	7870.4	5730.0	3813.3	7240.1
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5088.4	6062.3	7644.5	7514.9	8375.0	6461.3	9460.6	7289.2	7752.8	6913.3	5355.6
1155.4	6000.9	6579.7	7181.3	8796.0	6052.0	9283.6	7236.9	5634.7	3769.6	6170.0
1815.3	3735.7	3934.5	4734.4	5869.9	3897.7	6586.0	4811.8	3960.2	2434.4	4280.3
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3150.8	5423.0	6241.5	5734.0	5911.4	5155.5	6472.6	6714.8	5629.3	5235.1	6375.1
3898.3	11082.5	10656.9	12500.5	13349.8	10832.9	14278.1	10372.1	10399.9	6825.0	11418.0
564.7	4565.8	5173.1	5170.7	5484.2	4378.1	6183.9	4851.9	3405.6	1881.6	4399.4
1056.7	5985.6	5948.2	6482.0	5414.3	5699.7	7814.0	5869.2	5926.3	4777.4	5195.7
4476.6	3839.1	4865.4	5109.2	4448.0	4117.2	5354.9	4642.5	3425.9	2168.6	3208.9
616.1	6036.9	5730.7	7698.0	8045.5	7036.3	8782.4	6765.6	5299.1	4073.3	5761.7
1535.1	3686.8	3473.6	3296.2	3228.3	3360.2	3947.7	3356.3	3229.0	3059.4	4039.5
6502.8	8188.2	7213.8	5979.7	6875.1	7752.3	6820.6	5934.7	8321.6	8143.2	5441.8
768.7	2575.3	2510.1	2837.4	3246.7	2943.1	3283.6	2518.4	2258.1	2831.4	2390.0
9345.4	5896.1	5537.7	5535.5	5137.2	6000.0	5469.6	4998.4	7023.4	4967.0	7882.5
5612.1	5280.8	5287.2	6329.7	8305.0	5161.2	8569.2	5902.1	4099.2	4043.0	4269.3
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3101.2	9439.2	8704.6	9780.7	9759.5	9315.4	10767.4	7810.3	9484.2	5923.2	8374.6
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13831.3	9569.3	8215.5	8612.3	9648.9	9252.7	10192.5	8024.8	10549.7	6951.5	7725.5
11710.7	4234.4	4434.5	4300.6	4705.2	3636.9	4818.2	4085.8	4571.0	3887.9	5142.3
215.8	2344.3	2747.9	2814.1	3115.3	2505.2	3978.3	2713.6	1819.6	1142.6	2039.9
11295.7	6519.7	5083.8	4054.2	4555.2	5719.1	4728.6	4493.7	6819.2	5012.0	3395.3
231.0	4497.6	4996.5	4519.7	4361.6	4256.1	5005.4	4466.1	2583.2	2366.8	4042.1
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608.2	537.9	1779.1
3654.1	3152.4	3866.4
4099.5	5260.4	4581.5
7946.9	8071.3	12832.8
178.7	169.2	384.3
2823.9	3392.1	4404.7
8058.6	9064.6	8740.8
3637.2	5306.7	4089.0
2554.3	3124.1	4005.2
4577.7	5246.0	5089.9
4010.1	3424.2	5923.6
6362.9	7331.6	8476.0

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FJ152644.1 gg_id:322198 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX1A_ FJ1526
EU134886.1 gg_id:254415 tallgrass prarie soil clone FFCH1365 EU1348
EU134854.1 gg_id:240326 tallgrass prarie soil clone FFCH14573 EU1348
AY921936.1 gg_id:113023 farm soil clone AKYG548 AY9219
AJ347028.1 gg_id:60181 sponge symbiont clone TK19 AJ3470
GU118643.1 gg_id:557462 Threatened Corals Provide Microbial Habitats clone Mfav_E13 GU118
GU118605.1 gg_id:565653 Threatened Corals Provide Microbial Habitats clone Mfav_L08 GU118
GU118693.1 gg_id:544625 Threatened Corals Provide Microbial Habitats clone Mfav_D05 GU118
GU118648.1 gg_id:586196 Threatened Corals Provide Microbial Habitats clone Mfav_H20 GU118
GQ095375.1 gg_id:443417 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw4 GQ095
EF516463.1 gg_id:218620 grassland soil clone FCPU694 EF5164
EF516718.1 gg_id:217803 grassland soil clone FCPU461 EF5167
EU289488.1 gg_id:254895 metagenomic approach biosynthesis ansamycin endophytes or symbionts enriched s EU2894
AY921785.1 gg_id:113624 farm soil clone AKYH1201 AY9217
FJ152619.1 gg_id:356469 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX1A_ FJ1526
FJ152871.1 gg_id:322098 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX4CI FJ1528
FJ152673.1 gg_id:342606 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX1A_ FJ1526
GU083675.1 gg_id:585141 Microorganism Xiarinur soda lake sediment clone x271 GU083
EU374077.1 gg_id:267176 southern Cretan margin (eastern Mediterranean Sea) canyon and slope sediment clc EU3740
GQ143755.1 gg_id:373545 Level Continental Shelf Sediment and Phylum-level lineages Phylum Planctomycetes GQ143
AF317745.1 gg_id:136926 Nullarbor cave clone wb1_A18 AF3177
AM943577.1 gg_id:269262 Microbial dolomite formation Lagoa Vermelha Brazil carbonaceous sediments hyper AM943
AY592110.1 gg_id:99079 marine ANAMMOX sediment clone AY592110 AY5921
GQ262856.1 gg_id:554991 Structure Simulated Level Waste Site simulated level waste site clone F1_32X2 GQ262
DQ906881.1 gg_id:241659 Oman subsurface soil clone 11B-8 DQ906
EU682493.1 gg_id:530814 Four Primer Sets Detecting Anammox s estuary sediment Mai Po Nature Reserve clo EU6824
EU652631.1 gg_id:277923 Seasonal variation microbial Yel Sea sediment clone C8S-21 EU6526
EU245438.1 gg_id:237565 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M1-F03 EU2454
EU369136.1 gg_id:304950 libraries oyster shell clone MBIOS-20 EU3691
EU219931.1 gg_id:247892 study prokaryotic approach landfill soil 5.5 ft. depth clone C6B EU2199
EU369154.1 gg_id:317743 libraries oyster shell clone MBHOS-05 EU3691
EF125397.1 gg_id:182109 soil naked tidal flat sediment near mangrove clone MSB-1C5 EF1253
AB491850.1 gg_id:542631 affiliation (Litopenaeus vannamei) Banyuwangi East Java microbial flocs floating brac AB4918
EU134887.1 gg_id:252091 tallgrass prarie soil clone FFCH15678 EU1348
EU134863.1 gg_id:255390 tallgrass prarie soil clone FFCH17465 EU1348
GU056071.1 gg_id:579069 Biologic Techniques Applied Microbial Prospecting China: Ban 876 Gas Oil Field Bein GU056
FJ152883.1 gg_id:351400 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX4CI FJ1528
AB250557.1 gg_id:160916 and ecology Grotta Azzurra Palinuro Cape (Salerno Italy) microbial mat clone #2-2 AB2505
EU283598.1 gg_id:279155 Model Early Earth Harbors Deeply Divergent Divisions Anderson Lake clone A406 EU2835
FJ205371.1 gg_id:510313 Prokaryotic deep-sea hydrothermal region East Lau Spreading Centre deep marine se FJ2053
EU700157.1 gg_id:288295 Study on Shantou Bay Marine Sediments Microorganisms sediment clone STU15 EU7001

5943.8	5898.1	5728.8	6243.6	8458.1	5773.6	8703.8	6126.4	4639.5	4194.9	4268.0
457.8	4827.1	4800.7	5239.9	6798.3	5068.3	5979.7	4715.5	2645.5	1823.9	3610.7
1990.5	6435.5	5689.4	5874.0	8594.1	5618.0	7901.9	6221.0	4978.1	5471.4	5425.8
59.0	157.9	124.8	112.4	189.3	125.2	148.5	82.4	135.1	29.9	70.2
58.4	57.3	80.2	89.8	84.8	56.0	90.5	76.3	43.7	34.4	49.2
2280.2	2501.9	3324.4	3633.4	2908.8	2846.3	4211.5	4029.3	2015.1	1021.7	2642.3
354.5	2372.5	3354.9	3448.5	2942.2	3004.1	4985.2	3250.8	1766.6	638.9	2049.6
20829.7	6825.0	6252.6	6557.8	6117.5	6307.2	7569.0	6408.8	9479.3	7683.2	6969.7
5249.3	7309.8	7738.7	8393.4	8949.9	7617.9	9270.1	7994.7	8601.2	6214.9	9696.6
3652.7	7298.5	8166.5	7832.4	8664.5	7239.4	8259.2	7225.1	9129.1	7532.6	8120.1
75.1	280.3	249.1	290.6	285.5	223.5	241.9	152.8	92.1	108.6	118.8
39.7	174.3	233.8	76.8	216.0	211.8	244.0	202.1	58.4	79.5	115.9
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63.6	60.7	69.4	75.3	96.8	47.9	87.3	58.1	832.6	29.1	47.2
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7184.2	7934.8	7099.9	7377.0	7775.7	7272.1	8328.0	6765.3	8702.7	8349.1	7894.5
1930.2	4267.3	4111.6	4474.8	4989.3	4134.6	5748.0	3806.2	3629.5	3955.1	4296.4
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AF507713.1 gg_id:65673 forest soil clone S166 AF507
EU491859.1 gg_id:264825 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU491
GQ347441.1 gg_id:581615 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ347
DQ234160.2 gg_id:144617 determined library mangrove clone DS076 DQ234
DQ329577.1 gg_id:159133 Guerrero Negro hypersaline microbial mat clone 05D2Z07 DQ329
DQ397339.1 gg_id:159241 Guerrero Negro hypersaline microbial mat clone 02D2Z08 DQ397
AB192119.1 gg_id:142691 termite gut homogenate clone M2PT2-27 AB192
FJ791860.1 gg_id:571248 Unexpectedly archaeal species shift between rare and dominant over thousand year FJ7918
AY197400.1 gg_id:86409 Guaymas Basin hydrothermal vent sediments clone B02R018 AY197
FJ959985.1 gg_id:579816 bottlenose dolphin upper respiratory tract blowhole clone D940_045 FJ9599
AB232534.1 gg_id:154098 Prokaryotic gills deep-sea hydrothermal vent shrimp gill Alvinocaris longirostris clone AB232
EU052256.1 gg_id:256207 degradation kinetics and current efficiency cells supplied anode microbial fuel cell fe EU052
AF367482.1 gg_id:17620 deep-sea hydrothermal vent clone VC1.2-cl02 AF367
GQ349327.1 gg_id:562277 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ349
EU265935.1 gg_id:537633 transition and zone within near-shore anoxic basin: Nitinat Lake depth 20 m clone Ni EU265
EU101198.1 gg_id:237363 Sulfide/oxygen supply ratio predicts outcome competition among sulfur-oxidizing wa EU101
GU061180.1 gg_id:585963 Evaluation culturing methods cultivate previously Yel Sea intertidal beach surface se GU061
EU245804.1 gg_id:257757 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M6-F03 EU245
DQ330597.1 gg_id:159245 Guerrero Negro hypersaline microbial mat clone 09D2Z91 DQ330
FJ712458.1 gg_id:523166 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) K FJ7124
EU385807.1 gg_id:258358 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S EU385
EU245526.1 gg_id:256848 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M2-F08 EU245
FJ810558.1 gg_id:405181 Subsurface ecosystem resilience: Long-term attenuation subsurface contaminants su FJ8105
FJ416124.1 gg_id:357229 sediments sediment station NEC5 Northern Bering Sea clone 115O3 FJ4161
EU542519.1 gg_id:273867 Effects chemical structure concentration on pathways microbial during dechlorinatio EU542
DQ811954.1 gg_id:162191 mangrove soil clone MSB-5A5 DQ811
EU487916.1 gg_id:564815 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU487
EF203188.1 gg_id:204759 phylotypes sediments Lake Kastoria Greece sediment clone Kas139B EF2031
EU048677.1 gg_id:254199 and archaeal surface marine sediment Slope South China Sea clone MD2896-B18 EU048
EU487964.1 gg_id:573020 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU487
EU245855.1 gg_id:256405 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M7-C07 EU245
DQ329580.1 gg_id:159470 Guerrero Negro hypersaline microbial mat clone 062DZ43 DQ329
DQ154831.1 gg_id:138844 Diel Migration Restructures Hypersaline Microbial Mat hypersaline microbial mat cl DQ154
GQ246356.1 gg_id:548387 Temporal and spatial China North Yel Sea sediments clone Cm1-19 GQ246
FJ264777.1 gg_id:340190 Manganese and Iron Dependent Anaerobic Oxidation Methane methane seep sedim FJ2647
FM165273.1 gg_id:566144 seep chitineous tube vestimentiferan tubeworm Lamellibrachia sp. cold seeps clone FM165
FJ264598.1 gg_id:317416 Manganese and Iron Dependent Anaerobic Oxidation Methane methane seep sedim FJ2645
EU246145.1 gg_id:257436 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-P4-C07 EU246
EU245601.1 gg_id:257385 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M3-E09 EU245
DQ329606.1 gg_id:159400 Guerrero Negro hypersaline microbial mat clone 04D2Z65 DQ329
DQ329608.1 gg_id:159092 Guerrero Negro hypersaline microbial mat clone 05D2Z01 DQ329

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960.2	5722.8	4383.4	5709.4	2813.1	5021.7	6858.1	5819.6	3603.5	2799.2	5256.2
47.9	197.1	147.7	181.9	163.3	235.2	604.1	176.7	53.9	31.1	140.3
72.4	357.6	466.7	387.1	264.9	234.2	416.5	425.4	119.6	63.8	229.1
219.1	1375.4	1020.9	951.8	2347.2	1212.4	895.4	1225.5	2327.2	316.5	603.5
51.7	69.3	107.6	106.3	49.6	98.2	223.5	162.3	111.3	32.9	130.2
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341.9	3174.9	4210.3	4736.1	3032.1	3509.7	4280.7	4317.5	1890.2	1497.8	3911.3
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179.4	140.1	164.8
799.0	2415.8	1146.8
106.3	165.9	45.5
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144.2	63.6	76.5
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DQ329610.1 gg_id:159257 Guerrero Negro hypersaline microbial mat clone 062DZ28 DQ329
GQ472356.1 gg_id:546599 Microbial Dongping Lake lake sediment clone 3S4-17 GQ472
EU134901.1 gg_id:255924 tallgrass prarie soil clone FFCH3687 EU134
AB300086.1 gg_id:225464 Wide ancient microbial DNAs Quaternary sediments holocene mud sediment clone A AB300
EU134900.1 gg_id:248928 tallgrass prarie soil clone FFCH18260 EU134
FJ901586.1 gg_id:567970 phreatic limestone sinkholes northeastern Mexico biomat 30m deep cenote La Palita FJ9015
AB240362.1 gg_id:143463 microbial structure Phragmites rhizosphere biofilm reed bed reactor laboratory clone AB240
EU134904.1 gg_id:249081 tallgrass prarie soil clone FFCH18804 EU134
AY050577.1 gg_id:106690 MCB-contaminated groundwater-treating reactor clone GOUTA4 AY050
AJ543759.1 gg_id:95866 anoxic sediment Lake Cadagno clone 49 AJ5437
FJ746261.1 gg_id:567096 Microbial oligotrophic marine sediments: South Pacific Gyre ocean sediment 5306 m FJ7462
AB237732.1 gg_id:139838 microorganisms deep subsurface groundwater sedimentary rock milieu clone HDBW AB237
EU386097.1 gg_id:261462 Biogeographical and microbes sediments on subseafloor sediment South China Sea c EU386
EF688196.1 gg_id:351571 Detection microbial sludge anaerobic wastewater treatment system clone 4E1_cons EF6881
FJ645694.1 gg_id:550022 Microbial dynamics during -temperature biotreatment PCP-contaminated wastestrea FJ6456
EU622292.1 gg_id:298479 syntrophic partnerships deep-sea vents direct cell capture and metagenomics Eel Riv EU622
DQ415793.1 gg_id:158359 Dominant microbial limestone-corroding biofilms frasassi system Italy Frasassi sulfid DQ415
EF602489.1 gg_id:233633 metabolic phylum Planctomycetes anaerobic sulfide and sulfur-rich spring (Zodletone EF6024
EF687508.1 gg_id:283688 Biogeochemistry iron- and sulfur-precipitating microbial mats (Nile Mediterranean) s EF6875
GQ249498.1 gg_id:562766 Microbial anaerobic sediments Bay Cadiz (Spain) marine sediment: 0-2 cm layer clor GQ249
DQ329567.1 gg_id:159197 Guerrero Negro hypersaline microbial mat clone 08D2Z50 DQ329
DQ329541.1 gg_id:159505 Guerrero Negro hypersaline microbial mat clone 05D2Z11 DQ329
EU246164.1 gg_id:237663 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-P4-E12 EU246
DQ329542.1 gg_id:159334 Guerrero Negro hypersaline microbial mat clone 05D2Z93 DQ329
EU407206.1 gg_id:273907 household biogas digester clone GW-22 EU407
EU246196.1 gg_id:246894 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-P5-B01 EU246
FJ484771.1 gg_id:566342 microbial autonomous rover world's deepest phreatic sinkhole wall biomat El Zacator FJ4847
FJ484430.1 gg_id:513424 microbial autonomous rover world's deepest phreatic sinkhole wall biomat El Zacator FJ4844
FJ712497.1 gg_id:529594 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) k FJ7124
DQ811937.1 gg_id:162879 mangrove soil clone MSB-5B5 DQ811
EU617724.1 gg_id:346244 Seasonal variation microbial Yel Sea sediment clone C13S-9 EU617
AM086123.1 gg_id:149924 Abundance and archaea mesotrophic Lake Kinneret lake profundal sediment clone c AM086
FJ712479.1 gg_id:532343 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) k FJ7124
EU386122.1 gg_id:261859 Biogeographical and microbes sediments on subseafloor sediment South China Sea c EU386
AF286032.1 gg_id:26077 saltmarsh clone LCP-89 AF286
FJ716412.1 gg_id:562251 Uncultivated archaea sulfate-reducing biofilm Frasassi cave system anoxic lake water FJ7164
EU048684.1 gg_id:246605 and archaeal surface marine sediment Slope South China Sea clone MD2896-B27 EU048
FJ716279.1 gg_id:551134 Chlorobi dominate shal chemocline Bahamas Sawmill Sink column 10.3 m water dept FJ7162
GU363012.1 gg_id:532990 and archaeal biogeochemical cycling genes within Qiongdongnan basin Sea: pilot stu GU363
AY114321.1 gg_id:63785 anoxic marine sediment clone LD1-PA32 AY114
EU487944.1 gg_id:562517 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU487

53.3	109.0	129.9	146.4	119.7	84.6	142.1	123.3	40.2	21.1	65.9
573.8	4792.0	5838.6	7070.0	6114.8	6388.8	7468.0	5667.0	2690.2	1576.7	4060.8
857.5	2169.9	2150.8	1981.2	2827.5	2201.4	3635.0	2243.2	1508.8	1543.7	1826.2
52.8	327.4	378.4	465.0	785.5	303.8	867.7	318.6	61.8	41.7	105.3
3680.0	4267.6	3726.4	4134.2	5379.0	3718.5	5093.6	4314.1	3482.7	3304.3	3461.7
1943.9	6047.8	5332.3	5775.3	5627.3	5517.5	6659.8	5336.7	5062.2	4040.9	4799.3
86.1	219.4	451.3	495.5	435.5	571.8	756.7	435.7	128.0	59.3	177.3
38970.7	9013.3	9228.3	9364.1	9160.2	8763.8	10169.5	8279.5	12406.8	8573.7	12343.9
287.6	1617.2	1774.8	1349.6	1770.1	2527.5	2069.2	1664.7	1783.8	577.3	1284.0
41.5	85.3	89.6	152.3	154.1	75.2	239.9	112.1	40.4	18.8	48.6
499.3	1802.7	2038.6	1984.8	1507.0	1724.4	1779.7	1803.3	1212.9	1066.2	1358.9
40.1	240.2	236.8	266.2	194.7	180.8	203.5	244.3	58.4	48.8	190.2
6618.2	9056.9	7771.3	8972.5	7963.9	8663.2	8629.5	9520.8	9536.1	8132.3	10529.3
44.3	53.3	55.1	52.1	71.5	45.3	40.8	46.4	27.4	22.1	40.7
6855.1	7608.8	7316.6	8877.1	6976.2	6705.9	8296.5	7334.9	6844.7	7359.5	7890.9
36.1	113.2	121.6	131.9	77.9	105.8	132.2	154.3	130.8	34.8	82.7
130.2	1193.2	621.8	1191.1	817.0	726.5	1286.0	989.6	1210.5	276.4	605.6
43.3	168.0	335.5	338.8	195.8	185.8	308.3	325.5	183.1	36.9	161.3
18358.8	3863.7	5299.9	4979.7	6937.0	4815.9	6013.6	6264.4	3898.8	967.4	3548.7
826.5	7969.1	6902.7	7740.5	5413.9	6363.1	6921.3	7341.9	5925.8	6510.4	7674.4
32405.9	18586.2	15690.6	16310.0	16135.1	14798.3	16512.9	14649.5	22867.3	17845.0	20516.0
5696.5	5575.8	4471.4	4670.0	4406.8	4244.2	4970.3	4508.3	6829.7	4842.8	6070.4
11098.5	5807.3	4769.9	5040.8	4544.5	4420.5	5795.8	4243.9	7902.3	5228.4	5853.2
7768.8	10717.0	8898.7	8878.2	8294.0	7911.3	8501.0	8281.9	10243.3	7605.5	11786.8
887.7	5786.7	5443.5	6155.9	7147.6	5398.8	7523.6	6463.6	4466.0	1939.4	4785.4
5234.6	6217.8	4631.0	4563.0	4049.7	2343.3	4977.1	3575.3	5052.9	5300.6	6433.9
3954.4	8087.2	8113.0	9834.5	9855.7	8033.1	11446.3	8241.2	7750.8	7417.8	8713.9
5961.1	8930.5	10049.5	10192.3	10657.3	9542.5	12335.0	9534.7	9268.8	8136.2	10328.9
302.2	3222.3	3570.7	4124.5	5253.5	3199.8	5931.6	3284.3	2536.6	705.8	2286.7
61.7	86.3	145.3	171.9	97.1	93.0	103.9	131.1	47.2	35.2	71.0
669.2	6925.5	6990.7	8264.2	9303.1	7489.9	10608.1	8779.7	5686.8	1626.2	8530.7
672.3	3578.4	4437.0	5237.9	7008.3	4019.4	9020.7	4257.5	3021.0	1729.9	2782.8
768.9	6787.2	7810.1	7410.9	6753.2	6666.6	7836.9	7693.1	4927.4	5453.5	6977.7
4619.4	5253.4	5554.8	6316.6	6693.6	5317.6	7720.2	6092.6	5478.3	3073.6	5435.2
45.0	245.2	292.8	249.6	320.3	282.8	174.0	169.3	71.9	38.7	147.2
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3799.1	6748.3	6872.9	8012.4	7379.2	6520.1	9208.4	7571.3	3438.4	4197.0	5807.4
1525.0	9385.5	6816.9	8716.3	9354.1	7823.3	9389.7	8129.9	11529.6	5837.0	7299.8
500.9	5023.9	3997.0	4537.5	4442.0	3947.3	5466.5	4234.9	5269.9	2868.0	3428.9
2417.1	4914.0	5400.5	5666.8	6704.5	4698.7	6978.2	5392.3	5916.5	2043.7	4220.9
3273.6	11284.4	10918.4	11186.1	11333.9	9980.2	12138.4	9403.8	9993.6	8534.6	10859.2

118.8	236.7	175.7
4791.7	5884.1	7530.4
1787.4	3235.1	6057.4
167.0	242.2	1223.9
3840.8	5232.5	6686.8
4991.9	4850.6	7419.0
306.1	607.5	1203.9
8480.5	10165.3	9878.2
1752.8	2683.1	8796.6
73.2	155.9	89.0
1580.3	2197.0	1986.5
107.3	196.7	76.9
8307.9	9791.1	9396.5
53.8	70.3	34.4
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72.2	210.9	77.3
788.0	1840.5	1260.7
193.6	414.6	280.7
4599.5	5071.9	5927.4
5189.9	6015.4	5892.5
15032.6	15002.6	15232.8
4729.1	5679.6	4830.7
1944.7	5243.3	3991.2
7999.1	8237.6	7937.0
5797.6	5607.0	6739.9
3766.3	4697.7	3551.7
7789.8	8641.4	10055.7
9944.8	10546.8	12060.1
2742.5	3811.3	5008.3
94.0	208.8	128.6
6039.1	6536.4	9007.7
3114.3	5354.8	5877.2
6578.5	6673.6	8368.7
6299.4	6159.7	6843.9
163.4	413.6	495.3
6666.8	7339.4	9093.0
5078.2	6412.3	10107.2
8455.8	7920.7	9184.8
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NR_027571.1 gg_id:568139 Lentisphaera araneosa HTCC2155 str. HTCC2155; ATCC BAA-859 NR_02
EU050936.1 gg_id:237639 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_03_46 EU050
EU617881.1 gg_id:308950 Seasonal variation microbial Yel Sea sediment clone C13S-64 EU617
EU373977.1 gg_id:275456 southern Cretan margin (eastern Mediterranean Sea) canyon and slope sediment clc EU373
DQ903989.1 gg_id:243625 Cytophaga sp. PRPR22 DQ903
AB189358.1 gg_id:113979 cold seep sediment clone JT75-104 AB189
AJ431234.1 gg_id:79161 Cytophaga sp. str. Dex80-43 AJ4312
CU918294.1 gg_id:575335 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU918
EU236367.1 gg_id:299835 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg91E2 EU236
GU302469.1 gg_id:552105 Spatial structure and activity sedimentary microbial underlying Beggiatoa spp. mat h GU302
FJ172855.1 gg_id:349140 Qinghai Yak Ruminal and Fungi China rumen clone RB-3G5 FJ1728
DQ067008.1 gg_id:131533 Lake Washington sediment clone pLW-89 DQ067
FJ172836.1 gg_id:306087 Qinghai Yak Ruminal and Fungi China rumen clone RB-4D9 FJ1728
AB062771.1 gg_id:32071 termite gut homogenate clone BCf1-10 AB062
EU885059.1 gg_id:323370 microbial hindgut chamber Pomacanthus sexstriatus GI tract clone A2F3 EU885
EU491122.1 gg_id:266959 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak EU491
U81755.2 gg_id:1542 anaerobic digestor clone vadinHB65 U8175
AB009200.1 gg_id:14576 rumen clone RFN44 AB009
EU491130.1 gg_id:265874 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak EU491
EU850520.1 gg_id:342488 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF297 EU850
EF092196.1 gg_id:274447 Persistent Axinella corrugata Lentisphaerae clone Ax29_B12 EF0921
NZ_ABDE01000031.1 gg_id:235858 Victivallis vadensis str. ATCC BAA-548 NZ_AB
FJ833297.1 gg_id:551530 Microbial Ecology Crop Folivorous Hoatzin crop contents clone A3Q401_04D01 FJ8332
EU462436.1 gg_id:290815 Sumatran orangutan feces clone orang1_aai54e09 EU462
DQ353908.1 gg_id:148459 Fecal Wild Gorilla (Gorilla beringei) wild gorilla feces clone Z20 DQ353
EU465080.1 gg_id:288148 African elephant feces clone AFYEL_aaj67g06 EU465
CU920558.1 gg_id:551462 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU920
CU924053.1 gg_id:571561 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU924
EU459524.1 gg_id:287575 capybara feces clone CAP_aah99b07 EU459
AJ536842.1 gg_id:97002 chemocline clone 362 AJ5368
FJ755755.1 gg_id:563388 vertical archaeal water and Lake Taihu sediment clone LT-SB-B11 FJ7557
EU050937.1 gg_id:255593 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_08_35 EU050
GU196208.1 gg_id:584283 Bioaugmentation improved recovery digesters after toxicant exposure lab-scale ana GU196
EF602493.1 gg_id:233246 metabolic phylum Planctomycetes anaerobic sulfide and sulfur-rich spring (Zodletone EF6024
AJ431235.1 gg_id:79502 Cytophaga sp. str. Dex80-64 AJ4312
AY553939.1 gg_id:113934 Baltimore Harbor sediment clone FA6 AY553
EU048683.1 gg_id:251056 and archaeal surface marine sediment Slope South China Sea clone MD2896-B26 EU048
GQ246316.1 gg_id:511355 Temporal and spatial China North Yel Sea sediments clone Sd1-35 GQ246
GU180194.1 gg_id:547075 Impact coplanar PCBs on microbial activity anaerobic estuarine sediments sediment GU180
EU385673.1 gg_id:265544 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S EU385
DQ521806.1 gg_id:160216 Anaerobic Methane Oxidizing ANME-1b Archaea Hypersaline Sediments Gulf Mexic DQ521

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82.4	1811.0	1448.5	1784.7	1669.8	1389.4	2156.4	1887.4	662.3	1378.0	1747.2
57.6	841.6	871.8	858.9	1121.0	1146.3	693.4	321.8	629.9	75.0	504.6
7039.2	9889.3	9698.0	9144.0	9634.9	9898.3	10510.7	8753.4	12653.3	10068.0	10733.0
2075.4	7062.9	7738.1	7607.0	7574.3	6752.8	7775.7	7359.4	6679.2	4109.6	7156.0
206.6	1234.7	1128.2	899.0	975.3	1057.6	711.9	951.2	882.7	571.5	682.9
315.6	1961.8	2138.5	1692.1	1597.8	1708.8	1813.2	1615.4	1366.5	1680.0	871.8
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3996.7	7061.6	6488.9	6541.0	6793.5	6085.6	6054.5	6054.6	6245.5	6307.4	7598.2
32.9	65.7	99.6	99.4	131.2	102.7	412.3	140.1	21.4	26.4	29.5
3005.1	4533.9	5719.1	6700.7	5565.7	4492.8	5629.4	6432.9	3925.5	2979.3	5269.7
73.3	89.9	160.4	138.4	118.7	148.5	136.3	265.0	62.4	23.9	103.0
7766.6	5355.6	5302.3	5662.8	6210.8	5259.5	5954.7	5876.6	4642.0	3894.5	5645.0
64.6	178.7	421.0	419.7	185.2	280.1	165.1	477.5	127.1	50.4	201.7
5597.4	7260.8	7272.1	8047.0	7901.7	7096.4	8497.9	7462.6	6384.7	6242.2	6977.0
323.7	3211.3	3335.2	3666.8	4316.8	3625.6	6138.4	4390.8	2788.0	3167.2	3724.7
83.8	660.3	643.3	858.5	1195.5	507.9	671.0	729.2	141.2	135.7	262.4
208.6	331.1	419.4	604.1	729.9	370.3	500.4	637.0	303.5	72.1	210.0
5972.3	7533.2	8888.5	7790.7	7293.7	7754.0	8588.6	7446.7	6993.4	11214.7	8054.5
58.1	62.0	96.9	118.7	50.1	54.7	42.5	80.3	31.4	25.4	59.7
1373.2	6162.7	6157.2	5715.4	4897.0	5656.0	6978.3	5836.5	6083.5	4504.0	6317.0
62.8	439.1	473.4	562.4	198.1	327.8	432.7	435.4	161.3	67.9	288.2
11366.4	13443.4	12588.1	14576.3	13488.5	12332.2	14918.0	13385.3	14040.0	10849.0	16868.2
2237.2	4554.8	4363.4	4548.0	3930.1	3448.0	4860.8	3711.1	4590.8	4469.4	4979.4
54.2	60.3	114.0	72.6	68.5	58.0	50.3	96.1	53.7	34.6	49.7
3962.2	6299.3	6731.7	6751.7	7929.1	6502.5	8777.9	6880.2	6611.9	3652.5	7398.2
1107.4	6312.4	6776.0	7116.7	9130.7	6816.4	10182.3	6847.6	5414.9	5416.6	4717.2
2718.6	6860.8	6002.1	5635.2	5934.4	5626.8	6150.1	5326.1	5638.5	5720.8	3686.4
5789.9	7911.3	8490.7	9167.6	10371.0	8162.3	10727.1	8884.6	8984.3	6738.1	9178.4
34.5	214.4	394.7	266.1	88.9	162.9	710.5	227.7	44.9	23.1	109.4
77.9	2491.7	3380.5	3622.0	2734.1	2767.4	3391.2	3653.9	1765.2	1013.9	1902.3
21819.2	8455.4	7766.9	7647.4	6822.1	7028.3	7911.2	7632.6	9908.6	8010.4	8313.3
933.2	2282.5	3104.0	4338.2	4178.9	3761.7	4606.2	4698.4	2832.3	1530.3	5111.3
32.0	118.0	148.1	147.0	155.8	125.0	156.0	102.7	41.3	30.3	70.8
59.2	216.7	336.7	286.3	210.8	289.8	453.4	342.1	129.8	76.8	177.0
48.5	864.7	1324.6	1402.9	1124.3	1088.0	1617.2	1653.4	444.1	165.0	680.0
8643.5	7097.4	7920.0	8791.2	9608.9	7149.0	10038.1	7633.5	6360.0	3749.0	7836.2
6766.7	9748.7	8101.1	8718.8	8781.3	8292.4	8686.8	8094.4	14819.8	6659.9	9245.5
10188.4	2740.2	2111.5	2613.0	2741.3	2555.0	3120.5	2054.6	2881.6	1639.8	3194.6
25271.7	7174.0	6817.3	7423.6	7555.5	6676.0	7702.8	6348.9	10656.7	8162.8	9954.6
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44.1	52.8	76.3
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642.0	730.2	607.5
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EU181498.1 gg_id:251185 Prokaryotic enhanced organic matter remineralization continental margin marine se EU181
DQ521805.1 gg_id:160462 Anaerobic Methane Oxidizing ANME-1b Archaea Hypersaline Sediments Gulf Mexic DQ521
EF106489.1 gg_id:202958 microbial two endoevaporitic salt crusts evaporitic crust Guerrero Negro Baja clone 2 EF1064
AJ133617.1 gg_id:1688 brine sediment clone KTK 32 AJ1336
EU246019.1 gg_id:246314 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-P1-F02 EU246
FN393496.1 gg_id:552766 prokaryotic sediments two Tunisian multipond sediment solar saltern clone SFD1H1 FN393
GU390826.1 gg_id:526942 Dark hot springs: structure biofilms caves Acquasanta Terme (Italy) sulfidic cave stre GU390
AJ536840.1 gg_id:95720 chemocline clone 331 AJ5368
AB539947.1 gg_id:569847 Evidence syntrophic acetate oxidation coupled hydrogenotrophic methanogenesis -t AB539
CU921965.1 gg_id:554874 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU921
AY570581.1 gg_id:108459 -temperature biodegraded Canadian oil reservoir clone PL-11B10 AY570
GU476613.1 gg_id:515032 microbial biogas fermentation enrichment clone BBMC-13 GU476
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AB426199.1 gg_id:274653 -situ identification study benzene-degrading s under methanogenic condition anaer AB426
AB486305.1 gg_id:538794 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBAR AB486
EF492972.1 gg_id:257902 Iron-manganese Nodule and Its Surrounding Soil soil around iron-manganese nodule EF4929
AF351214.1 gg_id:71271 coal tar-contaminated groundwater clone 12-24 AF351
FJ621558.1 gg_id:561816 Enrichment and detection denitrifying methanotrophic NC10 phylum eutrophic fresh FJ6215
DQ837250.1 gg_id:239257 Archaeal and pristine National Park Spain Donana coastal aquifer clone 49S1_2B_43 DQ837
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DQ369742.1 gg_id:156874 microbial consortium couples oxidation denitrification anaerobic methane oxidation DQ369
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EU491416.1 gg_id:260370 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X4 clone EU491
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AF317743.1 gg_id:136988 Nullarbor cave clone wb1_A12 AF317
EU373968.1 gg_id:273635 southern Cretan margin (eastern Mediterranean Sea) canyon and slope sediment cl EU373
EU335184.1 gg_id:242324 Changes microbial metabolic and along hydrogeochemically variable profile saturate EU335
AF351231.1 gg_id:42281 upgradient coal tar waste-contaminated groundwater clone 4-29 sp. AF351
GU208486.1 gg_id:589700 Study on Sediment Dongping Lake sediment clone Shs2-20 GU208
DQ138963.1 gg_id:138815 rice straw paddy soil clone JG118 DQ138

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8681.1	5126.2	4946.8	5484.5	6366.8	5093.6	6447.1	5466.6	10310.9	5895.6	6256.5
95.0	335.7	368.3	388.4	496.3	334.0	740.8	706.2	2276.1	168.2	240.0
67.7	226.1	174.0	177.4	118.0	162.3	334.2	226.0	68.2	91.2	126.0
42.1	32.7	38.7	35.9	34.7	27.3	41.2	27.8	34.8	30.0	38.6
45.9	47.5	72.2	46.9	51.5	52.5	57.2	47.6	27.8	23.8	30.6
908.8	2559.6	2567.3	3018.8	3155.2	2196.2	3404.8	2289.0	1933.5	1118.5	2422.2
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5902.2	7101.2	6419.9	8025.4	7552.8	6577.6	8359.9	6757.2	8838.7	4402.0	7063.0
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6895.2	7612.1	7756.0	8758.0	9195.6	7619.3	8399.9	7768.2	7755.7	6171.7	8196.7
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6660.9	3422.9	4415.8	4454.2	4653.1	4201.8	5270.4	3844.6	5366.0	3523.4	5475.3
138.2	3328.6	3544.9	3716.0	5417.7	3776.3	6493.8	3153.7	1677.2	608.8	2550.0
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DQ138964.1 gg_id:138554 rice straw paddy soil clone JG325 DQ138
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DQ464149.1 gg_id:157346 acid mine drainage clone D1-90 DQ464
AF544226.1 gg_id:58150 acid mine drainage clone ASL9 AF5442
AB254780.1 gg_id:159816 Biogenic Fe-oxyhydroxides nodules (takashikozo) encrusted iron-oxide reducing sedi AB2547
EU372645.1 gg_id:564896 Evaluation Leptospirillum spp. Rio Tinto basin model interest biohydrometallurgy wa EU3726
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DQ464151.1 gg_id:158060 acid mine drainage clone D1-95 DQ464
EF409845.1 gg_id:211316 acid mine drainage clone FKBZ-53-06 EF4098
AF543509.1 gg_id:56204 acid mine drainage clone BA33 AF5435
FJ228276.1 gg_id:344157 sulfate-reducing enriched during bioremediation experiment sediments (Brandenburg FJ2282
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AF356833.1 gg_id:41859 Leptospirillum ferrooxidans str. BCT2 AF3568
X86776.1 gg_id:1509 Leptospirillum ferrooxidans str. L15 DSM 2705 X86776
GU168016.1 gg_id:565828 Leptospirillum ferrooxidans GU168
AF356839.1 gg_id:39980 Leptospirillum ferrooxidans str. Sy AF3568
AY952274.1 gg_id:153665 Leptospirillum ferrooxidans AY9522
EF025338.1 gg_id:191142 Leptospirillum ferriphilum str. ZTS EF0253
DQ659194.1 gg_id:221094 acid mine drainage clone DBS-Clone19 DQ659
GU168013.1 gg_id:571763 Leptospirillum ferriphilum GU168
DQ223208.1 gg_id:143919 subsurface water clone EV221H2111601SAH4 DQ223
EF018100.1 gg_id:203943 aspen rhizosphere clone Amb_16S_432 EF0181
AF155154.1 gg_id:1493 Nitrospira cf. moscoviensis str. SBR2016 AF1551
AJ617918.1 gg_id:110103 oxic-anoxic interphase flooded paddy soil clone D023010 AJ6179
AY555798.1 gg_id:106808 Bor Khlueng hot spring clone PK287 AY5557
EU287071.1 gg_id:237590 Pacific arctic surface sediment clone B78-107 EU2870
AM997652.1 gg_id:542056 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A AM997
EU803576.1 gg_id:332256 It's all ranking aquatic Lake Gatun clone 5C231165 EU8035
GQ249372.1 gg_id:583840 Research on biodiversity sludge bioflim Biological Aeration Filter clone B14 GQ249
DQ814725.1 gg_id:173004 zebrafish digestive tract clone aaa35h01 DQ814
AJ617920.1 gg_id:109789 oxic-anoxic interphase flooded paddy soil clone D023011 AJ6179
AY921743.1 gg_id:114282 farm soil clone AKYG586 AY9217
EU491464.1 gg_id:276859 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X4 clone EU4914
DQ128338.2 gg_id:183441 conventional tillage soil clone HSB CT52_D06 DQ128

1227.6	3614.1	3921.0	3823.0	3589.9	3583.3	4708.3	3367.8	2786.7	2560.3	2614.8
1191.0	6886.4	7269.6	8018.0	8192.0	7126.8	8561.7	6970.2	5609.4	3117.3	6721.6
272.9	3356.9	3115.1	3286.4	4143.6	2945.5	4659.2	2592.3	2412.8	1561.5	1644.2
120.7	604.4	710.0	802.0	819.8	708.4	623.8	693.5	241.2	159.9	365.5
1269.8	1804.1	2105.7	2135.1	2035.9	1897.7	3247.3	2071.7	1849.8	816.8	2245.8
1235.4	1155.9	1242.9	1323.1	1424.9	1358.6	1082.1	1251.8	872.2	732.2	1596.0
38321.4	9518.7	9073.5	10148.2	9555.9	9186.2	13750.9	8694.0	13162.5	10556.8	12387.8
472.2	1888.3	1876.9	1982.0	2678.6	2266.8	2826.4	1881.2	1921.3	934.8	1004.3
5842.6	3006.2	3166.0	3792.9	4103.8	3992.6	4532.3	3870.4	4085.0	3775.5	4952.4
42.4	1687.6	2211.8	2187.4	1427.3	1788.0	2710.3	1794.6	1922.7	1812.1	1037.6
13002.3	4384.9	4802.7	4784.6	4877.7	4802.0	4346.3	4603.3	5748.5	3555.4	7474.9
78.7	46.6	135.9	261.0	105.8	55.7	178.5	221.6	47.8	27.0	110.6
117.8	1952.4	2074.0	2672.6	2247.6	2410.9	2848.1	2635.7	897.4	652.1	1515.6
194.6	5323.7	4636.8	4665.5	5116.2	5892.1	5963.2	5147.2	3628.7	2109.2	6841.1
8160.6	7302.4	6203.7	6425.2	6851.2	6965.8	8029.5	5929.6	10157.8	4910.1	7148.8
115.9	876.7	978.0	933.2	823.8	1282.4	1293.0	1113.7	544.8	405.3	825.8
5111.5	6450.2	5734.5	7359.6	6293.8	6004.2	6315.4	5617.4	4309.7	4762.9	5887.2
30257.0	7759.5	7771.6	8281.9	7760.6	7332.6	9138.8	7116.5	10107.2	7254.7	11347.7
5485.1	4582.0	3170.9	4060.5	4636.5	4699.2	4068.9	4369.6	5110.9	2828.6	4071.4
10914.4	3744.2	4092.4	4707.5	3620.2	3760.6	3827.9	2883.8	6035.8	4280.2	5713.2
3747.8	1401.9	1704.1	1982.8	1545.9	1419.7	1905.7	1462.1	1787.8	1311.5	2423.6
392.4	1048.1	1211.2	1761.8	1481.5	1223.8	1442.8	1306.0	951.0	312.0	1311.6
58.2	242.0	405.3	473.6	317.7	250.3	376.8	293.1	178.3	71.0	375.4
475.4	2657.3	3055.7	3322.2	2811.4	2610.0	3471.6	2646.7	2071.9	1413.9	3680.6
155.4	3447.4	2702.2	3188.2	1896.4	2993.6	2204.1	2795.0	2754.2	2227.0	2604.6
712.4	1671.2	1381.6	1697.2	1837.1	1641.6	1830.8	1523.0	1460.8	714.0	1020.5
58.0	111.2	156.3	229.1	139.6	111.4	121.6	133.4	39.6	67.0	182.4
65.8	677.7	503.2	497.9	463.5	570.7	573.5	447.6	453.4	695.6	230.8
87.3	762.1	804.4	839.3	878.6	1210.1	981.1	982.3	301.0	198.1	755.1
341.7	2080.1	2708.8	2982.1	10761.9	2981.1	3288.9	4042.2	1464.9	193.1	1142.0
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49.7	1367.3	1518.1	2413.1	4633.2	1810.5	1408.0	1784.4	466.6	70.4	834.1
2299.4	4482.0	4497.2	5881.3	8766.8	5254.6	6129.3	4918.6	3420.7	1688.0	3588.2
37.9	16.1	22.8	15.4	21.0	17.9	20.6	13.7	16.6	11.9	13.9
469.0	5404.1	4081.2	4530.0	7887.2	5155.5	5199.8	4596.4	2956.6	1956.7	3798.0
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8223.8	4994.8	4044.6	5685.4	7774.7	5270.4	5928.0	4315.1	4272.8	2146.6	4346.7
57.6	296.7	363.2	429.3	1252.4	353.8	444.2	596.0	161.0	180.8	269.1
13588.2	8375.3	7727.4	9887.2	14242.2	9008.7	10413.0	8413.6	8442.6	6188.5	8844.5
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44.8	57.9	76.2	50.4	43.8	44.9	78.0	32.5	27.2	27.3	82.9

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2786.3	2881.2	4845.8
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73.7	143.2	488.8
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211.0	230.8	367.9
2053.0	2659.1	3043.5
2216.2	3453.2	3207.8
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6767.4	5563.3	7499.4
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GU118642.1 gg_id:549595 Threatened Corals Provide Microbial Habitats clone Mfav_D14 GU118
EF492939.1 gg_id:257467 Iron-manganese Nodule and Its Surrounding Soil soil around iron-manganese nodule EF4929
GQ848453.1 gg_id:588843 Microbial sediments vents along East Lau Spreading Centre deep sea hydrothermal GQ848
GQ500804.1 gg_id:586905 Surveys Biofilms and Sediments Mammoth Cave Karst Aquifers Bio-Sep beads conta GQ500
EF594048.1 gg_id:234702 mixed granule anammox reactor clone KIST-JJY015 EF5940
AY921494.2 gg_id:153641 Changes soils rice field soil clone AP19 AY9214
AY493911.1 gg_id:136740 Fingerprinting aggregates soil clone 1183 AY4939
NR_029287.1 gg_id:554350 Nitrospira moscoviensis str. NSP M-1; DSM 10035 NR_02
DQ451477.1 gg_id:156598 forest soil clone FAC38 DQ451
EU287156.1 gg_id:246040 Pacific arctic surface sediment clone P13-63 EU287
AJ863251.1 gg_id:120977 poplar tree microcosm bulk soil flooded clone 21BSF62 AJ8632
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GQ214107.1 gg_id:536771 China loess clone P859 GQ214
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AY328715.1 gg_id:88698 drinking water system simulator clone DSSD16 AY3287
EF612393.1 gg_id:246188 historic semiarid lead-zinc mine tailings site soil clone OS-C76 EF6123
FJ529312.1 gg_id:570363 Evidence vertical transmission symbionts adult embryo Caribbean sponge Svenzea ze FJ5293
EF092255.1 gg_id:260626 Persistent Axinella corrugata Nitrospira clone MAx27_C6 EF0922
EU652665.1 gg_id:279215 Seasonal variation microbial Yel Sea sediment clone D8S-37 EU652
DQ058679.1 gg_id:139106 Identification biofilm and bulk s nonchlorinated model system: detection large nitrit DQ058
AF317764.1 gg_id:136664 Nullarbor cave clone wb1_F07 AF317
EU491363.1 gg_id:274991 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X3 clone EU491
GQ472347.1 gg_id:545624 Microbial Dongping Lake lake sediment clone 3C2-9 GQ472
EF562103.1 gg_id:243273 Subsurface microbial deep-granitic-fracture water colorado Henderson Molybdenum EF5621
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GQ357017.1 gg_id:582662 Metal Dependent Marine Methane Oxidation methane seep sediment clone FeOrig_ GQ357
EU491391.1 gg_id:269847 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X3 clone EU491
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EU780676.1 gg_id:304501 magnetic-enriched magnetotactic Miyun reservoir Beijing China fresh water sedimer EU780
DQ478745.1 gg_id:157587 UASB reactor treating brewery wastewater clone CLONG59 DQ478
AB179690.1 gg_id:101911 groundwater 0.2 m-captured fraction clone KNA6-EB14 AB179

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AB240285.1 gg_id:142177 microbial structure Phragmites rhizosphere biofilm reed bed reactor laboratory clon AB240
GQ402751.1 gg_id:513871 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
FJ755775.1 gg_id:581592 vertical archaeal water and Lake Taihu sediment clone LT-SB-B104 FJ7557
GQ402791.1 gg_id:572073 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
DQ450806.1 gg_id:160776 Microbial Alpine Tundra Wet Meadow Soil: Chloroflexi Cold Water-Saturated satura DQ450
DQ395024.1 gg_id:151318 harbor sediment clone VHS-B5-55 DQ395
DQ138962.1 gg_id:138089 rice straw paddy soil clone JG131 DQ138
EU617719.1 gg_id:331634 Seasonal variation microbial Yel Sea sediment clone A13S-27 EU617
GU208367.1 gg_id:565006 Study on Sediment Dongping Lake sediment clone Td1-7 GU208
EF648166.1 gg_id:238866 dynamics during produced water treatment aerobic activated sludge clone XJ134 EF6481
DQ354748.1 gg_id:155453 subsurface water clone MS149BH1062003_38 DQ354
FJ484454.1 gg_id:540847 microbial autonomous rover world's deepest phreatic sinkhole wall biomat El Zacator FJ4844
AF286037.1 gg_id:51852 mercury and PCB contaminated saltmarsh sediment clone LCP-6 LCP-6 AF286
DQ811894.1 gg_id:171789 mangrove soil clone MSB-3B5 DQ811
DQ833491.1 gg_id:167800 detected analyses depth sediment Guanting Reservoir clone 35-52 DQ833
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EU592458.1 gg_id:594158 Seasonal changes Salton Sea hypersaline sediment clone SSS22N EU592
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GQ844371.1 gg_id:584184 Microbial anoxic tank full-scale water treatment plant influent produced wastewate GQ844
FJ638591.1 gg_id:511823 Temperature dependent succession sulfate reducing muddy southwestern Taiwan hc FJ6385
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AB021302.1 gg_id:1530 Thermodesulfovibrio sp. str. TGE-P1 AB0213
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EU735733.1 gg_id:320307 Biological Arsenic Remediation Project Groundwater Aquifer soil clone C_I55 EU7357
FJ497655.1 gg_id:590984 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun FJ4976
DQ640738.1 gg_id:232235 full-scale EBPR sludge clone Skagen116 DQ640
FM213079.1 gg_id:568248 Biodiversity and shifts assessment biology tools Biotrickling treating loads biotricklin FM213
FJ497309.1 gg_id:540736 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun FJ4973
FJ516826.1 gg_id:552017 semiarid 'Tablas de Daimiel National Park' wetland (Central Spain) unravelled lower s FJ5168
EF520619.1 gg_id:235051 structure lakes: what controls ? acid-impacted lake clone ACK-BTH02-32 EF5206

159.4	1772.0	2849.7	3408.7	1260.5	1526.9	2345.6	2812.0	716.8	357.9	1735.8
333.4	3002.1	3884.4	4180.9	2631.0	3842.9	3624.9	4305.8	1098.6	1219.8	2800.1
163.8	2566.3	1672.1	2077.6	2249.7	2140.8	1728.7	568.1	301.6	78.2	1428.0
886.6	4314.0	4380.3	5763.1	5092.7	4664.0	5322.7	4742.9	4037.7	1623.0	4805.9
507.0	5387.3	6435.3	8544.7	6705.8	6337.8	6761.5	5850.9	3175.8	2666.1	6335.1
1215.0	7021.5	7430.0	8243.6	7534.1	7674.9	7424.7	6754.6	10212.0	6053.4	7608.6
4862.4	4953.5	4546.9	5260.8	4904.7	4865.5	5363.0	4074.2	3530.7	3507.0	4855.3
8363.7	4674.4	5643.6	6161.9	4821.4	4581.2	5236.7	4400.0	4656.4	4598.4	6618.1
38.3	92.2	184.4	179.6	125.9	234.3	207.9	122.4	39.2	50.7	78.5
3264.6	4350.8	5818.4	6184.1	5750.0	5142.1	5985.2	5157.4	3442.7	2248.8	4863.2
4945.2	6644.6	8540.8	10498.5	9557.0	8683.8	10215.0	8979.0	8619.0	6217.4	10948.7
1750.8	3121.8	3603.5	4595.4	4410.8	3642.7	4403.8	3704.0	1728.5	1333.1	3146.8
366.0	2783.5	2931.9	3895.4	3029.9	3061.6	3246.9	2882.1	1409.2	2320.1	2758.8
33.3	70.9	154.9	192.4	90.5	26.0	24.4	165.9	41.6	21.9	54.8
44.0	91.7	80.8	105.7	116.6	87.4	246.7	91.7	38.7	30.9	69.7
169.2	552.3	866.4	764.7	653.9	496.8	733.9	599.2	228.2	94.0	147.7
105.0	739.0	762.6	728.2	835.9	620.6	1268.1	403.0	134.2	149.5	368.5
10139.3	6425.0	6700.3	6871.6	6627.6	6493.4	7707.7	5994.5	6201.3	5460.7	6909.3
3456.3	3698.9	4189.2	4786.5	4272.1	4282.6	5679.8	3908.3	3809.2	3413.7	4294.2
688.6	2970.7	3211.9	3434.5	2410.6	3177.4	2177.3	2284.1	3896.1	3477.2	2935.8
4284.1	6243.0	6500.5	7728.6	7708.2	6646.1	9186.1	6938.3	5690.3	2972.7	6952.1
77.3	1320.4	1551.9	1594.8	1685.6	1316.4	1586.8	1555.4	764.5	771.6	1425.9
2862.2	4168.2	4528.0	4664.4	4607.6	4394.4	4795.7	4601.0	5816.3	4820.3	5075.0
58.9	143.9	207.7	282.6	300.4	331.3	553.7	200.7	80.7	63.1	104.4
40.2	1998.1	2360.8	3233.7	3663.1	2334.5	2703.8	2542.6	688.3	342.3	2072.4
45.9	2489.2	3241.7	4124.3	2993.3	2489.0	3000.2	3569.4	880.8	771.0	1723.4
39.2	67.8	136.3	181.3	85.9	71.7	69.9	78.8	39.0	26.9	83.0
83.8	1590.7	1986.1	2132.8	2300.4	1683.7	2396.9	2083.0	796.6	774.6	1413.1
120.0	210.8	247.8	388.7	325.9	235.2	315.8	292.3	108.6	51.2	196.2
114.4	2777.7	2953.1	3363.4	3925.1	2735.8	3420.0	3418.9	1504.7	589.6	2123.2
31.1	45.9	114.4	47.3	61.3	42.5	45.3	47.5	42.3	24.4	50.3
55.8	59.6	82.6	75.2	92.4	57.5	79.8	91.2	47.7	40.1	50.2
61.0	125.2	250.8	217.6	490.9	939.2	1238.2	91.4	58.9	39.3	131.8
94.7	2654.6	2458.6	2908.0	3431.8	2983.5	3506.6	2182.3	502.9	769.9	1826.5
4461.7	4519.5	4852.3	5988.9	5323.4	4991.3	6752.1	4570.0	3135.9	3548.6	4979.0
1549.9	3605.2	4000.8	4427.2	3889.0	3816.3	5929.4	3953.5	2590.1	1377.3	2676.1
455.7	3304.1	2536.4	2915.6	2043.2	2343.2	2319.3	2493.8	2462.8	1806.6	1714.8
1295.3	4623.5	4438.2	5347.3	4176.7	4177.3	4583.8	4458.0	3151.5	3157.5	3232.5
4516.6	5608.6	4961.7	5462.4	4388.3	4941.8	6613.2	4888.9	4976.1	4673.0	5499.7
423.4	2870.8	3075.1	3275.1	3472.0	2953.4	4089.8	3337.4	1857.3	1305.9	2175.5
206.2	2908.6	3208.3	3371.6	1090.4	3614.0	3609.1	4952.5	2964.7	897.8	4738.8

1286.5	1574.5	1113.3
2453.0	3251.0	6369.8
510.2	224.9	733.8
4394.0	4998.6	4965.4
4234.3	2856.2	5487.8
6312.5	7846.8	7196.6
4057.2	4314.7	5034.7
3612.4	4702.2	4901.8
61.2	69.8	90.4
4328.6	4192.3	5475.1
7932.2	8439.3	10084.7
3039.8	3292.2	4687.7
1793.8	1842.6	2926.5
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34.3	69.2	80.5
489.3	142.1	602.6
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3999.5	4812.8	3833.9
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6266.7	6463.5	8350.0
1188.9	1340.4	1171.7
3781.8	5379.5	3610.5
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1952.7	2117.5	3088.0
2395.5	2761.3	3207.2
52.2	159.3	88.7
1926.2	1508.4	2216.0
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3375.4	2835.8	3205.4
29.0	44.4	54.9
82.1	134.4	111.0
268.9	273.3	177.6
1638.5	1176.7	2029.1
4201.3	4362.6	5920.0
3129.9	3720.0	5234.6
2225.7	2071.2	1871.9
4134.8	4170.8	4892.0
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GU208454.1 gg_id:562764 Study on Sediment Dongping Lake sediment clone Fr2-1 GU208
CU921757.1 gg_id:574695 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU921
DQ395545.1 gg_id:154578 deep-sea octacoral clone ctg_CGOCA85 DQ395
GU302451.1 gg_id:546200 Spatial structure and activity sedimentary microbial underlying Beggiatoa spp. mat h GU302
FJ497634.1 gg_id:570634 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun FJ4976
FJ497567.1 gg_id:539167 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun FJ4975
GQ246342.1 gg_id:566822 Temporal and spatial China North Yel Sea sediments clone Cm1-5 GQ246
EU617857.1 gg_id:306314 Seasonal variation microbial Yel Sea sediment clone C13S-3 EU617
FJ769506.1 gg_id:514019 Changes Methanogenic Microbial After Sludge Pre-treatment full-scale municipal ana FJ7695
EU245141.1 gg_id:238328 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-H2-H0 EU245
GQ848462.1 gg_id:591704 Microbial sediments vents along East Lau Spreading Centre deep sea hydrothermal GQ848
EU491069.1 gg_id:263387 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount South Rift X EU491
EU385825.1 gg_id:269047 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S EU3858
EU591656.1 gg_id:275968 Microbial Ecology Focused-Pulsed Electric Field Sludge Pretreatment Methanogenic EU591
AJ306780.1 gg_id:66921 DCP degrading consortium clone SHA-100 AJ3067
DQ067040.1 gg_id:132726 Lake Washington sediment clone pLW-99 DQ067
GU118009.1 gg_id:554824 Threatened Corals Provide Microbial Habitats clone Apal_G06 GU118
AY193179.1 gg_id:80983 thermal spring mat clone O1aA90 AY193
EU635936.1 gg_id:278503 Microbiology geochemistry great boiling and mud springs sediment hot spring; temp EU635
EU635935.1 gg_id:278911 Microbiology geochemistry great boiling and mud springs sediment hot spring; temp EU635
EU924242.1 gg_id:310156 Microbiology and geochemistry Little Hot Creek hot spring sediment temperature 8 EU924
DQ404838.1 gg_id:202174 contaminated sediment clone 655967 DQ404
FJ189542.1 gg_id:340415 digester anaerobic sludge clone EUB_21 FJ1895
AY218580.1 gg_id:82092 penguin droppings sediments clone KD2-26 AY218
AY218586.1 gg_id:82149 penguin droppings sediments clone KD2-5 AY218
AY188303.1 gg_id:80684 marine? clone KD3-145 AY188
EU542445.1 gg_id:264265 Effects chemical structure concentration on pathways microbial during dechlorinatio EU542
AY188301.1 gg_id:99822 marine? clone KD2-44 AY188
AF050600.1 gg_id:10566 contaminated aquifer clone WCHB1-07 AF050
EF019888.1 gg_id:210172 aspen rhizosphere clone Elev_16S_1253 EF0198
EU386078.1 gg_id:269947 Biogeographical and microbes sediments on subseafloor sediment South China Sea c EU386
EF019157.1 gg_id:206209 aspen rhizosphere clone Amb_16S_1804 EF0191
EU134976.1 gg_id:255464 tallgrass prarie soil clone FFCH9932 EU134
FJ479589.1 gg_id:509215 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4795
DQ298014.1 gg_id:142268 Microbial hydrocarbon contaminated soil clone UB12 DQ298
AF422676.1 gg_id:42849 TCE-sediment clone d153 AF422
CU924193.1 gg_id:534077 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU924
FJ710771.1 gg_id:593853 Abundance and microbial long-term operated anammox biofilm reactors initiated ino FJ7107
GQ356089.1 gg_id:556282 biomarkers ammonia oxidation activity anaerobic ammonium-oxidation (Anammox) GQ356
EU050864.1 gg_id:253554 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_08_10 EU050
EU386076.1 gg_id:274390 Biogeographical and microbes sediments on subseafloor sediment South China Sea c EU386

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47.9	236.4	546.1	569.9	138.3	295.9	234.9	774.5	753.6	80.3	334.4
974.6	4045.7	3660.1	4059.4	4597.3	4630.6	4307.5	4396.7	1759.3	3227.7	4289.6
8952.1	4654.4	5264.2	4898.1	6120.7	3702.0	6124.5	5322.6	4122.2	2288.3	4880.9
3656.0	4414.2	4354.3	4593.7	3994.4	3444.4	4388.2	3455.5	3612.7	3141.0	3861.8
3493.4	6524.9	6593.9	7063.8	7352.0	7736.9	8300.0	7915.4	6180.3	7988.1	7986.3
6139.8	10871.0	11308.8	12151.4	12031.9	10670.5	12529.7	10599.8	15122.1	11963.3	12321.2
9103.2	9444.5	7773.4	7229.0	7122.2	7371.8	7805.4	5996.4	10152.7	7555.9	6321.2
1096.9	6356.2	7213.4	6499.8	8145.1	6660.5	7701.8	6867.3	5319.1	7185.9	6642.6
813.1	7357.6	6869.4	7254.3	7814.6	7204.6	8442.2	6858.9	6156.4	6227.9	6238.7
3181.5	5169.0	5419.0	6523.8	6169.7	5431.3	6827.1	5691.8	5079.7	4324.6	6014.2
4732.6	6487.3	6318.8	7068.1	7420.8	6394.3	8091.9	6720.4	5692.1	5717.8	8124.2
136.7	3246.2	2917.2	2994.7	3193.5	3276.1	3352.2	4014.2	4527.0	3667.3	2464.3
795.4	6914.3	6860.0	7866.5	7937.0	7346.1	8829.9	7561.6	5424.1	3550.2	6078.6
5577.4	6893.5	6428.6	6950.4	7667.1	6645.6	8861.4	6678.6	5485.1	5408.4	6264.6
66.8	123.2	146.3	156.2	254.6	131.9	167.9	197.8	52.3	66.3	93.3
2004.4	9989.3	9017.5	10253.2	10453.6	9129.4	12416.8	8693.3	9715.2	9140.3	10283.0
86.6	1841.9	1793.4	2262.8	3214.1	1676.6	2987.0	1889.9	1059.4	338.7	928.7
686.8	4621.2	3491.9	5279.2	7457.9	5007.5	8141.5	3964.9	3576.6	1504.8	4190.6
310.6	2893.3	3407.6	3759.4	5923.0	3584.3	7192.1	2742.4	2184.1	770.6	1801.8
4404.8	4123.3	4044.7	4499.3	3630.8	3995.5	5124.5	4005.4	3157.7	1246.8	3715.0
3370.7	7126.1	6978.0	7397.2	4860.2	7386.7	8487.5	6283.9	2635.8	3782.8	7468.4
378.6	4907.8	4528.2	4731.0	3184.3	4249.6	4299.0	4126.1	1500.8	887.1	4688.3
53.7	1104.4	980.9	1240.6	190.6	260.3	1190.7	499.6	39.9	34.4	427.1
57.1	448.6	337.9	286.2	67.9	118.6	327.3	208.8	25.0	26.4	192.7
40.7	413.2	424.2	415.9	75.3	179.6	624.1	225.4	36.2	33.9	220.4
1948.6	4517.4	4583.2	5034.4	3719.8	4135.9	5225.5	4878.4	2330.9	1887.3	5087.7
377.9	3274.6	2870.7	3352.9	4084.7	2997.0	4350.7	3935.6	1608.9	1265.8	3033.5
56.2	901.4	1001.4	1047.3	659.8	813.6	1736.0	1348.4	159.6	128.5	795.7
89.5	6125.1	4226.2	4161.3	4449.8	6849.9	4829.7	3515.1	405.7	1446.5	4516.6
5691.6	8638.1	7835.8	8341.3	7113.7	7871.5	7952.8	7260.1	6966.9	4244.4	9196.2
162.2	7069.0	4494.4	4360.3	3548.5	5043.4	5292.6	4800.9	1891.5	2192.9	4418.5
70.1	8480.5	6267.6	6542.1	5859.1	6601.9	6518.2	5422.3	739.9	2294.9	6010.8
17815.3	10972.2	8851.9	9523.6	10993.9	10354.0	12412.7	8401.0	9827.7	7867.0	11710.4
21479.7	9103.3	9347.2	9307.8	9628.6	9350.5	11424.8	9258.0	11394.3	6464.1	10371.7
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227.2	5417.0	5362.2	5605.4	4583.4	4572.9	5710.7	5440.9	1517.9	2414.9	5216.6
5747.8	8526.2	8023.4	8683.5	7222.5	7420.6	8496.0	8968.1	8070.1	4370.5	9491.0
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EU386007.1 gg_id:266385 Biogeographical and microbes sediments on subseafloor sediment South China Sea c EU386
AB015559.1 gg_id:1665 deep-sea sediment clone BD4-9 AB015
EU385777.1 gg_id:271294 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S EU385
FJ746242.1 gg_id:511521 Microbial oligotrophic marine sediments: South Pacific Gyre ocean sediment 5306 m FJ7462
EU386085.1 gg_id:258248 Biogeographical and microbes sediments on subseafloor sediment South China Sea c EU386
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EU385956.1 gg_id:271229 Stratified microbes sediments Core MD05-2902 subseafloor sediment South China S EU385
EU800499.1 gg_id:331078 It's all ranking aquatic Delaware Bay NJ clone 2C228620 EU800
AM997403.1 gg_id:534821 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A AM997
AM991275.1 gg_id:279473 Microbial groundwater and their potential use biomonitoring karst spring water clo AM991
DQ676354.1 gg_id:226121 Archaeal sediment and plankton freshwater pond suboxic freshwater-pond clone M DQ676
AM997371.1 gg_id:538271 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A AM997
AF507707.1 gg_id:65679 forest soil clone S042 AF507
AY661975.1 gg_id:137070 uranium-contaminated groundwater clone 300E2-C09 AY661
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AM997579.1 gg_id:552101 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A AM997
GU208411.1 gg_id:592150 Study on Sediment Dongping Lake sediment clone Fh2-22 GU208
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DQ837261.1 gg_id:238430 Archaeal and pristine National Park Spain Donana coastal aquifer clone 49S1_2B_70 DQ837
AB232806.1 gg_id:138097 Microbial mesophilic chemostat cultivation propionate-degrading methanogenic con AB232
EF019262.1 gg_id:204198 aspen rhizosphere clone Elev_16S_444 EF0192
AB294344.1 gg_id:211556 Microbial structure deep coal seem groundwater stream clone SWB33 AB294
EU881347.1 gg_id:317758 (maize-sweet cropping field) Karst region maize-sweet potato cropland soil clone KM EU881
EU491266.1 gg_id:274405 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak EU491
EU373974.1 gg_id:272286 southern Cretan margin (eastern Mediterranean Sea) canyon and slope sediment clc EU373
FJ901639.1 gg_id:509494 phreatic limestone sinkholes northeastern Mexico biomat 30m deep cenote La Palita FJ9016
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DQ676379.1 gg_id:225089 Archaeal sediment and plankton freshwater pond suboxic freshwater-pond clone M DQ676
GQ356163.1 gg_id:534717 biomarkers ammonia oxidation activity anaerobic ammonium-oxidation (Anammox) GQ356
EF032777.1 gg_id:176040 cyanobacterial mat in lava cave clone HAVOmat111 EF0327
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EU385872.1 gg_id:263088 Stratified microbes sediments Core MD05-2902 subseafloor sediment South China S EU385
AY704402.1 gg_id:112300 oceanic crust clone FS142-68B-02 AY704
GQ143758.1 gg_id:395003 Level Continental Shelf Sediment and Phylum-level lineages Phylum Planctomycetes GQ143

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EU181480.1 gg_id:249848 Prokaryotic enhanced organic matter remineralization continental margin marine se EU181
EU245272.1 gg_id:252038 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-H5-B04 EU245
AB177161.1 gg_id:133316 seafloor methane hydrate clone ODP1230B18.23 AB177
EU385795.1 gg_id:269229 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S EU385
FJ746322.1 gg_id:551173 Microbial oligotrophic marine sediments: South Pacific Gyre ocean sediment 5306 m FJ7463
DQ811948.1 gg_id:170025 mangrove soil clone MSB-4A8 DQ811
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AB177172.1 gg_id:130540 seafloor methane hydrate clone ODP1230B20.28 AB177
EU385742.1 gg_id:266551 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S EU385
EU488093.1 gg_id:559670 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU488
DQ811949.1 gg_id:169350 mangrove soil clone MSB-3A8 DQ811
EU592453.1 gg_id:563387 Seasonal changes Salton Sea hypersaline sediment clone SSS83N EU592
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EU245402.1 gg_id:238714 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M1-C0 EU245
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FJ461971.1 gg_id:510303 Microbial ecology industrial digestor mesophilic anaerobic reactor fed effluent chemi FJ4619
DQ067009.1 gg_id:134526 Lake Washington sediment clone pLW-103 DQ067
EU399664.1 gg_id:273972 and localization microbial consortium full-scale granular activated carbon anaerobic EU399
AJ583209.1 gg_id:95059 radioactive site ground water clone S15B-MN72 AJ5832
AJ249097.1 gg_id:53679 DCP-dechlorinating consortium clone SHA-89 AJ2490
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EU290738.1 gg_id:257532 microbial structure biogeochemical contrasting shelf sediments Namibian upwelling EU290
FJ755774.1 gg_id:592094 vertical archaeal water and Lake Taihu sediment clone LT-SB-B88 FJ7557
AF449263.1 gg_id:61847 Riftia pachyptila's tube clone R76-B102 AF4492
CR933160.1 gg_id:110989 Evry municipal wastewater treatment plant clone 009E07_B_SD_P15 CR9331
EU721812.1 gg_id:575401 microbial production water Alaskan mesothermic petroleum reservoir two methods EU7218
EU358736.1 gg_id:315354 structure archaeal denaturing gel electrophoresis and sequencing mesophilic biogas EU358
EF559206.1 gg_id:225664 mesophilic anaerobic digester clone A35_D28_L_B_A04 EF5592
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AF419693.1 gg_id:74279 Guaymas Basin hydrothermal sediment clone C1_B023 AF4196
AB300125.1 gg_id:224659 Wide ancient microbial DNAs Quaternary sediments holocene mud sediment clone K AB300
AJ535219.1 gg_id:77784 marine sediment above hydrate ridge clone Hyd01-10 division AJ5352
AM745133.1 gg_id:289184 Impact oil er hydrocarbons on microbial and activity Gulf Mexico cold seep marine s AM745
AY542196.1 gg_id:112789 Gulf Mexico seafloor sediments clone GoM HDB-04 AY5421
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AB189340.1 gg_id:113184 cold seep sediment clone JT58-14 AB1893
FJ712453.1 gg_id:530784 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) K FJ7124
AF419682.1 gg_id:72683 Guaymas Basin hydrothermal sediment clone CS_B013 AF4196

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AB300107.1 gg_id:223917 Wide ancient microbial DNAs Quaternary sediments holocene mud sediment clone K AB300
EU386091.1 gg_id:273192 Biogeographical and microbes sediments on subseafloor sediment South China Sea c EU386
EU290732.1 gg_id:242377 microbial structure biogeochemical contrasting shelf sediments Namibian upwelling EU290
AF154105.1 gg_id:13713 hydrocarbon seep sediment clone GCA018 AF154
EU639265.1 gg_id:335164 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU639
CU919953.1 gg_id:542554 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU919
CU919427.1 gg_id:541379 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU919
CU920257.1 gg_id:539233 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU920
EF559042.1 gg_id:249738 Microbial functional groups solid waste digestor stable isotope probing thermophilic EF559
EF558973.1 gg_id:248313 Microbial functional groups solid waste digestor stable isotope probing thermophilic EF558
EU635950.1 gg_id:278345 Microbiology geochemistry great boiling and mud springs sediment hot spring; temp EU635
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AB195912.1 gg_id:109200 Anaerobic sludge clone N10 AB195
CU925213.1 gg_id:561559 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU925
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AY485295.1 gg_id:106114 marine sponge clone 232 AY485
AY627378.1 gg_id:103111 marine clone AY627378 AY627
GQ349157.1 gg_id:575293 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ349
FJ746128.1 gg_id:539443 Microbial oligotrophic marine sediments: South Pacific Gyre ocean sediment 5306 m FJ7461
EF076099.1 gg_id:238478 Sponge- microorganisms: ecology and biotechnological potential Bahamas: Little San EF076
EU617889.1 gg_id:327521 Seasonal variation microbial Yel Sea sediment clone D13S-68 EU617
FJ208807.1 gg_id:307010 Enrichment ANAMMOX Wastewater Treatment Plants Korea and Their Activity sludg FJ2088
FJ208813.1 gg_id:305954 Enrichment ANAMMOX Wastewater Treatment Plants Korea and Their Activity sludg FJ2088
GQ348002.1 gg_id:540414 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ348
FJ208832.1 gg_id:332638 Enrichment ANAMMOX Wastewater Treatment Plants Korea and Their Activity sludg FJ2088
DQ058681.1 gg_id:139290 Identification biofilm and bulk s nonchlorinated model system: detection large nitrit DQ058
BX294710.2 gg_id:84726 aerobic basin clone CY0ARA025G12 BX294
EF575301.1 gg_id:227921 site S25 near Coco's Island marine clone S25_1645 EF5753
FJ485411.1 gg_id:509346 microbial autonomous rover world's deepest phreatic sinkhole wall biomat El Zacator FJ4854
EU236408.1 gg_id:290327 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg92E7 EU236
EF208657.1 gg_id:201142 Vertical and horizontal structure microbial sandy carbonate sediment clone CI35cm.2 EF2086
GQ246374.1 gg_id:577122 Temporal and spatial China North Yel Sea sediments clone Cm1-37 GQ246
AM997498.1 gg_id:560658 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A AM997
FJ208809.1 gg_id:352790 Enrichment ANAMMOX Wastewater Treatment Plants Korea and Their Activity sludg FJ2088
L10943.1 gg_id:2910 Marine sp. (aggregate agg27) generated fragment L10943
EU478627.1 gg_id:339005 microdiversity study anammox Candidatus Scalindua phylotype marine oxygen minir EU478
AY907752.1 gg_id:137332 identification picoplankton contrasting waters Arabian Sea water clone A314014 AY9077
AM997936.1 gg_id:548511 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A AM997

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451.2	1049.5	1563.1	1361.4	1891.1	1301.9	2932.5	1238.8	750.6	423.4	1056.7
9950.8	3299.3	2925.2	3295.7	2986.0	3075.7	4532.7	2734.7	3022.7	2898.9	3459.5
305.2	679.3	725.8	791.7	598.0	656.8	790.8	662.5	490.3	238.1	299.3
54.3	429.5	432.8	475.8	590.6	481.0	506.6	480.1	363.8	294.3	889.0
11916.1	3273.9	3361.5	3540.8	2723.3	2879.5	3575.9	2757.3	4321.9	2816.5	4449.3
2488.3	6394.8	6016.6	6415.0	6555.1	6761.6	7453.7	5720.6	5559.3	3711.1	6295.1
1716.7	3674.6	3993.6	3351.3	3805.7	3372.8	4040.2	3187.4	3940.4	3347.2	4075.2
8218.3	7032.9	6407.0	6807.6	5634.6	6439.8	6497.0	5673.8	8753.7	7625.6	7129.1
8992.3	6229.8	6398.9	6579.7	6882.2	6699.4	7678.1	7815.6	8727.5	5997.6	6792.5
3562.1	2978.4	3229.2	3529.3	3613.1	3145.8	3479.7	2867.4	2326.4	2640.5	2438.1
1514.6	795.3	956.0	1350.8	1051.6	1047.1	898.1	1227.8	421.1	289.5	495.2
430.0	1016.5	1349.7	1199.0	1390.7	1178.9	1210.0	1085.4	1371.5	879.9	1283.4
35512.0	11360.0	10860.6	12023.9	10948.5	10972.4	11854.6	11448.1	14275.8	10554.3	14744.2
2470.8	6216.9	5250.7	5945.8	5397.6	6057.7	6340.6	6167.3	6214.8	3837.5	4628.4
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105.8	1475.4	1675.7	1675.2	1911.3	1562.2	2539.0	1372.5	1151.7	621.5	1170.2
1086.9	4182.3	4440.0	4566.1	4477.6	4349.6	5376.3	4338.4	4286.3	4720.0	4297.0
2082.2	6537.0	7765.5	7375.1	6331.2	5994.5	6610.6	6362.3	5406.0	4294.7	7229.0
94.0	243.6	261.1	372.5	384.0	250.7	286.6	292.3	91.1	54.1	148.0
2553.5	5734.7	4883.4	5513.2	5533.9	4904.2	6483.7	4829.2	6003.5	4735.1	4108.3
144.6	2385.5	2865.8	3150.1	3289.5	2596.8	4100.0	3700.5	1856.9	799.2	2137.1
13386.8	9805.0	10068.5	11510.7	12223.9	10099.0	13593.6	10920.9	11673.2	8391.8	11648.3
859.7	8405.8	8363.9	8315.9	8088.0	7756.3	9153.5	7897.7	7884.4	4479.7	6893.8
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32.5	192.0	146.7	143.6	388.4	140.2	265.1	453.1	71.1	32.7	59.2
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36.9	22.4	17.7	19.0	23.1	17.3	17.6	18.3	14.7	26.5	18.2
133.8	3322.8	4186.1	4626.8	5467.1	4077.0	6050.2	5949.9	2423.8	1546.2	3299.7
1054.1	6013.7	5539.3	5400.0	6489.3	4793.7	7177.0	6072.6	7023.5	6325.4	5108.2
88.0	37.3	32.3	30.6	43.0	31.7	34.7	35.3	39.8	23.8	34.2
2031.9	2147.9	2336.6	2497.8	3220.8	2478.7	3074.9	2643.0	2803.0	1996.1	1529.3
2534.5	5413.7	6197.9	6407.3	6035.1	5449.7	6770.1	5809.3	3082.6	4434.5	4434.4
15388.1	11002.5	11024.8	12863.1	12273.8	11300.0	14476.8	12377.8	12692.9	12106.3	14748.1
37.4	34.1	51.8	48.5	53.9	44.7	169.2	56.9	39.7	34.7	46.4
1699.5	7836.4	7702.0	8690.5	8789.3	7756.5	10020.2	7532.4	6777.8	4238.1	6821.9
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386.3	691.0	578.8
2402.7	3867.9	3120.8
5245.4	6643.0	8396.9
4033.6	3465.0	4050.6
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5726.9	6823.9	6197.2
3305.5	3836.6	3737.2
1134.3	1696.3	3753.4
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4861.4	4750.0	10559.8
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8122.0	8850.9	9699.2
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10677.5	11247.5	12932.0
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1287.0	366.8	425.2
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42.8	34.8	36.5
2890.7	3036.3	2939.5
6147.9	5438.5	7740.1
11741.3	12836.1	14538.3
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FJ652534.1 gg_id:570506 aerobic and anaerobic ammonia-oxidizing marine sponges Atlantic Ocean water colur FJ6525
DQ513072.1 gg_id:160383 Microbial life fluids ridge flank crustal fluid clone FS266-6B-03 DQ513
EF092217.1 gg_id:270621 Persistent Axinella corrugata clone B255_19a EF0922
FJ208822.1 gg_id:333159 Enrichment ANAMMOX Wastewater Treatment Plants Korea and Their Activity sludg FJ2088
FJ208814.1 gg_id:336106 Enrichment ANAMMOX Wastewater Treatment Plants Korea and Their Activity sludg FJ2088
FJ208815.1 gg_id:318107 Enrichment ANAMMOX Wastewater Treatment Plants Korea and Their Activity sludg FJ2088
EF516837.1 gg_id:223894 grassland soil clone FCPS655 EF5168
GQ349982.1 gg_id:579975 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ349
DQ513105.1 gg_id:161200 Microbial life fluids ridge flank crustal fluid clone FS275-24B-03 DQ513
EU373996.1 gg_id:270915 southern Cretan margin (eastern Mediterranean Sea) canyon and slope sediment clc EU373
EU491188.1 gg_id:266276 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak EU491
EU478635.1 gg_id:332383 microdiversity study anammox Candidatus Scalindua phylotype marine oxygen minir EU478
EF645945.1 gg_id:242961 Potential interactions particle- anammox and archaeal partners namibian Namibian u EF6459
GU118095.1 gg_id:584707 Threatened Corals Provide Microbial Habitats clone Apal_E05 GU118
EU050872.1 gg_id:237785 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_04_05 EU0508
DQ070801.1 gg_id:147446 Prokaryotic Structures Seafloor Basalts Varying Age and Juan de Fuca Ridge basalt gl DQ070
CU917688.1 gg_id:569653 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU917
AM056027.1 gg_id:137533 anammox wastewater treatment plant AM056
AM490671.1 gg_id:550928 Linking and functional nutrient spiraling mats (USA) microbial mat sulfidic cave sprir AM490
AY266450.1 gg_id:85294 Baltimore Harbor sediment clone B4 AY2664
EU478641.1 gg_id:338211 microdiversity study anammox Candidatus Scalindua phylotype marine oxygen minir EU478
FN396716.1 gg_id:565403 constant flux thermophilic cold seabed Arctic marine surface sediment clone s5_8_II FN3967
EU135126.1 gg_id:257290 tallgrass prarie soil clone FFCH12905 EU1351
FJ444691.1 gg_id:565666 Cotton Rhizosphere cotton rhizosphere clone 3h-166 FJ4446
FJ905739.1 gg_id:535979 s Tonga-Kermadec iron oxide sediments Volcano 1 Tonga Arc clone V1F106b FJ9057
GQ339140.1 gg_id:527968 Comprehensive Investigation on Iron Cycling Freshwater Seep ing Microscopy Cultiv GQ339
EU617888.1 gg_id:353402 Seasonal variation microbial Yel Sea sediment clone D13S-58 EU6178
EU638793.1 gg_id:340317 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU6387
GQ347619.1 gg_id:580887 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ347
AF314425.1 gg_id:39505 aerobic phosphorus-removal ecosystem clone PHOS-HE93 AF3144
EU478694.1 gg_id:312765 microdiversity study anammox Candidatus Scalindua phylotype marine oxygen minir EU478
FJ710640.1 gg_id:513938 Abundance and microbial long-term operated anammox reactors initiated inocula upi FJ7106
FJ710627.1 gg_id:534693 Abundance and microbial long-term operated anammox reactors initiated inocula upi FJ7106
GQ356125.1 gg_id:576581 biomarkers ammonia oxidation activity anaerobic ammonium-oxidation (Anammox) GQ356
EU661858.1 gg_id:292847 and kinetic research ammonia mixed sludge anaerobic ammonium oxidation reactor EU6618
AB057453.1 gg_id:28149 Planctomycete clone KSU-1 AB0574
GQ175284.1 gg_id:578161 nitrogen removal reactors lab scale SBR inorganic medium and glucose influence org GQ175
AY254883.1 gg_id:102606 rotating biological contactor clone EN 8 AY2548
AY257181.1 gg_id:92388 Candidatus Scalindua sorokinii AY2571
DQ386151.1 gg_id:206446 Anaerobic Ammonium Oxidizing Marine Widespread Occurrence but sea water Gulli DQ386
EF602038.1 gg_id:296196 Anammox marine sediments: cell numbers potential anammox activity and pore nuti EF6020

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127.7	1627.1	2862.9	2962.2	1813.5	2322.0	2942.1	1949.0	1006.0	325.8	1801.0
637.0	4342.7	3995.9	3471.7	3357.5	3445.4	3685.7	2847.2	2847.0	3456.5	4420.6
3842.5	6191.9	6076.8	6706.8	7699.1	6494.2	9032.4	6116.9	3536.7	3139.6	5312.5
3370.8	9204.2	8553.6	10038.8	8405.5	8585.4	9683.1	8711.7	8540.8	6752.1	10896.7
6627.6	8827.4	8944.2	10176.6	11421.8	9046.1	12970.0	8861.3	9169.3	7134.2	9680.4
39.4	144.6	152.4	167.7	385.9	196.0	2110.3	266.0	86.5	27.6	87.2
109.3	1280.5	1588.8	1614.4	1724.6	1073.4	1585.6	2211.7	904.0	155.3	952.9
79.3	988.3	1049.2	1137.6	609.0	178.2	1502.6	1015.1	292.3	295.4	1050.3
2473.9	7767.2	7536.6	8485.4	7861.6	8310.3	9170.2	7755.3	5845.3	6800.8	6508.7
1723.8	6090.3	5823.9	5896.6	8888.3	5744.2	8754.8	5507.1	6085.8	4744.8	5846.6
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1405.3	7386.5	7538.8	8037.7	8096.9	8424.7	9223.8	7304.1	6620.4	4517.0	11131.3
52.8	154.5	202.7	192.9	502.6	135.7	461.7	301.1	100.8	39.3	69.3
668.5	2112.3	2352.6	2561.6	3473.6	2482.7	3939.7	2550.9	1538.8	987.2	1834.4
62.3	58.1	88.9	51.8	97.5	57.1	137.5	48.2	33.8	28.5	33.6
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1529.0	6549.9	6339.1	8085.3	5042.0	6331.8	8269.2	6206.8	4991.0	3992.8	5959.1
36.5	43.5	35.0	40.6	43.8	54.0	37.5	19.7	18.7	13.0	32.9
1296.2	3704.1	4144.4	4256.2	5489.8	3975.1	5714.5	4513.7	3144.1	1849.6	3423.6
262.3	2316.7	2404.6	2276.8	3181.4	2411.8	3319.6	2758.9	2004.9	1076.9	2391.1
1694.9	6415.3	6271.1	7122.3	8379.8	6754.0	8343.5	6385.3	5228.3	2546.2	5589.5
214.2	4563.8	4308.2	4444.1	5114.3	3326.2	4387.3	4078.5	3525.2	1361.7	3095.2
2671.6	8886.0	8468.5	8950.8	9682.6	8073.3	10033.5	8461.8	8366.9	5081.7	7365.8
8241.5	7229.1	8007.1	7654.8	9823.5	7767.9	10880.3	8269.2	9728.5	5337.9	7245.2
1363.1	4412.1	5267.8	5620.9	5045.9	4886.7	6321.3	4715.3	3105.4	1413.5	3780.3
646.8	874.9	1349.7	916.6	977.3	964.2	844.6	982.4	1007.3	518.8	1051.1
1063.5	5679.5	5338.8	6084.8	6065.0	5428.1	6796.0	6934.3	3309.8	1462.0	5685.3
1426.1	6776.1	5966.1	6449.6	7481.5	6391.3	7133.8	6906.8	5937.3	3698.1	5450.1
65.3	740.3	1106.9	1323.4	853.5	1063.8	1019.3	1004.3	273.3	175.4	545.4
11928.5	5575.1	4711.3	6255.3	5200.3	4939.8	5719.1	5312.5	4251.0	3446.2	5661.1
3539.3	3914.6	3013.6	3155.2	3315.2	3171.6	3618.5	3351.9	3283.6	1807.5	2306.0
98.1	1098.3	1268.5	1184.7	1147.2	1298.8	2560.7	1235.2	495.5	223.1	458.9
74.2	307.0	652.1	484.5	500.5	646.1	648.0	466.4	162.0	86.3	199.8
34.7	915.9	1658.9	1817.2	1893.9	1679.3	2394.0	1092.1	272.5	34.4	376.3
38.9	147.6	199.2	210.3	231.1	337.5	417.6	258.0	33.8	34.3	80.7
5834.5	7568.2	7365.6	8214.4	10202.6	7530.4	9648.3	7395.4	8784.8	7183.4	6734.6
15487.5	8185.2	8080.6	9019.6	8853.9	8111.9	9849.2	7659.5	8715.3	6492.9	9682.4
118.6	2661.3	2347.7	1954.2	2330.7	2119.6	2647.0	2080.6	1286.7	1334.4	1697.4
2612.4	3540.2	3954.5	4347.7	5356.6	4550.7	6762.5	4023.1	2927.5	1801.8	3550.4

2516.5	2107.7	3038.4
1023.0	2311.4	4794.4
2961.1	3352.0	4050.8
6083.2	6468.0	8888.3
8136.3	8060.0	9321.7
9524.6	9669.2	11223.5
94.9	133.6	193.9
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2361.0	2438.5	3799.6
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3186.9	3233.9	3814.5
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4068.3	3669.8	6122.2
2482.2	2407.3	3217.0
6078.4	7519.8	9044.9
3763.0	3118.4	6141.5
8543.5	7879.3	9265.1
7813.4	8543.8	10350.1
4732.9	5336.7	7382.9
857.2	1151.1	806.1
5306.4	6909.6	8023.5
6552.0	6413.9	8219.6
1028.3	1336.0	4534.5
4385.6	5649.9	7499.3
2801.4	4001.5	4502.9
932.4	1516.3	4101.9
369.8	1037.2	1580.8
969.6	1421.5	3057.7
188.7	419.2	988.7
6547.5	7654.5	8724.8
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4816.7	4461.1	5381.2

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EU142947.1 gg_id:324638 Enrichment and two marine anammox involved nitrogen gas production anaerobic a EU142
AB300486.1 gg_id:219357 Detection Activity and Anammox Genes Coastal Marine Sediments Japan intertidal s AB300
AB281489.1 gg_id:194829 anaerobic ammonium-oxidizing planctomycete JMK-2 AB281
EU478593.1 gg_id:324123 microdiversity study anammox Candidatus Scalindua phylotype marine oxygen minir EU478
EU039861.1 gg_id:316215 Anaerobic Ammonium Oxidation Anammox Oxygen Minimum Zone Northern upper EU039
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EU039851.1 gg_id:334236 Anaerobic Ammonium Oxidation Anammox Oxygen Minimum Zone Northern upper EU039
EU478595.1 gg_id:335981 microdiversity study anammox Candidatus Scalindua phylotype marine oxygen minir EU478
DQ869384.1 gg_id:173040 evidence broad anaerobic ammonium-oxidizing freshwater and marine sediments B DQ869
EU039841.1 gg_id:338086 Anaerobic Ammonium Oxidation Anammox Oxygen Minimum Zone Northern upper EU039
EU478687.1 gg_id:306841 microdiversity study anammox Candidatus Scalindua phylotype marine oxygen minir EU478
EU039858.1 gg_id:318377 Anaerobic Ammonium Oxidation Anammox Oxygen Minimum Zone Northern upper EU039
EU039856.1 gg_id:305926 Anaerobic Ammonium Oxidation Anammox Oxygen Minimum Zone Northern upper EU039
GQ143786.1 gg_id:381880 Level Continental Shelf Sediment and Phylum-level lineages Phylum Planctomycetes GQ143
EU478661.1 gg_id:328021 microdiversity study anammox Candidatus Scalindua phylotype marine oxygen minir EU478
EU039855.1 gg_id:347502 Anaerobic Ammonium Oxidation Anammox Oxygen Minimum Zone Northern upper EU039
EU478664.1 gg_id:307650 microdiversity study anammox Candidatus Scalindua phylotype marine oxygen minir EU478
DQ534739.1 gg_id:229398 Anaerobic ammonium oxidation contributes significantly nitrogen loss Peruvian oxy DQ534
EU385873.1 gg_id:258876 Stratified microbes sediments Core MD05-2902 subseafloor sediment South China S EU385
EU385800.1 gg_id:262268 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S EU385
AB177204.1 gg_id:131205 seafloor methane hydrate clone ODP1230B31.20 AB177
EU050874.1 gg_id:239076 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_03_21 EU050
AB474364.1 gg_id:554768 Phycisphaera mikrensis str. NBRC 102668 AB474
FJ516779.1 gg_id:569736 semiarid 'Tablas de Daimiel National Park' wetland (Central Spain) unravelled biofilm FJ5167
EU236426.1 gg_id:302876 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg92H6 EU236
FJ202723.1 gg_id:356606 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2027
EU491354.1 gg_id:261113 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X3 clone EU491
AF445715.1 gg_id:44762 Planctomycetales clone SM2B12 AF445
DQ811901.1 gg_id:173711 mangrove soil clone MSB-4A3 DQ811
EF632950.1 gg_id:252359 Unique microbial contrasting aquatic altitude Andean Altiplano (northern Chile) fresh EF6329
AY344414.1 gg_id:91792 Lake Kauhako surface clone K2-S-7 AY344
FJ205228.1 gg_id:533393 Prokaryotic deep-sea region East Lau Spreading Centre inactive hydrothermal field se FJ2052
EU135058.1 gg_id:239668 tallgrass prarie soil clone FFCH1059 EU135
FJ205225.1 gg_id:568694 Prokaryotic deep-sea region East Lau Spreading Centre inactive hydrothermal field se FJ2052
EU801770.1 gg_id:341049 It's all ranking aquatic Chesapeake Bay MD clone 3C003141 EU801
FJ626886.1 gg_id:510050 Identification Phytodetritus Degrading Microbial Sublittoral Gulf Mexico Sands ocean FJ6268
EU135079.1 gg_id:247437 tallgrass prarie soil clone FFCH3889 EU135
AB430337.1 gg_id:276470 Removal Nitrogen Compounds Coupling Anoxic Ammonium Oxidation and Nitrate Re AB430

559.4	2865.4	2427.2	2652.1	2670.7	2475.6	2837.5	2885.4	1421.5	1032.6	1642.8
165.4	1681.2	2104.0	2407.0	1761.8	1923.0	2624.6	2313.8	1078.5	399.8	1417.0
2424.1	4839.3	5238.5	7472.4	6039.6	4617.0	6343.6	5305.2	3051.0	2248.2	4700.4
172.3	1291.0	1310.7	1526.5	2186.8	1575.3	1802.8	1652.9	1016.4	467.6	1031.8
3213.5	3194.5	3246.8	3639.0	3853.0	3827.1	4068.6	3802.8	3181.5	2273.7	3295.3
6618.8	5697.7	5481.4	5887.9	6497.2	5518.2	5886.1	5856.6	4642.7	3643.8	5396.6
7265.7	5381.8	5313.1	6150.3	7726.0	5213.5	7897.8	5501.4	5058.7	3639.5	5241.8
542.3	4698.7	4816.1	5700.3	8615.6	5410.8	8038.4	5603.6	2946.7	2234.3	3960.4
376.5	4868.8	4462.1	5500.3	5908.7	4514.3	5190.7	5257.1	4222.3	3496.0	3893.8
208.2	2633.6	2755.4	2924.6	3586.9	2776.6	3256.3	3161.4	3205.8	1927.9	2373.5
27863.4	8822.0	8442.9	9318.7	12643.9	9653.8	13085.7	8245.6	11372.8	8605.6	11399.3
1492.1	6164.6	6004.8	6813.8	6397.8	5696.1	7359.5	5469.6	4152.8	3326.3	5184.9
4429.6	4510.9	4810.7	5435.5	5540.8	4332.9	6014.7	3103.7	3844.8	4639.3	4780.4
4262.3	3927.7	4360.7	4098.3	4622.0	3456.5	4672.8	4303.2	3556.8	2627.5	3328.7
9600.1	6227.2	5981.0	6520.0	6659.8	6260.7	7586.1	6416.8	7370.3	4586.8	7618.3
6567.9	4509.2	4511.0	5288.6	6211.2	3792.2	5807.2	5133.7	5516.5	3068.0	4246.4
5709.1	8054.1	7977.0	9228.8	10330.2	7940.5	11359.8	8638.6	6764.3	5278.9	7695.3
10953.0	7289.3	6806.5	6736.4	7307.9	6501.0	7878.0	6434.2	6171.0	4773.6	7736.6
11561.3	5543.7	5468.4	5822.6	6470.9	6209.3	6457.9	5328.2	5847.7	4076.9	6756.7
2943.0	5936.4	6279.8	7178.1	9375.9	7263.8	11065.7	5224.3	4380.9	3208.3	6097.4
7889.4	4853.6	5357.5	5439.3	6500.8	4810.9	5977.6	5480.8	4222.5	5041.1	5311.3
584.6	5451.3	5329.1	5601.5	7724.7	6098.1	6833.0	7056.9	6469.7	2312.3	3744.2
2525.9	7959.3	8289.8	8401.6	10358.7	7893.4	10915.0	8176.9	8363.0	6371.1	6785.8
9050.8	10194.1	9677.3	10708.4	11106.3	9790.5	12010.3	10061.4	11791.7	8477.6	11958.6
4923.7	7661.3	6971.4	7714.3	7709.3	7484.6	9906.2	7533.3	6908.7	4730.5	7869.0
3952.4	5799.2	6989.3	7084.3	7829.6	5700.6	8141.8	6258.3	4374.7	900.4	5743.0
292.6	2180.3	2668.6	2862.8	2893.7	3202.5	4033.6	2873.7	2116.0	2919.0	2253.7
79.5	2309.9	2143.6	2110.4	3492.1	1056.3	3697.1	2114.6	1981.1	675.7	1528.2
36.3	54.7	61.0	45.1	64.5	57.5	115.1	81.5	22.2	29.1	28.5
379.9	4391.0	5532.4	5860.3	6154.8	4421.1	7779.1	5960.4	2886.7	1156.8	4224.5
43.9	91.8	124.6	114.1	143.7	119.3	135.0	142.3	57.1	40.4	89.0
45.9	126.1	144.3	148.9	163.3	122.9	171.1	121.2	49.2	33.0	65.4
273.5	2229.4	1875.4	1788.4	1409.8	1939.0	1773.3	2962.2	955.7	1263.1	1409.8
5162.5	3804.0	4207.8	3970.4	6369.8	3808.2	6475.6	4603.3	2813.0	3850.7	4897.2
109.1	1369.2	1082.3	1151.8	1463.2	1139.9	1582.7	1231.8	1007.0	510.7	818.6
48.8	965.0	1216.7	1126.3	4622.2	1631.2	2943.0	1869.0	372.4	136.8	280.0
33.2	21.3	21.1	20.5	27.0	15.8	34.4	19.3	22.3	15.2	18.9
70.5	31.3	42.3	43.1	71.8	30.5	54.0	50.8	26.8	20.2	21.7
82.3	1445.4	1412.1	1679.6	2034.9	1781.5	2178.4	1805.0	1255.8	291.7	1549.1
1537.5	2557.5	2522.6	3145.5	4376.0	2773.1	4111.2	2650.1	1382.7	787.5	2096.2
43.3	78.5	69.9	78.9	376.7	77.7	209.3	64.8	33.0	14.0	35.1

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1390.5	1842.9	3095.0
4087.0	4868.4	6027.9
1519.6	1738.2	2370.4
3368.5	4608.4	4496.8
5108.3	5902.6	6140.6
5312.5	6682.7	7988.2
5616.3	5439.9	6658.6
4628.9	4587.8	5976.6
2996.7	3522.9	3316.7
10630.1	11029.9	9184.8
4956.7	6029.0	8299.1
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3849.4	4716.4	4996.0
5696.2	7912.3	6801.1
5078.6	6473.0	4831.1
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5147.6	6880.3	6016.7
7295.0	6941.1	8542.5
5044.7	5762.2	5897.1
7282.3	5308.5	7712.8
8237.8	7557.1	10619.4
8922.7	10942.1	10974.3
7047.4	7975.0	9107.0
6479.9	6094.2	6897.4
2482.1	2357.3	3260.7
1865.9	578.9	2465.6
46.7	55.4	49.0
5787.3	4638.6	6491.2
113.7	105.7	151.4
93.8	89.0	159.4
1899.3	1401.6	2241.5
4238.2	5577.3	5123.3
1309.3	1186.7	1798.8
1665.5	546.7	551.9
14.3	16.0	17.7
41.2	35.5	51.7
1635.7	1588.7	2179.4
2442.1	2872.8	4161.8
57.8	51.8	81.3

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AB434262.1 gg_id:340702 Effect concentration on treatment non-woven biomass carrier sludge taken anammc AB434
DQ351812.1 gg_id:146588 Microbial Adherent Sediment Particles Heavy Metal Contaminated North Sea Surfac DQ351
EU236371.1 gg_id:294838 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg9F4 EU236
AM086132.1 gg_id:145659 Abundance and archaea mesotrophic Lake Kinneret lake profundal sediment clone (AM086
FJ612210.1 gg_id:561975 and Biogeochemistry Dongping Lake Ecosystems lake water clone DP7.3.10 FJ6122
DQ396220.1 gg_id:151370 deep-sea octacoral clone ctg_NISA377 DQ396
DQ513014.1 gg_id:160569 Microbial life fluids ridge flank crustal fluid clone FS140-16B-02 DQ513
AY162125.1 gg_id:135863 Cultivating Sargasso Sea clone GMD15D02 AY162
EF574227.1 gg_id:231309 site S25 near Coco's Island marine clone S25_571 EF5742
EF632831.1 gg_id:237452 Unique microbial contrasting aquatic altitude Andean Altiplano (northern Chile) sedir EF6328
AY957928.1 gg_id:115016 drinking water biofilm clone B3NR69D13 AY957
EU135121.1 gg_id:248077 tallgrass prarie soil clone FFCH5834 EU135
DQ450805.1 gg_id:200837 Microbial Alpine Tundra Wet Meadow Soil: Chloroflexi Cold Water-Saturated saturat DQ450
EU662552.1 gg_id:553506 Productivity- Chemolithoautotrophically Based Sulfidic Karst Systems floating microb EU662
EF515938.1 gg_id:218719 grassland soil clone FCPP573 EF515
FJ901683.1 gg_id:591480 phreatic limestone sinkholes northeastern Mexico biomat sediment cenote La Palita (FJ9016
GU359065.1 gg_id:531410 rhizosphere soil peanut clone 1S21 GU359
AF407717.1 gg_id:201735 microbial Australia's Great Artesian Basin 52 deg. C brown filament clone B16 AF407
GQ356133.1 gg_id:566719 biomarkers ammonia oxidation activity anaerobic ammonium-oxidation (Anammox) GQ356
EU881297.1 gg_id:304737 (maize-sweet cropping field) Karst region maize-sweet potato cropland soil clone KM EU881
AF312220.1 gg_id:199817 -based BTX-catabolizing microbial African sandy soil South Africa: KwaZulu-Natal Pro AF312
EF580964.1 gg_id:277693 Survey Microbial Freshwater Calcareous Mats freshwater calcareous mat clone CM1 EF5809
AF121889.1 gg_id:200587 analyses sulfidogenic and phenol-degrading microbial consortia 2-bromophenol-deh AF1218
DQ521520.1 gg_id:202207 Antarctic lake ice cover clone ANTLV2_E09 DQ521
AJ616270.1 gg_id:202670 and seasonal changes planctomycetales biofilms river biofilm clone DEL26 AJ6162
AB240380.1 gg_id:201941 microbial structure Phragmites rhizosphere biofilm reed bed reactor laboratory clon AB240
EF516039.1 gg_id:225108 grassland soil clone FCPN712 EF5160
EF125955.1 gg_id:581157 Biofilm-reactor Based Enrichment Utilizing Oligotrophic Concentrations Acyl-homose EF1259
FJ232661.1 gg_id:308368 Enrichment ANAMMOX Wastewater Treatment Plants Korea and Their Activity sludg FJ2326
AB486233.1 gg_id:540991 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC AB486
EU135254.1 gg_id:255557 tallgrass prarie soil clone FFCH8636 EU135
FJ479411.1 gg_id:572242 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4794
EU135178.1 gg_id:237749 tallgrass prarie soil clone FFCH7061 EU135
FJ232680.1 gg_id:333924 Enrichment ANAMMOX Wastewater Treatment Plants Korea and Their Activity sludg FJ2326
AY963421.1 gg_id:203044 analyses structures soils evergreen broad-leaved forests south-west China soil clone AY9634
FJ479427.1 gg_id:586523 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4794
EF580956.1 gg_id:279355 Survey Microbial Freshwater Calcareous Mats freshwater calcareous mat clone CM9 EF5809
DQ413078.1 gg_id:201687 Microbial -dependent and Approaches Anaerobic/Aerobic SBR Reactor EBPR sludge DQ413
EU881243.1 gg_id:312527 (long-term grazing and burned annual) Karst region serious disturbance field soil clor EU881
EU135175.1 gg_id:248027 tallgrass prarie soil clone FFCH6996 EU135
EU044117.1 gg_id:239077 luences structure fosters richness subtropical Altamaha Ohopee River Valley inland c EU044

5814.5	2134.7	2570.5	2306.2	2407.5	2593.7	2574.4	2569.2	2572.9	2261.2	2929.8
43.9	215.7	206.9	204.1	647.4	211.2	366.8	203.3	83.4	74.4	78.4
315.0	4337.7	3700.5	4291.2	5888.3	4293.1	5341.8	5380.1	4604.9	1785.8	3645.2
4393.1	3235.9	3437.8	3004.0	4235.3	3746.7	5030.6	3453.6	3186.9	3715.2	3173.3
1134.5	3708.2	3539.5	3835.9	3977.5	3977.5	5234.5	4305.6	5117.5	1886.8	4292.8
40.7	336.3	277.6	325.4	163.5	191.4	235.9	307.2	275.8	65.2	114.2
214.0	505.7	546.1	608.6	1050.2	585.0	1374.0	759.1	295.7	83.4	396.9
47.1	48.9	56.8	52.1	130.9	47.9	109.1	49.3	32.3	30.5	40.9
48.4	41.0	53.1	63.6	82.3	52.9	92.5	57.9	27.9	24.5	35.2
39.0	29.6	17.5	29.7	44.7	32.6	33.8	26.3	37.5	14.3	30.0
68.1	553.9	759.6	639.6	2212.6	874.8	1776.1	1418.5	490.7	102.0	407.9
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42.8	1247.5	1350.5	897.9	2560.5	1943.7	1766.3	1855.4	1059.8	617.3	677.6
1478.7	4432.3	4572.2	4773.0	7911.2	6060.4	7172.2	6061.2	2950.0	2878.1	2999.2
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97.1	2272.6	2298.3	1844.4	4536.2	3730.0	3557.3	3276.9	1332.2	826.6	1364.7
46.8	140.4	101.5	122.9	289.4	224.7	299.7	66.7	63.0	91.6	53.8
1956.2	7324.2	7008.9	7023.1	10674.4	8553.1	9871.6	8077.4	8251.6	3566.8	6684.3
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318.4	6974.8	6463.7	6049.0	11444.0	8540.1	9530.8	8281.8	4762.9	2768.5	4433.4
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117.8	1071.2	1123.3	846.6	2315.1	1800.2	2040.5	1142.1	389.6	305.1	661.5
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1688.9	1678.7	1480.0	1543.5	2974.2	2728.3	2768.0	1912.5	1156.2	858.8	902.7
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1218.1	1847.0	3133.5
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EU135265.1 gg_id:236310 tallgrass prarie soil clone FFCH18216 EU135
EU135274.1 gg_id:242459 tallgrass prarie soil clone FFCH18590 EU135
EU881267.1 gg_id:321885 (long-term grazing and burned annual) Karst region serious disturbance field soil clor EU881
FJ612288.1 gg_id:576167 and Biogeochemistry Dongping Lake Ecosystems lake water clone DP7.5.14 FJ6122
FJ466217.1 gg_id:563036 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea FJ4662
FJ536899.1 gg_id:590906 Linking performance microbiology biofilters treating dimethyl sulphide presence and FJ5368
FJ203423.1 gg_id:331911 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h FJ2034
EU135107.1 gg_id:249175 tallgrass prarie soil clone FFCH2726 EU135
FJ232673.1 gg_id:325828 Enrichment ANAMMOX Wastewater Treatment Plants Korea and Their Activity sludge FJ2326
EF516153.1 gg_id:220916 grassland soil clone FCPN669 EF5161
GQ093878.1 gg_id:397840 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ093
FJ652504.1 gg_id:593106 aerobic and anaerobic ammonia-oxidizing sponges marine sponge clone ML-Pla-38 FJ6525
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EU881193.1 gg_id:326719 Karst region natural restoration land soil clone KNR200711-121 EU881
EU135245.1 gg_id:250454 tallgrass prarie soil clone FFCH17044 EU135
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DQ814734.1 gg_id:200402 Reciprocal Gut Microbiota Transplants Zebrafish and Mice Germ-free Recipients Hos DQ814
AM902526.1 gg_id:250059 Singulisphaera acidiphila str. PO2 AM902
AY234528.1 gg_id:112330 soil isolate Ellin5111 AY2345
GQ402671.1 gg_id:552820 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
AB238776.1 gg_id:146076 shal subsurface Sarobetsu Mire peat soil clone HSM-SS-013 AB238
GQ264465.1 gg_id:545566 Structure Simulated Level Waste Site simulated level waste site clone WW3_167 GQ264
DQ986200.1 gg_id:186517 planctomycete member Isosphaera genus freshwater aquarium Isosphaera-like str. DQ986
EU669616.1 gg_id:340209 soil clone S22-2 EU669
EU289510.1 gg_id:246083 metagenomic approach biosynthesis ansamycin endophytes or symbionts enriched EU289
AJ252623.1 gg_id:20352 agricultural soil clone SC-I-20 AJ2526
EF515969.1 gg_id:220676 grassland soil clone FCPP710 EF5159
AB254788.1 gg_id:160585 Biogenic Fe-oxyhydroxides nodules (takashikozo) encrusted iron-oxide reducing sedi AB254
AJ867920.1 gg_id:202171 Fluctuations Significantly Influence Microbial Present Nival Lakes lake water clone C8 AJ8679
EU861926.1 gg_id:345379 effects chronic fertilization on alpine tundra microbial implications carbon and cyclin EU861
EF019037.1 gg_id:215283 aspen rhizosphere clone Amb_16S_1586 EF0190
X81959.1 gg_id:2877 Isophaera sp. str. 640 X81959
DQ532192.1 gg_id:170729 Geographical Variation Microbial Burden and Spacecraft Assembly Johnson Space C DQ532
AJ292683.1 gg_id:27191 PCB-polluted soil clone 2112 AJ2926
X81958.1 gg_id:2879 Isophaera sp. str. 666 X81958
EF492942.1 gg_id:249037 Iron-manganese Nodule and Its Surrounding Soil soil around iron-manganese nodule EF4929
AF465649.1 gg_id:35108 planctomycete clone YNPRH1A AF4656
EF516492.1 gg_id:222936 grassland soil clone FCPS404 EF5164
EU335237.1 gg_id:241588 Changes microbial metabolic and along hydrogeochemically variable profile unsatura EU335

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44.1	285.2	285.8	330.3	712.0	514.2	544.7	503.2	187.8	40.9	181.7
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34.9	159.7	116.5	86.9	255.6	244.2	156.6	72.7	48.8	39.0	136.9
71.7	1523.7	930.6	819.6	2829.6	1896.8	1647.0	2760.5	731.2	451.3	821.8
810.8	7297.4	7011.1	7197.1	9320.6	7274.7	10438.9	7049.1	5557.3	5435.0	5419.3
330.2	6276.7	6627.8	6816.9	8204.7	6844.0	8870.4	6646.9	3817.8	3259.0	5173.5
29.3	38.5	48.0	49.4	51.1	23.2	45.2	46.1	16.7	26.0	20.6
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42.1	124.4	169.9	136.1	183.7	148.5	199.2	656.3	88.8	68.4	138.1
62.3	895.6	1454.8	578.0	1478.9	2823.8	1488.3	3914.0	1250.3	1617.1	571.6
6008.7	5266.2	5192.4	5572.4	7406.8	6173.1	7073.3	6850.9	4143.4	3925.7	5090.9
554.4	4096.1	3682.4	3805.1	6233.9	4900.3	5383.5	5309.3	3145.4	1552.4	2764.8
49.0	101.0	217.8	91.4	140.4	322.7	157.3	537.3	181.7	208.8	43.1
165.2	4460.4	3660.8	3741.9	6639.1	5260.6	5386.4	6024.4	2887.0	1635.7	3034.7
35.3	119.1	102.5	114.6	638.8	235.1	211.6	108.3	32.3	29.9	42.0
153.0	3590.1	3534.3	3444.8	4840.4	4627.7	4637.9	5490.4	2883.4	1550.1	2701.8
44.7	253.0	315.1	274.3	355.3	406.8	399.0	258.0	80.4	110.3	179.7
493.4	4314.2	4672.5	4621.8	4622.0	4572.6	5229.7	5861.6	2463.8	1636.5	3186.6
241.2	1300.5	1474.8	1324.3	2341.6	2069.9	2210.0	2339.4	921.7	517.2	808.5
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374.6	3075.0	2739.3	2529.9	5088.8	3968.2	4294.0	4239.4	1905.3	1117.5	1838.3
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72.0	1448.1	1902.1	1844.2	2709.7	1748.6	2258.1	1343.7	602.9	218.0	743.2
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2678.5	7322.5	7121.6	7433.1	9583.4	7967.5	8995.3	8123.3	5208.1	5128.3	5953.5
141.6	1202.5	1048.8	1066.3	1821.4	1545.1	1401.8	1668.6	723.3	387.8	748.7
92.9	1010.0	1416.9	1510.7	1508.4	1345.6	2348.4	1291.9	420.7	502.1	988.1
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389.6	347.6	432.8
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EU135036.1 gg_id:241400 tallgrass prarie soil clone FFCH5359 EU135
EU135064.1 gg_id:252536 tallgrass prarie soil clone FFCH11875 EU135
FJ478520.1 gg_id:513639 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4785
AF234700.1 gg_id:35556 sludge clone A25 AF2347
GQ356088.1 gg_id:542965 biomarkers ammonia oxidation activity anaerobic ammonium-oxidation (Anammox) GQ356
EF516829.1 gg_id:219667 grassland soil clone FCPN696 EF5168
EU135135.1 gg_id:235394 tallgrass prarie soil clone FFCH1662 EU135
EU589315.1 gg_id:273690 China Ningxia rice paddy field soil clone 2_H12 EU5893
AF234760.1 gg_id:33376 sludge clone A17 AF2347
FJ232659.1 gg_id:322102 Enrichment ANAMMOX Wastewater Treatment Plants Korea and Their Activity sludg FJ2326
FJ543069.1 gg_id:531452 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone B FJ5430
X86391.1 gg_id:2815 Pirellula sp. str. AGA/M12 X86391
GQ264007.1 gg_id:509308 Structure Simulated Level Waste Site simulated level waste site clone WC3_03 GQ264
M34126.1 gg_id:2826 Pirellula staleyi M3412
AM902592.1 gg_id:245810 Acidobacteria and Planctomycetes radioactive mineral Central Alps Austria subsurfa AM902
AJ616292.1 gg_id:107831 river biofilm clone DEL77 AJ6162
EU135081.1 gg_id:257073 tallgrass prarie soil clone FFCH2281 EU135
AJ252628.1 gg_id:28765 agricultural soil clone SC-I-28 AJ2526
AF513967.1 gg_id:62476 planctomycete clone LA4-B40N AF5139
X62911.1 gg_id:2845 Planctomyces limnophilus X62911
GQ850548.1 gg_id:568227 surface water northern Bering Sea clone u78 GQ850
AJ231186.1 gg_id:2859 Planctomyces sp. str. 248 AJ2311
EF019893.1 gg_id:207109 aspen rhizosphere clone Elev_16S_1259 EF0198
AJ616272.1 gg_id:106693 river biofilm clone DEL30 AJ6162
EU236333.1 gg_id:288195 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg5a2A6 EU2363
AB286452.1 gg_id:205500 Reducing production and domination comamonadaceae reducing oxygen supply was AB2864
EU703485.1 gg_id:385507 lakes on Eastern Tin Plateau freshwater lake altitude 4279 masl clone XZZLH76 EU7034
GQ264049.1 gg_id:532634 Structure Simulated Level Waste Site simulated level waste site clone WC3_146 GQ264
EU135201.1 gg_id:246619 tallgrass prarie soil clone FFCH11725 EU135
EU135291.1 gg_id:243965 tallgrass prarie soil clone FFCH3333 EU135
FJ232636.1 gg_id:318175 Enrichment ANAMMOX Wastewater Treatment Plants Korea and Their Activity sludg FJ2326
GU118118.1 gg_id:577627 Threatened Corals Provide Microbial Habitats clone Apal_L16 GU118
GQ093884.1 gg_id:415267 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ093
DQ256391.1 gg_id:143227 Cloning and microorganism genes alkaline soil clone pGXAR2 DQ256
EF580936.1 gg_id:278198 Survey Microbial Freshwater Calcareous Mats freshwater calcareous mat clone CM4 EF5809
GQ202636.1 gg_id:576162 RFLP two library insect-resistant trans-genic and its control soil conventional cotton GQ202
FJ232624.1 gg_id:325188 Enrichment ANAMMOX Wastewater Treatment Plants Korea and Their Activity sludg FJ2326
FJ236055.1 gg_id:356355 three Parisian treatment plants approaches drinking water clone Joinville4 FJ2360
AJ576406.1 gg_id:105661 midgut homogenate Pachnoda ephippiata larva clone PeM40 AJ5764
GQ264445.1 gg_id:591299 Structure Simulated Level Waste Site simulated level waste site clone WW3_146 GQ264
AJ231185.1 gg_id:2863 Planctomyces sp. str. 423 AJ2311

272.3	3327.1	3472.9	2886.5	4782.1	3605.5	6254.1	4709.9	1278.5	1103.2	2070.7
8595.3	5614.7	5322.8	5083.5	6558.3	6496.5	8269.6	6938.8	3570.3	4971.8	5630.5
1024.5	6368.6	6722.7	6571.5	8988.3	6899.5	11114.2	7295.4	4680.3	2699.0	5643.4
39.1	2278.8	1698.6	1199.4	3161.0	2501.8	4717.9	3308.2	687.3	840.9	898.5
65.8	990.3	601.1	293.0	1232.6	1463.8	1495.8	725.7	278.3	138.3	334.5
49.7	789.7	920.1	681.3	1929.1	1066.3	2375.8	994.0	205.0	225.8	343.0
6044.7	2964.6	2881.1	3170.8	4535.0	3411.5	3377.3	2779.7	4069.4	3136.7	86.0
281.9	6276.0	5589.0	4551.8	9018.1	6709.5	9444.7	7035.6	3927.3	3754.0	4392.2
3953.5	7316.9	7430.2	7036.8	10589.7	7736.0	11324.4	8725.7	4941.2	4505.5	5557.2
74.9	2989.7	2473.2	1650.0	5149.3	3112.4	6534.8	3503.7	961.0	1049.5	1212.9
127.8	1574.5	1587.8	1931.1	1938.8	1657.5	2038.9	2318.3	836.7	1884.1	1294.8
41.2	102.6	129.4	103.2	164.3	129.8	228.6	196.5	55.9	41.7	58.5
548.3	2635.4	2853.9	2228.5	4659.2	3368.6	5191.1	2936.6	1263.6	1011.4	1517.5
77.3	796.0	661.8	773.3	2004.4	944.5	1056.6	1247.3	465.8	220.1	335.5
1275.9	4417.1	4335.2	4478.2	7028.8	4430.8	6896.3	4783.5	2408.7	1422.0	2710.5
142.8	1855.6	1784.2	1834.1	4227.5	1964.6	3067.2	2977.5	900.4	530.3	1180.1
182.6	3803.1	3275.7	3288.9	7444.6	3720.9	6708.7	4404.4	1799.5	1115.3	1850.2
53.5	753.5	528.0	734.7	4322.5	1147.1	1169.7	777.0	220.6	140.9	207.3
33.6	328.5	190.1	240.5	257.8	328.9	229.7	403.7	51.2	45.5	126.1
39.9	256.5	262.7	179.9	455.1	251.1	349.7	559.8	249.2	127.9	94.6
30.7	59.0	50.9	45.7	78.7	44.1	70.5	73.0	43.1	29.7	53.2
501.1	2887.6	3103.8	2910.2	3630.7	3093.3	3596.9	3040.9	1630.8	1486.8	2045.5
344.5	865.3	973.8	664.1	1642.5	1310.1	1355.0	1122.3	363.5	338.3	568.1
89.5	543.0	514.0	604.1	912.7	670.4	869.7	698.9	310.0	303.1	348.6
45.5	1093.9	1863.1	2035.3	1575.1	1299.1	1657.2	1989.9	1170.0	572.7	1157.7
440.8	1425.8	1553.0	1907.2	2294.0	1756.6	2857.7	2414.3	1284.2	452.0	1150.2
691.5	2692.9	2976.8	2982.2	4346.5	3131.3	4429.0	4918.8	2343.6	2791.4	4796.0
692.3	4554.2	3578.3	3949.3	5461.6	4871.2	6409.6	5269.1	2132.8	1832.5	3383.9
79.9	1946.1	2084.9	2707.1	3189.2	1870.2	3381.4	2838.9	1814.3	705.5	1231.6
1032.4	5097.1	5425.1	5801.1	8048.4	5497.9	9055.8	6289.6	5088.8	2581.0	4173.1
30.0	1243.4	1234.8	983.0	5386.1	964.2	5555.5	2726.3	359.7	477.2	466.7
41.2	203.9	186.7	194.9	378.8	270.6	327.1	318.3	84.0	55.3	126.6
1971.2	6753.7	7011.2	6948.9	8531.0	6796.1	8769.5	8309.8	7105.2	6292.8	6278.4
84.5	1041.4	1039.3	886.9	2093.0	1297.0	2024.2	848.7	562.0	247.8	735.5
70.4	681.8	859.5	892.3	1921.2	1478.2	1456.4	1232.5	502.3	380.4	348.9
1333.2	5261.0	5494.2	4943.2	7936.6	5582.0	8136.4	6058.6	3954.2	3066.7	3719.3
969.3	5447.0	5789.9	5759.0	7347.3	6383.5	7898.4	7474.4	4359.1	3386.9	8362.3
373.5	3034.3	3170.6	3624.8	4908.9	3232.5	4891.6	4020.2	3694.7	2265.4	2952.5
7468.7	8037.1	7771.6	7813.6	11108.1	8392.4	9248.5	9228.3	6916.1	5077.3	6871.6
99.8	1047.4	943.0	1015.6	2203.8	1292.2	1697.1	1168.9	411.1	278.1	456.9
147.4	712.4	603.0	628.1	760.2	496.1	764.7	790.9	547.3	364.3	408.8

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5920.6	4503.8	7931.1
6438.7	6038.0	10170.2
3866.2	1717.5	4266.0
621.4	927.5	2275.4
1651.1	510.7	1289.0
3200.8	2789.6	3324.6
7267.7	5337.6	10022.6
8987.6	7995.0	10464.0
4985.1	2668.0	7828.8
1929.4	1578.6	2754.9
201.6	226.4	149.8
3818.4	1908.6	3551.9
1234.7	456.6	406.6
4859.0	4463.6	6451.3
2527.4	1444.8	2111.0
4231.9	3360.4	5618.7
925.7	451.5	830.0
128.1	142.5	267.7
373.5	469.0	622.9
75.2	81.0	91.3
3063.2	3542.2	4545.5
964.0	1614.9	5261.9
622.8	840.6	1241.2
1524.4	1934.5	936.4
1985.7	1951.3	2695.7
4778.4	3041.1	4115.7
5298.3	5073.5	6326.0
1645.9	2648.6	2447.7
5239.5	5198.5	8987.9
2935.9	347.0	874.3
257.4	419.6	508.8
7940.8	6926.8	9947.5
908.1	855.8	673.6
1368.5	1067.1	3664.3
6606.5	5538.5	8374.6
6508.7	5216.7	7334.5
4188.1	3807.1	6095.3
8913.0	7910.4	12679.1
1226.0	966.3	1874.8
618.7	878.2	981.5

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s__unclassified	56604

AF029079.1 gg_id:2853 Planctomyces complete clone 7F15 AF029
EU332801.1 gg_id:368930 FACS assist identification TFO present aerobic enhanced biological phosphorus remo EU332
FJ232625.1 gg_id:337721 Enrichment ANAMMOX Wastewater Treatment Plants Korea and Their Activity sludg FJ2326
X81954.1 gg_id:2868 Planctomyces sp. str. 658 X81954
GQ487909.1 gg_id:585391 Microbial metal soil polluted heavy metals clone T1-58 GQ487
DQ228417.1 gg_id:199905 microbial compositions two subglacial possible role microbes chemical weathering p DQ228
EU979049.1 gg_id:308618 Effects intercropping Rhizobium inoculation on microbial biomass and rhizosphere b EU979
AJ252614.1 gg_id:46917 agricultural soil clone SC-I-11 AJ2526
EF157243.1 gg_id:255306 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon EF1572
GQ488002.1 gg_id:533542 Microbial metal soil polluted heavy metals clone V8-4 GQ488
FJ624888.1 gg_id:509799 Influence lead contamination on boreal pine forest soil clone HF_C_15 FJ6248
GQ994843.1 gg_id:588567 planctomycete bloom eutrophic and simulated blooms algal microcosms lake sedim GQ994
FJ542938.1 gg_id:517269 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone B FJ5429
EU491846.1 gg_id:270163 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU491
GQ487907.1 gg_id:589189 Microbial metal soil polluted heavy metals clone T1-42 GQ487
FJ437980.1 gg_id:545573 Benthic okenone production Fayetteville New York Green Lake surface sediments 16. FJ4379
EU617893.1 gg_id:314251 Seasonal variation microbial Yel Sea sediment clone D13S-21 EU617
DQ815011.1 gg_id:162552 zebrafish digestive tract clone aab56g07 DQ815
FJ542891.1 gg_id:521367 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone A FJ5428
GQ263999.1 gg_id:558118 Structure Simulated Level Waste Site simulated level waste site clone WC2_93 GQ263
GU183590.1 gg_id:556104 Structures Reduced and Oxidized Aquifer lower Aqueous Arsenic Titas Bangladesh a GU183
GQ009454.1 gg_id:500211 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw77 GQ009
AJ616260.1 gg_id:101336 river biofilm clone DEL04 AJ6162
BX294907.2 gg_id:84917 anaerobic digester clone CY0ARA056H03 BX2949
AY532587.1 gg_id:102577 uranium-contaminated aquifer clone 1013-28-CG52 AY5325
AY328798.1 gg_id:88168 drinking water system simulator clone DSSD101 AY3287
FJ230918.1 gg_id:339412 under Level Antibiotic Selection Pressures river water clone F45 FJ2309
DQ395915.1 gg_id:152923 deep-sea octacoral clone ctg_CGOF043 DQ395
GQ402618.1 gg_id:512701 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
EF589344.1 gg_id:231022 Rhodopirellula baltica str. OJF17 EF5893
EF421452.1 gg_id:211974 Rhodopirellula baltica str. OJF14 EF4214
EF421451.1 gg_id:215170 Rhodopirellula baltica str. OJF13 EF4214
EF589343.1 gg_id:227672 Rhodopirellula baltica str. OJF16 EF5893
EF012748.1 gg_id:192974 Rhodopirellula baltica str. OJF4 EF0127
EF012749.1 gg_id:180732 Rhodopirellula baltica str. OJF5 EF0127
EU236437.1 gg_id:297164 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg63H3 EU2364
AM259894.1 gg_id:212998 Spatial sponge- Mediterranean Tethya aurantia sponge cortex clone TAA-10-09 AM259
EU236342.1 gg_id:295035 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg5a2H2 EU2363
FJ624356.1 gg_id:440418 Rhodopirellula sp. str. SM50 FJ6243
DQ640663.1 gg_id:233756 full-scale EBPR sludge clone Skagenf17 DQ640
FJ624322.1 gg_id:448778 Rhodopirellula sp. str. CS14 FJ6243

63.5	274.7	239.5	273.6	350.1	313.5	277.1	486.9	139.1	84.0	186.4
51.8	425.7	620.9	807.5	1775.8	1008.8	702.5	2110.6	295.0	211.6	573.0
13968.8	13467.0	12424.3	13573.8	14701.2	11899.1	15054.3	12499.1	15459.0	9835.7	16049.3
120.5	1118.5	1032.2	919.8	1999.9	1393.9	2747.1	1069.4	443.0	308.3	484.3
60.9	573.4	826.3	584.4	1535.8	976.8	987.3	1731.2	423.8	345.0	323.0
40.2	472.3	509.2	490.9	1146.9	907.9	885.4	999.3	220.6	125.7	283.1
3667.0	5317.5	5215.6	5708.4	7690.1	5481.1	6796.4	5839.4	5207.4	2859.2	4149.0
46.8	48.9	47.2	54.8	89.4	57.7	88.1	45.7	40.8	30.1	40.2
6958.1	9919.0	7599.4	8197.7	9551.9	9000.1	9924.3	9177.7	11348.3	6371.4	9472.0
7347.4	4684.0	4395.1	4758.9	6418.6	5377.5	5986.8	5080.8	5046.6	4453.6	5047.9
101.0	722.1	887.0	830.9	2333.5	1111.4	1143.2	1490.7	596.3	410.8	607.9
43.1	152.4	240.3	208.5	513.2	306.5	508.2	145.7	38.6	49.0	144.3
3750.6	10159.7	10306.9	10251.5	14883.2	10673.1	14758.1	11652.9	9369.6	6241.4	8182.7
256.0	6701.4	6502.6	6799.7	8130.6	6903.6	9038.2	7250.1	3738.0	2634.0	6228.2
993.8	2500.5	3245.1	3783.0	3488.8	3451.1	4177.3	4479.7	1771.5	647.7	2413.1
43.7	1796.5	1748.0	1650.7	2992.1	1804.3	3486.1	5270.6	2014.8	1877.9	1150.8
30.3	39.2	43.6	33.7	86.3	30.2	60.1	107.3	55.0	30.0	26.3
51.1	508.9	503.1	394.4	890.4	825.1	1153.0	755.7	232.7	164.6	320.3
20880.5	9179.8	8471.1	9045.9	8502.7	8379.4	8892.5	8741.5	10918.1	9247.8	11586.2
17680.3	10027.5	9675.6	10463.4	10686.5	9356.5	10660.7	9500.7	8781.4	7994.7	11333.1
352.0	4098.2	4008.7	4596.7	5116.2	4506.2	4997.2	5094.9	2859.6	3021.5	4264.0
37.5	355.6	500.0	445.8	649.0	673.4	585.0	848.2	557.3	54.9	274.7
29.3	43.1	47.6	38.7	42.2	48.7	52.4	42.7	21.5	17.4	28.1
13988.9	6112.4	5438.7	5801.8	8126.2	5614.4	5910.7	6862.0	6913.0	4845.3	6782.5
52.7	89.4	72.2	45.6	246.9	129.0	54.5	94.0	71.7	41.4	23.7
76.6	355.3	413.8	417.8	967.0	505.2	1267.7	542.9	241.3	107.8	201.9
556.6	2919.1	2759.3	2662.5	4371.6	2422.8	4365.6	3473.0	2624.4	857.4	1944.4
20241.5	6801.5	5336.0	7546.4	7336.1	6570.0	8548.9	6865.5	8949.6	7978.7	9583.1
50.7	1789.4	2042.1	1979.8	2647.7	2368.3	2997.0	2353.7	850.0	577.1	1584.1
642.9	3383.1	3518.3	3737.5	4182.3	3138.6	4389.6	4646.4	2944.6	1687.7	2986.8
764.0	5575.8	7285.5	7791.0	6987.8	6093.3	7494.6	5976.4	6374.9	2334.3	6305.7
1927.5	3440.9	3872.7	4326.1	4854.8	3651.2	5095.3	5087.7	3388.4	2041.9	3466.0
38.5	328.1	226.2	366.1	372.0	187.3	416.4	928.8	344.0	142.9	198.7
2688.1	4367.5	4899.4	5295.8	5578.7	4390.4	5882.6	5978.5	4577.8	3325.8	4736.2
480.4	2240.2	2461.4	2731.0	2681.0	1960.6	2909.1	3801.7	2382.9	1208.0	2195.8
1189.5	2802.7	3014.4	2763.0	4024.0	3805.5	3860.0	2399.6	2902.8	1557.4	2862.9
56.6	558.2	547.0	570.0	604.7	722.8	956.2	748.6	325.1	239.0	374.2
40.9	444.2	525.9	521.8	333.5	497.4	584.2	613.6	92.3	176.5	368.9
126.4	725.4	1026.7	1000.6	1405.2	919.1	1442.2	1136.6	635.9	515.2	715.9
343.2	1382.5	1751.9	2404.4	1798.7	1500.1	2305.1	2909.4	989.5	358.7	1111.8
394.9	2134.0	2465.9	2546.5	3358.4	1926.0	2648.1	2569.6	3445.1	1142.8	1816.8

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2165.4	338.7	62.7
13113.2	12707.5	12886.1
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1630.1	762.9	2067.3
680.1	567.9	1862.0
6478.0	5614.5	6664.3
45.4	68.4	348.0
9191.7	9066.5	9946.4
3273.8	4890.7	6029.1
1268.2	1705.0	2420.5
312.9	181.3	355.5
12625.3	10568.5	14999.0
7178.8	5429.5	7401.3
3390.4	3446.9	4846.4
5550.2	815.9	1426.6
81.0	52.7	20.2
873.8	843.0	1586.5
7862.6	8638.0	7719.4
9230.3	8636.5	10252.6
5186.1	4232.2	6963.4
832.0	231.2	1624.9
48.6	47.1	62.6
7149.4	5111.2	5675.7
155.0	64.3	99.7
548.8	587.8	3055.4
3242.8	2807.1	3364.1
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1883.9	1766.2	2752.0
4379.6	3969.6	4360.7
5040.4	6275.9	8883.5
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2501.2	3192.0	3897.5
779.5	1076.2	876.2
867.0	364.4	602.6
1197.0	1370.9	1103.6
2987.6	2119.9	2419.1
2248.4	2624.3	2809.5

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GU305724.1 gg_id:558514 Research on changes structure during algae outbreak oligotrophic lakes (YangHe res GU305
X81942.1 gg_id:2801 Pirellula sp. str. 302 X81942
EU249951.1 gg_id:245163 Polyphasic description Pocillopora seawater adjacent Pacillopora meandrina coral co EU2499
EF157256.1 gg_id:245908 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon EF1572
FJ624353.1 gg_id:418512 Rhodopirellula sp. str. SM44 FJ6243
DQ986201.1 gg_id:190032 Pirellula sp. OJF3 DQ986
EF012750.1 gg_id:184921 Rhodopirellula baltica str. OJF6 EF0127
X81939.1 gg_id:2767 Pirellula sp. str. 140 X81939
EU812984.1 gg_id:323488 Microbial structure thermophilic reactors biogas reactor fed corn silage clone TUM-M EU8129
DQ499312.1 gg_id:159626 acidic cave snottite biofilm clone CV73 DQ499
GQ246290.1 gg_id:512628 Temporal and spatial China North Yel Sea sediments clone Sd1-9 GQ246
EU246802.1 gg_id:240923 polyphasic description Pocillopora meandrina Palmyra Atoll Calcinus obscurus abdon EU2468
AJ616261.1 gg_id:101508 river biofilm clone DEL05 AJ6162
AY907796.1 gg_id:136912 identification picoplankton contrasting waters Arabian Sea water clone A714001 AY9077
AB294955.1 gg_id:222378 -dependent & analyses hydrothermal system off Taketomi Island Japan microbial ma AB2949
GU061671.1 gg_id:549851 and function microbial mesoscale eddy perturbations South China Sea clone CE2-DC GU061
DQ903990.1 gg_id:235788 Microbes Hawaiian Marine Sponge Suberites zeteki USA: Oahu Hawaii clone PRPR39 DQ903
X81940.1 gg_id:2783 Pirellula sp. str. 516 X81940
FJ624355.1 gg_id:399640 Rhodopirellula sp. str. SM49 FJ6243
EF574895.1 gg_id:233369 site S25 near Coco's Island marine clone S25_1239 EF5748
FJ623363.1 gg_id:583343 Efficient polyhydroxyalkanoates production waste-activated submitted process seque FJ6233
FJ624354.1 gg_id:395015 Rhodopirellula sp. str. SM48 FJ6243
GU061406.1 gg_id:569946 and function microbial mesoscale eddy perturbations South China Sea clone CE1-5m GU061
EU037330.2 gg_id:269075 structure landfill sediments receiving long-term augmentations wastes chromium co EU0373
X81943.1 gg_id:2800 Pirellula sp. str. 382 X81943
X81941.1 gg_id:2787 Pirellula sp. str. 158 X81941
X81945.1 gg_id:2793 Pirellula sp. str. 139 X81945
FJ624364.1 gg_id:421926 Rhodopirellula sp. str. SM23 FJ6243
GQ302560.1 gg_id:542353 prokaryotic sediment Shawan methods cold spring clone sw-xj213 GQ302
EU703306.1 gg_id:435220 lakes on Eastern Tin Plateau polysaline lake altitude 3204 masl clone XZQH106 EU7033
AJ431347.1 gg_id:40268 Greenland:Ikka Fjord clone AJ4313
AF468237.1 gg_id:80863 Arctic pack ice; northern Fram Strait; 80 31.1 N; 01 deg 59.7 min E clone ARKCH2Br2-9 AF4682
EU491585.1 gg_id:271404 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR4C EU4915
FJ624347.1 gg_id:400480 Rhodopirellula baltica str. SH155 IFAM 1436 FJ6243
FJ205295.1 gg_id:557224 Prokaryotic deep-sea region East Lau Spreading Centre active hydrothermal field sedi FJ2052
EU050866.1 gg_id:237562 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_06_87 EU0508
FJ485080.1 gg_id:560755 microbial autonomous rover world's deepest phreatic sinkhole biomat El Zacaton 114 FJ4850
FJ197610.1 gg_id:338655 deep Pacific Ocean and Eastern Mediterranean Sea sediment clone ALVIN29a_5E_FL FJ1976
GQ143793.1 gg_id:403814 Level Continental Shelf Sediment and Phylum-level lineages Phylum Planctomycetes GQ143
GQ339128.1 gg_id:517627 Comprehensive Investigation on Iron Cycling Freshwater Seep ing Microscopy Cultiv GQ339
AB177200.1 gg_id:137395 seafloor methane hydrate clone ODP1230B30.13 AB1772

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41.0	202.9	386.8	414.5	244.9	345.1	379.4	829.9	217.7	118.6	157.1
41.1	72.8	67.3	72.5	314.5	130.0	136.9	157.6	41.3	19.5	48.4
1647.0	2303.9	2157.3	2290.9	3457.2	2410.1	3442.5	3699.7	1789.4	1036.6	1587.5
1185.2	3954.4	3951.0	3733.0	4071.1	3702.2	5436.1	3983.7	2891.8	1738.5	3026.4
1493.5	2768.4	3148.8	4000.9	2843.4	2614.5	4761.8	4014.7	3468.1	993.3	2764.2
2699.6	4356.1	4847.7	5331.7	5643.0	4600.9	6269.5	6333.5	4559.4	3462.7	4951.9
829.9	2655.4	2614.5	3021.7	3843.7	2392.7	3762.2	2905.4	2412.5	1651.7	2234.9
82.4	1864.0	2246.1	2205.1	2356.5	2136.5	2509.1	3411.2	1461.4	820.4	1559.0
42.2	175.3	169.1	207.3	431.2	280.2	260.9	504.7	115.1	58.0	77.4
64.8	736.3	596.0	830.6	864.8	542.7	1260.5	2169.2	633.2	468.6	343.4
544.3	2697.0	2325.4	2347.4	3482.9	2711.8	3615.0	4097.4	1787.1	1178.5	2269.0
46.1	883.5	664.8	918.2	735.0	980.9	808.4	1572.8	414.9	210.3	623.8
31.1	83.4	80.2	75.5	96.1	76.9	77.3	94.6	40.8	39.0	47.7
2972.7	1486.1	3192.9	2926.6	2991.4	3239.8	4072.1	3419.7	2556.9	2080.0	4074.0
50.6	182.7	240.5	264.2	237.2	139.7	288.9	334.4	55.7	58.1	57.7
310.3	3345.1	3397.9	3353.3	4168.0	3359.4	4677.6	3586.8	2670.3	1448.2	2504.6
92.0	461.8	554.6	644.8	680.7	761.0	951.8	770.6	309.3	145.3	537.0
530.5	2830.8	2844.9	2955.2	4028.2	3279.1	4189.9	3559.7	2065.6	1820.4	2624.0
60.9	3023.5	3157.2	3390.4	3596.1	3148.0	4203.2	4735.6	2152.7	1450.0	3245.3
576.4	2992.1	2963.8	3696.3	4170.8	2913.8	4200.3	3459.2	4139.3	1867.3	2039.6
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47.7	54.6	77.8	64.4	157.1	103.3	160.3	103.2	34.2	48.1	50.2
430.7	4746.5	4668.1	3840.3	8365.1	4932.1	7617.7	6369.9	3043.5	2729.8	3149.0
44.0	594.4	757.8	576.7	1272.8	669.7	1255.1	727.2	237.9	146.5	325.8
36.5	61.4	25.9	87.0	45.7	27.4	37.0	287.2	39.3	32.2	39.4
45.9	62.1	134.4	97.3	57.0	61.0	115.4	1058.4	228.0	119.8	156.7
14890.0	5673.8	6141.9	6989.1	6362.0	5947.5	7662.9	6352.4	7395.3	10890.7	7782.6
119.5	2648.5	2331.6	2422.9	4200.7	3038.1	3750.2	3187.7	1424.5	592.2	1226.1
980.5	2942.2	3029.8	3746.9	4692.4	3367.6	5592.2	4864.5	3433.6	1909.9	3128.4
341.5	1009.2	1137.5	1471.1	1197.2	1076.1	1510.2	1335.2	911.2	366.8	1035.6
3349.0	6878.9	8530.5	9079.7	8757.7	6856.0	8935.2	8313.3	8780.6	6819.0	8754.3
44.3	276.7	475.3	415.0	279.8	278.4	413.3	541.8	147.6	62.7	158.8
2602.8	4197.5	4237.1	4701.8	5653.4	4310.0	5816.1	5459.1	3029.1	3165.2	4206.8
1676.9	4010.7	4414.1	4846.5	4202.0	4440.8	5756.7	4527.7	2804.9	2718.8	4164.7
739.2	5495.5	6082.9	6888.6	6622.5	5939.0	7055.2	5740.3	4241.8	3182.2	5386.6
129.4	1985.6	2271.2	2005.2	2579.3	2124.2	2734.7	1602.5	762.0	820.1	1296.2
1862.5	5793.0	5715.6	6906.6	6993.3	5853.0	8255.4	6250.9	6001.4	3097.9	6632.3
2541.2	4953.3	5382.4	6636.4	8160.0	6024.9	8196.2	7023.3	4514.4	3420.1	4944.8
3338.6	6510.2	7168.7	7991.8	7910.4	6880.6	8726.5	7128.5	8177.1	5882.4	6926.4
15665.2	7003.8	6725.6	7801.5	7570.4	6985.3	7447.2	7274.8	10067.2	9674.2	11473.1

9464.1	5777.5	6057.3
755.2	495.3	244.2
81.7	64.4	80.2
3543.9	3050.2	3119.0
3836.3	3380.6	4042.9
2319.0	3754.7	3949.1
6557.7	5351.4	5806.1
2392.9	2674.9	3004.8
3154.8	2210.1	2605.6
249.8	316.5	446.7
2479.3	1780.3	752.5
3451.6	3158.1	3901.2
4163.8	956.2	777.5
64.5	71.8	71.2
3118.5	2394.7	3149.3
272.2	206.2	253.9
3521.3	4038.2	4556.9
1146.9	810.5	1473.5
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91.1	113.4	61.2
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815.4	621.9	1129.8
106.9	468.4	969.2
275.7	303.8	61.7
6258.7	6341.6	6963.9
3885.7	2508.4	4917.2
3963.8	3715.8	3612.8
1518.7	1204.1	1383.6
7071.6	8338.3	9161.6
663.8	432.8	466.5
4945.3	4453.9	5364.5
4714.3	4629.5	6156.7
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1465.0	2308.3	3693.2
5758.3	5994.0	7261.1
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DQ676328.1 gg_id:219735 Archaeal and plankton freshwater pond suboxic freshwater-pond sediment clone M DQ676
AY921874.1 gg_id:114298 farm soil clone AKYG1711 AY9218
GU444061.1 gg_id:523807 Effects amendments on fertility and microbial structure cucumber Cucumis sativus L GU444
DQ206406.1 gg_id:139615 microbial mediates arsenate reduction soda lake water clone ML--10 DQ206
AM997881.1 gg_id:576223 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A AM997
EF516155.1 gg_id:227320 grassland soil clone FCPT723 EF5161
AB530247.1 gg_id:544394 Monitoring Suez and Tokyo bays based on analyses marine sediment clone Tokyo..B AB530
AF507705.1 gg_id:65683 forest soil clone S165 AF5077
DQ450803.1 gg_id:161593 Microbial Alpine Tundra Wet Meadow Soil: Chloroflexi Cold Water-Saturated satura DQ450
FJ746253.1 gg_id:510156 Microbial oligotrophic marine sediments: South Pacific Gyre ocean sediment 5306 m FJ7462
EU048670.1 gg_id:257221 and archaeal surface marine sediment Slope South China Sea clone MD2896-B10 EU048
FJ873309.1 gg_id:562253 Vertical and archaea methane-rich cold seep located base sediments Okhotsk Sea clo FJ8733
EF688380.1 gg_id:237185 soil clone F6-89 EF6883
EU245970.1 gg_id:250462 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M8-H0 EU2459
GU322886.1 gg_id:548781 Metaproteomics -temperature anaerobic granular sludge cultivated temperatures c GU322
GQ246434.1 gg_id:594302 Temporal and spatial China North Yel Sea sediments clone Ld1-39 GQ246
AY493903.1 gg_id:136324 Fingerprinting aggregates soil clone 1430 AY4939
FJ264747.1 gg_id:311487 Manganese and Iron Dependent Anaerobic Oxidation Methane methane seep sedim FJ2647
CU923200.1 gg_id:550970 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU923
GQ246448.1 gg_id:576923 Temporal and spatial China North Yel Sea sediments clone Ld1-53 GQ246
AF507704.1 gg_id:55354 forest soil clone C167 AF5077
AY963300.1 gg_id:156060 structures and correlated ecological factors soils two evergreen broad-leaved forests AY9633
EU386080.1 gg_id:262812 Biogeographical and microbes sediments on subseafloor sediment South China Sea c EU386
FJ479214.1 gg_id:543366 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4792
U81656.2 gg_id:2794 anaerobic digestor clone vadinBA30 U8165
EF019225.1 gg_id:210216 aspen rhizosphere clone Elev_16S_394 EF0192
FJ712480.1 gg_id:518323 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) K FJ7124
FJ638603.1 gg_id:576295 Temperature dependent succession sulfate reducing muddy southwestern Taiwan hc FJ6386
EU622299.1 gg_id:296920 syntrophic partnerships deep-sea vents direct cell capture and metagenomics Eel Riv EU622
EF019958.1 gg_id:215591 aspen rhizosphere clone Elev_16S_1337 EF0199
EU245568.1 gg_id:248646 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M3-B0 EU2455
EU135296.1 gg_id:244874 tallgrass prarie soil clone FFCH4400 EU135
EU135033.1 gg_id:235601 tallgrass prarie soil clone FFCH5199 EU135
EF516309.1 gg_id:223655 grassland soil clone FCPT556 EF5163
EU245782.1 gg_id:251795 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M6-C0 EU2457
FJ264744.1 gg_id:327743 Manganese and Iron Dependent Anaerobic Oxidation Methane methane seep sedim FJ2647
EU385736.1 gg_id:271883 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S EU3857
AF423302.1 gg_id:35667 soil clone 96-2 AF4233
EU245905.1 gg_id:258094 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M8-A0 EU2459
DQ329791.1 gg_id:159475 Guerrero Negro hypersaline microbial mat clone 05D2Z14 DQ329
EF612394.1 gg_id:255351 historic semiarid lead-zinc mine tailings site soil clone OS-C18 EF6123

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290.8	930.5	1066.7	1154.1	1621.8	948.0	1856.1	779.2	717.7	392.8	1088.3
47.1	114.2	135.0	145.9	516.3	138.7	276.7	171.7	99.2	26.9	94.8
59.5	33.2	60.4	39.0	67.3	37.2	60.8	51.3	35.1	24.8	35.9
70.4	258.8	389.9	302.4	453.4	326.0	861.1	333.2	125.4	37.3	93.9
44.5	53.0	81.9	76.0	109.8	56.3	170.4	80.1	31.8	17.2	44.1
35.0	419.0	576.8	594.4	261.0	410.9	557.1	531.9	96.1	86.7	339.8
33.3	145.9	109.5	100.8	303.4	150.4	232.9	84.5	45.6	17.2	39.2
52.9	166.5	121.0	110.2	310.4	352.7	581.5	428.7	81.9	28.3	98.6
53.8	73.2	83.2	112.5	60.2	39.9	119.4	68.2	49.0	29.3	58.2
368.2	3204.5	3101.3	3514.9	5655.2	3676.5	8403.9	3308.3	1361.5	512.8	1535.2
13452.8	8594.7	7292.9	8327.9	8474.0	8196.0	7532.8	8864.2	6391.3	5786.7	11953.9
22716.0	6191.4	6413.2	6306.1	6664.4	5901.9	6772.8	6735.5	8904.2	8000.2	8697.3
9711.4	6054.1	6046.4	7365.3	7571.9	7145.1	7428.6	6802.5	5825.9	4917.3	6811.6
489.5	6131.4	6489.7	7414.0	11143.1	7500.2	10006.1	7865.7	5998.1	2511.0	5461.8
2353.9	6023.5	5018.2	5309.0	6299.2	5588.5	7460.3	4697.0	6144.5	5757.3	4870.9
180.7	525.3	370.4	413.9	722.9	312.6	847.4	207.2	236.6	80.7	276.5
108.2	1853.9	1382.4	1424.3	1941.0	1671.9	3408.3	1411.5	1263.7	576.6	819.8
29420.4	10357.1	10302.6	11514.7	11040.6	10044.2	11995.5	10078.4	13494.8	12900.5	13069.0
47.4	364.1	680.3	731.5	571.7	714.7	733.4	1060.3	325.4	275.6	367.6
473.3	655.2	620.2	664.2	828.5	679.4	1234.2	717.9	415.0	315.9	480.4
46.3	2371.7	2433.4	2539.5	4444.6	1870.5	4898.5	1826.7	640.1	367.8	1002.7
1101.5	4181.8	4444.4	4688.1	5801.8	4419.2	6211.5	4475.5	2823.3	1619.3	3542.0
5224.6	3262.9	2783.7	2761.6	4989.0	2818.7	5659.5	2638.8	2322.7	1900.8	2723.6
23801.8	10757.7	9592.3	10345.3	12203.3	10638.3	13564.8	9710.9	10925.9	10364.2	12189.9
45.3	111.9	69.0	63.5	113.4	82.1	251.9	64.7	35.8	19.0	49.8
378.9	4393.5	5682.3	4689.6	5561.2	4326.2	5487.8	4976.8	4132.3	5847.3	4125.0
7635.7	6255.7	6610.7	6906.2	8058.8	6413.5	9437.9	7113.3	4811.3	3349.8	4939.5
251.7	5782.5	6906.4	6809.8	7336.5	6119.1	9268.8	5844.0	4520.3	5924.0	6555.4
119.2	669.6	758.2	802.4	1446.2	812.9	1415.1	702.8	650.1	459.1	436.3
351.2	1858.2	1672.1	1977.6	2054.3	1604.4	1720.1	1860.5	1858.1	651.8	1257.6
68.1	1063.6	924.2	1011.0	2668.8	1174.1	3530.6	1373.7	416.4	157.9	509.2
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85.7	761.7	671.1	929.5	1628.5	693.8	1424.1	620.7	322.2	178.1	309.5
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32.1	1409.8	1281.9	1678.1	2445.2	2121.6	3795.6	1641.7	481.3	250.8	729.1
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220.0	1154.3	824.9	827.9	1608.0	847.6	1599.4	891.2	251.0	239.8	452.0
1529.9	3851.7	3913.5	5197.2	5137.1	4637.1	5033.6	4850.1	2839.0	1754.8	3248.8
28992.8	11864.1	11463.5	13463.4	12900.1	13067.0	13097.7	11309.8	14586.7	14395.3	17820.0
4263.0	3432.1	3673.6	4579.7	5268.9	3598.1	5524.1	3823.9	3344.1	2125.9	3357.3

6718.4	6707.1	7081.2
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182.4	184.8	222.3
35.0	82.7	1428.3
235.2	253.9	1055.3
37.3	41.3	55.9
269.3	324.6	423.2
64.7	55.4	70.2
305.2	147.8	47.5
68.3	64.4	112.5
2906.9	2373.8	6149.0
8041.5	9956.8	7505.6
5383.3	6410.7	4695.2
6636.2	6898.1	7180.8
8130.7	6655.5	11229.0
4619.9	4701.3	6207.4
268.3	262.6	261.6
1418.7	1297.8	2979.5
10056.8	10364.4	13205.2
932.0	1365.4	627.8
497.8	1085.7	671.7
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EU385723.1 gg_id:262361 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S EU385
CU919054.1 gg_id:548383 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU919
EU786130.1 gg_id:556144 cotton rhizosphere soil clone 3H-211 EU786
EF018222.1 gg_id:203959 aspen rhizosphere clone Amb_16S_572 EF0182
EU385921.1 gg_id:264090 Stratified microbes sediments Core MD05-2902 subseafloor sediment South China S EU385
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FJ485338.1 gg_id:571346 microbial autonomous rover world's deepest phreatic sinkhole wall biomat El Zacator FJ4853
EF540419.1 gg_id:220924 oil-shale semi-coke solid waste clone MK11 EF5404
EF032768.1 gg_id:181593 cyanobacterial mat in lava cave clone HAVOmat68 EF0327
EU245501.1 gg_id:245089 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M2-D0 EU245
AB177155.1 gg_id:136191 seafloor methane hydrate clone ODP1230B16.23 AB177
GQ844339.1 gg_id:543377 Microbial full-scale produced water treatment plant biofilm anoxic tank clone BB-B5 GQ844
GQ472311.1 gg_id:573896 Microbial Dongping Lake lake sediment clone 2B3-12 GQ472
FJ748808.1 gg_id:585249 Vertical and sulfate-reducing prokaryotes estuarine Southern China Pearl River Estua FJ7488
GQ143768.1 gg_id:454105 Level Continental Shelf Sediment and Phylum-level lineages Phylum Planctomycetes GQ143
EU386008.1 gg_id:273669 Biogeographical and microbes sediments on subseafloor sediment South China Sea c EU386
DQ811900.1 gg_id:163946 mangrove soil clone MSB-5C12 DQ811
FJ545451.1 gg_id:508778 Diveristy Seawater and Sediment Northern North Yel Sea sediment clone S1-19 FJ5454
EU245488.1 gg_id:235811 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M2-B0 EU245
EF208700.1 gg_id:200413 Vertical and horizontal structure microbial sandy carbonate sediment clone CI75cm.2 EF2087
EF516637.1 gg_id:225058 grassland soil clone FCPS673 EF5166
AJ292685.1 gg_id:44216 PCB-polluted soil clone WD283 AJ2926
FJ444683.1 gg_id:588682 Cotton Rhizosphere cotton rhizosphere clone 2y-55 FJ4446
GU056117.1 gg_id:554003 Biologic Techniques Applied Microbial Prospecting China: Ban 876 Gas Oil Field Bein GU056
FN563400.1 gg_id:556620 Impact changing HRT OLR on prokaryotes involved biomethanizitaion and fuzzy logic FN563
EF018678.1 gg_id:211992 aspen rhizosphere clone Amb_16S_968 EF0186
EF515994.1 gg_id:219383 grassland soil clone FCPT539 EF5159
EU181513.1 gg_id:237389 Prokaryotic enhanced organic matter remineralization continental margin marine se EU181
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EU491712.1 gg_id:272697 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU491
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FJ712491.1 gg_id:510851 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) K FJ7124
GQ356165.1 gg_id:573216 biomarkers ammonia oxidation activity anaerobic ammonium-oxidation (Anammox) GQ356
FJ478514.1 gg_id:544225 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4785
FJ232658.1 gg_id:353016 Enrichment ANAMMOX Wastewater Treatment Plants Korea and Their Activity sludg FJ2326
EU491293.1 gg_id:271990 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak EU491
EU135104.1 gg_id:243304 tallgrass prarie soil clone FFCH17847 EU135
EU374014.1 gg_id:271620 southern Cretan margin (eastern Mediterranean Sea) canyon and slope sediment clc EU374
AY592336.1 gg_id:104089 deep-sea mud volcano clone Amsterdam-1B-32; BC20-1B-32 AY5923
FJ203528.1 gg_id:337295 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h FJ2035

859.7	8096.0	8082.0	9529.4	11821.7	9480.9	10314.9	10969.2	8191.0	7320.7	9877.3
1886.1	4600.1	4507.5	5443.0	6458.1	4693.0	6951.1	4256.4	3387.4	3286.2	3936.9
5761.1	4816.0	4400.9	5901.7	6758.6	5885.5	6342.5	6042.2	4856.8	3801.7	4416.5
169.4	2351.5	2061.9	2102.4	1933.2	1732.1	2662.2	2478.5	1059.5	792.6	1668.8
33.1	195.4	136.6	147.9	445.8	135.6	523.7	102.1	64.6	14.3	66.8
58.7	45.3	67.4	58.8	41.8	38.0	46.1	57.2	27.4	20.1	38.2
87.0	2654.1	3086.8	2878.2	3173.9	2944.6	4080.6	3781.6	2179.0	1543.9	2009.7
7626.1	4394.0	4805.1	4287.8	5640.5	5155.4	6135.4	5040.5	3624.8	3033.2	3878.1
49.0	61.3	68.0	64.3	208.2	42.5	255.9	24.5	23.7	21.1	22.7
37.0	108.8	119.4	94.0	308.0	78.5	271.7	67.2	41.9	18.9	34.0
3730.1	4572.3	5313.1	4741.0	6544.8	5141.3	8383.3	5569.1	4576.8	3190.7	4347.8
30.7	82.9	50.0	63.0	55.7	48.8	88.9	105.7	41.2	38.0	32.6
5672.6	4056.5	4019.9	4341.1	5793.1	4539.8	5779.7	4192.6	2909.7	3450.4	3649.5
557.7	2475.9	2925.0	2642.5	2724.7	2453.8	3362.0	2648.0	1380.8	1315.9	2601.6
1844.1	1440.2	1444.8	1514.0	1573.4	1348.2	1870.7	2075.9	993.6	815.0	1002.7
277.2	3343.3	3195.7	3394.8	3362.5	3599.3	3969.7	3756.8	2894.3	4215.9	2358.4
36.5	119.7	372.3	323.6	51.2	63.5	225.7	176.5	43.7	28.2	61.5
39.5	159.3	126.2	202.6	39.3	78.5	49.2	175.3	16.8	18.0	119.3
2486.3	9810.6	9684.5	10393.9	10847.8	9282.8	12912.4	9412.9	10127.0	7236.1	11205.1
7840.2	7532.8	6260.4	6884.1	6258.8	6530.3	6446.5	6403.1	8279.0	5998.0	8133.7
36.7	81.4	137.7	195.4	246.7	279.9	136.6	204.9	59.6	133.0	71.2
71.8	182.0	228.5	204.8	1065.7	260.1	581.4	107.3	62.4	66.5	61.0
37.2	146.9	133.8	96.9	533.7	116.2	599.8	68.6	34.4	27.0	76.9
5486.2	8577.7	7700.1	8613.6	10525.5	7543.1	11021.9	7203.0	6553.4	3724.4	7691.4
889.1	2167.4	2807.8	2681.5	3519.3	2440.4	3060.4	2562.8	1479.3	2111.0	1922.5
111.0	4166.2	4312.4	4177.4	5144.8	4721.3	7020.1	4076.0	2603.9	1389.9	3020.7
33.5	141.7	116.4	113.6	584.9	106.2	349.5	112.8	37.8	30.0	57.6
6884.0	3789.9	4063.2	3861.7	4497.7	3932.6	5458.1	4249.0	7642.4	5112.6	5617.7
3134.8	5569.2	6715.2	5837.7	5557.0	5664.1	6919.2	5585.2	4900.6	4796.1	5586.7
38.5	539.0	620.9	607.9	1224.7	426.4	2454.3	458.7	81.2	74.4	108.6
1530.7	4335.8	3907.9	3253.4	3763.3	3483.9	5092.0	5030.8	3283.6	4277.0	3187.8
3108.6	4549.0	4708.0	4188.2	5122.2	4581.9	6482.7	5231.8	4472.5	4407.7	4153.8
118.6	7100.1	6227.0	5290.0	7639.3	6220.8	8786.2	6601.3	4669.0	3590.0	4639.4
760.2	8001.2	7170.0	7138.6	8367.0	7222.7	9469.2	8555.7	6506.1	7094.9	6128.2
1257.1	5585.3	5278.4	5694.2	6885.9	5209.7	8975.6	7640.3	4977.5	2513.6	4108.0
2268.5	4006.1	4261.4	4151.4	5341.0	4842.5	7358.8	5370.7	3327.6	2266.5	3579.0
5646.0	3725.1	3979.3	4248.8	5312.4	4112.6	5604.1	4774.7	3043.2	3238.5	2990.3
42.5	3805.7	3441.0	2841.1	7011.9	4090.0	8500.6	6043.2	1984.7	1602.9	2039.6
1598.9	8146.7	7553.6	8124.8	10526.5	8078.8	11771.0	9351.3	5631.4	5162.1	7171.0
404.8	4565.8	5036.0	5679.7	6758.2	5251.7	7421.4	5542.9	5993.5	7744.0	4632.9
218.8	1970.5	2193.9	1978.1	3509.3	2614.0	3080.3	2985.3	1362.6	709.2	1007.4

10841.1	10633.4	11771.0
4491.1	4803.3	7494.7
6007.9	6562.7	7655.1
1225.1	2214.5	1825.8
73.2	50.5	79.7
30.8	31.4	38.5
3483.6	3164.5	3889.9
4191.7	5702.6	6079.2
29.5	26.9	36.6
22.0	38.2	68.9
4666.2	5300.7	6785.2
42.9	58.1	56.1
2458.1	4183.6	5533.7
1914.4	2695.3	2974.1
1266.3	2235.0	2590.4
3014.2	3633.6	5034.4
83.5	52.8	109.4
32.9	22.7	54.7
9144.2	9803.5	10155.1
6622.1	5661.6	6154.0
120.3	190.2	168.5
153.6	220.4	136.8
89.4	62.4	103.2
7302.3	7214.6	8528.8
2537.0	2838.4	2920.9
3437.5	3097.5	6107.6
83.7	75.5	102.3
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4758.0	6370.5	6337.3
321.7	151.9	264.4
4448.4	3541.7	4298.6
4374.9	4422.6	6061.5
5783.7	5902.0	8198.0
8056.5	7128.7	9197.1
7746.7	5207.8	6558.7
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5036.5	5816.5	5611.6
6926.7	2510.8	4886.5
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FJ712558.1 gg_id:516943 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) k FJ7125
GU118019.1 gg_id:592923 Threatened Corals Provide Microbial Habitats clone Apal_F10 GU118
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GU118132.1 gg_id:588256 Threatened Corals Provide Microbial Habitats clone Apal_N24 GU118
DQ289921.1 gg_id:165216 Microbial Carbon and Nitrogen Cycling Sediments South Atlantic Bight Permeable Sh DQ289
FJ873317.1 gg_id:512846 Vertical and archaea methane-rich cold seep located base sediments Okhotsk Sea clo FJ8733
GQ356148.1 gg_id:571807 biomarkers ammonia oxidation activity anaerobic ammonium-oxidation (Anammox) GQ356
FJ516887.1 gg_id:535958 semiarid 'Tablas de Daimiel National Park' wetland (Central Spain) unravelled upper s FJ5168
EU843071.1 gg_id:348461 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
FJ652501.1 gg_id:582419 aerobic and anaerobic ammonia-oxidizing sponges marine sponge clone ML-Pla-33 FJ6525
AY114326.1 gg_id:71342 anoxic marine sediment clone LD1-PA40 AY1143
EU491864.1 gg_id:259028 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU4918
FJ203614.1 gg_id:306565 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h FJ2036
FJ203304.1 gg_id:323269 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c FJ2033
FJ232644.1 gg_id:337297 Enrichment ANAMMOX Wastewater Treatment Plants Korea and Their Activity sludge FJ2326
DQ396219.1 gg_id:152458 deep-sea octacoral clone ctg_NISA190 DQ396
EF573103.1 gg_id:229876 Coco's Island site 23 marine clone S23_1202 EF5731
GQ487912.1 gg_id:578134 Microbial metal soil polluted heavy metals clone T1-103 GQ487
FJ205299.1 gg_id:548823 Prokaryotic deep-sea region East Lau Spreading Centre active hydrothermal field sedi FJ2052
FJ203110.1 gg_id:337594 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c FJ2031
EU734992.1 gg_id:341990 assemblages sediment station DBSE Northern Bering Sea clone 086B35 EU734
FJ203078.1 gg_id:355875 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c FJ2030
GQ356114.1 gg_id:512540 biomarkers ammonia oxidation activity anaerobic ammonium-oxidation (Anammox) GQ356
AB486712.1 gg_id:589011 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCOR AB486
EF123574.1 gg_id:249219 Microbial disease microbial mats on Siderastrea siderea three regions wider Caribbea EF1235
EF125439.1 gg_id:179213 mangrove soil clone MSB-2E1 EF1254
GQ340148.1 gg_id:586939 Prokaryotic Marathonas Reservoir Greece water column clone B07-89-BAC GQ340
AM774187.1 gg_id:278832 lineages Planctomycetes densely colonize alkaline gut soil-feeding termites (Cubiter AM774
AB192132.1 gg_id:202625 termite gut homogenate clone M1NP1-64 AB192
AM086149.1 gg_id:149208 Abundance and archaea mesotrophic Lake Kinneret lake profundal sediment clone AM086
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AF234735.1 gg_id:50882 sludge clone A8 AF2347
EF020031.1 gg_id:216224 aspen rhizosphere clone Elev_16S_1426 EF0200
CU926663.1 gg_id:535989 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU926
EF125452.1 gg_id:190111 mangrove soil clone MSB-2F5 EF1254
GU118783.1 gg_id:558104 Threatened Corals Provide Microbial Habitats clone Mfra_K07 GU118
GQ340267.1 gg_id:579129 Prokaryotic Marathonas Reservoir Greece water column clone A08-139-BAC GQ340
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FJ203428.1 gg_id:327231 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h FJ2034
EF516721.1 gg_id:218584 grassland soil clone FCPU585 EF5167

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210.9	6355.8	5112.1	4987.4	6853.8	5529.0	6901.3	7545.8	3137.8	3070.0	4275.7
297.7	5639.5	6071.9	5602.6	6073.5	5469.6	6075.1	6018.0	3793.6	2179.1	5425.1
113.8	3316.1	3965.5	3493.3	5297.7	4179.8	7014.8	4456.3	1894.7	1148.3	2814.9
37.9	589.1	562.1	511.0	1265.9	667.5	1826.8	803.2	225.0	353.4	354.3
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211.9	5033.3	5409.8	4553.3	6661.9	4909.3	6893.8	5793.7	2411.4	1163.5	3145.0
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266.9	163.8	185.0
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7906.0	6065.3	9031.1
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EU245214.1 gg_id:237911 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-H4-B12 EU245
DQ329768.1 gg_id:201435 Guerrero Negro hypersaline microbial mat clone 02D2Z12 DQ329
EU386107.1 gg_id:265536 Biogeographical and microbes sediments on subseafloor sediment South China Sea c EU386
DQ070794.1 gg_id:147997 Prokaryotic Structures Seafloor Basalts Varying Age and Juan de Fuca Ridge basalt gl DQ070
FJ203440.1 gg_id:321503 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h FJ2034
AB486437.1 gg_id:552968 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC AB486
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FJ232648.1 gg_id:323064 Enrichment ANAMMOX Wastewater Treatment Plants Korea and Their Activity sludg FJ2326
EU135213.1 gg_id:244630 tallgrass prarie soil clone FFCH13721 EU135
GQ214098.1 gg_id:562881 China loess clone P818 GQ214
EF540354.1 gg_id:225493 oil-shale semi-coke solid waste clone 24B_MJK EF5403
AY704401.1 gg_id:112006 oceanic crust clone FS142-21B-02 AY704
FJ232639.1 gg_id:332829 Enrichment ANAMMOX Wastewater Treatment Plants Korea and Their Activity sludg FJ2326
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DQ404806.1 gg_id:155344 contaminated sediment clone 661261 DQ404
EF205581.1 gg_id:214356 among geographically regions central Tibet geothermal spring mat clone TP5 EF2055
GU118276.1 gg_id:548121 Threatened Corals Provide Microbial Habitats clone Dstr_C07 GU118
FJ232651.1 gg_id:351648 Enrichment ANAMMOX Wastewater Treatment Plants Korea and Their Activity sludg FJ2326
DQ404633.1 gg_id:152343 contaminated sediment clone 656078 DQ404
EF125406.1 gg_id:178940 soil naked tidal flat sediment near mangrove clone MSB-1E4 EF1254
FJ203554.1 gg_id:342344 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h FJ2035
EF208715.1 gg_id:200049 Vertical and horizontal structure microbial sandy carbonate sediment clone CI75cm.2 EF2087
DQ289931.1 gg_id:170286 Microbial Carbon and Nitrogen Cycling Sediments South Atlantic Bight Permeable Sh DQ289
EF208689.1 gg_id:200911 Vertical and horizontal structure microbial sandy carbonate sediment clone CI5cm.FC EF2086
AB240225.1 gg_id:142901 microbial structure Phragmites rhizosphere biofilm reed bed reactor laboratory clon AB240
AB270056.1 gg_id:170512 Influence temperature and humidity on heifers rumen contents Holstein heifer (Bos AB270
AJ290182.1 gg_id:200064 and seasonal changes planctomycetales biofilms extracted river biofilm s clone DSP2 AJ2901
EU381635.1 gg_id:264273 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid EU381
EF419414.1 gg_id:204219 Substantial alterations cutaneous biota psoriatic lesions human skin clone 6P2-75 EF4194
FJ516944.1 gg_id:509690 semiarid 'Tablas de Daimiel National Park' wetland (Central Spain) unravelled upper s FJ5169
FJ542842.1 gg_id:525666 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone A FJ5428
X81948.1 gg_id:2823 Pirellula str. 670 X81948
GQ246406.1 gg_id:536385 Temporal and spatial China North Yel Sea sediments clone Ld1-11 GQ246
DQ289943.1 gg_id:168811 Microbial Carbon and Nitrogen Cycling Sediments South Atlantic Bight Permeable Sh DQ289
EU488313.1 gg_id:555142 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU488
FJ232657.1 gg_id:342256 Enrichment ANAMMOX Wastewater Treatment Plants Korea and Their Activity sludg FJ2326
AY225652.1 gg_id:96259 Mid-Atlantic Ridge hydrothermal sediment clone AT-s2-38 AY2256
FJ437939.1 gg_id:544528 Benthic okenone production Fayetteville New York Green Lake surface sediments 16. FJ4379
DQ070834.1 gg_id:150611 Prokaryotic Structures Seafloor Basalts Varying Age East Pacific Rise and Ridge basal DQ070

68.4	525.1	785.9	894.7	817.4	638.7	898.2	976.1	341.2	249.6	319.4
11219.7	3772.4	3985.9	3987.7	4553.7	4184.4	6027.7	4662.2	5116.0	2811.8	4591.9
207.6	5329.3	5436.5	4867.0	6895.3	6308.1	8732.1	6157.5	2237.7	2004.9	4428.6
60.6	3033.8	3033.0	2816.1	3826.8	3821.4	4818.8	4150.9	1799.2	1656.3	2294.3
53.2	45.5	49.5	40.5	77.9	40.2	79.8	46.9	46.6	40.4	38.0
149.7	2331.5	2397.8	2189.4	3971.3	2690.9	4951.2	3438.9	1344.3	1234.2	1389.3
7694.7	10640.6	9911.9	10107.1	12112.6	10298.6	12351.0	9565.4	13127.9	8805.1	8252.8
18156.9	12764.8	12449.1	13010.7	15876.1	12539.2	16148.8	12962.7	14262.3	10585.4	13485.7
269.2	1748.7	2134.8	1694.0	4803.9	3146.3	3314.9	2101.0	658.3	491.7	903.2
1151.3	5743.6	7526.3	6662.8	7733.0	5994.2	8616.9	6820.4	3801.1	1789.2	5170.9
7564.7	11611.4	10934.7	11234.2	15366.4	11863.7	15750.4	12278.4	11939.6	7299.1	10825.6
67.6	2232.0	2482.3	2032.5	3761.6	2672.4	4549.8	3513.2	980.0	606.3	1136.4
33.2	196.6	267.6	138.9	216.8	167.6	487.8	345.5	30.2	34.7	79.4
78.0	2967.9	2720.2	2600.3	7233.4	3628.5	5869.0	5734.7	1768.5	1396.0	1146.7
167.9	1610.8	1718.4	2027.6	2590.5	1851.5	1948.9	2169.9	1278.4	336.2	1041.6
135.1	999.4	1181.9	745.5	3302.7	1331.3	4469.5	981.9	197.4	188.3	480.5
89.9	3270.7	2658.3	2045.2	4122.3	2979.1	4709.8	3478.6	1724.1	1848.0	1806.0
42.5	80.9	94.1	76.8	205.5	104.3	146.0	257.3	77.8	36.8	47.8
345.0	3781.1	3821.4	3680.8	4769.0	4043.3	5233.3	5090.9	1597.7	1274.6	3498.1
718.7	4952.1	5033.8	4998.2	8364.8	5659.8	8342.0	6143.1	6603.1	2110.5	4254.0
50.4	690.9	874.5	817.2	1493.5	1059.2	1611.9	1443.8	423.8	283.2	256.5
105.7	2731.0	3521.8	3043.0	4244.6	2780.3	5435.9	3627.0	1505.2	882.0	1442.1
71.2	1745.4	2321.3	2270.6	3367.1	1941.5	4002.4	2183.9	661.9	506.3	753.3
39.5	241.0	261.9	176.1	279.7	217.7	285.4	263.4	67.5	38.6	124.0
42.6	168.5	174.8	130.3	233.8	180.4	261.3	338.3	61.2	40.2	95.1
59.5	838.3	800.6	706.2	2018.3	1109.5	1997.7	1421.3	268.5	270.6	389.0
35.7	882.0	1416.2	1165.7	2078.1	2008.3	3466.1	2651.6	201.0	80.3	785.1
33.1	114.9	228.2	167.1	101.4	138.1	107.0	167.7	61.9	31.3	88.2
914.6	8012.0	7798.1	8049.9	10581.7	8582.5	12250.4	9417.9	5729.8	4892.4	6706.4
4622.9	3738.1	2865.4	4049.1	3981.6	3885.9	5180.2	4164.2	3533.8	2688.8	3523.4
537.7	5081.1	4035.7	3363.1	4070.7	5738.2	4221.4	4341.9	2811.8	6156.0	3605.4
685.3	7027.9	6788.2	6576.0	9105.0	7028.4	10442.2	7906.8	4028.2	2828.3	4927.8
1052.2	5917.9	5178.0	4301.2	6519.3	5188.5	6283.9	6262.5	4749.5	5500.7	3792.9
81.8	4511.4	3902.5	3489.3	7466.0	5115.2	5865.5	5452.4	3827.3	1981.5	2590.5
53.7	4437.2	4531.4	4755.0	7135.8	5111.5	7351.2	5403.2	2667.9	2856.5	3398.3
46.0	124.4	206.8	113.7	179.2	104.5	301.0	149.2	57.4	27.6	59.9
3350.7	9005.5	8217.6	7802.6	11336.2	8903.8	12494.4	9521.0	7177.0	5815.1	6604.2
7061.6	8959.6	8147.7	9350.2	11163.7	8025.1	9333.9	9092.9	7797.9	5084.0	9342.4
51.8	549.4	609.5	473.4	833.0	489.1	1143.2	618.4	291.9	192.9	303.5
774.0	4104.4	4594.7	4454.9	5688.3	4946.9	6416.8	5579.3	2801.8	1719.0	3789.6
56.7	438.1	443.4	310.9	1144.1	650.6	1156.0	662.2	110.7	93.0	133.9

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60.6	71.8	59.1
3503.9	1549.7	3200.8
9720.2	10177.6	10755.4
13917.0	12690.1	15493.6
2361.7	2348.3	3860.4
5749.6	5859.5	7311.0
12996.5	11521.1	14824.6
3147.1	2540.3	3722.8
100.8	140.5	246.0
6099.2	3612.1	5170.0
2396.9	2439.3	3234.2
1014.1	968.1	1627.9
3154.4	3004.7	5216.7
151.6	79.7	134.0
4152.4	3363.3	5338.9
6554.0	6065.6	8240.1
845.5	655.6	1442.9
2469.3	2857.6	3089.1
1659.9	1778.9	1887.3
157.3	156.9	251.7
156.9	127.4	675.0
1516.5	1053.0	1354.5
1084.6	961.2	2464.7
236.1	144.1	219.0
10143.3	7962.1	10732.7
4047.6	3973.0	4848.4
4170.3	4805.8	6030.0
7247.4	6976.2	9102.9
6769.9	5440.4	8694.0
5392.4	3932.9	8240.4
5245.4	4382.7	5606.5
114.5	143.0	144.3
10139.4	7642.2	11211.3
9253.0	7460.1	9393.7
656.7	1086.3	908.5
5508.6	4598.2	7079.9
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CT574224.1 gg_id:154335 evidence planctomycete Evry municipal wastewater treatment plant clone 029B06_F CT5742
FJ542996.1 gg_id:514874 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone B FJ5429
EU734986.1 gg_id:353483 assemblages sediment station DBSE Northern Bering Sea clone 080B24 EU7349
EU491549.1 gg_id:269000 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR4C EU4915
FJ172792.1 gg_id:344848 Qinghai Yak Ruminal and Fungi China rumen clone RB-2C12 FJ1727
FJ203088.1 gg_id:312705 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c FJ2030
EF494313.1 gg_id:224266 Nunnock River granitic landscape clone NR.4.006 EF4943
DQ984569.1 gg_id:245832 Mt. Nan-Jen soil clone IFD_124 DQ984
AB355065.1 gg_id:252268 Monitoring and archaeal two heavy polluted areas lake Egypt based on sediment Ma AB3550
EF515912.1 gg_id:217349 grassland soil clone FCPO648 EF5159
AB487699.1 gg_id:588740 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNSR0 AB4876
FJ208839.1 gg_id:351437 Enrichment ANAMMOX Wastewater Treatment Plants Korea and Their Activity sludge FJ2088
GQ402727.1 gg_id:545813 Accessing microbial biodiversity and metabolic potential tropical -based approach pe GQ402
FJ905699.1 gg_id:513469 s Tonga-Kermadec iron oxide sediments Volcano 1 Tonga Arc clone V1F13b FJ9056
FJ652511.1 gg_id:586795 aerobic and anaerobic ammonia-oxidizing sponges marine sponge clone ML-Pla-24 FJ6525
FJ208828.1 gg_id:315617 Enrichment ANAMMOX Wastewater Treatment Plants Korea and Their Activity sludge FJ2088
EU621897.1 gg_id:274014 and kinetic research ammonia mixed anaerobic ammonium oxidation reactor seedec EU6218
CU920107.1 gg_id:537364 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU920
FJ374260.1 gg_id:359089 Inter- and intraspecific humivorous scarab beetle larvae (Pachnoda spp.) larval hindgu FJ3742
AB234544.1 gg_id:145313 termite gut homogenate clone MgMjD-104 AB2345
AB234542.1 gg_id:149255 termite gut homogenate clone MgMjR-038 AB2345
EF032767.1 gg_id:178484 cyanobacterial mat in lava cave clone HAVOmat22 EF0327
AB252879.1 gg_id:171614 Identification Shibayama lagoon Ishikawa Japan iron-oxidation biofilm clone 018 AB2528
EU881130.1 gg_id:329424 Karst region primary forest soil clone KPF200711-199 EU8811
EU135304.1 gg_id:244428 tallgrass prarie soil clone FFCH773 EU1353
GU119349.1 gg_id:579236 Threatened Corals Provide Microbial Habitats reef water clone Reef_L13 GU119
GQ348014.1 gg_id:555348 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ348
EF032766.1 gg_id:189073 cyanobacterial mat in lava cave clone HAVOmat101 EF0327
EU617890.1 gg_id:309328 Seasonal variation microbial Yel Sea sediment clone D13S-65 EU6178
EU135137.1 gg_id:242995 tallgrass prarie soil clone FFCH15608 EU1351
EU478637.1 gg_id:324136 microdiversity study anammox Candidatus Scalindua phylotype marine oxygen minir EU4786
AY947993.1 gg_id:143867 Synchrony and seasonality two temperate rivers USA: Massachusetts Parker River cl AY9479
AJ247193.1 gg_id:25580 Asticcacaulis biprosthecium str. DSM 4723(T) AJ2471
AB016610.1 gg_id:5563 Asticcacaulis excentricus str. ATCC15261 AB0166
AF296688.1 gg_id:23972 Brevundimonas alba str. H12C5 AF2966
FJ950569.1 gg_id:436320 Brevundimonas diminuta str. c82 FJ9505
EU536433.1 gg_id:281870 profile human microbiota antecubital fossa (inner elbow) skin clone nbt213g08 EU5364
FJ658350.1 gg_id:568324 Metalworking Fluids and Aerosols Metallurgy Plant metalworking aerosol clone Winte FJ6583
DQ335215.1 gg_id:145289 Brevundimonas terrae str. KSL-145 DQ335
EU465068.1 gg_id:294281 African elephant feces clone AFYEL_aaj67e11 EU4650
FJ950592.1 gg_id:424138 Brevundimonas diminuta str. c94 FJ9505

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55.0	4023.1	3340.0	2955.8	6447.7	4288.9	7113.7	5064.6	1731.4	1527.7	2174.2
1086.0	2872.8	3218.9	3180.5	5039.1	3461.2	5669.0	3831.6	1048.4	779.3	2111.5
2150.7	5274.9	5188.8	5578.2	6844.3	5512.6	6745.2	5691.6	3971.7	3012.9	5518.1
107.8	347.4	465.0	386.5	673.1	383.7	600.2	757.1	169.3	74.0	125.9
40.9	1963.8	1306.4	1103.6	3863.6	1907.4	4700.1	2457.4	674.5	519.3	681.0
1260.5	3993.0	3409.7	3969.1	5002.0	3811.9	5367.9	4012.5	2628.7	801.1	2436.8
1929.8	4626.4	3598.2	3007.6	4501.4	4131.8	4879.5	4345.1	2545.1	1640.0	2437.6
13504.3	4080.2	3875.0	4213.8	3505.1	3935.2	5030.2	3648.3	9994.0	5942.2	6815.8
12125.7	9358.3	9282.5	9844.9	10379.5	9232.5	14276.2	9236.7	10253.4	6919.5	10238.9
6481.2	5936.8	5626.7	5516.1	6471.1	5501.0	7374.3	5409.7	4008.8	3335.2	4039.9
6428.4	7127.3	7311.2	8132.1	8061.3	7088.5	7984.5	7028.7	6119.9	5080.6	6964.5
332.9	3430.1	3824.6	3216.3	4415.0	3344.4	4402.8	3875.4	2281.3	1069.6	2641.7
1385.4	6799.5	6441.8	6933.5	8138.4	6297.2	9462.8	6184.9	4773.4	5256.6	6621.0
139.2	3806.2	4227.3	4616.7	4394.0	3801.4	4656.1	4186.1	2000.1	1590.6	4391.5
2210.3	6766.3	6900.2	7695.9	8538.8	7035.8	10030.6	8273.5	6149.0	3606.9	7243.3
9740.5	9470.4	9650.3	11113.3	11511.3	9627.3	12154.7	9606.5	11351.7	6457.8	11025.6
784.1	5372.6	7016.0	6062.6	5434.0	5501.1	6753.3	5459.4	4507.8	2699.6	6133.4
1057.1	3495.1	3738.2	3906.7	3429.4	3305.9	4063.6	3272.4	3681.5	6253.6	4312.1
595.4	2434.5	2793.9	2015.3	2395.1	2170.5	2353.2	2129.9	3041.2	3152.5	3353.1
44.4	103.8	96.2	58.2	193.0	90.2	138.7	62.7	25.3	21.4	28.4
47.3	121.2	137.9	169.5	98.4	132.4	252.6	90.7	33.8	27.8	60.3
199.6	1744.9	1904.1	2238.2	1818.3	1864.1	1866.7	2172.4	1124.1	744.4	1672.1
416.1	4054.2	3939.7	4630.1	4997.0	4159.5	5494.0	3808.0	3090.4	2837.1	4140.6
266.2	3871.4	5206.2	5325.4	6549.2	4266.8	6767.6	4593.6	3705.2	6018.2	3562.4
1720.6	4476.6	6644.6	4682.5	5712.1	4577.5	5871.9	4323.8	2777.0	2186.1	3069.1
1794.0	4703.2	6183.4	6607.7	8279.4	6139.0	9430.4	6528.1	3953.9	1971.4	5363.9
71.4	2017.9	2774.6	2890.2	3547.7	2440.1	3432.6	3895.8	2023.3	1476.4	1559.4
3522.5	2776.2	3097.4	2978.0	3855.4	3533.6	3425.8	3346.2	2503.3	1061.8	2959.1
6208.1	5937.3	6309.1	6361.6	6619.8	5995.1	7928.9	6975.8	6443.1	5418.0	6183.6
213.6	1351.8	2307.1	2264.3	1693.7	1750.3	1214.2	4518.7	1862.6	4084.3	1048.9
14707.7	4491.9	4843.3	4549.9	5320.4	4509.1	4513.5	6134.6	3975.4	5521.2	4438.7
3197.7	3706.5	4115.1	4377.9	6306.0	4178.5	6083.1	6045.8	4100.8	4965.4	2968.5
7076.9	6452.3	5477.1	6598.1	7349.4	5737.1	6986.0	6043.3	5524.9	4050.5	4351.1
4314.6	4209.6	3892.7	4369.1	4525.0	5013.3	4453.2	5101.5	3983.8	2999.5	3567.5
23099.8	11379.8	10427.8	11099.8	10300.9	11021.8	12597.4	9936.4	13004.1	12804.7	15134.6
13826.0	7966.5	7213.9	8103.8	7839.5	7747.8	8310.6	7217.4	7028.2	7465.6	8918.7
4482.4	5015.9	5000.5	5566.9	7361.1	6126.7	7329.5	6307.3	6581.6	6257.6	4298.9
2983.0	3208.9	3862.8	4418.9	5193.5	3805.9	5094.3	4635.7	2706.7	4640.8	2149.7
2933.9	2967.4	3747.7	3811.0	4924.3	4431.7	3608.3	5026.1	2931.9	6214.3	2341.1

5761.3	4706.1	7438.2
4613.0	3679.6	6519.8
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3578.3	2153.2	3643.7
5306.7	5169.4	8350.5
553.3	1059.0	621.4
2616.4	1293.2	2765.9
4792.6	3699.1	4719.6
3607.4	3857.4	5253.1
3618.0	5994.1	5064.3
9053.2	10218.4	12257.8
5318.2	6607.1	7608.4
6082.4	7030.5	8162.5
4021.3	3369.0	4229.6
6567.4	6028.0	7755.1
3159.4	3453.0	5223.6
7001.5	8858.6	9806.4
9313.5	9886.1	12539.2
5020.1	5792.1	6112.4
2958.8	3725.1	2816.7
2070.8	2405.6	2640.6
46.2	79.4	1820.1
59.0	113.5	495.8
1444.2	2099.3	4714.6
3788.8	4070.3	7200.1
3992.0	5080.6	6143.8
4302.8	5047.8	5181.3
6347.2	7033.5	8236.1
2925.1	3019.7	3171.0
2043.9	2862.3	5929.7
5929.3	7817.4	8360.3
5660.5	4882.3	3764.3
7253.1	5921.3	5321.1
6846.2	6185.6	4621.9
6793.7	6263.3	6058.1
5528.1	5752.6	4047.4
10481.9	11316.4	9906.8
7542.4	8177.4	7776.4
7058.3	5852.4	5092.8
6070.4	4567.2	3633.7
7047.3	5172.0	3322.7

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g__Brevundimonas
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s__Brevundimonas diminuta	59158
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EU434547.1 gg_id:262017 Brevundimonas diminuta str. b76 EU4345
EU465065.1 gg_id:301063 African elephant feces clone AFYEL_aaj67e08 EU4650
EU434576.1 gg_id:262199 Brevundimonas diminuta str. b108 EU4345
EU464720.1 gg_id:297700 Hartmann's mountain zebra feces clone AFZEB_aaj69f09 EU4647
FJ658310.1 gg_id:535144 Metalworking Fluids and Aerosols Metallurgy Plant metalworking aerosol clone Winte FJ6583
FJ658395.1 gg_id:540941 Metalworking Fluids and Aerosols Metallurgy Plant metalworking aerosol clone Winte FJ6583
EU434570.1 gg_id:265057 Brevundimonas diminuta str. b77 EU4345
EU464980.1 gg_id:290745 African elephant feces clone AFYEL_aaj66b08 EU4649
DQ824709.1 gg_id:183605 human fecal clone RL185_aaj72b02 DQ824
FJ657857.1 gg_id:537717 Metalworking Fluids and Aerosols Metallurgy Plant metalworking fluid clone Winter_ FJ6578
EU535556.1 gg_id:284254 profile human microbiota antecubital fossa (inner elbow) skin clone nbt27b12 EU5355
GQ280032.1 gg_id:588010 Brevundimonas sp. str. BJ-22 GQ280
FJ658136.1 gg_id:543663 Metalworking Fluids and Aerosols Metallurgy Plant metalworking aerosol clone Winte FJ6581
EU434575.1 gg_id:258759 Brevundimonas diminuta str. b124 EU4345
AB021415.1 gg_id:5595 Brevundimonas diminuta str. IAM 12691T AB0214
EU465159.1 gg_id:296763 African elephant feces clone AFYEL_aaj68h07 EU4651
FN433035.1 gg_id:559314 Brevundimonas terrae CCM24B FN4330
EU434509.1 gg_id:268353 Brevundimonas diminuta str. b215 EU4345
EU464952.1 gg_id:291623 African elephant feces clone AFYEL_aaj65f11 EU4649
AJ244706.1 gg_id:109577 Brevundimonas mediterranea str. V4.BO.18 LMG 22801 = MM_2367 AJ2447
AJ244707.1 gg_id:109696 Brevundimonas mediterranea str. V4.BE.56 LMG 22802 = MM_3001 AJ2447
AM402981.1 gg_id:162149 Brevundimonas sp. str. JO26 AM402
AY971369.1 gg_id:115361 Brevundimonas kwangchunensis str. KSL-110 AY9713
EU834791.1 gg_id:585677 Microbiology Aerobic Phosphorus Removal Process aerobic phosphorus-removing se EU8347
EF363713.1 gg_id:204302 Brevundimonas lenta str. DS-18 EF3637
GU321351.1 gg_id:547657 Brevundimonas sp. str. NMC11 GU321
AM412000.1 gg_id:198378 Brevundimonas nasdae Z66zhy AM412
AY328801.1 gg_id:90161 drinking water OR9 AY3288
EF157195.1 gg_id:241110 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon EF1571
AY169433.1 gg_id:82124 Brevundimonas vesicularis AY1694
AJ227782.1 gg_id:5579 Brevundimonas bacteroides str. CB7 AJ2277
AJ227797.1 gg_id:5583 Brevundimonas sp. str. FWC40 AJ2277
AJ227781.1 gg_id:5611 Brevundimonas vesicularis str. LMG 11141 AJ2277
AY293404.1 gg_id:87601 travertine terrace Yellowstone Hot Springs clone SM2A11 AY2934
EF546433.1 gg_id:219465 Brevundimonas nasdae str. P1 EF5464
EU182863.1 gg_id:247068 Brachybacterium sp. str. MH35 EU1828
DQ825663.1 gg_id:162728 Brevundimonas sp. str. 5420S-28 DQ825
AY328842.1 gg_id:89703 drinking water MB11 AY3288
AJ227786.1 gg_id:53033 Brevundimonas intermedia str. ATCC 15262(T) AJ2277
EU636022.1 gg_id:278329 Antarctic str. N97 EU6360
EU182890.1 gg_id:250309 Brevundimonas sp. str. MH62 EU1828

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13073.9	3783.6	4024.0	4141.0	4994.7	3864.8	5178.1	4330.9	3853.1	4133.6	2626.5
19042.1	7327.3	6971.5	7401.5	8506.6	7454.0	8567.8	7413.6	9225.7	8866.8	6284.5
10104.9	5301.1	5271.2	5657.7	5695.8	4949.1	5910.0	5301.6	6579.0	4818.1	3889.0
8339.8	5353.3	5042.1	5297.9	5922.2	5645.5	5774.3	5828.6	4885.0	6732.3	3842.0
5753.0	4627.9	4524.6	5125.7	5202.8	5466.8	5563.4	5349.5	4858.9	4648.8	4984.5
16122.0	6218.8	5604.9	6079.5	6371.4	5505.9	6073.6	6350.6	6730.6	7342.2	7604.4
8213.5	4577.3	4351.6	4487.7	4444.1	4274.4	4810.5	4260.9	4799.6	4920.8	5318.3
21353.5	6880.6	6380.3	6703.7	6994.4	6645.1	7704.9	6484.3	9379.7	9159.1	7360.8
9182.6	4856.9	5015.5	5343.7	6370.0	5911.5	5342.3	6000.4	6055.8	7429.2	3884.0
8487.3	4755.3	4855.0	5157.1	4966.4	6626.8	6236.7	7276.8	5215.0	7563.3	6813.3
5402.5	2913.6	3654.6	3625.2	4628.1	4055.1	3752.8	4218.5	2651.3	4109.1	1981.6
5625.0	5519.8	5416.7	5769.9	5645.0	5541.0	6716.5	5413.0	5641.1	6333.5	5937.8
4135.8	6907.2	5866.4	6359.4	7822.1	6044.3	7929.3	6995.2	7087.7	6369.9	4869.8
17486.4	7232.3	5979.3	6557.0	6823.8	6722.5	6703.6	5918.1	8069.4	6786.8	8506.7
20727.2	6581.2	7054.1	7164.0	6927.9	6394.9	7434.7	6250.6	5330.3	5732.1	5646.2
4402.8	2904.4	2698.5	3678.3	4493.0	3954.2	3674.6	4145.3	3928.6	4650.0	1718.7
20250.3	5732.2	6138.9	6148.7	7402.4	6033.5	8987.8	6388.1	7056.1	6862.0	6527.7
5067.4	3344.8	2800.4	3579.7	4102.9	3174.8	4053.7	3906.6	3597.1	2831.9	1721.7
1091.3	1217.5	2224.2	2454.4	3584.9	2665.3	1573.7	2961.0	2590.4	5503.3	834.5
346.0	939.9	1819.6	1966.5	2789.0	2041.4	1442.7	2448.5	1054.8	3077.7	696.1
602.5	530.2	841.4	786.1	727.7	650.1	763.4	1013.2	567.5	835.4	523.2
8288.4	5005.6	4881.7	5298.0	5852.3	6234.6	4937.4	8222.4	7992.4	5523.2	6738.5
9472.6	5942.2	5421.3	5599.5	7335.5	6277.0	6782.0	6164.0	6743.8	4953.2	5148.8
6002.4	3265.2	3150.0	3454.3	4408.6	3702.4	3671.7	4077.8	3774.4	4088.3	2542.3
2277.8	3424.3	2967.8	3871.3	5010.2	3775.3	5293.6	4657.7	3126.5	3927.2	2429.5
2452.2	1908.8	2908.6	3505.3	4543.5	3397.9	2492.8	3059.1	3221.6	7291.0	1724.9
19154.7	8165.0	7224.0	8874.5	8059.2	7507.3	9054.3	7815.4	12425.1	9312.1	9997.9
7239.2	3684.0	4108.4	4299.6	4761.2	4576.3	4038.4	4394.5	3465.6	5135.6	3724.0
18093.8	7367.1	7921.4	7854.5	8413.1	7528.1	7505.1	7536.3	10651.7	10735.2	7301.4
6176.1	6390.5	6071.1	6727.0	7564.8	6049.3	6960.3	6292.3	6845.0	5180.2	6617.0
3009.9	2383.3	3053.0	3358.9	3530.3	3087.3	3325.1	3339.7	2417.1	3269.5	1842.0
3260.7	2214.4	2958.6	3351.6	4299.6	3874.5	2289.5	3912.1	2352.5	6530.3	1105.0
6765.1	2252.4	2138.3	2643.3	4810.9	3226.2	3015.6	3039.7	3463.0	3474.0	1173.3
4143.6	2555.9	2405.3	3873.5	4450.9	4018.9	2840.8	4029.3	4535.3	6100.7	3315.3
8311.7	2822.9	3015.3	3540.0	4314.9	3635.3	2921.2	3669.1	4204.8	4725.3	2292.2
1631.9	1371.5	2284.8	2631.5	3463.9	2929.7	1414.1	2886.1	2768.5	6076.7	816.9
329.3	1359.6	1695.7	1835.2	2709.1	2179.9	2046.1	2497.5	1654.7	2850.7	694.8
1462.0	1250.5	2163.9	2525.3	3347.9	2761.5	1418.4	2677.8	2679.5	6285.3	759.2
5371.0	3365.1	3783.0	5074.4	5253.0	4044.7	4561.2	4998.6	4909.8	4981.8	2812.2
1137.1	1378.8	2213.8	2519.8	3323.6	2726.9	1655.3	2795.9	2112.0	5525.1	794.0

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5472.4	4461.6	3976.5
9300.8	8130.4	7617.6
6472.9	6205.9	5458.6
6457.5	6649.6	5740.4
5877.5	5258.1	5108.2
6845.3	7950.1	6133.0
5171.4	5298.2	3346.7
7428.0	9125.4	6512.4
7988.0	5912.5	5448.7
7062.8	8135.1	6284.5
5167.8	4206.5	3818.3
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8324.7	7279.7	7524.1
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4423.6	3010.5	1341.1
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7568.1	5708.9	5746.6
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5722.9	4186.1	3357.3
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7806.8	8516.8	8316.3
5920.9	4299.6	4036.6
9390.8	8038.3	7095.2
6731.2	6728.5	6049.0
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6757.7	3367.8	3096.7
4814.8	3292.8	3286.0
6828.4	4236.6	3359.4
6384.5	3405.4	2984.7
6678.6	2392.1	1501.6
3823.6	2300.7	1809.3
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EU143355.1 gg_id:238339 Brevundimonas sp. str. J22 EU143
EU580513.1 gg_id:543062 Benthic diatoms Constance: functional interactions regarding growth and EPS-secret EU580
AJ007808.1 gg_id:5626 Brevundimonas variabilis str. ACM 5107 (T) AJ0078
AB426562.1 gg_id:270554 Brevundimonas sp. str. HINF004 AB4265
DQ372984.1 gg_id:152214 Brevundimonas sp. str. EMB102 DQ372
AY328835.1 gg_id:89630 drinking water MA26 AY3288
EU379308.1 gg_id:274963 Brevundimonas intermedia str. 6R-J-7d EU3793
AJ007802.1 gg_id:5568 Brevundimonas intermedia str. ACM 2608 (T) AJ0078
AJ227784.1 gg_id:5617 Brevundimonas subvibrioides str. CB81 AJ2277
AJ495803.1 gg_id:63466 Brevundimonas sp. p22P AJ4958
AJ227783.1 gg_id:43186 Brevundimonas variabilis str. ATCC 15255 (T) AJ2277
EU434579.1 gg_id:266190 Brevundimonas aurantiaca str. e12 EU4345
AM183353.1 gg_id:167639 Brevundimonas sp. 1228-1II AM183
AB447548.1 gg_id:316703 Brevundimonas sp. str. SUWAF011 AB4475
DQ981459.1 gg_id:203778 Brevundimonas sp. SB4 DQ981
DQ442520.1 gg_id:191932 Streptomyces longisporoflavus str. NRRL ISP-5165T DQ442
FN397631.1 gg_id:452397 Brevundimonas sp. str. CM 272 FN3976
DQ413152.1 gg_id:152156 Brevundimonas sp. str. EMB 68 DQ413
AJ007803.1 gg_id:5518 Caulobacter fusiformis str. ACM 5108 (T) AJ0078
AB008533.1 gg_id:5557 Caulobacter fusiformis str. ATCC15257 AB0085
AJ007805.1 gg_id:5560 Caulobacter henricii str. ACM 5105 (T) AJ0078
AE005673.1 gg_id:209341 Caulobacter crescentus str. CB15 AE0056
AM921622.1 gg_id:248395 Caulobacter henricii PhyCEm-80 AM921
EF515958.1 gg_id:221595 grassland soil clone FCPT664 EF5159
DQ124680.1 gg_id:154386 Caulobacter tundrae str. Z-0024 DQ124
AF523036.1 gg_id:89365 natural mineral water clone D-1 AF5230
EU730905.1 gg_id:352383 Caulobacter vibrioides str. 156 EU7309
DQ532299.1 gg_id:164042 Geographical Variation Microbial Burden and Spacecraft Assembly Kennedy Space C DQ532
AY512823.1 gg_id:106146 Caulobacter vibrioides str. S13 AY5128
AB271055.1 gg_id:165771 Caulobacter ginsengisoli str. Gsoil 317 AB2710
AM940947.1 gg_id:278226 Caulobacter sp. ECN-2008 AM940
DQ404656.1 gg_id:151101 contaminated sediment clone 654987 DQ404
GQ396801.1 gg_id:538121 Functional unvegetated perhumid recently-deglaciated soils do not correlate shifts s GQ396
FN556568.1 gg_id:518192 Brevundimonas sp. str. JW23.4a FN5565
EU434505.1 gg_id:263790 Brevundimonas bullata str. b350 EU4345
DQ501309.1 gg_id:199553 Seasonal dynamics free-living and particle- four lakes northeastern Germany freshw DQ501
AY234477.1 gg_id:112129 soil isolate Ellin5060 AY2344
FJ197848.1 gg_id:313604 Brevundimonas sp. 39(2008) str. 39 FJ1978
AJ717391.1 gg_id:111099 Phenylobacterium falsum str. AC49 AJ7173
AJ582031.1 gg_id:93768 soil near uranium mill tailings clone JG36-GS-63 AJ5820
AY921824.1 gg_id:114202 farm soil clone AKYG696 AY9218

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1500.7	2494.9	3079.0	3231.6	5084.6	3708.2	4933.4	4711.7	2772.9	4543.8	2448.2
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1239.9	1959.3	2330.3	3101.3	3831.2	2635.3	2433.4	3107.9	2162.8	3296.5	1205.4
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GQ002488.1 gg_id:507172 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbu GQ002
AJ292592.1 gg_id:49162 PCB-polluted soil clone WD225 AJ2925
DQ202243.1 gg_id:140164 Enrichment s Type II Methane-Oxidizing Inhabiting Northern Peatlands peatland clo DQ202
GQ402724.1 gg_id:551851 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
AB473899.1 gg_id:554330 sequences endolithic and archaea Weissenstein (white rock) / Albula pass few millim AB4738
D49422.1 gg_id:5594 Brevundimonas diminuta str. IFO 3140 D49422
DQ984595.1 gg_id:240075 Mt. Nan-Jen litterfall clone IYF98 DQ984
GQ402558.1 gg_id:592079 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
DQ177484.1 gg_id:139814 Brevundimonas sp. str. Tibet-IK73 DQ177
EF516954.1 gg_id:226283 grassland soil clone FCPT726 EF5169
AJ292595.1 gg_id:30983 PCB-polluted soil clone WD233 AJ2925
AF289151.1 gg_id:70005 freshwater clone PRD01a003B AF2891
EU730914.1 gg_id:335822 Brevundimonas diminuta str. 207 EU7309
EU445215.1 gg_id:565413 Isolation Weight Forest Topsoil Metagenomic tropical forest topsoil clone R36 EU4452
GU118509.1 gg_id:573233 Threatened Corals Provide Microbial Habitats clone Gven_K20 GU118
DQ532251.1 gg_id:168212 Geographical Variation Microbial Burden and Spacecraft Assembly Johnson Space C DQ532
GU169058.1 gg_id:570254 Biofilms formed on substances: response f conditions and carbon concentrations sy GU169
FJ979845.1 gg_id:402409 Caulobacter sp. str. tsz12 FJ9798
AM697237.1 gg_id:227434 sequencing libraries indoor dust clone BF0001C078 AM697
AY922007.1 gg_id:113237 farm soil clone AKYG412 AY9220
GU118288.1 gg_id:568445 Threatened Corals Provide Microbial Habitats clone Dstr_G22 GU118
GQ402816.1 gg_id:589382 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
EU202832.1 gg_id:317304 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo EU2028
EU434454.1 gg_id:264269 Brevundimonas diminuta str. a229 EU4344
DQ177483.1 gg_id:140010 Brevundimonas sp. str. Tibet-IK53 DQ177
GU118656.1 gg_id:575957 Threatened Corals Provide Microbial Habitats clone Mfav_J15 GU118
DQ532201.1 gg_id:171288 Geographical Variation Microbial Burden and Spacecraft Assembly Johnson Space C DQ532
EU881329.1 gg_id:324088 (maize-sweet cropping field) Karst region maize-sweet potato cropland soil clone KM EU8813
EF520395.1 gg_id:235185 structure lakes: what controls ? acid-impacted lake clone ADK-BTe02-51 EF5203
EU784736.1 gg_id:336351 Brevundimonas sp. str. E8 EU7847
AY569007.1 gg_id:103285 Nitrobacteria hamadaniensis str. 104 AY5690
AB167225.1 gg_id:107935 Brevundimonas diminuta str. c66 AB1672
EF520409.1 gg_id:231965 structure lakes: what controls ? acid-impacted lake clone ADK-BTh02-54 EF5204
GQ402771.1 gg_id:587634 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
GU118170.1 gg_id:560087 Threatened Corals Provide Microbial Habitats clone Dstr_P10 GU118
AB473919.1 gg_id:573162 sequences endolithic and archaea Weissenstein (white rock) / Albula pass few millim AB4739
EU665093.1 gg_id:547599 Soil are Changed Agricultural Practices agricultural soil clone Plot22-C12 EU6650
AB374373.1 gg_id:272478 sequences Weissenstein (white rock) / few millimeters be surface rock called 'Weiss AB3743
AB167229.1 gg_id:107937 Brevundimonas diminuta str. c79 AB1672
AY734246.1 gg_id:133283 spring water of alpine karst aquifer clone SDKAS1_2 AY7342
DQ167245.1 gg_id:138986 Kopriimonas byunsanensis str. KOPRI 13522 DQ167

13141.4	5724.9	5549.5	5875.8	5486.2	5072.3	5642.0	5234.2	7104.8	4654.5	6172.4
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8822.3	2561.4	2625.9	3133.6	3239.5	2899.2	2960.2	4135.4	2322.5	2129.5	1463.9
7124.6	3051.9	3062.1	3035.4	4810.7	3400.4	4584.7	3577.5	2254.7	2194.4	2026.2
910.6	1846.8	1970.8	2247.4	4237.2	2448.4	3045.4	3516.9	2309.5	1499.6	1182.9
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14921.4	4356.8	4228.8	4428.7	4924.6	3925.5	4946.0	4898.4	6323.8	4514.5	3302.2
9389.8	2943.9	3294.1	3350.0	3623.5	3344.1	3522.4	3843.0	4409.7	4506.7	3120.3
100.4	459.5	543.6	662.4	893.2	612.4	575.9	875.6	282.3	369.9	229.6
67.2	121.5	228.2	203.1	61.3	237.8	663.4	211.6	124.5	341.6	24.6
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5447.1	3717.6	3074.8	3746.8	4162.7	4159.0	3158.0	4207.9	3580.3	3151.6	2875.0
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11959.2	4044.9	4146.8	4181.7	5049.5	4632.8	4979.6	4775.2	4422.6	4259.3	4199.2
10027.7	3381.4	3375.0	3596.5	5135.9	3767.3	3852.9	4211.9	2435.8	1793.8	2094.9
14474.4	5765.9	5286.7	5846.2	6997.6	5832.6	6968.1	5533.8	8128.2	5844.1	7724.4
7596.4	4150.8	5033.1	5719.5	6376.4	5874.8	5603.3	6301.3	7538.2	6809.5	4653.6
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10292.0	4664.5	4920.2	5706.2	6263.7	5126.0	6827.4	5676.4	5549.2	2426.1	4917.9
36161.4	9589.1	9931.7	10157.9	10128.7	9413.9	10715.0	9527.0	15253.6	11373.9	11824.5
5158.7	2986.7	2832.7	2722.3	4286.9	3380.0	3407.8	3558.4	3072.0	1990.4	1577.5
1558.3	3742.0	3451.1	3355.7	4842.8	4414.4	3868.6	3709.4	2494.4	3439.2	1337.8
2012.1	992.1	1444.9	1631.4	1894.1	1610.6	1662.3	2625.1	1753.9	1794.6	757.8
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1735.5	2352.4	2696.4	2725.6	3943.5	3380.4	3751.6	3806.7	3765.5	3116.0	1903.4
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13569.9	7325.9	6682.6	6950.9	9327.4	7942.5	8091.1	7982.7	6558.1	9020.4	7163.7
280.4	2552.0	3470.8	3863.2	3614.6	3152.0	3385.7	3893.1	1888.4	2739.0	1835.8
1295.1	739.8	1072.7	1136.8	2112.2	1160.3	1326.1	1576.6	755.0	704.6	466.0
124.8	49.0	49.1	38.5	26.9	85.5	88.1	56.5	36.3	27.8	25.3

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412.0	161.5	104.8
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2162.6	1709.1	1940.9
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AM749667.1 gg_id:566744 Kiloniella laminariae str. LD81 AM749
EF437150.1 gg_id:208597 Thalassospira nitroreducens str. TN1 EF4371
FJ210804.1 gg_id:346096 Thalassospira sp. str. QDHT-08 FJ2108
AB373113.1 gg_id:277271 Thalassospira sp. str. N5EA13-1A AB3731
AB373114.1 gg_id:265832 Thalassospira sp. str. G12-1 AB3731
AF358664.1 gg_id:35557 Thalassospira lucentensis AF3586
FJ202650.1 gg_id:316411 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2026
AB006768.1 gg_id:4594 Terasakiella pusilla str. IFO13613 AB0067
AY922191.1 gg_id:112927 whalefall clone 131616 AY9221
EF092208.1 gg_id:260078 Persistent Axinella corrugata clone Ax36_F7 EF0922
AJ633974.1 gg_id:114828 host's accessory nidamental gland clone 6ANG531 AJ6339
EF629835.1 gg_id:258350 Changes marine Mycale laxissima on transfer aqua sponge tissue EF6298
AY922227.1 gg_id:113991 whalefall clone 131732 AY9222
GQ169074.1 gg_id:592716 Thalassospira lucentensis str. TVGB18 GQ169
AY162078.1 gg_id:135758 Cultivating Sargasso Sea clone GMD37B4 AY1620
EU880514.1 gg_id:352101 Thalassospira lucentensis str. P44 EU8805
FJ952806.1 gg_id:399348 Thalassospira sp. str. 2ta2 FJ9528
AF143826.1 gg_id:25696 hydrocarbon-degrading consortium clone 4-Org1-58 AF1438
GU118853.1 gg_id:541338 Threatened Corals Provide Microbial Habitats clone Mfra_C21 GU118
EU268103.1 gg_id:254391 summer Dalian and Liaodong bay determined sea water clone L0603 EU2681
AY682384.1 gg_id:100730 Parvulomonas gwangyangensis str. GW14-5 AY6823
DQ917818.1 gg_id:221237 Microbial profiles bleached and wild-type Muricea elongata Kordiimonas clone BME DQ917
GU119022.1 gg_id:554110 Threatened Corals Provide Microbial Habitats clone Past_K19 GU119
EU287361.1 gg_id:252140 Pacific arctic surface sediment clone S26-61 EU2873
AB537162.1 gg_id:517870 Preparation single species magnetotactic multiple-displacement sediment water we AB5371
X81185.1 gg_id:11274 magnetic coccus MP17 str. TB24 X81185
X61607.1 gg_id:11262 magnetic coccus MP17 X61607
AAAN03000028.1 gg_id:130031 Magnetococcus sp. str. MC-1 AAAN0
DQ785314.1 gg_id:166095 magnetotactic sediments Jiaozhou Bay sediment clone QH-1 DQ785
EF371486.1 gg_id:214607 magnetotactic China Jiaozhou Bay clone M-40 EF3714
EF379386.1 gg_id:211078 magnetotactic China Jiaozhou Bay clone XSE-4 EF3793
AJ863157.1 gg_id:111324 marine microcosm clone CF24 AJ8631
GQ468519.1 gg_id:540513 Temporal variation magnetotactic two freshwater microcosms fresh water sedimen GQ468
Y13213.1 gg_id:11268 magnetic coccus MP17 str. pa19 Y13213
AJ863155.1 gg_id:109702 freshwater microcosm clone CF22 AJ8631
Y13210.1 gg_id:11281 Magnetic strain clone rj517 Y13210
X81184.1 gg_id:11271 magnetic coccus MP17 str. CS981 X81184
X81182.1 gg_id:11270 magnetic coccus MP17 str. CS92 X81182
EU570899.1 gg_id:543851 transition and zone within near-shore anoxic basin: Nitinat Lake depth 13 m clone Ni EU5708
EF370485.1 gg_id:205086 Morphology and wild type magnetotactic Miyun reservoir near Beijing China fresh w: EF3704
EF371485.1 gg_id:212269 magnetotactic China Jiaozhou Bay clone M-52 EF3714

8484.2	4134.7	3832.2	3762.9	4175.1	3880.7	4600.8	3732.9	2718.1	1879.5	2293.4
7429.5	6210.9	5850.7	6111.3	6273.5	6704.1	6739.1	6223.1	7644.7	7299.0	5888.5
1297.9	4994.9	4708.5	5065.8	6151.8	5370.0	5287.4	5544.7	3833.2	10695.6	4456.5
9605.9	8770.2	7554.9	7622.5	9392.5	9337.7	8763.4	8158.9	10750.8	8812.7	6028.7
4602.2	7547.1	7198.2	7661.6	8315.7	7781.4	8032.9	7762.9	7796.1	8352.3	6650.3
14213.7	8009.9	7314.2	8448.7	8829.9	8650.9	8813.9	7624.5	10530.9	9361.3	9023.8
384.5	1433.2	1429.0	1535.7	1489.3	1213.2	1566.2	1613.1	760.8	1244.2	715.0
65.1	268.0	433.4	694.4	424.3	298.5	310.2	436.3	201.4	162.0	192.9
215.8	1485.9	1644.5	1457.2	1560.5	1347.1	1661.9	1333.0	1775.3	2220.6	1200.0
1534.1	5218.3	5778.5	5202.1	5716.2	5701.4	5652.9	5630.1	5354.9	4205.5	4838.4
271.4	3663.6	2382.7	2328.2	4588.8	2023.4	2575.7	2493.8	3900.8	1116.3	932.1
2251.7	3502.5	2489.8	1849.4	3875.6	2696.1	2014.7	2264.6	1159.1	874.3	1346.6
63.4	89.1	119.7	126.8	129.5	90.9	102.1	118.4	69.2	60.6	72.8
838.9	3308.1	3140.5	2959.1	3716.6	3652.6	3053.1	3339.6	2767.1	6934.5	2521.6
7458.3	5186.7	4551.0	3602.2	4118.7	5692.9	3438.1	4135.9	5739.1	4123.9	3011.2
604.8	1565.5	1682.3	1856.8	2225.0	2334.9	2054.0	1854.3	1851.0	2428.3	1319.2
650.0	5655.2	4052.2	4083.8	4343.9	3730.2	3753.7	3980.2	2591.8	1837.0	2828.3
3663.8	4975.2	5306.5	5149.2	7966.1	6373.0	5478.5	6089.0	5329.9	6685.9	4447.3
47.0	76.9	184.9	94.7	134.9	98.3	110.8	324.9	65.7	88.3	173.4
3593.9	2700.3	2813.6	2856.7	3145.5	3954.9	2782.2	2955.7	2318.2	2642.2	1871.0
50.0	196.7	285.3	160.7	265.4	191.3	179.5	235.0	159.0	61.0	103.0
2492.5	1949.4	1339.6	1502.6	1754.5	1730.7	2667.9	1889.5	531.7	752.1	629.4
7381.4	5721.8	4052.0	4063.7	5408.3	5128.2	3950.5	5002.2	4596.8	4271.1	3392.8
68.0	59.3	86.5	94.4	86.0	87.5	82.5	105.3	49.0	33.3	63.3
829.0	1681.7	1976.9	2247.1	2959.6	1914.6	2357.1	4295.2	1956.9	806.2	1426.3
1424.1	2439.1	2289.2	2365.9	2744.5	2305.5	2690.6	3785.5	2350.5	856.6	1889.4
2834.8	1205.6	2956.1	2479.7	3118.0	2463.3	3210.9	3660.2	1877.6	1247.0	2622.7
290.8	1711.5	1176.5	1193.7	717.5	1074.9	1194.7	1456.6	564.3	437.3	532.5
704.1	3700.3	3294.0	3388.9	3415.5	3408.0	3663.8	3782.5	3228.2	2459.8	2835.6
3404.6	1773.5	1416.1	1825.6	3154.2	2057.7	2904.7	2132.8	968.5	484.0	1452.9
1038.9	4048.0	4222.9	4647.4	5232.6	3971.5	5550.5	4645.1	4796.1	2727.7	3465.0
57.7	302.7	572.6	582.6	555.4	471.8	467.8	1426.0	225.4	130.0	424.5
268.1	2842.7	3126.4	2948.2	1611.7	2419.9	2127.3	3345.3	1936.5	1213.9	3233.7
365.0	912.3	1120.4	1131.1	1091.4	1256.2	937.3	1827.5	536.5	1121.0	943.9
35.7	125.3	159.1	174.6	93.2	131.2	117.4	241.9	58.3	35.3	78.9
309.9	5252.5	3574.4	3770.8	4664.2	3979.8	4670.4	3822.5	3042.4	2314.8	2544.6
14230.0	6403.3	6507.6	7445.2	7963.2	7651.2	7946.1	7158.0	8103.1	5381.3	7250.9
52.0	229.6	474.0	297.4	255.1	176.9	502.1	279.9	76.0	73.4	128.2
5031.5	4417.9	4100.4	4103.0	4401.6	4451.1	4555.6	4466.6	4765.3	3175.4	3191.1
43.7	641.5	1092.1	724.2	488.9	488.2	540.9	1250.5	255.4	128.4	575.4
1769.6	3321.2	3488.1	3819.8	4673.7	3732.1	5005.0	4429.9	4112.9	1949.1	3151.7

4631.2	4245.3	4268.7
6235.9	6878.1	5537.3
5711.0	6322.0	6621.0
9153.8	8016.9	7297.0
7548.3	8709.4	7269.9
7756.9	8490.0	7878.8
1572.3	1774.6	1470.2
226.3	366.9	172.4
1493.1	1925.7	1677.4
5842.1	5362.2	5850.2
2375.5	2786.4	3242.7
2514.8	2355.0	3248.4
116.2	151.0	105.2
3189.8	3160.1	3110.8
4438.7	3811.5	3291.7
2093.8	1947.1	1849.2
4122.8	3848.0	4745.4
5645.5	5815.9	5822.2
358.0	450.4	225.8
3032.0	3815.9	3587.3
237.8	378.1	455.9
2880.0	1843.1	2775.0
5666.1	4923.2	5394.8
92.4	97.6	48.2
2818.0	2504.5	2714.3
2216.8	2745.5	2538.2
2676.6	3243.8	3516.6
1105.8	989.5	1163.8
3440.5	3430.6	3941.0
2535.9	2437.6	2832.9
5433.1	3684.4	5433.2
772.6	845.8	529.9
2090.9	2514.3	2256.0
1551.7	1650.9	1160.4
129.6	105.6	103.6
3867.7	3465.3	4180.8
6931.2	7873.2	7063.7
152.0	205.4	202.8
3895.2	4858.5	4712.1
752.2	922.4	778.7
4669.5	4132.8	4514.5

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k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria

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o__Magnetococcales	f__Magnetococcaceae
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g__Magnetococcus
g__Magnetococcus
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g__Magnetococcus
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s__unclassified	61826
s__unclassified	61888
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s__unclassified	62621
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s__unclassified	62935
s__Bartonella bacilliformis	61846
s__Bartonella clarridgeiae	61576
s__Bartonella elizabethae	62149
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s__Bartonella grahamii	61673
s__Bartonella grahamii	61827

X81183.1 gg_id:11265 magnetic coccus MP17 str. TB12 X81183
EF371491.1 gg_id:209788 magnetotactic China Jiaozhou Bay clone M-67 EF3714
Y13208.1 gg_id:11266 Magnetic strain clone rj53 Y13208
Y13212.1 gg_id:11267 magnetic coccus MP17 str. pa11 Y13212
GQ468507.1 gg_id:593515 Temporal variation magnetotactic two freshwater microcosms fresh water sedimen GQ468
AY328711.1 gg_id:88630 drinking water system simulator clone DSSD12 AY3287
GQ500720.1 gg_id:561524 Surveys Biofilms and Sediments Mammoth Cave Karst Aquifers Charon's Cascade sa GQ500
AF544015.1 gg_id:111917 Parvularcula bermudensis str. HTCC2503 AF5440
AY625140.1 gg_id:104892 perchloroethylene-contaminated ground water clone I-6 AY6251
AM934846.1 gg_id:544221 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM934
FM242322.1 gg_id:318593 sequences sediment clone 63 T9d-oil FM242
EF530680.1 gg_id:226147 Extremely acidic pendulous biofilms Frasassi cave system Italy microbial biofilm clone EF5306
AY193164.1 gg_id:80157 marine tidal mat clone BTM11 AY1931
GU370118.1 gg_id:530853 Rhodovulum sulfidophilum str. P721(3) GU370
EF173322.1 gg_id:185425 Sinorhizobium sp. MKI8 EF1733
EU544515.1 gg_id:272510 Aurantimonas altamirensis str. IFP14.1 EU5445
EU442518.1 gg_id:275257 Aurantimonas altamirensis str. NML 070722 LSPQ no. ID089387 EU4425
EF512716.1 gg_id:218585 Aurantimonas coralicida str. JL661 EF5127
AY178863.1 gg_id:77748 Fulvimarina litoralis str. HTCC2156 AY1788
AJ508755.1 gg_id:110301 marine str. V4.MO.18 AJ5087
AJ508754.1 gg_id:110412 marine str. V4.MO.17 AJ5087
EF423363.1 gg_id:206636 Aurantimonas sp. str. N1 EF4233
EF373540.1 gg_id:206133 Aurantimonas kwangyangensis str. CW5 EF3735
AY178861.1 gg_id:77696 Fulvimarina pelagi str. HTCC2615 AY1788
GQ009485.1 gg_id:500180 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw77 GQ009
AM746691.1 gg_id:241968 etiology rosy discoloration ancient wall paintings rosy-discoloured mural clone A13 AM746
FJ357425.1 gg_id:363192 Aurantimonas sp. str. YIM J01 FJ3574
FM872739.1 gg_id:365130 occupant source house floor dust clone FB01C04 FM872
EF489025.1 gg_id:221997 Bacillus sp. str. HB01085 EF4890
FM872541.1 gg_id:368575 occupant source house floor dust clone FA01H06 FM872
FN421693.1 gg_id:536202 proteogenomics physiology phyllosphere soybean clone 3_E11 FN4216
GQ115503.1 gg_id:421082 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw686f02 GQ115
AB257635.1 gg_id:262792 Microbial few millimeters be surface dolomite rock 'Val Piora' Alps 1965 meters abov AB2576
GQ009554.1 gg_id:500111 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw77 GQ009
DQ883810.1 gg_id:164020 Aerobacter ureolyica str. 5715S-12 DQ883
Z70003.1 gg_id:5472 Bartonella bacilliformis str. LA6.3 Z70003
X89208.1 gg_id:5476 Bartonella sp str. ATCC 51734 X89208
AB246808.1 gg_id:149483 Bartonella elizabethae str. Q-4 AB2468
AB246801.2 gg_id:147120 Bartonella elizabethae str. R-5 AB2468
AB440632.1 gg_id:338719 Bartonella sp. str. Fuji 18-1 AB4406
AB242293.1 gg_id:141840 Bartonella sp. str. Fuji 12-1 AB2422

73.8	124.6	194.3	268.2	229.6	188.9	145.5	302.5	99.9	65.2	125.9
2402.1	4306.1	4383.5	4815.4	4509.2	5226.5	5077.0	5304.0	4200.7	1863.0	3935.7
158.8	1309.4	1121.4	1466.4	1993.3	1189.5	2842.6	2155.3	888.1	314.6	757.6
6108.6	4803.4	5600.7	6706.9	7353.6	5252.2	5994.8	6151.4	8550.7	4940.5	7404.7
6259.6	4342.1	4511.4	4581.2	5031.2	5152.7	5382.5	5483.5	5093.1	3684.2	6172.4
114.1	1281.9	1069.5	1187.0	1327.4	1800.1	927.7	2229.1	1878.6	487.2	904.4
5691.6	3119.1	3665.3	3629.2	3743.7	3366.5	3000.0	4814.6	3011.2	2559.0	2577.5
7402.2	4598.1	5212.6	5651.6	5753.5	4492.2	6186.9	5346.6	5261.1	3359.8	4793.9
2778.9	3826.0	3929.8	4443.5	5178.5	4282.1	4081.5	4941.1	5373.6	3459.3	6277.8
6044.4	1886.4	2332.1	2678.4	3220.1	2356.0	2584.9	2994.8	1887.8	1657.3	1978.3
1017.7	1234.0	1040.7	1120.8	1446.9	1086.8	1308.1	1333.4	1569.4	775.1	1058.4
1741.2	4654.2	4688.1	4837.1	5677.5	5192.8	6296.9	5562.2	3969.0	1093.7	2838.8
470.3	1427.2	1555.5	1531.7	2321.7	1281.9	1852.5	1829.1	701.4	500.5	841.8
2216.6	4561.3	4646.1	4679.4	4298.3	3983.1	2903.3	4789.7	3943.4	2375.9	6221.4
42.9	1306.5	2102.4	1270.9	2111.0	1494.1	1481.0	2034.9	850.7	1553.6	1032.1
8388.1	6756.8	6329.8	6780.0	9628.2	7602.7	8518.4	8369.9	9000.7	7486.4	6132.4
848.0	3382.0	3579.0	3511.0	5815.8	3606.7	4988.5	4492.1	3969.6	3958.2	2193.1
963.3	1099.4	1503.8	1430.0	2725.9	1426.4	1690.1	2601.1	1292.4	2026.8	1272.6
2393.9	2417.3	3214.5	4118.9	3208.6	3124.6	2885.3	4067.9	2795.8	6161.4	2573.8
3145.7	2271.4	2544.0	2921.7	4594.1	3095.5	3179.7	3451.4	3578.8	3473.0	2224.7
10290.7	4109.6	4618.0	6377.3	4951.3	4625.1	5083.7	5063.5	5862.0	5427.1	4524.4
7201.4	3036.8	3643.8	3963.5	5040.6	4041.9	5068.4	5275.0	3193.8	4638.7	3657.6
9017.7	6558.2	7482.6	8792.7	8191.1	6400.9	7214.9	7845.8	7930.2	6581.9	6424.7
10784.5	4179.1	4849.8	5749.3	4757.6	5737.5	4273.2	5989.2	4467.3	4604.4	3328.4
8967.4	4623.5	3027.1	3373.5	6001.3	3570.7	4498.2	4395.9	5037.0	3227.6	1768.3
15180.2	5651.6	6774.8	6845.9	7049.2	5917.2	6276.6	7191.4	6531.3	6574.8	9642.3
2545.4	3921.5	3397.8	3281.9	4863.0	4274.0	4536.0	4412.2	2733.4	6531.5	2453.5
9240.9	9664.2	7266.9	7204.6	10565.0	7952.9	6835.8	7241.9	9054.5	8238.0	8668.1
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20610.2	6381.6	6640.2	7138.2	8050.0	7078.4	8137.0	9199.3	8520.1	9057.4	8250.2
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4590.3	5028.9	3978.0
4516.6	5201.1	5636.4
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3730.3	3508.0	3149.1
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AB426630.1 gg_id:276614 Bartonella grahamii str. Hokkaido 48-1 AB426
AB529507.1 gg_id:594215 Bartonella grahamii str. cg147up AB529
AB529498.1 gg_id:578474 Bartonella grahamii str. Korea 4-1 AB529
AY513504.1 gg_id:103693 Bartonella henselae str. 882_ANT5 AY513
U87831.1 gg_id:5492 aortic heart valve patient with endocarditis clone v9 U8783
Z11684.1 gg_id:5473 Bartonella henselae str. BA-TF Z11684
EU111755.1 gg_id:273803 Bartonella queenslandensis str. AUST/NH5 EU111
EU111749.1 gg_id:270242 Bartonella rattiaustraliensis str. AUST/NH4 EU111
EU111754.1 gg_id:263406 Bartonella queenslandensis str. AUST/NH12 EU111
NC_005955.1 gg_id:129029 Bartonella quintana str. Toulouse NC_00
AJ278187.1 gg_id:25998 Bartonella schoenbuchensis str. R1 AJ2781
AB519061.1 gg_id:550137 Bartonella washoensis str. DR1-1 AB519
AB519065.1 gg_id:548080 Bartonella washoensis str. SR25-1 AB519
AB519062.1 gg_id:548956 Bartonella washoensis str. DR3-1 AB519
EF682085.1 gg_id:331242 'Candidatus rudakovii' detected voles Western Siberia Candidatus Bartonella rudakov EF682
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FJ177634.1 gg_id:353598 Bartonella sp. str. HMD-3 FJ1776
EU294521.1 gg_id:244723 Bartonella volans str. FSq-1 EU294
Z70001.1 gg_id:5501 Bartonella sp str. R-phy2 Z70001
EF616480.1 gg_id:249397 Bartonella silvicola str. Cul-9 BAA-1453 EF6164
AB292597.1 gg_id:211030 Bartonella washoensis str. Sb944nv AB292
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Z70008.1 gg_id:5483 Bartonella sp str. C5rat Z70008
EU111759.1 gg_id:268319 Bartonella coopersplainensis str. AUST/NH20 EU111
AF204274.1 gg_id:46747 Bartonella birtlesii str. 325 AF2042
X89110.1 gg_id:5486 Wolbachia melophagi str. MO6 X89110
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DQ645425.1 gg_id:161188 Bartonella henselae str. M7SHD DQ645
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NR_029368.1 gg_id:541643 Bartonella doshiae str. R18; NCTC 12862 NR_02
AY254309.1 gg_id:104973 Bartonella chomelii AY2543
L01260.1 gg_id:5502 Bartonella elizabethae L01260
DQ538394.1 gg_id:227943 Bartonella australis str. Aust/NH1 DQ538
AY515118.1 gg_id:100352 Bartonella rattimassiliensis str. 16115 AY515
AJ002139.1 gg_id:5462 Bartonella alsatica str. 382 AJ0021
NR_029366.1 gg_id:571234 Bartonella grahamii str. V2; NCTC 12860 NR_02

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3651.5	6282.2	6055.5	5633.5	8679.3	6508.4	7280.7	6561.5	5571.0	8158.1	3788.7
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2384.7	3375.4	3246.9	3307.1	4404.9	3379.8	3861.2	3734.0	3239.6	6310.4	3280.2
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4890.7	4682.4	2163.9
3823.6	3741.4	1751.5
3150.9	3235.5	1441.6
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6571.7	5811.2	4958.3
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6948.6	6443.6	4811.7
7902.4	5532.1	4498.3
5918.0	5290.7	3643.0
7619.5	6530.2	4979.6
5406.4	2717.2	1569.6
4196.5	3825.3	2930.6
9010.2	7710.2	6355.1
7460.8	7693.2	6776.6
5149.9	4366.2	2961.0
2996.0	3356.0	1934.4
8138.7	6743.0	5919.6
4455.4	5487.4	4413.3
5598.0	5200.5	3049.4
3980.8	3527.4	2281.9
11223.3	9457.5	8839.5
8552.2	9975.9	7805.4
4617.6	4236.6	3179.9
4321.9	4217.4	2485.1
7969.6	6908.2	5339.8
5909.7	4594.3	4633.1
8872.5	7845.2	7695.0
7322.5	6788.7	4696.7
3951.9	3497.6	2412.1

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AB119197.1 gg_id:106044 Beijerinckia indica str. ATCC 9036 AB119
AB119199.1 gg_id:106358 Beijerinckia indica str. ATCC 19361 AB119
AJ563932.1 gg_id:100451 Beijerinckia mobilis str. DSM 2326 AJ5639
AB119210.1 gg_id:106197 Beijerinckia sp. str. TB16 AB119
AB119203.1 gg_id:101664 Beijerinckia sp. str. TB9 AB119
EF584507.1 gg_id:232942 Chelatococcus daeguensis str. K106 EF5845
AM162441.1 gg_id:155035 and situ identification acidic sphagnum peat bog clone B56 AM162
AJ563926.1 gg_id:104947 Methylocella palustris str. Ch3 AJ5639
CP001280.1 gg_id:527956 Methylocella silvestris str. BL2 CP001
AJ555244.1 gg_id:83530 Methylocella tundrae str. T4 AJ5552
DQ450165.1 gg_id:155167 (Uruguay) Atlantic coastal lagoon clone R7C54 DQ450
EU131038.1 gg_id:252176 alkaline China coal mine soil clone SIP CM24 EU131
GQ402592.1 gg_id:584864 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
FJ719048.1 gg_id:530044 Protozoan grazers alter metabolically active aquifer aquifier sediments clone p03_D0 FJ7190
EF064161.1 gg_id:225511 Microbial sediment bottom AMD pool acid mine drainage clone Sed3 EF0641
X97076.1 gg_id:4762 peat bog clone TM9 X97076
EU133271.1 gg_id:246401 tallgrass prarie soil clone FFCH2375 EU133
AF407384.1 gg_id:27469 MCB-contaminated groundwater-treating reactor clone RB7C5 AF4073
FM253682.1 gg_id:348953 Rock gold mine unusually microbial biofilm clone H09-2 FM253
AF200697.1 gg_id:32333 13C- extracted 13C-methanol exposed soil clone UP3 proteobacterium AF2006
AB119198.1 gg_id:106192 Beijerinckia derxii str. ATCC 49361 AB119
FM253655.1 gg_id:349812 Rock gold mine unusually microbial biofilm clone E02-2 FM253
FN433469.1 gg_id:562500 Methylocapsa sp. str. KYG FN4334
CU926994.1 gg_id:551719 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU926
DQ837242.1 gg_id:252587 Archaeal and pristine National Park Spain Donana coastal aquifer clone 49S1_2B_23 DQ837
GU205295.1 gg_id:524604 unusual Microbial Venezuelan Tepui (Orthoquartzite) Cave: Dominance Chloroflexal GU205
AY913393.1 gg_id:112985 forest soil clone DUNssu187 (-7A) (OTU#034) AY9133
DQ451456.1 gg_id:156677 forest soil clone FAC17 DQ451
U87759.1 gg_id:4967 Afipia broomeae str. F186 U87759
AY513503.1 gg_id:103555 Afipia felis str. 2002033830 AY5135
U87764.1 gg_id:4964 Afipia genosp. 2 str. G8965 U87764
EU499727.1 gg_id:276997 Field-based laboratory stable isotope probing surveys identities both aerobic and an EU499
GQ032540.1 gg_id:375131 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ032
DQ222224.1 gg_id:140520 Bradyrhizobium sp. str. CCBAU 71283012 DQ222
AY568510.1 gg_id:102699 Afipia massiliensis str. NW-12 AY5685
AY029562.1 gg_id:58038 Afipia massiliensis str. 34633; CIP 107022; CCUG 45153 AY0295
AY547290.1 gg_id:99065 Bradyrhizobium sp. str. CCBAU 7128301 AY5472
AF288304.1 gg_id:41002 Afipia birgiae str. 34632 AF2883
AB099659.1 gg_id:77914 Oligotropha carboxidovorans str. S23 AB0996
FJ193001.1 gg_id:304744 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior FJ1930
FJ165544.1 gg_id:559211 Microbially-enhanced Dissolution Karst Carbonates microbial biofilm Sonterra #8 well FJ1655

3218.8	3445.3	3274.2	3145.4	4640.5	3699.3	4013.4	3573.4	2981.0	4056.3	3725.3
8983.3	5621.1	4908.8	4926.1	7315.1	6514.1	6834.6	5412.9	6379.2	3697.8	4771.8
21561.4	8640.0	7204.5	7306.6	9546.8	7611.3	10444.0	7308.3	7467.1	5898.7	6436.6
3889.1	4394.8	3568.1	3554.5	3995.8	3744.6	3574.6	3999.4	3700.3	2902.5	2141.4
985.7	4533.6	2137.0	1896.8	2982.2	3546.6	2988.5	2277.6	2676.4	1154.8	1298.0
13488.8	5354.4	4602.1	4940.8	7137.1	5193.2	6733.0	5116.7	3028.1	3156.2	3288.5
3091.9	9227.9	3096.2	3228.8	5318.9	5166.0	4986.9	3418.1	1547.7	1557.8	1575.0
5971.6	10207.3	4652.5	5351.8	7138.6	6912.3	6314.5	4770.7	4156.6	2838.0	3349.4
2123.7	3132.3	1388.8	1738.6	2294.1	1952.1	1773.8	2107.2	692.7	474.3	658.4
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1302.3	4614.8	2171.2	2231.0	3699.2	3007.8	4204.1	2628.9	2357.5	1516.6	1433.5
5761.4	6311.7	5063.0	5269.2	7126.0	5825.6	6819.1	4958.7	4777.2	5789.9	6002.5
11786.3	5757.0	4289.2	4441.1	7718.3	6709.0	7342.9	5234.0	4056.5	2634.7	3289.6
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4951.3	5291.7	5372.6	5596.2	6027.2	5704.1	5981.7	5012.2	5190.6	4431.3	6073.2
2366.1	5336.4	3872.0	3920.9	5519.5	5570.1	5637.7	5762.3	3832.2	4757.8	3862.4
4916.4	4029.9	3008.3	3051.5	5205.3	4137.3	4354.3	2421.6	3121.7	2243.9	2542.7
10233.6	4759.9	4140.7	4224.1	6255.1	4936.3	5689.6	5144.6	4455.7	5494.2	3581.0
4077.3	4788.3	4116.9	4303.0	5243.4	4379.3	5010.3	4866.2	2692.2	1799.0	3545.2
343.6	3390.2	1002.1	744.0	2030.3	1354.0	1637.1	1128.1	620.2	463.7	415.2
6177.5	6112.3	4637.3	4282.2	7593.7	5983.0	6707.5	4758.4	2875.0	6097.1	3029.2
14121.6	7114.0	5465.1	5873.5	9476.5	8015.5	8305.6	6303.6	4619.5	4855.2	4085.9
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15244.3	4648.2	3872.2	3733.5	6142.2	5231.1	5414.2	5410.4	3508.9	2871.7	2887.6
23911.3	6381.8	6733.3	6462.4	8468.7	6877.7	9276.3	7493.8	8383.4	6904.9	7347.9
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AY238503.1 gg_id:92573 Bradyrhizobium sp. str. 1 AY2385
AJ295483.1 gg_id:40221 rape rhizosphere clone wr0024 AJ2954
U87761.1 gg_id:4971 Afipia broomeae str. G5958 U8776
AY568503.2 gg_id:106979 Afipia broomeae str. C-12 AY5685
EF203409.1 gg_id:261125 Bradyrhizobium sp. str. URBM1 EF2034
EF520400.1 gg_id:231834 structure lakes: what controls ? acid-impacted lake clone ADK-BTh02-40 EF5204
EU308573.1 gg_id:243951 Deinococcus sp. str. 4A4 EU3085
DQ838529.1 gg_id:161809 Methylobacterium sp. str. WSM3686 DQ838
AJ871433.1 gg_id:111252 Chelatococcus asaccharovorans CP141b AJ8714
DQ298340.1 gg_id:151224 studies on and nifH Lasiurus sindicus Sewan grass Thar Desert Rajasthan India rhizos DQ298
FM160634.1 gg_id:292268 Microvirga sp. PCA19 PCA 19 FM160
AB098515.2 gg_id:78887 Balneimonas flocculans str. TFB AB0985
GQ103792.1 gg_id:446977 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ103
AY776209.1 gg_id:108377 Methylobacterium sp. str. AC72a AY7762
AF338176.1 gg_id:68816 Blastobacter denitrificans str. IFAM 1005; LMG 8443 AF3381
X66025.1 gg_id:5058 Blastobacter denitrificans str. LMG 8443 X66025
AF288306.1 gg_id:24179 Bosea vestrisii str. 34635 AF2883
GU377117.1 gg_id:526769 Afipia sp. str. sptzw29 GU377
EU325943.1 gg_id:255748 Bosea sp. str. fei-4-9 EU3259
DQ377760.1 gg_id:153195 Bosea sp. PD 19 DQ377
AJ968692.1 gg_id:165499 Bosea sp. str. STM 358 AJ9686
AJ250796.1 gg_id:4822 Bosea thiooxidans str. DSM 9653 AJ2507
DQ104985.1 gg_id:136035 Bosea thiooxidans str. JS 11 DQ104
EU730912.1 gg_id:324973 Bosea thiooxidans str. 187 EU7309
AJ250797.1 gg_id:4823 Bosea thiooxidans str. RpPI5-VS AJ2507
DQ303323.1 gg_id:149709 Bosea sp. TM19_7 DQ303
EF114681.1 gg_id:194437 Bosea sp. str. SJH07 EF1146
AF288307.1 gg_id:27298 Bosea massiliensis str. 34649 AF2883
EU130951.1 gg_id:243491 Afipia sp. BAC312 EU1309
AF288309.1 gg_id:47211 Bosea massiliensis str. 63287 AF2883
EU584530.1 gg_id:263418 Afipia sp. str. Everest-gws-91 EU5845
NR_028787.1 gg_id:583653 Bosea minatitlanensis str. AMX51; DSM 13099 NR_028
EU561082.1 gg_id:273777 Bradyrhizobium sp. str. CTFI54 EU5610
FJ390904.1 gg_id:589546 Bradyrhizobium canariense str. SEMIA 928 FJ3909
GQ899183.1 gg_id:569090 Bradyrhizobium canariense str. L-2 GQ899
EU561083.1 gg_id:273925 Bradyrhizobium sp. str. CTFI410 EU5610
EU420082.1 gg_id:569322 Bradyrhizobium canariense str. Cy-1 EU4200
AY649429.1 gg_id:99495 Bradyrhizobium elkanii str. BR2001 AY6494
EU170546.1 gg_id:251540 Bradyrhizobium elkanii str. CCBAA 05065 EU1705
FJ192710.1 gg_id:319167 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior FJ1927
AY904753.1 gg_id:111860 Bradyrhizobium elkanii str. SEMIA 6148 AY9047

10560.0	2265.9	1506.6	1215.1	3581.9	1867.5	3472.4	1897.2	959.4	380.0	721.0
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38436.4	7351.8	7568.3	7829.6	11205.1	8095.2	10294.2	8452.5	8152.2	6693.6	5893.4
42632.2	5006.3	4837.1	3955.1	8983.1	5611.8	7802.2	5348.7	3980.3	2036.1	2727.3
5569.4	2733.1	2003.4	1323.3	3215.2	2332.6	3466.9	1651.0	596.6	559.6	666.6
30697.0	2670.5	3029.8	2764.0	5221.9	3163.3	5240.4	3408.6	2040.3	1784.5	1789.3
675.1	1593.5	1641.4	1532.7	2751.6	1652.1	2015.0	2380.7	1128.3	829.7	934.0
1499.8	2578.4	3186.1	2114.5	5541.2	3198.3	2536.9	2910.8	1407.6	832.7	1041.0
1749.2	4147.3	4585.5	3929.7	5843.6	3821.8	5028.8	4608.2	2653.9	2054.9	2968.5
5263.2	4073.5	4785.0	4360.2	4600.5	4124.4	4190.6	4818.0	4009.0	2520.6	2840.3
1133.3	3220.4	2073.7	2113.7	4777.9	3376.4	3355.3	2749.3	1411.6	973.9	992.6
800.4	1700.0	1366.1	1307.2	2075.7	1398.1	1964.3	1535.2	1249.6	865.4	1204.2
3123.9	3001.4	2948.0	3002.9	4749.6	3186.0	3957.0	3367.6	1890.5	1277.3	1927.2
699.8	1519.2	1335.1	1245.0	2871.7	1748.2	2090.8	1522.9	882.9	924.1	724.3
14744.1	2000.2	2746.1	1305.5	4537.0	2579.1	4749.8	2106.2	983.1	508.5	581.5
26810.2	3820.6	4086.8	3307.4	6604.4	4662.8	6526.9	4336.7	3249.3	1515.4	2120.7
9743.5	6238.5	5704.3	5619.3	7833.8	6265.5	7246.6	6048.2	7722.2	4296.3	6056.2
11863.8	6672.4	5825.7	5799.8	8612.0	6902.4	7893.5	6995.1	6355.9	6196.6	5116.8
2359.4	4574.9	3917.4	3768.9	6500.7	4558.1	5406.3	4655.8	4012.7	2691.4	2781.5
2298.7	4561.7	3842.0	3680.6	6379.4	4390.0	5646.7	4776.9	3964.0	2660.9	2897.0
5493.7	6727.6	5810.6	5833.1	8165.8	6223.2	7362.9	6321.9	6914.5	4131.3	5100.2
1938.3	3945.8	3565.3	3311.1	5327.5	4168.3	4268.3	3909.1	4442.5	2484.0	2836.4
6477.8	6368.7	3756.9	2981.1	7153.7	5008.9	6547.0	4643.4	3751.0	2197.0	2057.5
9841.0	6305.0	5700.5	5695.1	7693.3	6107.6	6930.3	5992.6	7773.7	4275.0	6067.3
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747.8	5071.5	3788.8	3857.2	6129.0	4022.9	5546.1	4943.1	3987.3	1998.2	1970.0
9326.1	5088.2	4833.1	4827.8	6883.9	5429.3	6231.0	5200.2	6442.2	3192.8	5160.0
29809.3	11426.9	9819.0	10477.8	11978.9	10946.3	12465.0	11019.5	13322.4	9852.7	13649.2
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19434.8	8254.3	7290.4	7933.4	8766.5	8315.7	8894.5	8610.8	8168.3	7865.4	9183.8
1992.2	3779.4	3186.6	3299.9	4929.5	3727.3	4439.9	4178.1	3263.6	1798.4	2419.2
32172.7	7562.4	7684.9	7462.9	10502.1	7372.1	10614.8	7130.4	10494.4	6663.7	8780.8
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16615.7	2209.7	3491.6	1802.8	6205.6	2836.2	6865.0	2532.2	896.9	539.3	873.6
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57698.4	4624.2	4000.1	3576.5	10842.0	4986.0	8457.3	4489.8	2178.1	1782.1	1725.5
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10405.8	10823.9	10942.1

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FJ418920.1 gg_id:362396 Bradyrhizobium sp. str. PC28 FJ4189
U35000.3 gg_id:4946 Bradyrhizobium elkanii str. USDA 76 U3500
AY904788.1 gg_id:112273 Bradyrhizobium elkanii str. SEMIA 6425 AY9047
AY904762.1 gg_id:111745 Bradyrhizobium elkanii str. SEMIA 6160 AY9047
AF417554.1 gg_id:21176 Bradyrhizobium elkanii str. DASA37005 AF4175
AF208516.1 gg_id:55735 Bradyrhizobium elkanii str. USDA 46 AF2085
FJ193395.1 gg_id:328559 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior FJ1933
DQ786801.1 gg_id:169640 Bradyrhizobium elkanii str. HaE4 DQ786
FJ193017.1 gg_id:353693 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior FJ1930
AF417553.1 gg_id:49609 Bradyrhizobium elkanii str. DASA38001 AF4175
AY904736.1 gg_id:112163 Bradyrhizobium elkanii str. SEMIA 696 AY9047
AY904748.1 gg_id:112153 Bradyrhizobium elkanii str. SEMIA 6100 AY9047
FJ193380.1 gg_id:324669 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior FJ1933
AF417556.1 gg_id:44293 Bradyrhizobium elkanii str. DASA35013 AF4175
GQ129847.1 gg_id:465190 Genetic inventory 'JPL-SAF' during MSL mission spacecraft assembly clean room floc GQ129
EU399711.1 gg_id:271806 Bradyrhizobium elkanii str. CCBAU 05041 EU3997
AY039016.1 gg_id:64297 Bradyrhizobium sp. ORS3260 str. ORS 3260 AY0390
AF417555.1 gg_id:21431 Bradyrhizobium elkanii str. DASA35011 AF4175
AY904744.1 gg_id:111950 Bradyrhizobium elkanii str. SEMIA 6028 AY9047
EU170551.1 gg_id:242313 Bradyrhizobium elkanii str. CCBAU 23109 EU1705
AY649433.1 gg_id:103679 Bradyrhizobium elkanii str. BR3279 AY6494
AY904789.1 gg_id:112254 Bradyrhizobium elkanii str. SEMIA 6440 AY9047
FJ192573.1 gg_id:321198 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior FJ1925
FJ540914.1 gg_id:586787 Bradyrhizobium yuanmingense str. DTB8 FJ5409
FJ540920.1 gg_id:578473 Bradyrhizobium yuanmingense str. DTC5 FJ5409
AF417549.1 gg_id:20737 Bradyrhizobium japonicum str. DASA24015 AF4175
AY904774.1 gg_id:111573 Bradyrhizobium japonicum str. SEMIA 6319 AY9047
AF193818.1 gg_id:49866 Bradyrhizobium yuanmingense str. B071 AF1938
FJ540960.1 gg_id:585297 Bradyrhizobium yuanmingense str. TSC9 FJ5409
AF417548.1 gg_id:45495 Bradyrhizobium japonicum str. DASA03183 AF4175
EF070133.1 gg_id:196710 Bradyrhizobium yuanmingense str. CCBAU 43022 EF0701
EF061098.1 gg_id:183640 Bradyrhizobium yuanmingense str. CCBAU 45079 EF0610
AY649439.1 gg_id:104594 Bradyrhizobium japonicum str. BR3267 AY6494
AY162036.1 gg_id:135634 Cultivating soil clone PI_GH1.1.B1 AY1620
AF417543.1 gg_id:71773 Bradyrhizobium japonicum str. DASA12006 AF4175
DQ303328.1 gg_id:146763 Dynamic during maturation Tuber magnatum Pico ascoma Bradyrhizobium clone TM DQ303
DQ133341.1 gg_id:137967 Bradyrhizobium liaoningense str. GXD1 DQ133
DQ786798.1 gg_id:168591 Bradyrhizobium liaoningense str. DdE3 DQ786
AB240363.1 gg_id:144998 microbial structure Phragmites rhizosphere biofilm reed bed reactor laboratory clone AB2403
AF239843.2 gg_id:32699 Bradyrhizobium japonicum str. PRY40 AF2398
EF221623.1 gg_id:207870 Bradyrhizobium sp. str. JR008 EF2216

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48107.1	4520.3	4667.6	4381.6	6754.8	4846.1	7248.7	5347.4	3281.4	2687.4	3062.9
46926.3	5768.2	4986.2	4423.6	8609.6	5524.1	8905.7	4982.6	2563.3	2123.8	2693.3
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40785.1	5134.6	5173.2	5131.4	6017.1	5371.1	6962.4	6045.6	5255.6	4247.9	4783.9
51838.3	4136.7	4698.5	4379.1	7506.2	4370.8	8124.9	4636.6	2088.7	1784.5	3045.4
39267.1	4850.3	4184.0	3575.3	5196.7	4226.0	6389.7	4416.3	2200.8	1825.4	2644.9
31517.0	6222.7	5103.1	4609.6	6762.5	5584.6	6755.7	5085.2	6193.3	7489.7	4569.1
28346.9	3233.1	4372.2	4167.5	4751.2	3519.6	5593.4	4426.0	1387.2	1229.3	2555.6
44785.6	4875.8	5813.6	4708.9	7106.5	5251.4	7522.1	4986.7	6986.3	9124.3	5853.0
58788.6	5859.2	5578.0	6043.7	7789.9	6026.6	7912.8	6675.1	6566.6	8033.0	6723.1
43815.4	7023.6	7248.2	7812.4	8327.2	6902.6	7886.8	7445.1	7349.2	4363.3	7888.7
24065.0	4681.6	4063.1	3445.4	5223.7	3559.2	4662.0	3804.3	3182.3	3056.5	1948.0
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38537.2	5827.8	5733.7	5850.5	10740.4	6184.1	10374.0	5551.9	3715.8	2327.0	3401.5
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6639.5	5634.2	5435.4
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5760.8	6338.0	5866.2
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4336.0	4062.6	3764.7
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5555.2	4896.7	6526.4
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7314.9	9995.9	8305.5
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DQ303349.1 gg_id:149227 Dynamic during maturation Tuber magnatum Pico ascoma Bradyrhizobium clone TM DQ303
U69636.1 gg_id:4932 Bradyrhizobium lupini str. FN 13 (USDA 3505) U69636
AY904778.1 gg_id:112228 Bradyrhizobium elkanii str. SEMIA 6387 AY9047
AY904757.1 gg_id:112271 Bradyrhizobium japonicum str. SEMIA 6155 AY9047
DQ303324.1 gg_id:147536 Dynamic during maturation Tuber magnatum Pico ascoma Bradyrhizobium clone TM DQ303
EU145989.1 gg_id:236262 Bradyrhizobium liaoningense str. CCBAU 83684 EU1459
EU170561.1 gg_id:245983 Bradyrhizobium elkanii str. CCBAU 41236 EU1705
EU399713.1 gg_id:258733 Bradyrhizobium japonicum str. CCBAU 43170 EU3997
AF417544.1 gg_id:32002 Bradyrhizobium japonicum str. DASA12007 AF4175
GQ181045.1 gg_id:563588 Bradyrhizobium elkanii str. LN5 GQ181
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FJ025097.1 gg_id:348667 Bradyrhizobium japonicum str. SEMIA 6153 FJ0250
EF394156.1 gg_id:210105 Bradyrhizobium japonicum str. CCBAU 65068 EF3941
FJ390914.1 gg_id:591406 Bradyrhizobium japonicum str. SEMIA 512 FJ3909
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X70403.1 gg_id:4945 Bradyrhizobium sp str. LMG 9566 X70403
AB179515.1 gg_id:100954 sedimentary rock clone MIZ24 AB1795
AF363138.1 gg_id:24680 Bradyrhizobium japonicum str. MSDJ G94 AF3631
EF394146.1 gg_id:214964 Bradyrhizobium japonicum str. CCBAU 53135 EF3941
FJ418696.1 gg_id:364095 Bradyrhizobium japonicum str. CCBAU 33175 FJ4186
AY904746.1 gg_id:111411 Bradyrhizobium elkanii str. SEMIA 6069 AY9047
DQ517956.1 gg_id:159686 Bradyrhizobium japonicum str. HHL-01 DQ517
GQ181034.1 gg_id:510301 Bradyrhizobium elkanii str. LNW14 GQ181
EU133476.1 gg_id:237433 tallgrass prarie soil clone FFCH17074 EU1334
EF070138.1 gg_id:195443 Bradyrhizobium liaoningense str. CCBAU 33158 EF0701
DQ303346.1 gg_id:145143 Dynamic during maturation Tuber magnatum Pico ascoma Bradyrhizobium clone TM DQ303
AY904756.1 gg_id:112304 Bradyrhizobium japonicum str. SEMIA 6152 AY9047
DQ303348.1 gg_id:147522 Dynamic during maturation Tuber magnatum Pico ascoma Bradyrhizobium clone TM DQ303
AF239844.2 gg_id:51967 Bradyrhizobium japonicum str. PRY42 AF2398
AY568513.2 gg_id:103141 Bradyrhizobium elkanii str. NW-6 AY5685
DQ303379.1 gg_id:146676 Dynamic during maturation Tuber magnatum Pico ascoma Bradyrhizobium clone TM DQ303
EU335263.1 gg_id:257149 Changes microbial metabolic and along hydrogeochemically variable profile unsatura EU3352
DQ303343.1 gg_id:148707 Dynamic during maturation Tuber magnatum Pico ascoma Bradyrhizobium clone TM DQ303
DQ303364.1 gg_id:148890 Dynamic during maturation Tuber magnatum Pico ascoma Bradyrhizobium clone TM DQ303
EF512281.1 gg_id:223867 Bradyrhizobium japonicum str. CCBAU 45002 EF5122
AF363135.1 gg_id:18027 Bradyrhizobium japonicum str. MSDJ 5697 AF3631
EF394151.1 gg_id:211052 Bradyrhizobium japonicum str. CCBAU 65619 EF3941
DQ786799.1 gg_id:170123 Bradyrhizobium liaoningense str. BqE4 DQ786

51021.3	8290.2	8509.9	9166.9	14867.0	9064.3	13562.3	9955.2	6592.1	3746.4	7083.4
41228.2	6305.1	6177.8	6493.5	11428.3	6708.7	10728.3	7316.0	5018.2	2705.4	5589.9
37129.8	7976.0	8474.2	7793.0	12131.2	7811.4	10192.4	7821.2	7605.2	4516.0	7585.0
42549.6	8097.6	6788.8	7309.9	9400.8	7334.6	7754.4	7143.8	7503.8	5488.7	7594.7
35847.6	5332.6	5252.3	4246.1	9374.3	5538.4	10173.8	4961.1	3051.5	3056.7	2896.6
3634.5	274.2	320.2	274.8	735.7	372.9	589.7	352.8	263.8	163.9	171.3
31652.3	3509.0	4374.0	3116.9	7114.6	3782.6	7701.3	3472.9	1517.9	1332.9	1731.5
51687.7	6101.2	5230.6	4225.6	10163.0	5912.0	9612.1	5191.8	3058.9	2567.2	3123.5
30529.3	4746.1	6225.3	4187.1	8620.3	4790.2	9069.6	4810.7	3391.7	2761.9	3384.6
1493.2	127.9	118.6	109.3	307.0	129.7	278.9	136.1	84.5	66.4	89.5
51869.2	5731.3	5043.6	4899.5	7553.6	5544.3	7685.0	6089.5	5109.9	3956.7	4070.5
3119.4	1025.6	1056.2	1258.3	1965.7	1340.1	1803.2	1278.6	2009.5	826.4	1214.0
3063.9	1238.8	1740.3	523.9	2210.8	1275.6	2924.4	799.6	418.8	427.5	295.4
20493.2	2223.4	4115.3	1422.2	5934.7	2282.3	6302.2	2360.4	636.9	491.7	685.6
45121.4	6011.5	6175.9	5182.0	10404.7	6258.9	10149.2	5899.3	4033.8	2888.1	3540.3
19795.9	2542.6	3754.2	1547.1	6613.0	2936.0	8170.4	2092.4	733.6	650.5	724.5
27930.5	3468.0	4126.4	2411.3	8185.7	3860.5	8641.0	3144.2	1313.7	1192.4	1260.8
49817.3	5801.2	5011.3	4207.0	9200.2	5559.8	8854.9	5296.0	3104.3	2417.1	3130.8
54661.5	6243.9	5553.6	4506.7	10228.5	6119.7	9752.6	5744.2	3035.5	2439.7	3203.6
17174.0	5175.8	4600.7	4898.3	7277.3	5551.3	7391.0	5549.7	2608.4	1194.2	3155.6
42762.2	5498.0	5578.9	3823.2	10088.5	5534.1	9648.6	4645.5	2704.5	1801.8	2336.7
32220.4	4114.4	4914.1	3089.3	9476.2	4987.5	8205.4	4032.4	2349.6	1473.9	1528.1
25591.4	2832.6	3694.2	1953.8	7338.0	3354.4	8212.7	2531.6	1012.3	767.5	955.5
35849.3	4170.9	4780.2	4754.2	6424.8	4717.0	5886.2	5303.7	2952.7	2973.7	3621.5
17980.3	4139.7	5083.3	3148.9	7581.7	4705.6	7706.7	4200.8	3884.7	1662.5	1769.6
50986.4	6241.1	5251.2	4375.7	9886.7	5966.0	9534.1	5276.1	3044.4	2408.7	3136.0
11656.0	3339.2	2850.3	2688.6	4153.3	2546.2	3814.8	2656.2	1987.3	2282.0	1501.6
31593.8	3412.5	4007.1	3095.9	6974.0	3700.2	7268.9	3481.7	1505.1	1335.2	1732.3
21629.7	3855.9	3540.3	3584.3	6920.2	3706.3	6312.1	4314.8	3812.9	1364.3	2592.9
46691.0	7212.9	6922.3	5525.7	10997.6	7010.0	10833.1	6262.3	5109.7	3888.1	4233.5
32779.8	5569.3	5268.2	5076.2	8543.3	5353.2	7769.2	5335.5	6209.2	4760.6	5466.7
29716.3	3749.6	4210.9	2670.6	8524.5	4215.7	9186.6	3442.2	1519.7	1276.0	1419.3
53795.9	5028.1	4916.1	4110.8	9957.9	5232.2	9684.5	4951.3	1969.6	1742.8	2710.8
18715.0	4398.4	2446.2	1884.1	5753.3	3902.4	5659.0	2518.4	875.1	723.7	1007.3
13725.9	1197.7	1083.8	924.1	3068.8	1498.9	3130.6	2056.0	362.9	399.1	445.5
46991.4	3880.3	4427.5	3719.4	11378.5	4840.8	8003.3	5148.8	1590.7	1525.1	1784.1
676.2	468.5	356.6	368.7	812.1	468.4	834.9	394.3	147.3	154.4	172.1
16926.6	1454.1	2238.8	1134.1	4456.9	1919.0	5261.6	1517.3	477.8	307.7	451.7
7655.1	1533.8	2584.8	850.3	3494.4	1743.6	4809.9	1399.0	414.7	269.0	414.8
26521.7	3247.4	3804.8	2436.3	7578.6	3777.6	7169.1	3179.3	1201.4	756.9	1201.0
39774.2	4500.5	4978.9	4376.1	8704.5	4789.7	8215.4	4647.8	2555.7	2000.0	2556.9

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8792.7	9157.5	9522.4
7503.1	7998.3	7227.3
6371.0	5833.4	7101.2
396.7	476.6	471.1
4218.8	3278.2	4569.6
6380.1	5513.4	7094.2
6368.8	5532.9	5294.2
155.6	296.6	235.7
6185.7	5518.3	6256.9
1050.5	1779.7	1302.7
1514.9	1808.6	1217.8
3782.7	2930.0	2338.8
6579.9	5402.6	7421.9
3574.2	2355.0	3460.6
4546.4	3630.7	4634.2
6129.9	5419.9	6628.9
6642.0	5555.3	7257.7
6231.5	5001.9	7870.5
6393.2	5605.5	6436.9
5190.6	4282.3	7148.5
4003.1	2939.0	4044.8
5142.4	5566.1	5619.4
5383.4	4322.9	6454.5
6439.9	5588.2	7205.9
2859.6	3227.7	3381.9
4092.3	3303.7	4449.4
4467.1	4233.8	4298.7
7842.4	6893.1	7831.0
6200.1	6079.8	6286.6
4934.9	3936.8	5203.6
5827.2	5149.3	6264.9
3338.6	4276.4	5021.6
3372.1	1537.6	4629.0
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410.2	751.3	804.4
2075.9	1665.7	2402.1
2400.9	1795.8	1972.0
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FJ390900.1 gg_id:545943 Bradyrhizobium liaoningense str. SEMIA 5062 FJ3909
DQ303374.1 gg_id:146501 Dynamic during maturation Tuber magnatum Pico ascoma Bradyrhizobium clone TM DQ303
EU074195.1 gg_id:250401 Bradyrhizobium liaoningense str. CCBAU 03282 EU074
DQ303326.1 gg_id:149079 Dynamic during maturation Tuber magnatum Pico ascoma Bradyrhizobium clone TM DQ303
AF417541.1 gg_id:54256 Bradyrhizobium japonicum str. DASA02007 AF4175
AF363133.1 gg_id:37117 Bradyrhizobium japonicum str. MSDJ 5718 AF363
AY599677.1 gg_id:104113 fungal ascocarp clone Cl-19-TB8-II AY5996
AF417545.1 gg_id:49277 Bradyrhizobium japonicum str. THA7 AF4175
EU333380.1 gg_id:268064 Bradyrhizobium japonicum RLA09 EU3333
EU083497.1 gg_id:240912 Evidence Carboxylation During Degradation Hexadecane Denitrifying Consortium he EU083
DQ303335.1 gg_id:148648 Dynamic during maturation Tuber magnatum Pico ascoma Bradyrhizobium clone TM DQ303
AY904773.1 gg_id:111438 Bradyrhizobium elkanii str. SEMIA 6208 AY9047
EF018750.1 gg_id:211106 aspen rhizosphere clone Amb_16S_1209 EF0187
DQ517958.1 gg_id:160432 Bradyrhizobium sp. str. HMS-O1 DQ517
EF019158.1 gg_id:204406 aspen rhizosphere clone Amb_16S_1805 EF0191
U69637.1 gg_id:4921 Bradyrhizobium lupini str. KM50 90 (USDA 3514) U69637
NC_010725.1 gg_id:289367 Methylobacterium populi str. BJ001 NC_01
AF069958.1 gg_id:111772 Nitrobacter alkalicus str. AN4 AF0699
AF069957.1 gg_id:73775 Nitrobacter alkalicus str. AN2 AF0699
NC_007964.1 gg_id:156705 Nitrobacter hamburgensis str. X14 NC_00
AM292301.1 gg_id:254106 Nitrobacter vulgaris str. BB3 AM292
AY055796.1 gg_id:17737 Nitrobacter winogradskyi str. ATCC 14123 AY0557
AM286382.1 gg_id:220346 Nitrobacter vulgaris str. K55 AM286
AY055798.1 gg_id:56503 Nitrobacter sp. str. KB212 AY0557
EU528247.1 gg_id:284778 Seasonal Dynamics Mudflat Mouth Major Kentucky Lake Reservoir Tributary sedime EU528
L11661.1 gg_id:4840 Nitrobacter winogradskyi str. W L11661
AM286390.1 gg_id:223530 Nitrobacter vulgaris str. 329 AM286
L11662.1 gg_id:4842 Nitrobacter sp str. LL L11662
AF529115.1 gg_id:62406 trichloroethene-contaminated site clone FTLM116 proteobacterium AF5291
AB241411.1 gg_id:223626 Rhodopseudomonas lichen O5 AB2414
AB196356.1 gg_id:109667 Rhodopseudomonas palustris str. LW-RE AB1963
AF487428.1 gg_id:68786 Rhodopseudomonas palustris str. Wai1S1 AF4874
U09829.1 gg_id:4878 marine sediment clone JAP850 Rochelle U09829
X87279.1 gg_id:4854 Rhodopseudomonas palustris str. DSM 126 X87279
EU018457.1 gg_id:252635 Rhodobacter sphaeroides PSB07-19 EU0184
CP000463.1 gg_id:183860 Rhodopseudomonas palustris str. BisA53 CP0004
AB167545.1 gg_id:100949 Rhodopseudomonas palustris str. KP0014 FERMP-19432 AB1675
AJ968691.1 gg_id:166553 Rhodopseudomonas sp. 1416ri str. ORS 1416 AJ9686
CP000301.1 gg_id:153177 Rhodopseudomonas palustris str. BisB18 CP0003
EF515308.1 gg_id:224099 Electricigen Enrichment MFC upf microbial fuel cell anode clone 22f08 EF5153
AB167544.1 gg_id:100793 Rhodopseudomonas palustris str. KP0003 FERMP-19430 AB1675

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52399.6	7465.3	7162.4	7358.3	13477.0	7788.2	11630.7	8132.0	5693.1	3694.7	5559.8
30768.5	5624.8	5112.0	3577.6	8943.7	5928.3	8529.7	4595.8	2607.0	1773.5	2217.0
58108.8	6381.1	6292.2	5803.1	13442.0	7016.7	10317.4	6775.8	4602.0	3394.3	3217.7
21892.1	2757.4	3871.0	1998.3	5530.6	2993.0	6275.9	2730.8	1436.9	773.5	980.1
22483.5	4220.2	5110.6	3232.0	7996.7	4724.0	7280.7	4296.5	3909.5	1702.2	1793.1
11341.3	3284.9	2877.4	3242.1	6245.7	3594.0	5707.5	3470.6	2609.9	3062.5	2288.7
36575.5	3491.1	4589.5	2594.3	8658.4	4013.6	9083.9	3477.5	1093.8	979.0	1393.9
24121.6	2367.9	3359.9	2005.8	7287.0	2941.3	5599.2	3040.7	883.5	688.1	1091.0
21574.5	4532.8	2892.2	2761.9	6452.6	3120.1	6071.2	2406.3	1475.0	979.6	1774.6
56434.2	7511.2	6970.5	7036.3	11956.7	7609.4	9665.8	7715.1	6686.0	6066.7	6323.1
50993.7	5889.4	5067.1	4215.5	9403.7	5693.8	9032.5	5322.4	3026.4	2398.8	3145.8
29291.6	5007.3	5748.8	5265.3	9649.9	5413.7	9946.0	6210.5	2619.3	2164.2	4157.7
7241.8	4397.2	4807.6	3759.8	4772.2	4082.1	6349.5	3220.4	4776.8	2311.7	4712.9
45111.7	5097.5	4886.4	5389.7	11139.8	5649.8	8500.4	5872.7	4555.2	3948.4	3929.5
20757.9	2399.1	3073.5	2034.6	5046.5	2670.6	5038.3	2393.6	1853.4	1223.8	1546.4
62138.0	13221.1	10070.4	9670.6	15443.1	11539.4	15354.2	10085.4	9372.2	7658.8	8633.2
19300.9	2942.3	3436.6	2450.3	6458.2	3308.6	6416.3	3349.5	2071.9	1671.9	1494.5
25761.5	4238.2	4133.4	3312.7	7359.0	4259.0	7472.0	4245.9	3711.1	2616.8	2078.5
18208.1	1205.7	1928.0	1083.4	2992.0	1535.6	4259.2	1434.8	359.0	291.4	432.2
11809.3	2671.0	2545.3	1431.4	5698.1	2402.4	6082.9	1989.9	2355.0	1229.5	683.3
2451.3	2197.4	1435.3	1295.0	1288.0	1185.7	1421.1	1518.8	2879.0	824.1	1387.4
14806.9	2337.7	2866.5	1536.6	5064.1	2330.4	5765.8	2043.9	2133.4	1300.3	801.6
6572.7	1127.5	1073.8	860.0	1640.7	1794.7	1503.2	1260.8	1629.3	677.8	759.4
11414.4	5953.7	5533.6	5768.6	6969.6	5402.8	8095.5	5375.6	6448.9	5012.9	5326.8
9790.2	1288.8	1333.6	1048.4	2438.7	1469.5	2180.3	1322.0	821.7	811.0	695.4
18077.9	5320.7	5360.1	4875.6	7136.1	5087.6	8176.7	4682.1	4350.5	2783.5	3989.3
5912.9	771.1	589.1	399.1	1663.9	676.4	1761.6	603.8	209.0	152.1	111.9
10455.8	4808.7	4761.8	5063.8	8005.0	5569.7	8995.8	4726.7	2871.7	2246.5	3535.0
35174.2	3705.7	4377.4	3298.6	8481.3	4444.7	9253.4	3866.0	1670.5	863.0	1647.7
14087.7	4691.6	5550.6	4594.9	7586.9	4741.7	8339.9	4776.9	4093.9	3222.1	2702.9
22974.3	2982.6	3415.5	2692.5	4573.3	2970.8	6820.8	3213.9	2751.8	1853.1	1444.3
12899.9	3301.2	2181.0	1991.9	4157.3	2709.7	3560.9	2458.2	2172.9	857.0	1666.1
2419.0	766.2	1320.5	784.0	3388.1	986.2	1989.8	1284.5	926.1	223.4	347.4
22050.9	6596.6	6938.7	7128.5	7989.4	7374.7	7396.4	7406.7	6020.5	5962.7	6016.6
20554.7	5709.9	5075.4	3283.9	6690.8	5050.1	7681.3	3876.7	5113.3	3437.0	2923.1
24678.3	5577.9	5066.0	5086.0	6676.7	5447.6	8271.0	5542.2	5283.7	3980.2	3359.0
10131.4	2811.4	2582.1	2313.4	5433.0	2868.6	6013.2	3177.4	1403.4	914.6	1149.2
30954.0	5249.1	5154.0	3264.6	6062.0	4851.7	6851.5	3754.4	5634.8	2873.8	3003.9
16512.8	2835.0	2241.2	3050.6	4192.8	2870.8	4299.7	2775.3	2408.2	847.3	2326.5
474.6	685.7	910.2	777.0	1301.1	684.8	1537.7	853.3	751.5	70.9	695.8

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8520.5	6839.6	9122.2
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7713.2	6529.4	8684.5
4239.7	4008.9	2921.4
5475.1	4616.1	6458.3
3719.6	3410.5	3149.2
4900.5	3599.0	4529.5
4201.4	4013.5	2855.8
2831.6	3433.0	3849.5
8495.8	8113.6	10060.3
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6733.6	5544.7	7126.8
4355.0	5028.6	3226.9
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12054.7	10930.4	14008.7
4289.3	2663.2	4006.0
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1972.9	1179.4	1499.7
3068.4	1905.6	2244.9
1188.3	2157.1	1455.5
3278.3	1985.7	2419.9
1275.0	1201.0	941.1
5121.0	5230.4	5836.0
1725.7	1206.3	1127.6
5812.7	4767.9	5316.2
440.2	809.2	661.3
4384.6	4714.1	5955.2
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5253.1	4427.1	5702.3
3779.8	3258.6	2839.5
2912.8	2630.5	2570.5
2170.9	1335.9	1820.5
7452.1	7154.5	8818.6
4607.5	4385.8	4624.9
5570.3	4796.2	6147.5
3867.4	2909.7	3724.5
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EU221585.1 gg_id:253925 Rhodopseudomonas palustris str. DX-1 EU221
AF509907.1 gg_id:111553 Bradyrhizobium sp. str. CMI23 AF509
AB079634.1 gg_id:62340 Rhodopseudomonas palustris VA2-2 AB079
L11664.1 gg_id:4866 Rhodopseudomonas palustris L11664
DQ126338.1 gg_id:138381 Rhodopseudomonas sp. str. PSB-O DQ126
EU531568.1 gg_id:514717 Rhodopseudomonas palustris str. J EU531
EU018458.1 gg_id:248384 Rhodopseudomonas palustris PSB07-21 EU018
GQ036328.1 gg_id:384524 Topographical and Temporal Human Skin Microbiome skin palm clone nbu362h08c1 GQ036
DQ984578.1 gg_id:245601 Mt. Nan-Jen litterfall clone IYF09 DQ984
DQ497243.1 gg_id:157613 Chelatococcus sp DQ497
GQ421849.1 gg_id:550491 Microvirga sp. str. 5420S-16 GQ421
FJ025099.1 gg_id:308491 Bradyrhizobium japonicum str. SEMIA 6396 FJ0250
AY904750.1 gg_id:112390 Bradyrhizobium japonicum str. SEMIA 6144 AY904
AJ009451.1 gg_id:4819 anaerobic TCB-transforming consortium clone SJA-9 AJ0094
EF121353.1 gg_id:216650 microbiota uninfected and Rickettsia-infected colonized cat fleas Ctenocephalides fel EF1213
EU861833.1 gg_id:309753 effects chronic fertilization on alpine tundra microbial implications carbon and nitrog EU861
FJ478995.1 gg_id:579612 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4789
FJ025100.1 gg_id:309477 Bradyrhizobium japonicum str. SEMIA 6154 FJ0251
GU455366.1 gg_id:523224 Understanding short-chain fatty acids accumulation enhanced alkaline digestion: kir GU455
AM412118.1 gg_id:247879 Chelatococcus sp. str. P-117 AM412
EU256461.1 gg_id:256534 Bradyrhizobium sp. str. CCBAU 85044 EU256
AM990457.1 gg_id:279499 Chelatococcus sp. str. I-21 AM990
DQ303342.1 gg_id:150032 Dynamic during maturation Tuber magnatum Pico ascoma Bradyrhizobium clone TM DQ303
EF394148.1 gg_id:205693 Bradyrhizobium japonicum str. CCBAU 43277 EF3941
X87272.1 gg_id:4980 Bradyrhizobium japonicum str. DSM 30131 T X87272
AF530465.1 gg_id:61023 Bradyrhizobium japonicum JZ1 AF5304
DQ129309.1 gg_id:138424 microarray level air two cities Texas urban aerosol clone AKIW763 DQ129
EU276558.1 gg_id:362293 -DGGE and Approaches Analyze Effect Agricultural Practices on Soil agricultural soil c EU276
AF417550.1 gg_id:48037 Bradyrhizobium japonicum str. DASA01059 AF4175
EF018822.1 gg_id:204655 aspen rhizosphere clone Amb_16S_1300 EF0188
FJ716001.1 gg_id:579890 Diet- gut microbiota Lumbricus rubellus fingerprinting technique and cloning intestina FJ7160
AY345540.1 gg_id:91124 Lake Wai'ele'ele water clone LWSR-28 AY3455
GQ129955.1 gg_id:434250 Genetic inventory 'JPL-SAF' during MSL mission spacecraft assembly clean room floc GQ129
AF417547.2 gg_id:33185 Bradyrhizobium japonicum str. DASA38025 AF4175
GQ389009.1 gg_id:587997 quality deterioration drinking system during serious red water outbreak clone J57 GQ389
DQ432334.1 gg_id:156941 prokaryotic alkaline hypersaline lakes Wadi Natrun Egypt Lake Hamra water clone W DQ432
EF394142.1 gg_id:204550 Bradyrhizobium japonicum str. CCBAU 41267 EF3941
AY649440.1 gg_id:99283 Bradyrhizobium japonicum str. BR3288 AY6494
AB187010.1 gg_id:101203 Suiyo seamount hydrothermal vent water 0.2micro-m filterable fraction clone SSM-M AB187
AB195991.1 gg_id:130287 Bradyrhizobium japonicum str. MH615 AB195
AJ867909.1 gg_id:143411 Fluctuations Significantly Influence Microbial Present Nival Lakes lake water clone B6 AJ8679

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11920.4	4210.8	3730.9	3013.4	4749.1	3998.3	5997.4	3636.9	3024.1	1939.4	2028.9
17064.6	4846.7	5703.8	4640.5	7802.2	4961.0	8655.1	4794.6	3633.2	3075.3	2804.2
17632.0	2114.7	2170.3	1250.0	4276.6	2367.5	7215.1	2431.8	832.3	880.5	983.2
27888.9	9519.3	9674.4	10381.9	11489.5	11000.0	10390.3	10033.2	12290.5	10172.2	12807.6
18154.0	7845.9	7986.9	8520.1	9364.4	8641.3	10195.0	8579.4	8120.8	6261.5	7793.0
10850.6	4034.3	4529.7	3586.9	6040.5	4084.7	6890.2	4021.2	3196.0	2925.7	2567.4
13863.7	6116.0	4359.0	3388.7	4147.6	4633.9	4546.5	3634.6	5703.0	2501.7	2517.6
10384.7	3462.5	3408.6	3184.3	5397.5	3510.2	5509.6	3754.2	3651.2	2460.8	2273.6
16925.9	4780.1	3733.5	3994.0	5179.4	4603.7	4632.6	4727.4	2856.7	2656.8	4288.2
2649.1	1918.4	1384.3	1670.1	4280.0	2217.7	2544.1	2221.0	1416.7	804.8	1012.8
22910.6	4055.8	4296.1	2853.3	7084.9	3956.5	8178.4	2954.9	1601.1	895.0	1251.4
40192.4	5834.6	5428.6	3846.5	11267.1	6120.8	11300.9	4835.7	2155.8	2196.8	2039.3
67.7	124.7	121.5	102.5	204.8	219.5	226.5	145.0	56.6	45.5	73.8
105.0	486.9	141.0	150.3	281.2	249.6	246.9	170.4	59.4	43.1	69.5
17653.3	4451.5	4230.5	2972.4	5324.3	4404.9	5408.9	3354.2	3173.3	1797.0	2325.5
35245.2	7613.8	6715.7	6670.9	11196.0	7968.6	10777.5	7031.9	5864.2	3977.0	4826.9
44165.2	6688.7	6599.3	5292.1	10456.1	6645.7	10414.0	5914.2	5208.6	3875.7	4125.1
11932.5	3670.0	3553.4	2929.7	5294.4	4323.5	4906.5	3613.9	3262.5	1696.1	1737.4
7279.7	4580.0	3610.6	3469.7	6084.3	5096.7	5909.3	4693.4	2489.3	2042.3	3707.0
13121.9	6242.2	5721.1	5808.6	7462.2	6150.6	7131.7	5924.9	7126.5	6025.7	5814.6
9795.2	9062.6	6663.8	6643.1	9514.5	7597.3	9482.9	7254.9	6373.0	6713.2	7452.7
42486.1	4050.0	4829.6	4034.3	10212.4	4891.0	7629.9	5848.3	2059.9	1584.2	2399.2
28170.5	4457.1	5205.6	3951.7	9140.1	5033.7	7910.7	4985.3	4312.5	2027.4	2026.3
22575.7	4534.5	5500.3	3357.6	8254.0	4984.8	7622.1	4277.9	3331.2	1421.6	1983.4
31394.4	3589.8	4345.3	3672.1	7213.1	3924.6	7325.2	3869.4	2375.0	1873.0	2217.8
65.8	819.7	831.2	808.0	1843.6	948.9	1238.8	937.3	455.3	496.1	702.0
4387.4	3141.5	3297.8	2550.2	5164.5	3519.1	3812.6	3537.3	2350.4	2075.0	2131.5
20091.2	4238.8	3762.4	2376.3	7133.4	4037.2	7317.1	3015.6	1509.6	2202.7	1446.7
29785.3	4272.2	4392.2	3943.9	9350.2	4615.1	8191.8	4835.6	3967.3	2215.3	3431.6
31663.1	3973.2	4471.0	3676.9	9375.6	4685.0	6085.0	5508.9	2036.7	1445.0	2326.2
3944.5	2864.8	2176.7	2332.9	3871.5	2821.8	3688.7	3420.5	1755.6	1817.2	1132.1
322.2	4463.0	1666.0	1281.9	3242.0	2273.7	2981.6	2422.7	1891.2	729.2	824.2
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1953.8	5750.2	2740.6	5852.9	5005.6	5434.2	4862.9	4512.2	3805.9	2153.2	4438.2
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31516.4	4260.5	4626.9	3290.8	7459.0	4175.8	8048.1	3696.5	1608.9	1564.9	1855.8
600.3	3078.8	3062.1	3302.6	4496.8	3230.8	3993.1	4244.5	3836.0	3385.1	1636.7
44069.5	9089.5	11597.6	9838.4	15574.4	8975.2	14126.6	10077.6	12068.3	9281.4	10079.4
2444.0	2323.4	2436.1	2625.4	4226.7	2914.3	3681.5	3159.6	2882.2	1096.5	1408.0

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3925.4	4063.2	4785.8
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3762.2	2310.0	2033.4
9588.5	11430.0	10341.8
8055.9	8262.5	10031.6
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3502.0	4072.5	3824.2
4293.4	4346.1	4180.8
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2515.4	2836.0	2810.9
4916.7	4237.7	4922.2
6624.9	5795.3	7980.2
144.1	242.5	233.5
174.2	148.0	221.6
3742.7	4225.8	5077.1
8547.2	6724.0	10288.8
7487.3	6647.0	7297.6
4412.7	3414.6	4202.1
4870.5	4513.7	5485.8
6455.9	7274.5	6826.2
7321.4	7577.0	8355.9
6141.2	5644.5	5583.0
5534.9	5230.0	7773.5
5557.2	5045.1	7361.5
4302.3	3683.6	4508.3
614.4	1068.1	1094.6
4025.4	3518.1	3994.6
4619.9	4120.5	4854.2
5360.2	5010.1	6436.0
6188.6	5141.1	4988.3
3730.4	3867.7	4761.4
2258.3	2481.8	2804.7
1421.1	2069.3	1282.2
4393.4	3944.8	5592.9
3086.8	1991.6	1389.7
5366.9	4966.6	7408.5
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AJ968693.1 gg_id:167720 Bosea sp. str. ORS 1414 AJ9686
EU878006.2 gg_id:576097 Salinarimonas rosea str. YIM YD3 EU878
GQ103050.1 gg_id:397383 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ103
FJ479132.1 gg_id:512302 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4791
AM292299.1 gg_id:242856 Nitrobacter hamburgensis str. Y AM292
AB195986.1 gg_id:128373 Bradyrhizobium canariense str. MH547 AB195
EU029133.1 gg_id:244029 Deinococcus sp. str. 5A4 EU029
AM411919.1 gg_id:253138 Bradyrhizobium sp. str. P-44 AM411
AB300992.1 gg_id:223242 Bradyrhizobium iriomotense str. EK05 (= NBRC 102520) AB300
EF394144.1 gg_id:214300 Bradyrhizobium japonicum str. CCBAU 53152 EF3941
AY963315.1 gg_id:154614 structures and correlated ecological factors soils two evergreen broad-leaved forests AY9633
AB426223.1 gg_id:263163 -situ identification study benzene-degrading s under methanogenic condition anaerc AB426
AJ785294.1 gg_id:211869 Rhizobiales genosp. AL ARRI 185 AJ7852
CU927551.1 gg_id:545730 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU927
DQ351924.1 gg_id:173105 manganese oxidation soil clone JH-GY18 DQ351
AF417552.1 gg_id:27428 Bradyrhizobium japonicum str. DASA37011 AF417
AY372184.1 gg_id:94343 Bradyrhizobium betae str. PL7HG1 AY372
EF516928.1 gg_id:222831 grassland soil clone FCPN762 EF5169
AF208509.1 gg_id:56515 Bradyrhizobium japonicum str. USDA 129 AF2085
AY904764.1 gg_id:112297 Bradyrhizobium japonicum str. SEMIA 6163 AY904
FJ382130.1 gg_id:582075 Potentially pathogenic and air stem cell transplant summer hospital shower water BM FJ3821
AF417551.1 gg_id:45827 Bradyrhizobium japonicum str. DASA37026 AF417
AY904758.1 gg_id:112060 Bradyrhizobium japonicum str. SEMIA 6156 AY904
FJ528273.1 gg_id:573764 Bradyrhizobium sp. str. Mf253 FJ5282
AF234889.2 gg_id:77279 Bradyrhizobium japonicum str. SEMIA 5080 AF2348
AY904765.1 gg_id:112064 Bradyrhizobium japonicum str. SEMIA 6164 AY904
FJ382683.1 gg_id:510366 Potentially pathogenic and air stem cell transplant summer hospital shower water BM FJ3826
AY904743.1 gg_id:111821 Bradyrhizobium japonicum str. SEMIA 6002 AY904
AF502220.1 gg_id:55851 EBPR sludge lab scale clone HP1B78 AF5022
EF032655.1 gg_id:198655 structure riverine biofilms river biofilm clone SepB-6 EF0326
FJ380996.1 gg_id:549917 Bradyrhizobium sp. str. BQN4T-01d FJ3809
AY178079.1 gg_id:100322 Bradyrhizobium sp. Cmey1 Cmey 1 AY178
AY904732.1 gg_id:111515 Bradyrhizobium japonicum str. SEMIA 656 AY904
AF409021.1 gg_id:98929 Bradyrhizobium sp. str. Ellin179 AF409
D13430.1 gg_id:4937 Bradyrhizobium japonicum str. USDA 110 D13430
AB220164.1 gg_id:153145 Bradyrhizobium sp. QC1 AB220
AF508112.1 gg_id:66234 Bosea thiooxidans TJ1 AF508
GU377100.1 gg_id:514335 Balneimonas sp. str. sptzw09 GU377
AY169423.1 gg_id:81409 Bradyrhizobium japonicum AY1694
D78366.1 gg_id:5055 Agromonas oligotrophica str. JCM1494 D78366
GQ389186.1 gg_id:582505 quality deterioration drinking system during serious red water outbreak clone D59 GQ389

84.1	3498.4	614.7	570.9	1857.1	1031.5	1213.9	1263.0	692.6	221.8	399.8
6911.8	3590.4	3286.4	2897.4	5354.1	4275.9	4968.4	3449.8	3305.7	2018.9	3140.0
16596.1	5490.8	4719.2	5206.9	6751.9	5183.9	6690.4	6113.6	6518.8	4923.4	4978.8
5720.6	2756.7	2878.1	2682.0	3005.0	2530.9	3353.4	2491.0	2833.6	2757.7	3925.4
26171.7	4020.2	3947.5	3808.3	6370.4	4260.5	6177.0	4585.1	3058.9	2187.0	2565.4
3594.1	1027.0	1842.2	400.8	3227.0	1435.1	3753.4	690.4	143.6	190.5	251.9
2089.5	2597.5	1898.9	1652.0	3395.0	2867.5	2410.0	2674.1	1202.7	1227.0	1176.3
26708.7	3534.4	2731.1	2541.5	5750.6	3020.4	5302.2	2397.2	1426.4	818.9	1109.4
12385.4	4237.8	4496.8	3732.6	5740.6	5159.3	4900.9	4747.2	3391.3	2599.0	3001.1
20407.4	4061.1	4643.9	3714.4	8667.3	4627.1	8089.5	4142.5	3563.2	2198.1	1852.9
38619.5	6416.6	5791.5	6277.5	10402.7	6208.5	9091.5	7073.3	4284.3	4371.2	4724.2
536.2	1816.2	1224.0	1525.2	4312.4	2013.1	2052.9	1911.2	1164.2	539.0	640.5
1210.5	6704.6	5802.3	5682.2	7416.0	6316.4	7174.8	6826.3	4717.9	3748.1	6178.6
337.4	1019.1	679.2	1000.0	2122.4	1207.6	1721.8	1469.4	510.8	335.7	395.9
147.6	3062.8	1150.0	1245.8	2931.1	1773.0	2535.6	2235.1	843.1	701.6	742.8
17453.2	5505.3	3894.6	3364.1	6104.4	4763.9	5530.4	3842.2	5311.5	2481.3	2564.0
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18816.6	7020.1	6220.2	5978.4	6886.5	7460.5	7404.3	6344.8	8223.3	6442.3	6999.0
17318.4	4612.8	4758.6	4050.1	7383.9	5159.4	6521.5	4198.0	3751.1	1467.1	2091.2
3612.4	2930.8	3257.9	3050.5	2893.9	3219.5	2703.4	3222.3	2347.5	2778.9	2339.2
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24802.9	3945.4	4743.4	2716.0	7942.1	4178.7	9055.0	3217.9	1430.8	1131.0	2051.8
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44490.7	6074.6	5737.9	4529.0	11770.0	6505.5	11393.1	5698.8	2498.0	2547.8	2472.8
40.7	863.0	1259.5	1957.7	2855.4	1421.9	1555.9	2629.8	6292.8	767.5	873.0
157.2	583.3	628.8	654.3	844.3	766.5	1008.7	812.5	1131.9	571.5	382.7
15367.5	3610.7	2870.9	2865.1	4800.5	3738.8	3567.9	3636.0	2765.8	1701.7	1787.3
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AM490612.1 gg_id:249691 Ochrobactrum anthropi str. LMG 401 AM490
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EU352762.1 gg_id:268033 Ochrobactrum tritici str. NK 2.X-2 EU352
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EF028152.1 gg_id:179539 Ochrobactrum sp. str. xll-3 EF0281
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AM180484.1 gg_id:145855 Pseudochrobactrum saccharolyticum str. CCUG 33852 AM180
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FJ493040.1 gg_id:589752 Pseudochrobactrum asaccharolyticum str. 2G-2 FJ4930
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AY914071.1 gg_id:113751 Ochrobactrum sp. R-3 AY914(
AB369864.1 gg_id:253214 Pseudochrobactrum glaciale str. KMM 3858 (= Pi 26) AB3698
AM114407.1 gg_id:151281 Ochrobactrum anthropi str. CCUG 34735 AM114
FJ887929.1 gg_id:551972 Ochrobactrum intermedium str. AR9 FJ8879
AF526514.2 gg_id:62908 Ochrobactrum intermedium ADV21 AF5265
EU352758.1 gg_id:271007 Ochrobactrum intermedium str. NK 2.HA-1 EU3527
GQ280047.1 gg_id:591634 Ochrobactrum intermedium str. BJ-37 GQ280
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AJ519939.1 gg_id:76582 Ochrobactrum gallinifaecis str. Iso 196 AJ5199
AM041247.1 gg_id:133461 Ochrobactrum aqua-oryzae str. MTCC 4195 AM041
FJ202509.1 gg_id:345537 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2025
DQ446093.2 gg_id:172411 Surface Mucopolysaccharide Layer and Band Microbial Mat Black Band-Diseased Sid DQ446
GU118085.1 gg_id:560738 Threatened Corals Provide Microbial Habitats clone Apal_L09 GU118
FJ202721.1 gg_id:319280 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2027
GU118071.1 gg_id:567305 Threatened Corals Provide Microbial Habitats clone Apal_M03 GU118
D25314.1 gg_id:4687 Blastochloris viridis str. ATCC19567 D25314
AM502287.1 gg_id:261580 Blastochloris gulmargensis str. JA248 AM502
AF084509.1 gg_id:200193 Blastochloris viridis str. B9 AF0845
AJ401203.1 gg_id:78031 Blastochloris sp. AT2101 AJ4012
AY117148.1 gg_id:63558 Blastochloris sulfoviridis str. OK3G7 AY1171
AJ012089.1 gg_id:4711 Blastochloris sulfoviridis str. ToP1 AJ0120
AJ548824.1 gg_id:82396 Candidatus Devosia euplotis str. CAMP4.4 AJ5488
EU589260.1 gg_id:260684 China Ningxia rice paddy field soil clone 1_C6 EU5892
EF433460.1 gg_id:212196 Devosia sp. str. IPL15 EF4334
EU812979.1 gg_id:311842 Microbial structure thermophilic reactors biogas reactor fed corn silage clone TUM-M EU8129
EF540476.1 gg_id:224522 Devosia sp. 6_4V EF5404
FJ807418.1 gg_id:550842 Presence and iron oxidizing landfill leachate impacted groundwater surface water int FJ8074
EU362140.1 gg_id:355188 and Mesquite Flats Site Death Valley dune sand clone 11 EU3621
DQ125710.1 gg_id:130155 uranium contaminated soil clone AKAU3805 DQ125
EF612399.1 gg_id:255206 historic semiarid lead-zinc mine tailings site soil clone OS-C20 EF6123
GQ396877.1 gg_id:573755 Functional unvegetated perhumid recently-deglaciated soils do not correlate shifts s GQ396
AY512822.1 gg_id:105993 Devosia riboflavina AY5128
DQ279337.1 gg_id:144518 Dynamic during maturation Tuber magnatum Pico ascoma Xanthomonas clone TM1 DQ279
EF067859.1 gg_id:174315 Devosia terrae str. DCY11 EF0678
FN421512.1 gg_id:573013 proteogenomics physiology phyllosphere Arabidopsis thaliana clone 12_F07 FN4215
EU289427.1 gg_id:245814 metagenomic approach biosynthesis ansamycin endophytes or symbionts enriched s EU2894
GQ472390.1 gg_id:544772 Microbial Dongping Lake lake sediment clone 4D3-5 GQ472
FM253613.1 gg_id:333986 Rock gold mine unusually microbial biofilm clone F07-1 FM253

46722.0	12142.6	10302.5	11895.4	14607.9	11442.6	13231.2	10065.7	14659.5	11969.3	15759.1
3417.1	4691.0	3671.1	3844.8	5290.2	3810.7	3675.9	5004.5	3186.1	4175.3	2323.4
10018.3	5124.5	4884.6	5043.4	6201.6	6321.9	4872.8	6268.7	5012.9	7089.4	4050.6
6943.7	5478.4	5116.0	5165.4	8816.0	6493.3	8174.2	6096.8	4226.1	6140.5	3707.7
5849.6	6031.1	4337.7	4240.0	5322.9	5227.5	4132.9	5614.8	3992.8	3975.7	3117.8
310.7	3635.7	1977.7	1855.2	2523.3	2621.7	2248.2	2553.7	1490.1	1926.7	1115.3
4515.0	4664.5	2833.4	2744.7	3567.2	3416.7	3208.2	3495.9	2229.1	3459.2	1914.9
23312.7	7849.9	7224.7	6877.4	8311.4	7020.0	8254.3	7444.2	4060.8	8430.4	6078.2
2424.9	2186.9	2088.6	1855.5	2889.5	2488.1	3043.6	2685.0	1508.7	1984.7	1307.9
392.2	3876.1	2471.5	2248.1	3040.3	2936.7	2869.8	3058.1	1712.7	2466.0	1303.6
360.7	3815.2	2270.5	2144.8	2765.3	2778.4	2408.1	2818.4	1583.3	2456.3	1265.8
4320.6	2883.0	3192.3	3186.8	4607.9	3415.5	4357.2	3126.2	1969.3	2489.9	1934.3
14742.5	4707.5	4634.9	4704.2	7313.0	5153.0	5588.0	5119.2	3381.6	4760.8	3734.9
2059.1	3094.6	3570.2	4380.3	5590.7	4237.3	4793.0	4727.4	3704.8	2884.8	2343.8
11610.4	6440.6	5940.5	5868.4	6263.1	5745.6	5831.3	5691.2	6467.1	6402.0	6078.1
9147.1	5211.1	5406.8	5652.9	6791.2	5753.7	6767.8	5290.8	6038.5	6539.0	6937.1
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6012.2	4708.1	3783.2	4077.0	5271.6	4596.8	4645.4	4656.1	3855.5	3293.4	3905.1
3052.4	2667.4	3070.8	3368.0	4657.8	3518.6	5004.2	4084.5	2208.8	1682.0	1766.6
12216.8	3949.6	3885.1	4114.5	4391.2	4050.2	6081.3	5048.6	4593.0	3134.0	3005.1
7062.1	4896.7	4257.7	3829.2	5610.3	4754.3	6024.1	4366.1	4225.4	2152.6	2866.7
324.6	1779.5	2266.7	2232.3	3795.1	2647.2	5583.9	2718.8	2062.0	771.3	972.1
619.1	1315.0	2045.1	2477.4	3318.7	1805.3	3459.3	3173.3	8176.3	1614.6	1075.0
8620.2	3322.6	3670.3	4038.5	5588.4	4692.4	6325.5	4796.6	5023.6	4209.2	3649.1
11193.4	6512.9	5002.3	5629.2	6579.0	4879.1	7329.9	5857.2	6405.3	5548.7	6417.4
1309.4	2720.0	3549.6	3537.6	4793.2	3449.3	4100.9	3809.5	2984.3	1832.5	3071.5
1387.0	2830.6	3317.9	2997.9	4707.4	3116.4	3883.7	4256.2	2745.5	4094.3	1998.2
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12987.9	6086.7	5206.1	5061.0	7183.7	6890.1	7206.8	5277.4	5759.0	5126.0	4390.3
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7950.7	5046.4	5128.4
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3284.5	2626.3	2498.2
4343.9	3877.0	2933.9
8812.3	8300.2	7128.1
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3633.3	3026.8	2311.0
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5972.6	5356.9	6545.1
5901.5	5306.4	4369.0
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6063.1	7234.2	5656.2
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5498.0	3705.1	3357.2
8610.5	4524.2	6168.4
9851.7	6116.4	6402.1
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7460.6	5628.7	5654.7
404.5	348.9	591.4
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6488.3	3337.9	3415.5
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5588.6	3348.4	3032.5
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GQ006663.1 gg_id:502999 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu86b10c GQ006
FN594684.1 gg_id:559356 and arsenic mobilization rock biofilms ancient biofilom gold mine Zloty Stok clone f1- FN594
EF018449.1 gg_id:215447 aspen rhizosphere clone Amb_16S_1074 EF0184
GQ263214.1 gg_id:581749 Structure Simulated Level Waste Site simulated level waste site clone F3_19X GQ263
EU709017.1 gg_id:301593 Devosia sp. str. B2 EU709
FJ560749.1 gg_id:550691 Prosthecomicrobium mishustinii str. 17 FJ5607
EF540486.1 gg_id:227483 Devosia sp. c4M EF5404
AM293857.1 gg_id:237298 Devosia subaequoris str. HST3-14 AM293
GU444083.1 gg_id:516056 Effects amendments on fertility and microbial structure cucumber Cucumis sativus L GU444
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AJ318163.1 gg_id:25284 Waste-gas biofilter clone BIri24 AJ3181
AY695724.1 gg_id:107598 USA: New Mexico Carlsbad Lechuguilla Cave Rainbow Room clone RR3A4 AY6957
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EU937979.1 gg_id:332501 Biogeochemistry Iron Oxidation Circumneutral Freshwater Habitat riparian iron oxidi EU937
CU918672.1 gg_id:552248 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU918
GQ396880.1 gg_id:560208 Functional unvegetated perhumid recently-deglaciated soils do not correlate shifts s GQ396
DQ814270.1 gg_id:163314 zebrafish digestive tract clone aab66c07 DQ814
EU133360.1 gg_id:257399 tallgrass prarie soil clone FFCH11455 EU133
DQ248307.1 gg_id:142990 carbon tetrachloride contaminated soil clone TF11 DQ248
GQ093782.1 gg_id:453654 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ093
Y14309.1 gg_id:4622 Hyphomicrobium facile str. H-526 Y14309
FM877980.1 gg_id:553425 Microbial iron redox cycling circumneutral-pH groundwater seep Hyphomicrobium c FM877
Y14307.1 gg_id:4627 Hyphomicrobium methylovorum str. DSM 5458 Y14307
AB016812.1 gg_id:4626 Hyphomicrobium methylovorum str. MBIC3196 AB0168
AF235089.1 gg_id:29178 Hyphomicrobium sulfonivorans str. S1; ATCC BAA-113; DSM 13863 AF2350
FJ536921.1 gg_id:594171 Linking performance microbiology biofilters treating dimethyl sulphide presence and FJ5369
Y14305.1 gg_id:4632 Hyphomicrobium zavarzinii str. ZV-622 Y14305
AB252934.1 gg_id:167855 Identification Shibayama lagoon Ishikawa Japan iron-oxidation biofilm clone 225 AB2529
EF019299.1 gg_id:210886 aspen rhizosphere clone Elev_16S_489 EF0192
AF198623.1 gg_id:47454 Hyphomicrobium chloromethanicum str. CM2 AF1986
AF234719.1 gg_id:52859 sludge clone A27b AF2347
AY328655.1 gg_id:88846 drinking water system simulator clone DSSF33 AY3286
Y14302.1 gg_id:4636 Hyphomicrobium vulgare str. IFAM MC-750 ATCC 27500 Y14302
DQ814327.1 gg_id:172883 zebrafish digestive tract clone aab67a09 DQ814

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12699.1	5311.8	5335.6	5460.7	5645.1	4878.4	4731.2	5059.2	6735.1	6598.9	7939.2
846.7	3250.8	4469.7	4975.9	4596.0	3605.1	4136.3	5248.1	3987.3	1657.8	2663.9
180.7	1436.0	1553.8	1268.2	5532.3	2854.6	4349.4	2199.8	693.8	874.7	787.2
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87.6	2076.2	2240.9	2092.6	3722.1	2673.3	3077.3	3297.6	1321.5	1980.9	1501.8
735.2	1807.3	2048.5	2163.7	3686.6	2654.6	2656.3	3130.8	1553.1	2689.4	1119.3
712.7	2742.9	3293.2	3224.8	6177.8	3725.4	4625.3	4750.6	2206.3	3293.0	1993.3
1841.8	2042.5	1960.4	1833.2	2883.3	2287.6	2963.6	1870.6	1669.8	1743.7	1572.9
93.4	1132.8	1559.5	1628.5	2615.7	1689.3	1905.1	2280.0	1302.0	1701.7	717.9
311.0	1369.9	1953.5	1855.5	2806.7	2318.4	2805.6	2534.5	1158.0	1098.1	1168.5
31903.3	9969.1	9616.7	9989.7	11797.2	10047.8	12432.3	8847.3	9683.1	6571.9	12416.3
1221.7	2252.8	2425.5	2323.4	4327.7	2448.2	3853.3	2841.6	2127.7	1423.6	1434.5
6208.3	5450.6	5353.2	5577.3	7731.1	6165.8	7379.8	5895.7	4893.9	4383.0	3954.9
2253.5	3287.2	3643.4	3520.5	4241.6	3396.9	3494.7	3760.4	2995.8	3626.4	3676.9
78.8	799.9	711.4	858.6	1680.8	1092.5	1277.3	1401.7	645.6	922.1	458.3
1661.3	3169.8	3077.8	3249.1	3703.3	3801.0	3398.5	4666.6	3086.9	2737.3	2366.1
35.5	93.3	219.9	258.2	497.4	413.9	130.0	244.7	97.3	251.5	80.8
13961.3	5430.5	4995.7	5121.5	8244.8	5534.7	8417.1	6275.0	4644.4	4423.6	4273.2
8404.4	7457.2	7622.1	7163.8	8260.5	7412.8	8036.3	7427.7	7952.9	6027.4	8761.6
1089.2	2955.7	3309.4	3165.8	4191.9	3845.0	4043.8	4684.1	2784.0	1956.1	2363.8
6141.6	5271.9	5654.8	5412.5	5650.2	6098.8	5242.0	6212.4	6125.4	5557.1	5789.6
21725.5	4221.4	4016.4	4405.0	5751.1	4817.8	4705.7	4830.3	4058.5	4545.1	4042.0
11553.7	4195.5	4061.3	4324.1	4856.8	4561.8	5038.2	5555.8	3374.3	2475.0	3072.1
15580.5	4665.5	4381.5	4929.2	5923.7	5076.7	6328.6	5471.7	5152.8	7413.0	5383.8
281.4	2021.8	2111.6	2158.5	2911.7	2423.4	3123.7	2213.0	1367.3	808.7	1312.8
179.4	675.6	589.5	680.1	1263.3	636.6	749.5	663.6	411.4	221.2	478.9
6625.6	3690.7	3140.8	2946.7	3797.2	3276.7	3794.1	2691.4	3506.3	3281.5	4783.0
4975.5	3849.6	4119.2	4466.7	5326.4	4094.1	5084.8	4671.3	4885.6	2360.5	3261.6
37.2	105.9	229.4	264.2	965.9	249.8	567.6	544.7	46.4	45.9	91.1
121.1	2206.9	2618.1	2813.4	5095.1	3155.8	4727.1	4446.2	1807.4	1637.5	1857.1
7911.4	2433.9	2656.1	2591.1	3390.6	2522.4	3806.4	2672.6	2041.0	1642.5	2177.4
372.1	1421.2	1644.6	1451.7	2448.1	1441.5	2716.6	2138.6	647.6	867.3	747.7
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2044.7	784.3	868.2	944.2	1260.6	907.3	1268.4	978.1	1018.5	809.9	1068.9
2090.0	2672.9	2021.2	1874.5	3986.8	2433.5	3661.3	2895.6	1198.1	1457.8	1301.7
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3989.6	3465.1	3829.3
4471.2	1742.3	2018.7
4907.4	3410.8	3046.2
7365.1	3982.8	3832.2
3032.7	2313.0	2724.3
4501.0	2506.2	1091.6
3819.1	2154.3	3577.0
10660.9	10136.9	12334.3
3932.2	3166.6	2951.7
8735.7	5749.9	7901.8
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1547.6	1424.3	1435.4
3578.8	4360.6	4085.4
1024.4	154.4	189.3
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8082.9	7694.2	6832.8
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6863.3	5226.4	5907.3
5765.7	4936.3	4281.4
5581.0	5553.8	5739.5
6596.5	5065.5	7284.4
2898.0	2292.0	3121.1
553.8	799.1	1079.8
3293.8	3693.4	4472.6
4562.8	4927.9	5682.4
275.7	243.7	283.3
5191.2	2984.9	3186.3
2581.4	2522.4	2470.5
1831.6	1490.2	1440.8
1326.4	723.6	1789.2
3852.7	3482.7	5802.5
876.3	946.4	982.2
2811.3	2938.7	4101.0
9138.1	9097.4	8560.6
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AY957933.1 gg_id:115024 drinking water biofilm clone B3NR69D18 AY9579
Y14303.1 gg_id:4630 Hyphomicrobium hollandicum str. IFAM KB-677 Y14303
Y14304.1 gg_id:4635 Hyphomicrobium aestuarii str. DSM 1564 Y14304
CU918149.1 gg_id:539592 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU918
AY328697.1 gg_id:88935 drinking water system simulator clone DSSF75 AY3286
AY328659.1 gg_id:89720 drinking water system simulator clone DSSF37 AY3286
AF097815.2 gg_id:4640 activated sludge clone 49520 AF0978
AF279787.1 gg_id:26693 Hyphomicrobium sp. str. PMC AF2797
AY328635.1 gg_id:89164 drinking water system simulator clone DSSF12 AY3286
AY328650.1 gg_id:90267 drinking water system simulator clone DSSF27 AY3286
GQ500789.1 gg_id:573659 Surveys Biofilms and Sediments Mammoth Cave Karst Aquifers Bio-Sep beads conta GQ500
X53182.1 gg_id:34344 Hyphomicrobium vulgare str. MC-750 X53182
GQ263780.1 gg_id:558638 Structure Simulated Level Waste Site simulated level waste site clone WC1_b17 GQ263
CU918043.1 gg_id:568017 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU918
AF097824.2 gg_id:4624 activated sludge clone 4953 AF0978
DQ814766.1 gg_id:172128 zebrafish digestive tract clone aab53a04 DQ814
CU920885.1 gg_id:547603 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU920
GQ264377.1 gg_id:513073 Structure Simulated Level Waste Site simulated level waste site clone WW2_57 GQ264
AY328683.1 gg_id:88276 drinking water system simulator clone DSSF61 AY3286
DQ815221.1 gg_id:168134 zebrafish digestive tract clone aab51g05 DQ815
FM253620.1 gg_id:324555 Rock gold mine unusually microbial biofilm clone G04-1 FM253
Y14308.1 gg_id:4619 Hyphomicrobium denitrificans str. DSM 1869 Y14308
GQ500820.1 gg_id:591347 Surveys Biofilms and Sediments Mammoth Cave Karst Aquifers Bio-Sep beads conta GQ500
FJ152725.1 gg_id:336999 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX5A_ FJ1527
GQ281066.1 gg_id:586097 Hyphomicrobium facile str. NBCS23 GQ281
GQ500792.1 gg_id:579761 Surveys Biofilms and Sediments Mammoth Cave Karst Aquifers Bio-Sep beads conta GQ500
EF019856.1 gg_id:207848 aspen rhizosphere clone Elev_16S_1214 EF0198
FJ439830.1 gg_id:550289 Investigation estrogen-degrading bioreactors membrane bioreactor biofilm clone M2 FJ4398
AY328674.1 gg_id:90421 drinking water system simulator clone DSSF52 AY3286
EF125445.1 gg_id:198749 mangrove soil clone MSB-2E9 EF1254
DQ814141.1 gg_id:172266 zebrafish digestive tract clone aab60d07 DQ814
GU269548.1 gg_id:579387 Pedomicrobium ferrugineum str. ATCC 33119 GU269
GQ339120.1 gg_id:529888 Comprehensive Investigation on Iron Cycling Freshwater Seep ing Microscopy Cultiv GQ339
GQ264219.1 gg_id:585537 Structure Simulated Level Waste Site simulated level waste site clone WW1_b13 GQ264
FJ478816.1 gg_id:573426 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4788
FJ479530.1 gg_id:554597 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4795
AY921654.1 gg_id:113465 farm soil clone AKYG1791 AY9216
FJ478521.1 gg_id:556996 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4785
GU269549.1 gg_id:571598 Pedomicrobium manganicum str. ATCC 33121 GU269
EF019229.1 gg_id:207866 aspen rhizosphere clone Elev_16S_398 EF0192
EU644219.1 gg_id:285061 and Samoylov Island Lena active layer -centred polygon near surface horizon; Rim_T EU6442

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203.1	2356.1	2533.5	2805.3	5332.1	2992.6	5089.2	3416.6	1328.6	1554.0	1794.7
1945.4	3654.2	4046.4	3495.5	4058.6	3928.5	5246.5	4425.1	2350.6	1490.7	2687.6
7051.2	4897.3	4850.1	5104.4	5999.2	4865.2	5579.6	5329.9	4879.5	3807.0	5012.6
18228.6	3058.4	3010.6	2954.9	5808.0	3385.0	4928.7	3268.7	4112.9	1722.3	2051.1
26391.7	8327.9	8854.6	8447.6	8693.5	8881.5	8911.9	8684.7	13642.4	11334.3	9610.3
8193.1	5162.7	4339.9	4386.8	4974.0	5802.4	4874.2	5234.6	4882.7	3883.3	3460.2
1737.5	3768.0	3659.6	3390.0	5909.5	4518.1	5150.5	5356.0	2462.6	2295.6	2895.0
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13291.4	5921.9	6317.8	6145.5	5559.5	5703.7	5717.0	5835.0	6676.6	6663.9	6319.8
9162.2	4863.4	3963.0	4497.8	5500.0	4875.1	5411.8	5204.4	5250.4	3721.1	4410.9
1883.9	1809.4	2097.6	2066.0	3563.5	2199.6	2549.1	2788.1	2050.6	1746.3	1446.9
10725.6	5464.1	5439.6	5775.7	7240.4	6058.3	7932.3	6083.0	6152.4	5373.4	6364.4
7448.9	2355.3	2247.1	2759.6	4002.7	2577.0	3176.4	2955.0	1998.7	1791.4	1409.6
261.8	2423.0	1731.5	1600.7	3826.9	2470.5	3524.4	3180.8	651.4	618.5	689.7
1183.6	4873.5	4477.9	4738.8	6928.3	5430.2	6505.6	5295.9	3763.8	3645.6	3175.7
2188.7	3028.6	3166.1	2935.7	4685.5	3709.8	5299.2	3662.3	2422.7	2312.3	2333.8
7795.2	5341.7	5287.8	4519.2	7997.1	6422.2	7040.5	6168.1	4696.1	3481.6	3849.9
8261.8	4273.4	3432.5	3830.2	4765.1	4355.9	4607.0	4524.0	3402.6	2201.9	3388.9
3186.2	3997.4	2856.6	3494.8	3972.0	3068.9	4120.8	3170.0	2859.7	3443.8	2296.7
788.2	2521.4	2474.1	2290.3	4092.2	2277.2	4302.5	3127.2	1907.8	1450.2	1288.9
154.2	692.9	775.9	845.7	2285.6	968.1	1482.3	1439.7	335.7	219.1	512.8
683.3	6113.2	4810.1	5145.2	6402.2	7127.3	5928.6	5654.3	3595.0	2880.9	3162.9
14829.5	4830.3	4332.8	4421.2	6978.2	6297.7	5706.4	5942.6	4102.4	3561.9	3910.5
51.1	618.5	677.8	706.9	1913.0	865.7	987.2	1478.5	302.5	177.8	385.0
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9039.0	3088.3	3385.2	3565.0	6178.7	3715.2	6085.3	4969.9	3946.9	3440.0	3932.0
13260.4	4988.3	4717.7	4608.4	5200.5	5033.9	5320.8	5124.5	4875.6	3769.3	4462.3
7041.1	5738.8	3984.5	3920.9	5580.7	6541.7	4883.1	4671.2	3766.6	3149.3	3341.3
936.8	2981.0	2904.9	3219.2	5008.6	3292.3	5426.7	4041.6	1865.7	1499.6	2282.6
2116.3	5788.4	4744.5	5281.7	7556.3	6511.9	7446.2	5852.2	4051.2	3594.1	4133.5
8274.9	3947.8	3143.8	3228.8	5158.8	4230.8	4562.5	4213.7	2960.1	1601.1	2181.9
4057.1	3167.9	2828.7	2723.0	4312.5	2924.8	4092.0	2570.7	2386.3	2140.1	3376.9
2288.1	5533.8	5038.5	5112.6	6343.1	6375.8	7075.1	6040.7	6911.5	4052.5	4369.0
1030.1	4958.2	4854.1	5641.4	7300.9	5349.6	7111.7	6105.1	3379.6	2490.6	4021.0
323.2	1167.4	850.4	955.9	2713.3	1257.6	2200.6	1262.1	568.2	695.5	513.7
6766.6	7247.6	7130.4	7449.1	10465.2	8418.2	10052.4	8753.7	7910.1	7621.7	6849.6
2045.0	4492.0	3486.4	4184.7	6530.6	5429.0	5773.9	5207.4	3116.4	2639.4	2745.2
1294.1	1825.5	1921.5	1817.5	3786.9	2474.5	3284.0	2832.7	1049.0	889.5	907.2
6483.5	3808.5	3386.3	3378.6	6162.7	4990.4	4971.7	5030.0	2956.7	2204.7	2095.4

2642.6	1838.6	2310.1
3917.3	2482.8	3016.5
3916.5	3149.9	5699.2
5306.3	5811.3	5354.5
4318.6	3698.7	4408.5
10357.6	9566.3	7642.8
5456.7	4710.2	6045.7
6042.1	4141.2	7112.8
4437.4	6242.9	4414.2
6399.9	6372.5	5462.2
3185.3	5018.6	7414.1
2549.7	2919.4	2526.3
5910.6	6612.4	7906.5
3122.6	2756.4	2924.5
2496.9	1983.7	2854.3
5646.9	5698.3	6952.1
3169.1	3511.1	4227.5
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5222.1	4649.4	4453.8
2968.2	3592.7	2703.7
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5317.9	4777.9	7000.3
6006.3	5791.6	7736.9
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10309.2	9028.3	9507.6
1236.4	2382.5	3156.7
4218.2	3861.6	4995.1
5943.6	5892.4	5613.5
4987.7	5302.9	5454.9
3892.4	3998.6	3926.9
6663.2	5892.5	8634.7
3555.6	3786.0	6187.7
2866.2	3095.1	4018.9
5136.8	6273.7	7765.4
6172.1	6625.1	8648.7
1775.5	1670.8	1694.6
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EF153296.1 gg_id:187340 Rhodomicrobium sp. str. ShRmc01 EF1532
EF650482.1 gg_id:238973 Rhodocista sp. str. GP-7 EF6504
D25313.1 gg_id:4680 Rhodoplanes roseus str. 941 D25313
AM712913.1 gg_id:247905 Rhodoplanes piscinae str. JA266 AM712
EF019983.1 gg_id:212484 aspen rhizosphere clone Elev_16S_1370 EF0199
EU133616.1 gg_id:254348 tallgrass prarie soil clone FFCH2026 EU1336
EU335329.1 gg_id:245987 Changes microbial metabolic and along hydrogeochemically variable profile unsatura EU3353
AY921820.1 gg_id:113474 farm soil clone AKYG712 AY9218
AY922092.1 gg_id:114396 farm soil clone AKYH1064 AY9220
EF018397.1 gg_id:208293 aspen rhizosphere clone Amb_16S_1010 EF0183
GQ263521.1 gg_id:534454 Structure Simulated Level Waste Site simulated level waste site clone FW2_47B GQ263
EU335450.1 gg_id:235975 Changes microbial metabolic and along hydrogeochemically variable profile unsatura EU3354
EF020096.1 gg_id:210974 aspen rhizosphere clone Elev_16S_1506 EF0200
GQ500727.1 gg_id:576799 Surveys Biofilms and Sediments Mammoth Cave Karst Aquifers Charon's Cascade sa GQ500
AY622245.1 gg_id:107444 subsurface soil clone B-L17 AY6222
FJ479010.1 gg_id:561693 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4790
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EF019513.1 gg_id:207374 aspen rhizosphere clone Elev_16S_1015 EF0195
EF032737.1 gg_id:179877 cyanobacterial mat in lava cave clone HAVOmat148 EF0327
EF018835.1 gg_id:215423 aspen rhizosphere clone Amb_16S_1316 EF0188
AY234497.1 gg_id:111439 soil isolate Ellin5080 AY2344
EU937846.1 gg_id:315986 Biogeochemistry Iron Oxidation Circumneutral Freshwater Habitat riparian iron oxidi EU9378
AY921720.1 gg_id:113725 farm soil clone AKYH1040 AY9217
FJ807419.1 gg_id:570413 Presence and iron oxidizing landfill leachate impacted groundwater surface water int FJ8074
EF020128.1 gg_id:215872 aspen rhizosphere clone Elev_16S_1545 EF0201
DQ537531.1 gg_id:163571 manganese oxidation soil clone JH-GY22 DQ537
FJ152854.1 gg_id:316335 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX5A_ FJ1528
DQ984560.1 gg_id:237595 Mt. Nan-Jen soil clone IFD_31 DQ984
AY326602.1 gg_id:136172 Amazon soil clone 711-1 AY3266
AJ581617.1 gg_id:93792 soil near uranium mill tailings clone KCM-C-24 AJ5816
FJ479160.1 gg_id:551343 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4791
FJ479575.1 gg_id:585582 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4795
AB286367.1 gg_id:204919 Reducing production and domination comamonadaceae reducing oxygen supply was AB2863
EF018437.1 gg_id:212776 aspen rhizosphere clone Amb_16S_1057 EF0184
AY395414.1 gg_id:105676 pasture soil clone EB1095 AY3954
EF019188.1 gg_id:208963 aspen rhizosphere clone Amb_16S_1857 EF0191
DQ451455.1 gg_id:156816 forest soil clone FAC16 DQ451
EU133294.1 gg_id:251152 tallgrass prarie soil clone FFCH12843 EU1332
AY913382.1 gg_id:113588 forest soil clone DUNssu176 (-7A) (OTU#160) AY9133
AY963313.1 gg_id:151184 structures and correlated ecological factors soils two evergreen broad-leaved forests AY9633

7565.9	5532.0	5321.3	6367.3	7733.3	5816.4	7432.3	6429.4	4912.9	2855.6	4946.8
8366.2	4581.6	5007.5	5467.0	7126.4	4894.1	5698.5	5453.0	3842.9	3697.9	4506.0
13261.5	7842.8	7504.9	7701.6	7883.1	7874.3	8527.7	7297.6	9715.1	7325.8	9990.3
7664.1	5007.2	5621.2	6173.4	7394.3	5990.2	5961.1	5918.3	5241.8	6188.2	4821.8
3328.2	3839.8	2706.1	2584.9	3908.9	3806.3	4403.7	2966.8	915.3	555.6	1340.7
2100.3	2780.4	2442.4	2103.9	4852.4	2840.2	3591.7	2774.4	2514.4	1447.2	1490.6
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6930.3	2602.4	2156.5	2127.1	3974.4	2704.1	3438.1	2547.2	1595.6	1150.7	1533.8
14509.9	3676.7	3354.8	3505.5	5621.8	4088.1	5096.6	4680.0	4003.4	2036.4	2607.4
27302.5	9460.0	6283.0	5741.6	11791.7	8257.7	11594.1	6447.2	3776.8	4169.8	4070.9
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9300.0	5481.5	5293.9	5449.4	4958.8	5624.2	6526.1	5437.7	5079.6	4794.6	6576.1
202.2	4116.3	4124.4	4363.5	6530.8	4413.6	5352.3	4233.8	2098.6	744.6	2876.5
13572.8	6872.2	4890.1	5007.0	5400.5	5328.5	5735.0	4832.5	7131.0	2539.5	3452.2
7746.5	3835.7	3801.6	3861.6	4236.5	4227.3	4078.1	4129.6	3266.7	1985.6	3691.8
510.2	4394.2	3474.6	3936.3	3672.6	4137.4	4716.5	4045.9	1331.9	936.2	2879.7
12483.9	2895.3	2030.1	2100.8	3992.3	2704.4	4886.4	2037.1	511.4	388.8	948.7
15702.0	11443.6	10584.0	11855.0	13568.3	11578.6	13840.0	10870.5	11094.0	7536.1	13364.2
84.7	447.7	340.0	478.1	646.8	685.6	592.2	547.3	257.3	117.8	290.5
3878.0	2465.2	2188.3	2337.6	4033.9	2988.2	4539.3	2480.2	1061.0	745.3	1437.6
22766.1	4064.3	3816.7	4232.4	5339.6	3769.2	5389.0	4098.0	3765.7	4919.3	3562.4
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966.5	3376.1	2952.3	3103.6	4920.9	3805.7	5004.7	3255.6	1932.6	1496.7	1593.2
4331.4	4585.1	3380.1	3243.6	6214.0	4092.7	6628.9	3677.9	2998.3	1842.4	2718.8
40.9	272.9	253.3	227.5	338.4	581.3	630.9	336.2	110.2	52.1	147.1
5980.4	2953.0	2709.2	3492.4	4032.7	2381.1	6204.1	2940.4	1941.0	2093.8	1519.0
2142.9	2743.5	1912.1	1969.5	3619.2	2822.4	3637.6	1962.6	1694.3	1565.4	1009.1
339.9	3432.3	2177.4	2162.8	4367.5	2988.5	3628.5	1905.2	536.3	523.3	1376.5
4331.6	5029.9	3804.4	5658.7	6165.8	5258.1	5122.1	4123.9	1623.9	1548.8	2567.2
225.0	388.3	412.3	499.8	619.5	517.8	642.0	429.7	371.4	242.4	307.1
9668.9	3625.7	2912.5	2643.3	3665.4	3373.6	3831.1	2892.1	4146.2	3728.9	2746.4
24618.0	5959.5	5371.7	6164.6	6162.2	6372.4	6547.0	6212.3	7434.3	6629.1	7133.0
702.6	710.3	446.2	429.0	1307.5	897.8	1158.6	721.0	207.9	187.7	179.4
8090.4	2634.4	2779.1	3234.5	3561.9	3011.8	2565.0	2986.9	2111.3	2113.1	2290.8
20020.6	3845.9	2596.4	2344.3	5366.3	3331.0	4839.5	3128.8	1744.1	1338.4	1570.2
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204.7	696.7	721.9	789.0	1825.7	887.7	1395.3	907.6	415.6	186.0	372.3
3925.9	4824.0	4475.0	4687.0	6384.2	4926.4	6080.7	5254.6	3831.1	3062.7	3789.8
25880.1	8081.8	7706.2	6922.1	10936.5	7555.3	9889.0	7536.3	11017.2	7276.0	7453.5
9917.9	5422.7	4347.0	3452.0	6672.7	5683.0	6257.2	5144.4	4379.1	4667.1	3704.9

6995.0	6075.1	7728.6
5516.5	4588.8	4019.0
7437.9	8973.1	8246.1
8012.1	6275.2	6622.9
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3809.8	3089.3	4088.3
4269.8	4351.5	8535.2
8277.2	10820.6	8429.0
2765.1	2390.1	3500.8
4960.1	4784.2	3965.4
7529.0	8278.0	11467.9
5173.5	4446.3	7017.8
4653.9	7021.8	5729.6
4429.3	3673.0	8380.1
4618.6	5201.2	6421.4
3376.8	4705.5	4994.8
3783.0	3202.9	4824.5
2331.9	2409.0	4682.2
10923.0	10492.3	12234.9
441.0	676.7	1048.0
3057.2	2819.9	4671.1
4284.8	4650.4	4428.2
4233.3	4292.9	5892.0
3290.1	3752.7	6103.9
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410.4	352.9	649.5
2836.3	2926.0	3087.9
2453.7	3171.7	4417.1
2211.0	3003.5	5794.2
4341.2	5683.1	7310.2
478.3	967.3	714.0
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6264.7	7046.0	7168.2
1017.0	866.1	1610.4
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GQ262926.1 gg_id:566311 Structure Simulated Level Waste Site simulated level waste site clone F1_73X GQ262
DQ837247.1 gg_id:244310 Archaeal and pristine National Park Spain Donana coastal aquifer clone 49S1_2B_37 DQ837
FJ478974.1 gg_id:584077 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4789
EF540400.1 gg_id:217826 oil-shale semi-coke solid waste clone 4_24MK EF5404
AY724055.2 gg_id:111888 soil clone DUNssu006 AY724
AB121773.1 gg_id:98457 Bradyrhizobium sp. str. Shinshu-th2 AB121
AY921846.1 gg_id:114139 farm soil clone AKYG1898 AY921
GQ397068.1 gg_id:575164 Functional unvegetated perhumid recently-deglaciated soils do not correlate shifts s GQ397
EU335327.1 gg_id:250714 Changes microbial metabolic and along hydrogeochemically variable profile unsatura EU335
AJ810382.1 gg_id:159481 Rhizobiales genosp. AB CsBT10/2 AJ8103
EU429497.1 gg_id:544454 producing pigmented colonies aerosol and soil remote glaciated areas (Antarctica Al EU429
EF516064.1 gg_id:218539 grassland soil clone FCPS586 EF516
GU444101.1 gg_id:515709 Effects amendments on fertility and microbial structure cucumber Cucumis sativus L GU444
GQ402598.1 gg_id:566207 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
EF018075.1 gg_id:211128 aspen rhizosphere clone Amb_16S_400 EF018
DQ404666.1 gg_id:152904 contaminated sediment clone 654997 DQ404
EU644207.1 gg_id:282627 and Samoylov Island Lena active layer -centred polygon near surface horizon; Rim_T EU644
GQ264285.1 gg_id:555816 Structure Simulated Level Waste Site simulated level waste site clone WW2_06 GQ264
EF019849.1 gg_id:205156 aspen rhizosphere clone Elev_16S_1206 EF0198
DQ125920.1 gg_id:136171 uranium contaminated soil clone AKAU4191 DQ125
EU669630.1 gg_id:314708 soil clone S22-33 EU669
EF020062.1 gg_id:213736 aspen rhizosphere clone Elev_16S_1469 EF020
AY426439.1 gg_id:101471 full-scale anaerobic UASB bioreactor treating paper mill wastewater clone B14 AY4264
EF018152.1 gg_id:216748 aspen rhizosphere clone Amb_16S_487 EF0181
CU918797.1 gg_id:534993 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU918
EU133549.1 gg_id:253944 tallgrass prarie soil clone FFCH2918 EU133
AB240329.1 gg_id:144888 microbial structure Phragmites rhizosphere biofilm reed bed reactor laboratory clon AB240
GQ264159.1 gg_id:584598 Structure Simulated Level Waste Site simulated level waste site clone WW1_a15 GQ264
GQ263836.1 gg_id:592746 Structure Simulated Level Waste Site simulated level waste site clone WC1_b83 GQ263
EU289423.1 gg_id:256335 metagenomic approach biosynthesis ansamycin endophytes or symbionts enriched s EU289
GQ500841.1 gg_id:546305 Surveys Biofilms and Sediments Mammoth Cave Karst Aquifers Bio-Sep beads conta GQ500
EF019976.1 gg_id:206188 aspen rhizosphere clone Elev_16S_1362 EF019
EU335194.1 gg_id:256477 Changes microbial metabolic and along hydrogeochemically variable profile saturate EU335
GQ093920.1 gg_id:452881 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ093
EU289515.1 gg_id:256361 metagenomic approach biosynthesis ansamycin endophytes or symbionts enriched s EU289
EF520408.1 gg_id:228499 structure lakes: what controls ? acid-impacted lake clone ADK-BTh02-5 EF5204
AY921875.1 gg_id:112834 farm soil clone AKYH1162 AY921
EU133623.1 gg_id:254308 tallgrass prarie soil clone FFCH929 EU133
EU881166.1 gg_id:317632 Karst region primary forest soil clone KPF200711-134 EU881
DQ125603.1 gg_id:136238 uranium contaminated soil clone AKAU3608 DQ125
DQ269121.1 gg_id:191415 marine macro-alga surface clone DPC255 DQ269

11810.3	4769.0	3127.0	2980.2	6172.0	5092.3	5663.9	3660.1	1930.7	1265.5	1794.4
23732.1	5629.0	4582.3	4281.4	7927.3	5405.6	7841.0	4555.2	5263.7	3167.1	3809.5
2992.1	3692.0	3028.6	3033.7	4370.2	3996.1	4682.9	3309.0	1279.4	642.7	1800.0
6533.0	7126.6	6205.4	6539.3	7684.2	6828.8	8197.2	6443.0	7417.6	6509.9	7511.7
6294.3	3962.5	4072.1	3527.7	4177.9	3728.4	4349.7	2530.2	5115.4	5009.8	5564.6
10256.7	1877.1	2249.9	2411.7	3891.0	2129.3	3614.5	2441.5	1310.5	609.8	1096.8
3242.6	4121.1	1205.5	956.3	2727.6	1558.2	1929.8	2758.2	731.3	660.8	1133.2
6676.4	3639.0	2531.0	2574.3	5345.1	3308.8	4221.9	3009.6	3200.0	1353.8	1849.4
19695.1	9349.3	8020.2	8828.0	9114.3	8344.6	10906.8	7184.6	9224.9	10308.5	11460.4
4674.0	4825.3	5051.5	5483.6	6083.1	5724.8	6628.1	6130.3	4281.9	3328.0	6538.5
1878.3	10699.6	7292.7	7481.0	8529.3	7975.7	9762.8	7557.1	6898.1	5597.1	6274.8
44.3	420.4	126.1	102.7	211.0	152.6	254.4	283.8	256.5	28.7	63.2
10166.3	5913.6	5007.1	4856.0	6555.4	5852.9	6512.5	5181.6	4836.1	4057.5	3439.4
4076.1	2926.8	2182.8	2968.5	3995.2	3353.5	3537.7	2559.9	1870.9	2001.1	3019.3
14517.5	5154.4	4671.2	4852.1	6507.9	5091.2	6080.0	4722.2	4789.8	4000.0	3126.9
3217.2	2854.2	2262.6	2460.6	4908.4	3434.6	4745.8	3104.2	1774.1	1419.4	1581.7
204.8	1695.4	1290.7	1243.5	2667.8	1717.6	2931.2	1402.9	492.6	419.2	542.8
6174.0	4320.7	4007.2	3482.8	6833.5	4720.0	6251.9	3845.4	2100.3	1448.2	1860.0
5297.7	2583.0	2508.7	2523.6	5581.5	3263.7	4825.6	2748.1	1589.2	796.7	1263.0
12704.9	3694.0	3714.8	4106.0	5919.7	4566.7	5611.7	4846.1	3663.9	3057.4	2882.8
5903.7	4106.8	3736.3	3756.3	5741.2	4251.3	5643.4	3769.9	2867.6	2756.4	2707.8
175.7	1521.9	764.5	481.8	1043.0	967.5	943.4	1278.9	411.7	349.4	600.2
5953.8	3359.1	2665.9	2925.3	4978.4	3803.9	5388.5	5461.9	3151.7	3219.6	1984.3
10594.6	3367.7	3742.8	3149.8	3855.6	3384.4	5572.9	3227.4	4005.6	4134.1	3045.7
1099.2	2224.9	1744.0	1617.2	2216.6	1998.5	2128.4	2297.3	2131.4	1177.6	864.4
1523.0	5253.7	3471.8	3592.6	5076.4	4038.4	4479.1	3599.7	4112.2	2329.3	1699.4
358.6	2360.4	1122.6	1152.7	2527.4	1789.9	2990.1	1731.6	520.7	355.2	367.9
28925.5	8239.4	6621.5	6770.2	9847.2	8765.1	9474.9	7619.9	7004.3	5101.7	5928.5
6961.3	2349.6	2131.7	2377.4	4124.2	3011.3	3293.6	2376.2	1781.2	1638.0	1813.4
8461.8	6761.4	5638.5	5495.2	7632.0	6590.6	8120.9	5615.5	5284.7	4947.6	4679.2
312.5	1363.1	1023.7	1026.1	3163.2	1952.6	3253.5	1389.0	288.8	212.7	462.5
58.6	1549.3	763.7	661.0	3781.0	1700.5	2742.4	755.8	225.4	140.0	299.7
879.6	2973.5	2467.5	2481.1	2835.4	3015.2	3205.2	3132.4	1958.1	1277.6	1918.0
19474.0	5507.1	4786.3	5473.3	7259.8	5700.6	7909.4	5593.9	4475.7	4826.8	4030.5
1117.6	2007.0	1778.4	1853.4	3126.7	2655.9	2839.6	2826.4	1800.9	1793.2	832.8
8463.6	5734.2	4943.3	5562.9	8550.6	5877.4	8338.1	6666.3	4184.0	3378.2	4007.0
1260.6	2833.5	2834.7	2563.8	4630.3	3523.4	4318.9	3696.3	1952.0	2133.9	1374.5
33770.3	5326.8	5188.7	4523.2	7320.2	4992.1	7124.8	4519.9	5093.4	1588.7	4852.0
6200.5	5631.9	5132.8	6120.7	7935.8	6554.7	7366.1	6633.1	4801.4	4611.2	4696.2
1764.8	1889.9	1994.9	1755.3	4242.5	2473.2	3916.2	2306.1	995.0	872.3	874.7
507.4	3080.1	3671.4	4016.3	4633.6	3792.9	4554.4	4449.3	2606.5	1974.8	2300.3

4210.4	4220.7	7514.8
4876.5	5905.9	7723.7
3667.2	3178.4	5104.3
6890.6	6904.0	7071.6
3772.9	4537.3	4142.8
3392.2	2439.6	2260.2
1258.3	1455.0	1550.7
3612.5	3464.2	5238.3
7224.9	9063.2	8332.0
6289.6	6384.0	6970.9
8269.6	6185.9	7536.4
44.9	739.0	153.6
5868.8	5668.4	8147.8
2520.1	3570.3	5651.8
5142.5	6280.1	7868.5
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1909.1	1971.3	3519.7
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4217.5	4473.5	7444.2
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EU703268.1 gg_id:547851 taxon richness -altitude lakes eastern tin plateau predominance Bacteroidetes and S EU703
AB240517.1 gg_id:141913 microbial structure rhizosphere biofilm Sapporo root-base (80 160 mm) Phragmites S AB240
EF520393.1 gg_id:233793 structure lakes: what controls ? acid-impacted lake clone ADK-BTh02-93 EF5203
AY934488.1 gg_id:138039 Hyphomicrobium sp. str. WG6 AY9344
GQ397055.1 gg_id:583185 Functional unvegetated perhumid recently-deglaciated soils do not correlate shifts s GQ397
AM934937.1 gg_id:572993 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM934
EU491418.1 gg_id:263450 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X4 clone EU491
AM935138.1 gg_id:564931 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM935
GQ264131.1 gg_id:588269 Structure Simulated Level Waste Site simulated level waste site clone WC3_68 GQ264
EU881135.1 gg_id:318155 Karst region primary forest soil clone KPF200711-156 EU881
DQ413077.1 gg_id:151855 Microbial -dependent and Approaches Anaerobic/Aerobic SBR Reactor EBPR sludge DQ413
EU491437.1 gg_id:274058 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X4 clone EU491
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EU491407.1 gg_id:260794 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X4 clone EU491
Y14313.1 gg_id:4638 Filomicrobium fusiforme str. DSM 5304 Y14313
FJ203575.1 gg_id:338671 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h FJ2035
CU927236.1 gg_id:567895 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU927
DQ860029.1 gg_id:248682 anchovy intestinal microflora clone F1W DQ860
FM242368.1 gg_id:305774 sequences sediment clone 64 T9d+oil FM242
GQ264526.1 gg_id:589466 Structure Simulated Level Waste Site simulated level waste site clone WW3_80 GQ264
DQ125521.1 gg_id:136194 uranium contaminated soil clone AKAU3482 DQ125
FM253663.1 gg_id:344787 Rock gold mine unusually microbial biofilm clone F01-2 FM253
EU488066.1 gg_id:552142 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU488
EU491718.1 gg_id:262760 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU491
GU362945.1 gg_id:572272 and archaeal biogeochemical cycling genes within Qiongdongnan basin Sea: pilot stu GU362
EU491544.1 gg_id:260534 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR4C EU491
CU926506.1 gg_id:549098 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU926
FM872754.1 gg_id:363198 occupant source house floor dust clone FB01E01 FM872
EU246798.1 gg_id:256471 polyphasic description Pocillopora meandrina Palmyra Atoll Calcinus obscurus abdon EU246
AB453748.1 gg_id:550276 Sulfur-Oxidizing Deep-sea Sponges deep-sea Poecilosclerida sponge clone GM-BSS-B AB453
AB487448.1 gg_id:574086 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNIR0 AB487
EF117253.1 gg_id:178313 Hyphomicrobium sp. str. SLG5B-19 EF1172
FJ264674.1 gg_id:306677 Manganese and Iron Dependent Anaerobic Oxidation Methane methane seep sedim FJ2646
AB099999.1 gg_id:150659 Microbial dead chimney structures systems Mid-Okinawa Trough and Indian Ocean F AB0999
EF018886.1 gg_id:205881 aspen rhizosphere clone Amb_16S_1374 EF0188
EU753663.1 gg_id:353953 modern freshwater stromatolites Ruidera Pools Natural Park Spain dry stromatolite EU753
EF540511.1 gg_id:226508 Devosia sp. 4_C16_46 EF5405
AM162442.1 gg_id:156227 and situ identification acidic sphagnum peat bog clone B60 AM162
EU335176.1 gg_id:238442 Changes microbial metabolic and along hydrogeochemically variable profile saturate EU335
EF644804.1 gg_id:303233 genes and citrate lyase deep-sea microbial MAR Logatchev hydrothermal vent syster EF6448

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1607.9	3640.5	3575.0	3191.8	4380.9	3350.1	4689.0	3813.3	2794.8	2904.6	3271.1
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20583.3	10793.5	8263.1	8425.6	11171.5	10618.4	10246.0	9501.4	8929.1	6906.5	7315.7
2154.5	5746.4	4707.3	5147.6	6047.7	5676.2	5531.9	5714.2	5373.9	5042.9	3946.6
9348.1	3862.9	4207.5	4028.7	5859.0	4452.8	6129.9	4180.8	3451.8	2915.3	3452.1
1754.0	3321.2	3372.6	4067.8	6691.5	4065.9	4672.1	4915.4	2585.3	1720.2	2111.2
19263.4	8788.4	8532.9	9139.8	9754.9	9983.8	9612.3	9152.0	9017.7	8966.6	9285.9
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677.8	3582.2	3618.7	4105.0	5147.4	3796.4	4959.0	4251.6	5196.6	2001.2	3168.0
4195.6	3560.3	3277.3	3667.2	5600.9	3781.5	6320.1	4059.2	2585.4	1897.5	2239.1
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1611.7	6114.4	5097.4	4569.6	7646.2	6319.6	6968.0	5693.4	3345.6	3221.7	4136.3
423.9	2123.3	1551.8	1834.4	2460.8	2062.2	1873.6	2251.8	1445.2	1353.1	1191.2
3794.6	1192.0	1283.0	466.2	2178.6	1344.1	2002.6	1639.6	762.0	180.6	945.5
9745.8	3607.1	3445.9	3265.4	6851.8	4726.5	5590.8	4681.2	3354.4	3069.1	2454.5
1612.6	3561.5	2921.8	2857.2	5599.8	4080.2	5213.4	4358.6	1835.9	1477.9	3311.2
416.5	2013.9	1649.0	2035.1	3095.7	1985.5	2286.3	2437.4	1218.0	849.0	1013.9
15332.8	9138.8	7498.9	8016.5	10278.5	9252.3	10137.2	8968.6	7990.6	7667.9	8106.0
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931.7	3106.1	2883.3	3194.4	4939.5	3905.6	5169.8	4620.1	2472.5	2809.5	2577.0
7156.0	8336.9	7269.0	8518.3	9966.6	9221.1	10593.6	8538.0	7895.3	7246.9	8181.2
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482.1	1792.1	1373.2	1444.3	1850.6	1657.2	1665.2	1865.7	2357.9	1611.2	1287.4
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12337.5	5803.3	5813.7	5932.2	10063.7	6669.7	11552.2	6992.6	4491.6	5175.9	4427.2
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7851.1	6940.5	6746.2	7315.0	9189.8	7306.6	9277.7	8219.5	8196.9	6454.0	6831.0
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4869.1	3920.5	5452.7
5886.9	5224.9	7306.4
7776.4	7437.5	8072.1
3797.6	3513.1	4267.0
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3908.5	3607.2	6708.3
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4636.4	4088.1	6556.3
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3663.3	3517.5	5557.0
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EF020326.1 gg_id:203923 aspen rhizosphere clone Elev_16S_1905 EF0203
FJ157965.1 gg_id:583678 Methylobacterium sp. str. 5a.1.5 FJ1579
AB220073.1 gg_id:131580 Methylobacterium sp. str. PB20 AB2200
AJ635303.1 gg_id:106826 Methylobacterium aquaticum str. GR16 AJ6353
AB252205.1 gg_id:238917 Methylobacterium brachiatum str. Hojyo2 AB2522
EF116592.1 gg_id:190418 Methylobacterium fujisawaense str. TNAU14 EF1165
FJ382176.1 gg_id:574655 Potentially pathogenic and air stem cell transplant summer hospital shower water BM FJ3821
GQ181028.1 gg_id:588577 Methylobacterium fujisawaense str. LNW7 GQ181
EF015477.1 gg_id:189399 Methylobacterium fujisawaense str. MP1 EF0154
EU379265.1 gg_id:266548 Methylobacterium hispanicum str. 2N-2A EU3792
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AJ888240.1 gg_id:132019 Methylobacterium sp. str. AR25 AJ8882
AY169421.1 gg_id:81189 Methylobacterium fujisawaense AY1694
GQ113305.1 gg_id:404095 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor GQ113
FJ593719.1 gg_id:528281 midgut tropical caterpillars fed on diets egg clone 298EGG8 FJ5937
AB252202.1 gg_id:250748 Methylobacterium persicinum str. 002-165 AB2522
AB252201.1 gg_id:237732 Methylobacterium komagatae str. 002-079 AB2522
NZ_ABIP01000058.1 gg_id:251181 Methylobacterium nodulans str. ORS 2060 NZ_AB
EF019402.1 gg_id:208196 aspen rhizosphere clone Elev_16S_637 EF0194
AB024616.1 gg_id:4808 Methylobacterium sp. str. MBIC4305 MIF2 AB0246
AY468364.1 gg_id:99777 Methylobacterium podarium str. FM3 AY4683
ABFR01000001.1 gg_id:238083 Methylobacterium populi str. BJ001 ABFR01
NC_010725.1 gg_id:289369 Methylobacterium populi str. BJ001 NC_010
GU294326.1 gg_id:574537 Methylobacterium radiotolerans str. 5310 GU294
AB175637.1 gg_id:152031 Methylobacterium organophilum str. DSM 760 AB1756
GQ077459.1 gg_id:411824 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1209a(GQ077
EU730904.1 gg_id:305729 Methylobacterium fujisawaense str. 151 EU7309
NC_010505.1 gg_id:264722 Methylobacterium radiotolerans str. JCM 2831 NC_010
GQ281074.1 gg_id:545132 Methylobacterium radiotolerans str. NBCS05 GQ281
AB175641.1 gg_id:154811 Methylobacterium radiotolerans str. IAM 12098 AB1756
AB175646.1 gg_id:151826 Methylobacterium thiocyanatum str. DSM 11490 AB1756
GQ281068.1 gg_id:543707 Methylobacterium extorquens str. NBCS12 GQ281
D32230.1 gg_id:4776 Methylobacterium zatmanii str. JCM 2819 D32230
AB175647.1 gg_id:150755 Methylobacterium zatmanii str. DSM 5688 AB1756
GU294335.1 gg_id:543270 Methylobacterium zatmanii str. 6012 GU294
EF682985.1 gg_id:242745 Eastern Mediterranean atmosphere clone F13_9A_FL EF6829
GQ084916.1 gg_id:374179 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw26 GQ084
U58018.1 gg_id:4788 Methylobacterium thiocyanatum str. ALL/SCN-P U58018
AY741725.1 gg_id:101778 Methylobacterium sp. str. SKJH-20 AY7417
DQ507203.1 gg_id:159608 Methylobacterium sp. str. K611B DQ507

10208.0	3559.6	3881.4	5051.2	4462.8	4073.0	5677.8	4204.9	3001.4	2414.6	3179.2
5221.6	1808.9	3098.9	2143.5	3942.5	2048.9	3108.1	3100.3	1887.5	1039.7	1971.3
1905.9	1643.1	1784.0	1835.8	5311.7	2016.4	2115.3	2116.1	1355.8	785.2	1196.2
5949.4	4968.1	3738.1	3515.5	5427.6	4436.4	4916.8	3540.2	1959.9	1792.6	1990.2
2038.5	1331.2	1041.3	1144.5	3384.4	1474.3	1731.5	1078.1	900.5	398.8	492.8
18719.8	5512.7	5547.9	5629.5	6600.1	5334.6	6431.6	4946.2	7394.6	5388.9	6263.3
12900.2	5171.6	6129.8	5310.6	7601.2	5673.5	6696.0	6856.7	5648.3	5482.0	5901.8
4756.6	1453.2	1355.9	1442.3	3770.8	1550.8	2245.2	1339.1	1512.2	741.8	797.3
7347.7	4518.5	3497.2	4384.4	6613.9	4365.5	5007.4	4852.1	4292.5	2536.6	3110.6
3636.4	2124.3	2053.0	2334.6	5045.3	2716.0	2101.1	2736.5	1846.5	1137.3	1594.1
3518.7	1960.2	1928.7	2060.0	4177.3	2248.1	2441.9	2228.8	2730.5	1572.2	2576.1
1387.0	871.1	966.2	918.8	1569.7	867.2	897.7	653.5	1268.8	877.9	1245.4
1719.0	1619.3	1649.7	1362.8	2698.1	1793.6	2102.7	1738.6	1174.3	1118.6	837.0
25816.4	10205.7	10578.9	9769.8	13353.0	11134.7	12443.2	9260.3	9875.4	7593.2	13922.5
10971.2	3213.7	3154.7	3491.9	5293.7	3629.2	4426.2	4031.2	2298.9	1884.1	2107.9
16951.7	3050.8	2869.2	2755.9	6710.0	3401.2	4184.5	2853.7	2974.8	1544.0	1575.8
15610.0	4165.5	3751.7	3290.2	6845.3	4390.0	4584.1	3566.6	3856.4	2639.9	3342.1
7620.1	2168.0	1278.3	1329.1	2604.6	1971.1	1546.4	1499.9	807.1	681.9	676.5
1404.7	1256.6	1051.8	1142.5	2261.6	1325.4	1611.7	1330.9	1179.2	842.7	961.0
481.6	1513.9	499.4	686.2	1127.2	690.0	819.9	710.3	244.5	81.0	210.5
263.3	866.7	433.4	337.3	1517.7	1231.3	721.5	683.4	389.9	163.4	204.9
5548.6	4565.1	4317.6	4643.9	7506.1	4964.3	4748.1	4297.7	4257.5	3954.3	4168.5
4995.4	4107.4	3631.2	4014.1	6152.7	4262.9	4171.7	3537.9	3799.1	3747.6	4042.7
4527.5	3791.8	3176.8	3444.0	5222.5	3365.8	3358.4	3148.1	3464.5	2286.8	4078.5
5307.2	2450.4	2519.4	2268.2	4891.5	2549.7	3115.2	3285.3	1715.9	1780.0	1789.4
5514.4	2511.2	2735.8	2562.1	5022.3	2643.0	3420.4	3608.4	2105.7	1829.3	1929.1
5187.4	1988.0	2291.8	2131.5	4111.3	2226.2	2960.4	3021.6	1721.2	1379.9	1688.9
21449.8	7131.1	7412.5	7576.9	9063.3	7094.9	9180.1	8023.9	7026.4	5845.1	8232.3
4851.0	2319.7	2635.7	3163.6	4672.6	2812.9	3556.1	3385.1	2302.3	4112.6	2589.8
5008.1	1850.2	2011.5	1836.5	4161.0	1915.2	2781.5	2408.6	1703.1	1134.2	1253.3
4385.5	1723.0	2115.5	1891.9	4146.0	1756.1	2601.0	2661.0	1435.5	1115.5	1487.1
1099.3	2294.3	1950.9	2174.1	4201.5	2459.0	2103.7	2327.0	1806.0	2034.0	1452.3
7157.9	5357.1	4513.6	4846.6	6252.9	4975.2	5513.2	4764.0	6139.5	4900.5	5982.8
6936.8	3091.0	2801.0	2739.7	5890.5	3506.6	3296.2	2704.4	2806.9	2599.4	1716.0
7168.0	3006.7	2857.7	2666.1	5774.6	3408.3	3246.3	2828.3	2789.7	2283.7	1709.1
1013.9	2326.2	1830.4	1934.6	3844.5	2216.2	1928.6	1944.8	1866.7	1481.9	1435.0
7511.3	2892.1	2725.0	2706.9	4932.8	2964.3	3132.0	3495.8	2111.2	2172.2	1458.2
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5596.5	6103.5	5495.2	5722.7	6018.5	5475.2	5786.5	5628.7	6723.3	5481.6	4975.5
16715.9	5507.4	5348.9	5922.8	6300.1	5925.8	6019.5	5266.4	8206.5	4858.4	7498.4
1506.7	3081.8	2786.3	3087.7	4984.3	3488.2	4193.1	3140.3	2614.8	1374.8	2310.3

3579.0	4010.5	5401.5
4014.6	2741.0	2674.9
3616.3	2849.7	1775.4
4626.4	4623.2	5081.5
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7298.8	8623.5	9067.5
3277.3	1962.0	1231.9
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3868.9	3220.2	2485.1
3481.6	2646.0	2441.4
927.1	1257.9	485.4
1944.6	2201.1	2392.2
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5254.9	4874.9	4550.9
5842.7	3795.6	3164.8
6128.1	3862.2	3394.0
3753.0	1609.2	2131.3
1298.7	1519.8	1949.8
1189.1	764.5	650.1
865.0	683.3	609.1
5625.6	5438.6	5396.6
4333.4	4693.5	4864.9
3250.4	3697.7	3975.4
4239.9	2979.1	2526.7
4377.4	3294.3	2666.7
3937.5	2644.3	2421.8
8295.0	9641.8	10510.3
4342.7	4332.4	3342.0
3804.2	2401.7	1646.8
3853.8	2600.0	2189.5
2989.8	2341.4	2230.0
5191.5	5925.0	5306.0
4056.4	3512.9	2962.7
3978.9	3355.6	3081.7
2670.1	2027.3	2136.1
3276.4	3365.6	2808.0
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6514.7	6303.1	6484.4
5766.4	6467.4	5780.4
4515.4	4319.9	4108.8

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EF116586.1 gg_id:178333 Methylobacterium thiocyanatum str. TNAU8 EF1165
AY436812.1 gg_id:105470 Methylobacterium sp. str. ST4.9 AY4368
AY616142.1 gg_id:110238 Methylobacterium radiotolerans str. P AY6161
EU528225.1 gg_id:284643 Seasonal Dynamics Mudflat Mouth Major Kentucky Lake Reservoir Tributary sedime EU5282
AB220086.1 gg_id:134057 Methylobacterium sp. str. PB140 AB2200
AB175635.1 gg_id:154997 Methylobacterium lusitanum str. NCIMB 13779 AB1756
GQ002387.1 gg_id:507275 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu176g11 GQ002
AY838487.1 gg_id:109372 fruiting body Pleurotus eryngii clone PE31 AY8384
EU379312.1 gg_id:277255 Methylobacterium fujisawaense str. 7RN-5A EU3793
M95654.1 gg_id:4785 Methylobacterium sp str. PK-1 M9565
EF015479.1 gg_id:196467 Methylobacterium lusitanum str. MP2 EF0154
DQ339624.1 gg_id:146461 Methylobacterium sp. str. Ens25 DQ339
EF116591.1 gg_id:177690 Methylobacterium aminovorans str. TNAU13 EF1165
AM910532.1 gg_id:268349 Methylobacterium aminovorans str. F13 AM910
GQ008625.1 gg_id:501040 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ008
NR_029082.1 gg_id:584448 Methylobacterium populi BJ001 str. BJ001; ATCC BAA-705; NCIMB 13946 NR_029
AF198624.1 gg_id:52319 Methylobacterium chloromethanicum str. CM4 AF1986
EF116585.1 gg_id:191242 Methylobacterium thiocyanatum str. TNAU7 EF1165
NZ_ABEX01000007.1 gg_id:239664 Methylobacterium chloromethanicum str. CM4 NZ_AB
EF015478.1 gg_id:187464 Methylobacterium aquamaris str. MRT EF0154
AY366072.1 gg_id:93863 Methylobacterium extorquens str. UCM B-3368 AY3660
AF267912.1 gg_id:43152 Methylobacterium extorquens str. DSM 13060 F AF2679
EF116584.1 gg_id:190499 Methylobacterium suomiense str. TNAU4 EF1165
EF116583.1 gg_id:180676 Methylobacterium populi str. TNAU3 EF1165
FJ225120.1 gg_id:332818 Methylobacterium sp. str. DDW-1 FJ2251
DQ223682.1 gg_id:161482 Methylobacterium sp. zf-IVRht11 DQ223
EF426729.1 gg_id:204294 Methylobacterium sp. PMB02 EF4267
AB252208.1 gg_id:253017 Methylobacterium tardum str. RB677 AB2522
AY365229.1 gg_id:93518 Methylobacterium extorquens str. UCM B-3362 AY3652
AB252209.1 gg_id:246889 Methylobacterium gregens str. RB678 AB2522
GQ002395.1 gg_id:507267 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu176h08 GQ002
AB369041.1 gg_id:555620 and microbial oils produced Asia petroleum crude oil (Qatar Land Light) clone PT-QTL AB3690
EU250227.1 gg_id:249628 acid mine drainage clone GXDC-13 EU2502
AB220102.1 gg_id:138655 Methylobacterium sp. str. PB236 AB2201
FJ192175.1 gg_id:329760 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior FJ1921
EF116582.1 gg_id:182127 Methylobacterium populi str. TNAU1 EF1165
AY741717.1 gg_id:105899 Methylobacterium sp. str. SKJH-15 AY7417
D32228.1 gg_id:4786 Methylobacterium rhodesianum str. JCM 2810 D32228
AJ851087.1 gg_id:112210 Methylobacterium variabile str. GR3 AJ8510
GQ059305.1 gg_id:374704 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw: GQ059

11874.1	5251.9	5511.5	5718.3	7176.6	5898.2	7035.2	5432.1	5438.4	3635.1	4812.8
5053.6	3265.5	2668.7	2796.3	3674.5	2641.5	2652.6	2416.6	2338.8	3363.6	2752.7
25486.0	10604.0	9792.8	10472.4	9662.1	8841.0	10791.9	9101.5	13231.4	10067.3	12704.7
6121.4	2695.5	2601.5	2377.9	5062.8	2664.4	3084.2	3436.0	1946.1	1679.9	1781.1
2881.1	2256.0	2299.3	1630.7	3877.8	2340.7	2545.5	1670.4	2048.2	1029.3	1112.2
12392.2	1856.5	2333.7	1992.4	4699.1	2195.9	2600.8	1834.2	1661.6	839.4	1748.6
4218.4	1248.6	998.9	1473.2	2019.6	1260.8	896.7	1108.1	1703.2	443.8	930.5
14432.7	3562.5	2083.6	1657.0	4183.3	2918.6	4079.9	2134.6	1131.0	1317.8	947.8
1944.2	611.7	519.9	491.9	2150.0	1067.7	1376.2	838.5	322.6	139.4	183.4
8370.5	3121.3	3040.1	3298.9	5733.2	2831.8	3899.0	3206.0	3034.8	1515.0	2254.4
1322.5	3030.8	1753.9	1970.2	2665.3	2064.5	2351.3	2345.9	1941.9	940.8	1534.0
4840.9	3480.9	3193.9	3435.0	6494.4	3940.5	3511.1	3292.8	2905.5	3017.8	2518.0
6916.5	5266.5	3548.9	3644.1	6910.4	4447.1	5051.8	4006.3	3124.5	2913.9	2980.6
24858.2	6728.8	6224.8	7276.5	9229.4	6963.8	7689.1	6807.7	7710.2	6048.4	6384.3
5264.6	3876.4	2718.9	2692.6	5586.8	3407.4	3601.2	3108.9	2445.0	2059.1	2012.1
10565.5	1569.8	1978.6	1721.1	5140.5	1929.5	2379.5	1381.4	1345.9	776.2	1450.5
15974.7	7055.9	4977.4	5513.7	6834.8	6331.9	5558.2	5890.5	6623.3	4128.5	4488.8
11208.4	1206.0	1067.1	1032.0	2108.1	1369.9	1942.3	1400.9	1352.2	661.5	702.3
11342.2	5017.9	5386.5	5202.3	6983.9	4776.4	6598.1	4899.9	4661.0	5959.0	4182.3
2081.5	2467.6	1972.8	2139.8	4813.9	2323.3	2139.3	1800.3	1911.5	1175.0	1782.5
9418.5	4518.4	5071.7	4724.8	7361.2	4892.6	6693.9	6016.3	4907.2	4361.8	6604.3
37326.9	9165.5	9061.9	11397.7	10987.9	9993.1	10068.1	9178.6	10804.7	7216.5	9319.4
8064.9	5213.1	4831.7	4767.3	6914.6	5213.4	5223.2	4354.0	6917.6	5075.4	4250.9
6118.4	2552.4	2296.8	2198.4	2962.1	2491.4	2118.5	2226.2	3048.5	2234.6	2128.7
8115.4	5488.8	4687.1	4285.1	6055.5	4796.1	4513.5	5225.4	4011.2	3305.3	2930.4
5468.8	5453.9	5070.1	5016.6	7000.0	5072.8	5815.0	4855.7	4920.8	3180.7	3679.7
997.5	952.0	721.3	675.3	1350.4	852.0	1039.6	1103.7	1296.0	624.8	707.6
16539.9	4710.8	5058.0	5432.2	7629.5	5147.5	6106.5	4710.2	4967.5	3551.8	6169.5
4406.6	1889.3	1979.4	1800.6	3955.7	1868.7	2877.1	2174.6	1628.5	1061.3	1299.0
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8796.3	6514.3	6870.3	6414.9	8399.0	6427.5	7244.3	7604.3	7275.5	5349.2	9839.5
7384.4	2855.4	2029.9	2132.5	6005.5	2535.7	3116.1	2393.9	1196.7	1046.4	1079.1
187.9	1402.3	970.1	920.3	2943.9	1286.3	831.9	846.1	539.8	311.7	478.3
5266.0	1898.9	2256.9	2065.1	4090.5	2165.0	3055.2	2940.6	1707.6	1372.3	1692.2
4895.8	2023.1	1925.9	1653.7	5024.7	2222.3	2731.2	1834.6	1025.5	658.2	909.9
20179.9	7023.7	6187.1	6892.9	7780.7	7015.1	7882.2	7263.2	6429.5	5810.7	7970.5
28707.6	12088.0	9802.0	10504.2	10892.1	9956.8	10955.4	9119.9	14931.2	12982.7	12022.4
3901.2	4853.6	4975.5	5019.4	6663.2	5326.9	5075.8	5538.7	5024.6	4963.1	4673.8
1043.1	2377.3	1875.3	1969.9	4071.9	2262.1	1962.7	2073.8	1875.0	1487.8	1438.6
2369.6	833.7	1195.9	981.3	3742.4	1350.2	1204.6	955.7	801.9	323.0	636.4
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4699.2	4390.9	4068.6
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3241.5	2314.6	1949.2
6167.3	7131.7	4889.3
1300.5	1425.0	1024.5
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8945.0	9753.7	9942.6
5597.2	5669.2	5046.5
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5346.3	4982.3	6175.6
1249.9	1227.8	844.0
5344.5	5514.5	5668.2
3835.4	2202.4	1764.7
1571.4	1732.9	1495.8
7510.0	7351.5	6825.4
3242.0	3306.3	2523.9
1631.8	1069.6	1049.9
3779.5	2484.9	2239.0
3842.0	2603.9	2278.0
6351.9	7405.1	8111.6
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2921.5	1220.3	1012.7
1908.3	1862.3	1432.5

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DQ471331.1 gg_id:157883 Methylobacterium jeotgali str. S2R03-9 DQ471
AF409010.1 gg_id:102764 Methylobacterium sp. str. Ellin168 AF409(
Z23159.1 gg_id:4797 Methylobacterium sp. str. PC30.44 (pale pink colony type) Z23159
AB252204.1 gg_id:312016 Methylobacterium sp. Hojyo1 AB252
D32229.1 gg_id:4784 Methylobacterium rhodinum str. JCM 2811 D3222
DQ129299.1 gg_id:138274 microarray level air two cities Texas urban aerosol clone AKIW886 DQ129
DQ532273.1 gg_id:164604 Geographical Variation Microbial Burden and Spacecraft Assembly Johnson Space Ce DQ532
FJ193768.1 gg_id:341095 Genetic inventory 'KSC-Astrotek' spacecraft assembly clean room during DAWN missi FJ1937
EU289454.1 gg_id:256447 metagenomic approach biosynthesis ansamycin endophytes or symbionts enriched s EU289
AF107461.1 gg_id:32547 Methylosinus pucelana str. MTS AF107
AJ458508.1 gg_id:64197 Methylocystis parvus str. 57 AJ4585
AF150805.1 gg_id:4738 Methylocystis parvus AF1508
DQ852349.1 gg_id:176777 Methylocystis sp. str. m1511 DQ852
AJ458510.1 gg_id:72367 Methylocystis sp. str. 50/54 AJ4585
AJ458467.1 gg_id:64230 Methylocystis sp. str. 495/4 AJ4584
FJ502233.3 gg_id:558957 Methylopila sp. str. JZL-4 FJ5022
DQ404188.1 gg_id:212879 Schlegelia plantiphila str. S1 DQ404
AB007842.1 gg_id:58407 methylotroph str. Hohenstaufen AB0078
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AJ458495.1 gg_id:111428 Methylosinus sporium str. KS16a AJ4584
M95664.1 gg_id:4735 Methylosinus sp str. LAC M9566
AJ458481.1 gg_id:64219 Methylosinus trichosporium str. 33/1 AJ4584
AF150804.1 gg_id:4739 Methylosinus trichosporium AF1508
L20845.1 gg_id:4736 methanotrophic str. IMV B-3060 L20845
AJ458483.1 gg_id:64217 Methylocystis sp. str. Pi5/4 AJ4584
AY921958.1 gg_id:113362 farm soil clone AKYG1554 AY9219
AJ431385.2 gg_id:64234 Methylosinus trichosporium str. KS21 AJ4313
AY922142.1 gg_id:113005 farm soil clone AKYH643 AY9221
EF515258.1 gg_id:224728 Electricigen Enrichment MFC upf microbial fuel cell anode clone 22a11 EF5152
AY297803.1 gg_id:89669 waterlogged archaeological wood clone pACH83 AY2978
EF515279.1 gg_id:220495 Electricigen Enrichment MFC upf microbial fuel cell anode clone 22c11 EF5152
CU924338.1 gg_id:560880 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU924
AB127972.1 gg_id:101532 Kaistina koreensis str. Y9 AB1279
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GQ064493.1 gg_id:418162 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw7 GQ064
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AB095950.1 gg_id:87497 Ancalomicrobium adetum AB0959
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CU925731.1 gg_id:548842 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU925

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16453.4	4744.6	5550.7	5765.2	7158.9	5193.6	6112.6	5379.4	4655.8	3058.1	4741.3
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35.1	50.0	86.5	77.2	124.4	45.6	95.7	99.0	39.5	32.7	26.7
9946.4	5790.4	4986.8	5447.7	9180.4	5829.0	6993.2	5238.6	3960.9	2781.8	4039.1
1409.7	3283.9	2811.6	3168.6	5210.5	3409.5	4728.2	4052.3	2124.9	1376.6	1899.6
11239.3	6412.3	6265.1	6517.2	7852.7	6998.5	8915.3	6882.2	6604.3	6291.0	6067.9
9515.3	5462.4	5064.6	5239.0	6559.7	6382.1	6892.1	7028.9	6609.3	2745.9	4364.3
6795.8	4545.6	4607.7	4747.9	5586.8	5192.4	6089.9	5330.8	4224.8	4136.4	5081.0
12228.6	6025.7	4610.4	6006.2	5433.0	5706.0	6713.3	5319.4	5177.0	4109.4	7417.2
340.7	4739.8	3153.0	3216.3	4830.7	4764.3	4573.5	3839.7	2671.7	1347.6	1854.6
2762.1	4229.6	2477.5	2390.3	4727.3	4268.5	5418.9	2970.1	1102.9	875.7	1469.6
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258.5	173.6	176.6	154.4	418.5	206.1	260.7	184.3	113.4	67.7	83.2
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14769.0	9271.8	5022.9	5562.4	9229.7	7354.3	9290.1	6679.5	4728.7	3518.6	3823.5
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14418.3	5703.4	3157.0	3101.2	6146.0	4061.7	6128.9	3399.6	2408.1	2119.4	1546.6
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56.0	581.5	349.3	289.9	783.4	583.0	654.3	611.4	299.5	156.1	180.3
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4600.2	4689.6	5010.2
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4726.0	4168.5	5275.9
9790.2	10763.6	11166.4
83.4	144.9	53.6
7066.2	6212.1	6312.5
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3861.3	3359.9	6066.0
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3964.9	3445.4	5353.2
5481.6	4761.2	7369.7
7841.9	6822.4	4887.9
6109.0	5658.4	5770.5
5390.3	6161.4	5599.4
6757.1	6152.3	5944.4
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1329.2	1347.5	1210.0
4874.5	4781.4	4260.9
1892.7	1195.7	2491.5
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DQ202244.1 gg_id:140112 Enrichment s Type II Methane-Oxidizing Inhabiting Northern Peatlands peatland clo DQ202
GQ221762.1 gg_id:582735 Prosthecomicrobium hirschii str. 6 GQ221
AM162434.1 gg_id:156044 and situ identification acidic sphagnum peat bog clone B112 AM162
AY138237.1 gg_id:107461 human stomach biopsy clone Sto3-1 AY138
AJ458473.1 gg_id:56422 Methylocystis echinoides str. IMET 10491 AJ4584
GQ402774.1 gg_id:537864 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
AM283543.1 gg_id:165785 Methylocystis heyerii str. H2 AM283
FJ478572.1 gg_id:541918 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4785
EU979087.1 gg_id:304412 Effects intercropping Rhizobium inoculation on microbial biomass and rhizosphere b EU979
GU208455.1 gg_id:591539 Study on Sediment Dongping Lake sediment clone Fr1-9 GU208
GQ500824.1 gg_id:540718 Surveys Biofilms and Sediments Mammoth Cave Karst Aquifers Bio-Sep beads conta GQ500
GQ500812.1 gg_id:556729 Surveys Biofilms and Sediments Mammoth Cave Karst Aquifers Bio-Sep beads conta GQ500
AM934956.1 gg_id:546522 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM934
FJ755762.1 gg_id:552837 vertical archaeal water and Lake Taihu sediment clone LT-SB-B39 FJ7557
CU923583.1 gg_id:566212 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU923
FJ542854.1 gg_id:530919 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone A FJ5428
CU921271.1 gg_id:550854 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU921
CU926316.1 gg_id:532947 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU926
EF019602.1 gg_id:214638 aspen rhizosphere clone Elev_16S_1127 EF0196
AY921960.1 gg_id:113860 farm soil clone AKYG1560 AY9219
FM874050.1 gg_id:362109 occupant source house mattress dust clone MB05G07 FM874
EF032656.1 gg_id:182489 structure riverine biofilms river biofilm clone SepB-8 EF0326
EU589298.1 gg_id:272318 China Ningxia rice paddy field soil clone 2_D3 EU589
GQ093788.1 gg_id:382544 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ093
EF590055.2 gg_id:230239 changes structure sediments Songhua River contaminated nitrobenzene -DGGE cloni EF5900
AF370880.1 gg_id:66822 Nordella oligomobilis str. N21 AF3708
DQ984605.1 gg_id:236172 LY oil-contaminated soil clone LYC075 DQ984
AJ582085.1 gg_id:102514 Ahrensia sp. DFL-33 AJ5820
AJ582087.1 gg_id:95153 Ahrensia sp. DFL-44 AJ5820
AJ582086.1 gg_id:94505 Ahrensia sp. DFL-42 AJ5820
AJ582084.1 gg_id:95110 Ahrensia sp. DFL-13 AJ5820
L20802.1 gg_id:5138 Aminobacter ciceronei str. ER2 L20802
DQ196478.1 gg_id:139758 Aminobacter sp. str. MI-p2a DQ196
GQ254285.1 gg_id:544184 Aquamicrobium sp. str. H15 GQ254
FJ167676.1 gg_id:307902 Chelatovorus multitrophus str. LPM-6 FJ1676
EF457242.1 gg_id:237931 Chelatovorus oligotrophus str. LPM4 EF4572
GU111569.1 gg_id:537767 Nitratireductor sp. str. SL014B-25A2 GU111
EF157205.1 gg_id:249985 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon EF1572
EU564843.1 gg_id:267825 Nitratireductor sp. str. CC-MHSW-5 EU5648
EU281628.1 gg_id:243131 Bacillus sp. B2(2007b) str. B2 EU281
EU024398.2 gg_id:238204 Isolation cyclohexylalkyltetralin degradation sediments marine sediment clone WBI3 EU024

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7745.5	3479.9	2305.1	2490.3	4319.7	2834.3	4265.7	2859.2	2085.2	1987.1	1423.3
1225.5	3873.4	2622.2	2321.8	3622.6	3425.5	2988.4	4215.5	3187.2	715.0	1553.5
1660.3	2177.8	2011.8	1917.6	3328.8	2580.8	3255.5	2845.0	1186.7	1299.6	1110.1
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2775.1	5364.3	5617.3	6024.3	7228.5	5839.8	6725.2	6354.3	3698.7	5754.7	5904.0
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DQ311089.1 gg_id:149931 Mesorhizobium sp. str. CCBAU 61156 DQ311
GU201842.1 gg_id:516545 Rhizobium leguminosarum str. Qtx-1 GU201
AJ487829.1 gg_id:66200 Mesorhizobium ciceri str. Rch9816 AJ4878
FM209490.1 gg_id:314928 Mesorhizobium ciceri str. TS56 FM209
U07934.1 gg_id:5127 Mesorhizobium ciceri str. UPM-Ca7 U07934
X67230.1 gg_id:5122 Mesorhizobium loti str. LMG 4284 X67230
EU256435.1 gg_id:251597 Mesorhizobium plurifarium str. CCBAU 85060 EU2564
EF061111.1 gg_id:186691 Mesorhizobium huakuii str. CCBAU 25053 EF0611
EF061107.1 gg_id:198842 Mesorhizobium amorphae str. CCBAU 45122 EF0611
GU083820.1 gg_id:593690 Mesorhizobium amorphae str. DBT14 GU083
DQ310706.1 gg_id:186218 Mesorhizobium loti str. U261 DQ310
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EF061106.1 gg_id:194940 Mesorhizobium amorphae str. CCBAU 45139 EF0611
EU399717.1 gg_id:273591 Mesorhizobium huakuii str. CCBAU 03094 EU3997
EU849580.1 gg_id:554748 Mesorhizobium sp. str. CCNWYC132 EU8495
EU410952.1 gg_id:276865 Mesorhizobium temperatum str. CCNWSX0012-2 EU4109
AY195843.1 gg_id:82201 Mesorhizobium mediterraneum str. PECA03 AY1958
EU074171.1 gg_id:253654 Mesorhizobium mediterraneum str. CCBAU 01409 EU0741
AF508208.1 gg_id:102422 Mesorhizobium temperadae str. CCBAU 11018; SDW 018 AF5082
AY725261.1 gg_id:136815 decayed velvetleaf seed clone S1-4-CL6 AY7252
FJ234902.1 gg_id:352327 Microbial structure mesophilic biogas mesophil anaerobic reactors fed corne silage cl FJ2349
AF410897.1 gg_id:20161 Mesorhizobium sp. str. Lo7-12 AF4108
FJ550306.1 gg_id:512978 Mesorhizobium tianshanense str. BIHB 4151 FJ5503
FJ025121.1 gg_id:324436 Mesorhizobium tianshanense str. SEMIA 3012 FJ0251
EU707156.1 gg_id:290008 Mesorhizobium tianshanense str. CCBAU 15528 EU7071
Z94807.1 gg_id:5084 Mesorhizobium genosp. T str. BDV5908 Z94807
DQ407284.1 gg_id:156049 Mesorhizobium tianshanense str. RCAN08 DQ407
GQ500629.1 gg_id:558777 Mesorhizobium sp. str. S948 GQ500
FJ544261.1 gg_id:580951 Mesorhizobium sp. str. CA17 FJ5442
DQ100068.1 gg_id:135924 Mesorhizobium plurifarium str. CCBAU 51276 DQ100
AY922072.1 gg_id:113594 farm soil clone AKYG882 AY9220
FJ025123.1 gg_id:306937 Mesorhizobium amorphae str. SEMIA 849 FJ0251
AF325770.1 gg_id:47902 Rhizobium sp. str. TM-5 AF3257
AY688622.1 gg_id:136093 Mesorhizobium plurifarium str. Sp42 AY6886
DQ859034.1 gg_id:204637 Mesorhizobium plurifarium str. ORS 3324 DQ859
FJ550307.1 gg_id:548722 Mesorhizobium tianshanense str. BIHB 4154 FJ5503
D14514.1 gg_id:5142 Mesorhizobium loti str. ATCC33669 D14514
EU256441.1 gg_id:248289 Mesorhizobium loti str. CCBAU 85068 EU2564
D14511.1 gg_id:5149 Rhizobium sp str. TAL 1148 D14511
GQ088394.1 gg_id:443339 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw: GQ088
AF508207.1 gg_id:102269 Mesorhizobium nortea str. CCBAU 11014; SDW 014 AF5082

2700.3	1692.8	2131.7	1920.3	3432.3	2293.9	2439.4	2619.6	1627.1	2831.2	1171.9
6420.3	6561.2	4967.7	5331.3	8286.0	7288.0	7822.2	6332.0	5314.2	5341.4	4632.0
9790.8	2412.6	2590.3	2235.3	6604.6	3281.8	4389.4	2906.9	1678.1	1365.2	1401.3
2699.8	2311.6	2279.1	2321.0	7355.7	3491.9	5168.8	2899.8	1461.1	1518.4	1292.7
9083.9	2384.2	2642.2	2229.8	5664.4	3053.3	4209.3	2899.6	1726.7	1351.9	1366.9
3628.9	2317.2	2452.0	2216.8	4834.6	2533.6	3951.6	2860.2	1474.2	1152.7	1355.4
5402.3	2283.7	2287.2	2180.7	4784.9	2822.0	4233.5	3153.4	1715.1	1995.1	1304.0
4848.9	2404.3	2411.3	1987.6	3251.3	2233.6	2633.3	2984.4	2062.0	1447.2	1327.9
5994.5	3395.1	2847.6	2782.9	5244.9	3312.3	4199.2	3673.1	2601.3	2678.8	1804.3
5600.1	3923.9	2956.8	2926.3	4925.6	3429.7	4273.2	3771.5	2665.2	2685.6	1904.9
123.5	160.9	265.4	190.6	389.1	228.3	304.3	242.3	115.0	210.7	131.2
5512.9	3053.2	2236.1	2194.6	4191.2	2455.9	3407.8	2937.6	2057.5	1926.9	1455.0
5555.1	3668.9	2640.8	2551.9	4901.4	3128.9	4022.6	3435.8	2480.6	2421.8	1709.5
5573.4	3504.3	2965.8	2923.4	5288.1	3363.6	4394.7	3725.3	2741.9	2518.9	1889.8
443.1	1827.8	1097.0	978.1	3322.6	1582.0	2265.4	1605.5	1610.0	768.8	656.2
1796.9	3529.5	2781.2	2998.8	4874.2	3876.5	4209.8	3127.2	3745.7	3463.5	2486.5
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293.9	2340.5	2572.5	2512.0	5402.4	3050.2	4112.1	3376.1	2358.8	3046.1	1337.7
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4667.5	4568.0	4531.9	4346.4	4828.0	4146.3	5225.3	5630.3	4433.7	2589.6	5175.1
4683.9	5517.4	4722.4	4626.7	7811.8	4952.3	6374.8	5386.0	3692.2	2714.4	5205.4
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1149.0	3566.8	2716.9	2896.8	4251.5	3220.6	3286.5	4298.7	3533.4	2187.2	2201.3
1213.8	3969.5	3389.9	3640.4	5482.3	4145.5	4461.0	4389.6	4433.8	3796.7	2641.6
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5432.4	2326.3	2707.5	2382.7	3503.4	2731.7	2641.1	2997.4	2394.6	2133.0	1781.4
25741.8	7560.9	6948.4	7860.0	9576.2	7444.1	8825.1	7428.1	7855.8	7470.1	7498.5
3143.6	1585.5	1510.2	1597.1	2625.4	1772.5	2476.5	2000.1	902.5	620.6	812.6
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21753.7	4334.1	3638.3	3508.3	5465.3	5418.1	3647.3	4299.4	2255.5	3787.6	1776.7
9730.9	6476.6	4731.6	4344.4	9098.2	5815.3	8908.1	6145.7	3305.0	3905.0	2697.9
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3195.5	2644.1	2750.3
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GQ221766.1 gg_id:575053 Prosthecomicrobium sp. str. ATCC 27825 GQ221
D13431.1 gg_id:5091 Mesorhizobium huakuii str. IFO15243 D13431
U50166.1 gg_id:5085 Mesorhizobium loti str. ICMP3153 USDA 3455 261 U50166
CU919824.1 gg_id:566028 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU919
AB166876.1 gg_id:99830 Mesorhizobium sp. str. M01 AB1668
AF041447.1 gg_id:5146 Mesorhizobium tianshanense str. -1BS; USDA 3592 AF0414
AY195844.1 gg_id:81838 Mesorhizobium mediterraneum str. PECA20 AY1958
AF325769.1 gg_id:23504 Rhizobium sp. str. E-13 AF3257
AY490116.1 gg_id:109828 Mesorhizobium sp. str. lema-2 AY4901
FJ544258.1 gg_id:563420 Mesorhizobium sp. str. CA9 FJ5442
EU410950.1 gg_id:271237 Mesorhizobium amorphae str. CCNWGS0015-1 EU410
EU867314.1 gg_id:556935 Phyllobacterium sp. str. CCGE2278 EU8673
EU074176.1 gg_id:236357 Mesorhizobium ciceri str. CCBAU 01466 EU0741
AJ785293.1 gg_id:159531 Mesorhizobium genosp. AA Cs6145 AJ7852
Z94819.1 gg_id:5097 Mesorhizobium genosp. U str. BDV5514 Z94819
AY509218.1 gg_id:99286 Mesorhizobium loti str. S139 AY5092
EU256445.1 gg_id:235712 Mesorhizobium loti str. CCBAU 85074 EU2564
EU256442.1 gg_id:252097 Mesorhizobium mediterraneum str. CCBAU 85070 EU2564
EU074175.1 gg_id:240934 Mesorhizobium loti str. CCBAU 01465 EU0741
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FJ542962.1 gg_id:511099 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone B FJ5429
AJ295079.1 gg_id:74017 Mesorhizobium plurifarium str. ORS1096 (LMG 15298) AJ2950
EU874893.1 gg_id:308046 Mesorhizobium sp. W12 EU8748
CU915140.1 gg_id:466324 and dynamics adapted microbiota during degradation Tunisian zarzatine enriched se CU915
CU915133.1 gg_id:381876 and dynamics adapted microbiota during degradation Tunisian zarzatine enriched se CU915
EU440986.1 gg_id:317496 Nitratireductor aquibiodomus str. PR57-9 EU4409
EU874875.1 gg_id:344328 Mesorhizobium sp. W66 EU8748
CU915137.1 gg_id:413807 and dynamics adapted microbiota during degradation Tunisian zarzatine enriched se CU915
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CU915166.1 gg_id:423734 and dynamics adapted microbiota during degradation Tunisian zarzatine enriched se CU915
CU915156.1 gg_id:377929 and dynamics adapted microbiota during degradation Tunisian zarzatine enriched se CU915
CU915082.1 gg_id:409815 and dynamics adapted microbiota during degradation Tunisian zarzatine enriched se CU915
EU143347.2 gg_id:253753 Nitratireductor sp. str. J3 EU1433
DQ659453.1 gg_id:160997 Chelatobacter sp. Pht-3B DQ659
GU447302.1 gg_id:518497 Nitratireductor sp. str. C115 GU447
FJ182044.1 gg_id:313217 Parvibaculum sp. str. P31 FJ1820
DQ015855.1 gg_id:139871 Antarctic lake water clone WLB16-101 DQ015
FJ536887.1 gg_id:563896 Linking performance microbiology biofilters treating dimethyl sulphide presence and FJ5368
AB186821.1 gg_id:101714 polychlorinated dioxin dechlorinating microcosm clone TSAC02 AB1868

3022.1	3100.9	3384.7	3684.7	5284.0	3889.3	4396.4	4183.4	2744.2	4410.1	1893.8
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4504.8	2327.7	2319.4	1891.0	2963.7	2139.9	2426.3	2792.1	1857.0	1423.4	1375.9
3460.4	1997.9	1532.6	1544.6	2724.2	1926.6	2335.1	2112.0	1172.3	909.1	979.9
260.5	1209.6	1051.5	981.1	2377.3	1253.0	1714.3	1628.2	695.0	1140.7	574.5
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2239.6	4374.9	3300.5	3543.6	5516.7	4723.9	5061.1	3921.0	4449.4	4140.0	2897.7
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2753.9	5388.8	4553.5	4217.4	7655.6	4853.9	4267.1	5033.6	3738.1	6834.8	3094.3
5519.4	2578.3	3070.1	2590.6	5624.9	3351.0	4215.2	3704.7	2053.9	2484.6	1663.2
4363.6	2616.1	2849.9	2422.9	3954.8	2954.6	2982.9	3304.8	2049.4	2333.3	1546.1
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9942.3	4905.9	4081.0	4267.1	6834.4	5354.4	6237.4	4780.5	4051.0	4523.1	3155.1
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FM242452.1 gg_id:311978 sequences sediment clone 9 T12d+oil FM242
AY387398.1 gg_id:101358 Parvibaculum lavamentivorans str. DS-1; DSM13023; NCIMB13966 AY3873
FN430653.1 gg_id:537152 Parvibaculum sp. str. MBNA2 FN4306
FJ154092.1 gg_id:333292 Phyllobacterium ifriqiyense str. CCNWGS0184 FJ1540
EU169165.1 gg_id:236290 Phyllobacterium myrsinacearum str. B65 EU1691
EU420076.1 gg_id:541971 Phyllobacterium myrsinacearum str. Sp-0 EU4200
AY636000.1 gg_id:104486 Phyllobacterium callistus str. CSC19 AY6360
DQ917820.1 gg_id:219107 Microbial profiles bleached and wild-type Muricea elongata Phyllobacterium clone B DQ917
FJ405362.1 gg_id:367932 Phyllobacterium myrsinacearum str. SPc FJ4053
EU169173.1 gg_id:253647 Phyllobacterium myrsinacearum str. B18 EU1691
AY785319.1 gg_id:144696 Phyllobacterium brassicacearum str. STM 196 AY7853
AJ011330.1 gg_id:5118 Phyllobacterium myrsinacearum HM35 AJ0113
EU928863.1 gg_id:345333 Phyllobacterium sp. str. T1018 EU9288
X98418.1 gg_id:5120 Nanobacterium sanguineum Seralab FBS batch 901045 X98418
AY785329.1 gg_id:142779 Phyllobacterium myrsinacearum str. STM 958 AY7853
EF364390.1 gg_id:225459 Phyllobacterium sp. str. Hue-5 EF3643
AY635999.1 gg_id:107799 Phyllobacterium callistus str. CSC32 AY6359
AY512821.1 gg_id:105844 Phyllobacterium myrsinacearum AY5128
GU257961.1 gg_id:593356 Bartonella elizabethae str. HXG-C15 GU257
AY331575.1 gg_id:91742 Pseudaminobacter sp. str. mp-1 AY3315
D32248.1 gg_id:5112 Thiobacillus sp. str. THI 051 D32248
FJ203076.1 gg_id:337809 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c FJ2030
FJ203650.1 gg_id:356370 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h FJ2036
GU118765.1 gg_id:542574 Threatened Corals Provide Microbial Habitats clone Mfra_M12 GU118
FJ203080.1 gg_id:338592 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c FJ2030
FJ203059.1 gg_id:303869 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c FJ2030
FJ203057.1 gg_id:350236 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c FJ2030
DQ396147.1 gg_id:155758 deep-sea octacoral clone ctg_NISA060 DQ396
AB099936.1 gg_id:79338 inactive deep-sea hydrothermal vent chimneys clone IheB2-3 AB0999
EU491659.1 gg_id:270912 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU4916
AF358017.1 gg_id:26724 peat soil microcosm clone LO13.3 AF3580
EU491413.1 gg_id:269457 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X4 clone EU4914
EF572341.1 gg_id:228614 Coco's Island site 23 marine clone S23_440 EF5723
DQ351777.1 gg_id:147394 Microbial Adherent Sediment Particles Heavy Metal Contaminated North Sea Surfac DQ351
GQ250606.1 gg_id:545163 bulk sea water column Gulf Mexico clone GOM_WB10-41 GQ250
EU246807.1 gg_id:248919 polyphasic description Pocillopora meandrina Palmyra Atoll Calcinus obscurus abdon EU2468
EU488046.1 gg_id:568753 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU4880
FJ478659.1 gg_id:548335 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4786
FM253615.1 gg_id:337543 Rock gold mine unusually microbial biofilm clone F09-1 FM253
EU735674.1 gg_id:343405 archaeal structures oil contaminated and soils China pristine soil Jidong Oilfield clone EU7356
AY913401.1 gg_id:113418 forest soil clone DUNssu195 (-7A) (OTU#173) AY9134

41.6	381.3	523.9	455.6	547.8	495.5	679.2	1398.3	376.7	1340.6	506.9
25950.4	7419.5	6365.0	6814.7	11180.9	8505.5	9091.8	7603.0	6777.6	5473.2	5030.6
2031.4	2606.0	2635.3	2594.4	3403.6	3516.4	3046.7	2925.9	3222.8	1900.5	1813.5
112.8	546.3	614.5	586.1	2343.9	1042.1	1485.2	1079.3	281.7	382.6	343.9
7495.5	2290.8	3088.6	3154.4	4385.9	3300.1	3510.7	3785.9	3941.4	4263.3	2346.0
15856.2	6073.8	6592.6	6904.1	8935.2	7209.6	8641.7	8180.0	6491.6	10747.2	5011.3
1327.7	1797.8	2334.3	2292.9	3419.8	2631.7	2048.2	3453.1	1906.0	4036.2	1676.1
1340.6	1365.8	1401.7	1208.8	1628.0	1261.0	1625.6	1353.2	1294.6	1202.8	1462.2
382.6	806.0	1355.2	1020.9	1319.0	1029.1	1103.2	1400.2	1078.7	1056.1	759.9
755.2	1233.1	1216.4	1364.7	3593.8	1756.3	1636.9	1529.2	1021.1	826.4	674.5
1025.6	2320.7	2732.4	2650.6	5321.9	3494.8	3616.8	3656.6	2190.8	3722.5	1771.0
8621.1	3438.4	3437.0	3674.8	5266.7	4000.0	4686.1	4309.1	3730.1	4726.8	2622.9
4367.9	3051.4	3471.4	3877.0	7526.3	4002.2	5096.8	4926.5	2971.0	3129.0	2269.1
8179.5	5282.0	4461.9	4651.8	4847.4	4750.4	5787.2	4454.8	5684.5	4780.0	6276.2
15792.3	4463.4	4389.2	4527.9	6266.7	4664.6	6715.7	4937.2	4624.7	5207.5	3874.0
9861.9	4399.9	3953.9	3855.2	5581.0	4982.8	5311.5	4751.1	4114.0	5683.1	3158.2
25214.6	7176.5	6535.7	7593.9	7847.4	6853.3	7628.8	6435.7	11454.2	10061.5	8634.5
3607.8	2725.9	3088.9	3652.4	5031.0	3285.5	3495.8	4412.6	3165.3	2781.4	2117.5
51.5	1150.9	1782.6	1460.5	3018.7	1902.7	1527.3	1795.8	1217.6	3221.0	831.8
1368.5	2427.6	2508.0	2425.4	4838.5	3932.7	3772.3	3115.4	1991.6	2969.9	1597.9
3536.3	5213.1	4961.0	5468.3	8146.9	7759.4	7613.3	6635.6	4389.1	5664.8	4312.6
1880.8	5416.6	4339.6	4425.0	6222.7	6862.6	4980.5	5045.4	3129.1	2506.0	3189.0
21884.5	6515.4	5524.5	5324.2	6612.9	7920.1	6024.5	6400.0	5863.1	6068.5	6327.5
3816.4	4388.1	3174.7	2875.0	4328.7	5108.3	3413.6	3808.9	3182.9	3034.1	3107.6
8309.1	5717.9	4532.0	4519.8	5578.9	6742.2	5102.1	4777.3	4994.6	4632.1	5297.2
8573.3	2646.8	2635.3	2753.1	4408.8	3001.2	4613.6	3367.9	1907.4	1175.7	1545.0
5167.0	4456.2	3064.3	2907.8	4469.0	5460.9	3374.9	3984.1	2973.6	2605.3	2578.2
80.2	89.3	146.5	117.6	101.9	123.5	191.7	386.7	61.0	95.7	70.2
3199.2	1368.1	3383.2	3964.7	1688.9	1588.3	2098.0	3454.7	3155.4	783.3	1779.0
148.1	3489.7	3388.7	2853.3	2523.4	4401.0	3189.7	3782.7	3923.9	947.0	2534.8
26029.7	9464.2	8873.9	9464.8	9647.8	8965.1	10373.7	8454.9	12808.5	9607.6	10189.2
3074.4	6037.8	5644.1	6330.2	7856.6	6319.4	7000.7	6853.4	5576.4	4514.3	4474.9
672.2	5964.8	5881.7	6764.2	8325.9	7671.6	6824.0	7731.8	9140.5	4400.4	5366.3
591.3	3802.8	3831.5	4494.0	4418.5	3228.7	5246.2	4888.6	1820.2	1532.8	2563.8
127.8	2680.8	2762.4	1843.7	1039.3	2042.2	1031.8	2327.0	970.3	883.4	1530.4
9637.0	7545.9	8351.7	8481.4	8486.3	7424.4	8291.7	8133.5	8551.5	8738.4	7027.5
20545.5	11256.6	10190.9	12100.3	11864.0	10463.9	13134.2	11155.6	16887.4	14757.0	13115.9
14064.9	6653.0	5486.0	6184.3	9070.1	6408.3	7615.3	5922.6	5145.2	3594.4	4086.1
8561.6	5883.8	5924.3	5625.5	6977.4	5711.2	7354.9	5737.5	5137.3	3380.8	5107.8
136.5	1815.3	1229.8	1391.0	3180.4	1911.1	2265.7	2084.9	619.3	570.9	975.9
12735.5	4060.2	4046.7	4067.1	4518.5	4395.6	4230.6	4991.4	4100.8	3328.5	4093.7

1215.5	634.8	409.2
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4854.5	4577.6	2832.5
10495.8	9157.4	6721.8
4300.7	2960.9	2208.4
1365.4	2015.0	1420.2
1333.7	1612.0	1100.8
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5854.2	2970.7	3059.5
5457.8	5052.3	4196.5
6485.4	3612.7	4025.8
4366.8	6055.3	4423.4
6491.7	6146.0	5603.2
5784.7	4312.2	3912.6
6613.4	8702.3	7036.4
5087.8	3756.5	3753.6
3424.1	1275.6	999.8
4341.4	3078.9	3601.5
8233.1	5534.7	4617.3
5952.3	4265.6	4152.8
6237.4	6737.6	5216.6
4295.5	3783.6	2973.3
5647.1	5760.6	4574.0
3585.6	3355.8	4031.5
4717.2	3505.3	3042.2
226.3	200.0	125.5
2247.2	2946.8	1602.8
3098.7	2695.8	2343.8
8785.1	9950.8	10651.5
7282.8	6237.7	6389.4
8550.3	6911.0	7218.8
4818.4	2825.1	3394.2
2459.7	2968.3	1127.5
8307.6	8944.6	8836.9
12077.7	11578.0	14109.1
6733.1	6586.0	7179.8
4667.1	6488.4	8055.7
1719.7	1562.0	1787.3
4407.6	5740.9	4584.8

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AY923020.1 gg_id:114265 Sargasso Sea waters clone D92_92 AY923(
AY922026.1 gg_id:112779 farm soil clone AKYG492 AY922(
AY913262.1 gg_id:113787 forest soil clone DUNssu042 (-2A) (OTU#176) AY913
GQ263181.1 gg_id:510769 Structure Simulated Level Waste Site simulated level waste site clone F3_139X GQ263
EU881134.1 gg_id:308120 Karst region primary forest soil clone KPF200711-010 EU881
EU236381.1 gg_id:288220 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg91H4 EU236
AY913338.1 gg_id:114183 forest soil clone DUNssu131 (+7A) (OTU#177) AY913
EF019626.1 gg_id:215375 aspen rhizosphere clone Elev_16S_770 EF0196
EU488067.1 gg_id:548592 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU488(
FJ152813.1 gg_id:308393 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX5A_ FJ1528
EU386115.1 gg_id:270010 Biogeographical and microbes sediments on subseafloor sediment South China Sea c EU386
GQ262947.1 gg_id:549426 Structure Simulated Level Waste Site simulated level waste site clone F1_85X GQ262
AJ633940.1 gg_id:114727 host's accessory nidamental gland clone 52ANG2 AJ6339
EU386026.1 gg_id:272493 Biogeographical and microbes sediments on subseafloor sediment South China Sea c EU386(
AY913351.1 gg_id:112770 forest soil clone DUNssu144 (+7A) (OTU#173) AY913
FJ479146.1 gg_id:588630 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4791
EU491428.1 gg_id:260972 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X4 clone EU491
DQ070827.1 gg_id:147965 Prokaryotic Structures Seafloor Basalts Varying Age East Pacific Rise and Ridge basal DQ070
GU369888.1 gg_id:529803 and mats vents Arc white filamentous microbial mat photic shal hydrothermal vent GU369
AB491708.1 gg_id:559688 Microbial control lamina formation Crystal geyser central Utah travertine clone CG1(AB491
DQ814512.1 gg_id:161858 zebrafish digestive tract clone aaa30b10 DQ814
GQ262857.1 gg_id:567747 Structure Simulated Level Waste Site simulated level waste site clone F1_33X GQ262
EU491525.1 gg_id:271177 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR4(EU491
AY162106.1 gg_id:150582 Cultivating Sargasso Sea clone GMD21A06 AY162
AY913263.1 gg_id:113892 forest soil clone DUNssu043 (-2A) (OTU#173) AY913
GQ262821.1 gg_id:534554 Structure Simulated Level Waste Site simulated level waste site clone F1_12X GQ262
EU735621.1 gg_id:339556 archaeal structures and pristine soils China oil contaminated soil Jidong Oilfield clone EU735
EU799979.1 gg_id:351580 It's all ranking aquatic Newport Harbour RI clone 1C227658 EU799
EU491596.1 gg_id:264919 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU491
FJ745115.1 gg_id:575156 Transporter genes expressed coastal response dissolved organic carbon surface wate FJ7451
EU385898.1 gg_id:259577 Stratified microbes sediments Core MD05-2902 subseafloor sediment South China S EU385
EU181478.1 gg_id:245815 Prokaryotic enhanced organic matter remineralization continental margin marine se EU181
AF406520.1 gg_id:106379 complex marine community d at depth 200 m North Aegean Sea (Station 3) clone AE AF406
GQ262936.1 gg_id:575894 Structure Simulated Level Waste Site simulated level waste site clone F1_79X GQ262
AM936572.1 gg_id:547134 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM936
GU369924.1 gg_id:518338 and mats vents Arc white microbial film on pebble aphotic zone shal hydrothermal v GU369
AM936135.1 gg_id:553156 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM936
AM712634.1 gg_id:257971 Anderseniella baltica str. BA141 AM712
GU220743.1 gg_id:571033 Microbial mineralization and involved microbial Basin field temperature hydrotherm GU220
FJ152698.1 gg_id:346361 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX1A_ FJ1526
DQ334628.1 gg_id:176463 Impact metals on sediments heavy metal polluted marine sediment clone HB2-33-2 DQ334

1404.4	4114.6	4107.8	4815.3	6114.0	4917.2	6726.9	5595.5	3615.1	3865.3	3606.8
40.7	493.2	241.5	209.8	409.9	489.9	422.3	216.6	60.2	37.5	138.4
5360.4	7859.3	7140.1	6723.8	9613.5	7545.0	9003.8	7815.8	6160.6	6275.0	5513.4
7086.8	4147.5	4758.6	4261.9	4683.3	4032.4	4760.8	4312.0	3792.3	3245.0	4132.5
125.7	3760.9	2495.3	3520.1	7029.0	3884.8	4925.2	3393.0	1193.7	700.5	1839.6
544.3	1129.5	1044.7	1213.9	2338.9	1948.5	1693.2	1741.7	878.0	764.8	943.0
10877.9	5370.7	6030.8	5635.3	7101.8	5789.0	6713.1	6073.6	6779.0	6121.6	5204.1
1338.1	2943.0	2259.8	2247.6	4213.8	3153.2	4226.9	2986.7	1761.6	1300.1	1455.0
25780.8	7496.3	7076.9	7459.5	7273.4	7548.4	8240.2	6902.3	8923.2	10249.4	10182.7
4961.9	4974.0	3870.4	3519.1	6546.9	4914.2	6592.0	4657.5	1883.8	1206.7	2128.2
3990.5	1181.9	1339.4	1518.5	3386.9	1701.4	3088.5	2653.8	864.7	671.7	669.2
3916.9	5136.1	5274.8	5867.2	6357.1	5554.1	6671.0	5826.0	4671.9	2737.8	3543.2
6267.5	2859.3	2266.6	2503.1	4365.8	3075.2	4779.6	3886.0	1324.7	2211.6	1533.9
385.7	1580.6	1820.9	1962.3	2839.4	2263.6	2443.3	2117.6	885.6	1924.1	854.1
5121.5	3301.1	3444.8	3135.9	3622.6	3076.4	3395.0	3695.4	3132.4	3543.2	2916.0
11640.9	5070.9	4339.4	4640.8	6618.9	5085.4	6746.6	4645.7	3584.5	2385.7	2969.2
32769.5	8750.1	8106.1	8193.2	8581.5	7873.9	8121.6	7468.8	9509.1	9657.4	9499.6
77.1	123.8	214.0	163.5	196.0	176.8	161.6	250.4	64.1	62.9	93.9
13089.9	9386.6	8777.4	9466.6	11365.0	9310.3	11859.7	9559.0	12038.7	9167.8	9137.2
870.5	3375.0	3403.6	3149.8	5106.0	3897.8	3132.8	3777.0	2255.3	1672.2	1531.5
674.7	5111.1	3978.3	4523.7	7038.2	5620.2	6775.6	4670.7	3165.5	2494.4	2636.9
1735.4	4399.8	3559.5	3713.3	5050.7	4449.2	5053.4	4727.3	2518.5	2152.3	2591.9
12383.6	4865.0	4457.4	5566.6	6245.3	6139.2	6014.4	4185.9	5675.0	5156.2	4665.0
4861.1	1202.8	1392.4	1211.7	2023.4	1378.7	962.4	1798.0	1331.2	728.2	1115.2
9851.1	5312.4	4978.2	5327.3	6602.3	5460.3	6332.9	5220.9	6168.3	3626.4	5375.2
664.3	4201.5	2048.8	2005.9	5122.2	4280.2	5070.1	2765.8	2346.5	477.6	1125.3
19513.4	4393.0	4220.3	4898.0	3590.1	3938.4	4408.4	5223.6	5067.1	7564.5	4292.5
2893.8	1388.6	1857.6	1953.1	2279.0	1804.0	1641.1	2713.3	2782.1	1209.4	1021.6
2344.7	2600.7	2405.5	2687.4	2594.3	3228.2	2740.3	3236.1	2794.8	2436.4	2538.6
12366.4	5524.7	5256.5	5775.4	5695.3	5035.7	5565.8	5502.2	6045.6	4859.7	5903.0
10259.7	5768.0	5192.5	5999.9	6197.5	5284.4	6919.2	5500.9	4807.4	4883.0	5844.2
2023.4	3893.9	4016.1	3685.5	4323.8	4527.4	4425.2	4099.0	2377.9	3192.5	2643.8
1159.0	2213.6	2326.7	2381.5	3250.8	2835.9	2781.4	2929.8	1753.5	1990.3	1637.2
3544.6	5966.5	5586.7	5756.6	5819.4	6732.8	6622.1	7334.2	5562.7	9746.0	6384.3
6982.0	4613.7	3935.3	4387.7	7439.9	5246.9	7031.0	4553.7	2542.4	1509.0	1957.1
12442.9	5138.2	4103.2	5121.6	5389.5	6357.6	5475.2	5985.9	5432.4	5710.2	5244.8
10925.1	9893.2	8009.2	7903.4	10629.0	9045.9	10884.0	8358.1	8568.9	7247.3	7692.2
14025.3	7096.3	6141.9	6555.8	10112.1	7310.8	11102.8	8089.8	6521.5	6457.1	6506.3
7376.6	3032.2	3269.4	3209.1	4959.1	2897.1	4558.7	4634.1	3423.1	2603.8	2301.0
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3473.6	2806.9	7048.0
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4663.3	6135.9	9920.3
4931.8	5451.2	5970.5
6852.0	5440.6	5945.4
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5613.0	5248.5	5792.2
2346.3	4137.4	9234.2
4415.1	5173.1	3856.5
2731.8	2920.6	1669.8
3337.3	2947.4	3546.5
5623.1	5254.9	4352.7
5552.9	5430.3	6247.7
4331.7	4748.9	7011.1
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6970.1	7787.4	6897.2
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5718.7	5539.5	4436.6
9434.3	8289.4	10615.4
9973.5	8134.9	7821.7
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EU236304.1 gg_id:289355 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg1a1A9 EU236
EF208711.1 gg_id:201560 Vertical and horizontal structure microbial sandy carbonate sediment clone Cl75cm.2 EF2087
EU881167.1 gg_id:342537 Karst region primary forest soil clone KPF200711-032 EU881
GQ347790.1 gg_id:592876 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ347
AF382114.1 gg_id:79210 bacterioplankton clone ZA3318c AF382
FJ203577.1 gg_id:322591 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h FJ2035
GU118597.1 gg_id:581316 Threatened Corals Provide Microbial Habitats clone Mfav_F16 GU118
FJ152626.1 gg_id:304121 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX1A_ FJ1526
FJ024326.1 gg_id:358115 Prokaryotic and their role biogeochemical cycling marine basalts basalt Juan de Fuca I FJ0243
DQ395471.1 gg_id:156247 deep-sea octacoral clone ctg_CGOAA69 DQ395
FJ203565.1 gg_id:315490 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h FJ2035
EU491292.1 gg_id:276298 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak EU491
GQ848473.1 gg_id:538386 Microbial sediments vents along East Lau Spreading Centre deep sea hydrothermal GQ848
FJ152991.1 gg_id:340224 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX4C FJ1529
GQ009791.1 gg_id:499876 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw77 GQ009
DQ104986.1 gg_id:137534 Mesorhizobium sp. str. JS 12 DQ104
EU332813.1 gg_id:360547 FACS assist identification TFO present aerobic enhanced biological phosphorus remo EU3328
FJ167442.1 gg_id:342632 microbiology granular sludge under autotrophic mixotrophic and heterotrophic denit FJ1674
AB374372.1 gg_id:259747 sequences Weissenstein (white rock) / few millimeters be surface rock called 'Weiss AB3743
FJ203570.1 gg_id:316649 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h FJ2035
AB246806.1 gg_id:146335 Mesorhizobium sp. str. Q-2 AB2468
DQ001642.1 gg_id:158376 Microbial seeps asphalt seep clone E101-27 DQ001
EF471634.1 gg_id:269321 Fast Screening and Estuarine Operon Libraries whole surface water Chesapeake Bay EF4716
AF234721.1 gg_id:32754 sludge clone A7 AF2347
AJ864462.1 gg_id:109471 Mesorhizobium thiogangeticum str. SJT AJ8644
FJ674841.1 gg_id:529939 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6748
CU922361.1 gg_id:547097 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU922
AY598817.1 gg_id:105079 Hoeflea marina str. LMG 128 AY5988
NR_025411.1 gg_id:547162 Mesorhizobium chacoense str. PR5; DSM 17287 NR_02
GU118307.1 gg_id:538811 Threatened Corals Provide Microbial Habitats clone Dstr_L15 GU118
GU118284.1 gg_id:589090 Threatened Corals Provide Microbial Habitats clone Dstr_M18 GU118
AF280865.1 gg_id:72907 bioreactor clone mle1-44 AF2808
AB167198.1 gg_id:107911 Rhizobium sp. str. c19 AB167
AF150703.1 gg_id:24111 Elbe River snow isolate Iso26 Iso26_1389 AF1507
FJ670878.1 gg_id:524118 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6708
EF019808.1 gg_id:206948 aspen rhizosphere clone Elev_16S_999 EF0198
FJ152680.1 gg_id:332848 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX1A_ FJ1526
FN436146.1 gg_id:554537 Molekularbiologische Charakterisierung der bakteriellen Populationsdynamik eines t FN436
AY942778.1 gg_id:145164 but species richness marine sponge Cymbastela concentrica clone Cc173 AY9427
AM934887.1 gg_id:573454 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM934
AY690674.1 gg_id:99235 Mesorhizobium sp. str. GC08 AY6906

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23965.8	6521.1	4769.5	5282.5	7739.0	6184.2	8265.6	5183.0	4194.4	3384.1	3574.7
4509.4	4232.1	3787.2	4083.4	5944.9	5410.0	4464.4	4660.7	6341.9	4016.2	3342.4
172.8	1307.2	1107.3	1432.8	2040.5	2150.5	1310.4	1659.3	1953.0	713.0	756.8
293.1	2056.2	1765.5	1478.9	2205.7	2017.4	2074.2	1419.0	784.8	591.1	829.1
232.4	1257.3	1437.5	1815.8	2300.7	2838.4	2137.7	2202.6	1681.6	264.6	912.4
3458.2	3989.3	3952.5	4366.8	5338.9	4071.1	4663.9	4435.6	4913.9	3885.0	5799.2
187.3	1546.3	2008.1	1501.2	1489.9	1997.7	1412.0	1576.9	1815.8	872.1	1032.1
551.5	2464.6	1551.5	894.2	1580.1	2190.8	1287.1	1509.3	1179.7	1575.3	617.7
166.2	536.0	310.1	280.4	639.3	563.2	1280.9	322.2	85.2	52.6	137.3
4820.3	4766.2	5236.5	5858.4	4976.1	5608.8	6181.2	6216.5	6427.2	7575.7	6474.0
4275.5	2778.8	3005.3	2956.9	2795.6	2985.6	3648.3	3036.5	3043.0	2716.9	3111.7
2291.6	2339.9	2851.8	2977.8	5907.5	3403.0	4248.4	3453.9	3030.4	3340.1	1753.0
480.9	1676.4	1838.1	1789.2	4793.3	1972.7	3546.8	2399.2	1795.0	1212.3	984.7
1729.2	2929.8	2792.2	2943.0	4583.3	2860.9	4131.5	3283.7	2332.9	2459.0	1685.7
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14371.9	3895.6	4445.4	4888.8	6311.2	4921.0	6607.3	5394.4	3657.7	3509.4	3837.8
6221.2	3185.5	3378.0	3224.5	4125.2	2980.3	3882.1	4090.7	1785.2	3421.0	3234.3
1227.0	2480.7	2553.8	2482.4	3483.4	2873.1	3960.6	3022.8	1460.0	1699.5	1340.1
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532.0	1603.8	1839.0	2073.1	2747.7	2213.9	2604.1	2460.7	1341.6	1815.1	1458.9
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18918.1	4092.4	4158.0	3975.1	5259.5	4429.5	4919.3	4729.6	4743.4	4753.0	4578.0
231.6	3237.1	3414.5	3330.4	4547.2	3756.3	4395.7	3591.2	3077.1	2750.2	2255.7
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28232.0	5780.8	6136.7	6257.0	9705.9	7014.6	10277.2	6993.3	6071.7	6187.6	4929.9
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5738.5	2325.8	2444.7	2533.7	3947.5	2620.2	3731.2	3241.3	1435.5	1911.6	1486.8
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219.2	2681.7	3262.7	2984.5	4447.3	3405.4	4519.6	6200.7	2462.8	4414.1	2159.2
110.1	1365.3	1857.1	2208.5	2819.7	1977.2	2453.9	2470.6	1687.3	2655.6	1070.9

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7299.4	5335.7	4984.3
3588.4	2886.5	2529.9
5005.5	4454.6	4874.0
5881.4	5767.4	6062.4
3862.5	3429.2	3747.0
3422.0	3460.1	3708.0
2469.2	1507.6	2073.4
5570.3	4890.4	4043.1
2869.5	2083.0	2603.3
3772.8	2065.4	2061.9
6058.2	4975.1	5599.6
4354.5	2934.5	1695.8
4737.6	3844.0	3106.8
6706.0	4613.6	3136.7
5301.0	4567.6	2662.8
5097.7	5768.8	3732.7
4407.2	5191.4	3587.5
1321.9	1521.1	830.1
9051.6	6509.7	8086.7
4963.2	4538.4	5567.7
3746.0	2882.1	3885.9
2047.0	1743.2	1131.8
293.6	334.9	202.8
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3323.3	5584.3	2222.1

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AY332151.1 gg_id:100524 Mesorhizobium sp. str. GWS-SE-H103 AY3321
FJ671077.1 gg_id:519193 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6710
AB265157.1 gg_id:164464 Mesorhizobium sp. str. E11 AB2651
AJ318199.1 gg_id:73511 Waste-gas biofilter clone BIwii1 AJ3181
FJ542875.1 gg_id:521776 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone A FJ5428
FJ203541.1 gg_id:316301 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata I FJ2035
GQ263841.1 gg_id:548137 Structure Simulated Level Waste Site simulated level waste site clone WC1_b89 GQ263
EU287328.1 gg_id:243907 Pacific arctic surface sediment clone S26-28 EU2873
FJ671628.1 gg_id:529153 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6716
FJ675300.1 gg_id:527154 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6753
DQ860072.1 gg_id:170119 Symbiotic aerobic anoxygenic phototrophic colonial tunicate clone L9 DQ860
AY307924.1 gg_id:90640 Aminobacter sp. str. COX AY3079
EU236387.1 gg_id:287433 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg92A11 EU2363
EU223941.1 gg_id:246412 -RFLP microbes Qinghai-Tin rail soil clone 56 EU2239
FJ671907.1 gg_id:514109 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6719
DQ814869.1 gg_id:162010 zebrafish digestive tract clone aab54f12 DQ814
GU454867.1 gg_id:523337 Understanding short-chain fatty acids accumulation enhanced alkaline digestion: kir GU454
DQ364238.2 gg_id:157010 Rhizobium sp. str. WH2K DQ364
FJ542989.1 gg_id:528720 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone B FJ5429
Y15403.1 gg_id:5113 Aquamicrobium defluvii str. DSM 11603 Y15403
DQ860063.1 gg_id:167582 Symbiotic aerobic anoxygenic phototrophic colonial tunicate clone C7 DQ860
FJ674998.1 gg_id:518661 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6749
FJ907162.1 gg_id:552671 Aminobacter sp. str. Sokolova FJ9071
FJ542969.1 gg_id:531912 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone B FJ5429
AB257631.1 gg_id:267976 Microbial few millimeters be surface dolomite rock 'Val Piora' Alps 1965 meters abov AB2576
AY515416.1 gg_id:99884 bulk water German Wadden Sea May 1999 clone GWS-BW-H52M AY5154
AB257653.1 gg_id:273074 Microbial few millimeters be surface dolomite rock 'Val Piora' Alps 1965 meters abov AB2576
EU404018.1 gg_id:306709 Microbial septic tank effluent and soil biozone infiltrative surface clean water clone C EU4040
EU769196.1 gg_id:329286 velvetleaf seed clone S4-6-CL4 EU7691
Z30542.1 gg_id:5416 Agrobacterium larrymoorei str. 3-10 Z30542
D14503.1 gg_id:5409 Agrobacterium rubi str. IFO13261 D14503
X67228.1 gg_id:5430 Agrobacterium rubi str. LMG 156 X67228
D12787.1 gg_id:5414 Agrobacterium rubi str. IAM 13569 D12787
AJ389912.1 gg_id:33557 Agrobacterium vitis str. CFBP2736 AJ3899
DQ466575.1 gg_id:156733 Agrobacterium tumefaciens str. B8LH DQ466
FJ493020.1 gg_id:556421 Agrobacterium tumefaciens str. T0H5 FJ4930
EU295450.1 gg_id:241317 Agrobacterium sp. str. LKXJ-3 EU2954
AB208737.1 gg_id:115126 Agrobacterium sp. AEOC022 AB2087
DQ803328.1 gg_id:190446 human fecal clone RL311_aam24b01 DQ803
EU652866.1 gg_id:280086 Agrobacterium sp. str. ZY068 EU6528

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266.5	5461.9	2974.6	3340.4	6717.3	4590.8	4849.7	4173.4	3467.2	2740.0	2374.9
1287.3	159.5	298.1	206.3	2502.6	448.8	501.3	536.0	100.7	88.8	120.8
1176.4	1340.7	1293.9	1307.2	2711.8	1878.1	1157.0	2009.0	819.1	1266.4	771.3
3476.9	600.8	876.0	534.4	1805.1	735.5	1764.7	974.2	246.5	197.5	192.5
147.9	966.2	696.2	626.3	1348.2	942.5	1420.5	908.3	353.9	540.8	336.5
319.8	1236.2	1398.4	1168.4	2542.6	1573.7	2234.8	1573.8	785.1	1010.7	647.8
740.5	1822.4	1788.5	1794.7	2709.7	1921.7	2092.9	2235.3	1768.4	2229.5	1137.4
16139.3	7502.6	8006.9	8178.7	11246.3	8411.8	11864.7	9040.8	10676.7	10136.2	8406.6
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21352.0	3883.7	3212.3	3509.7	4244.8	3730.7	3994.6	3621.6	3411.1	1846.3	2569.6
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21377.5	7516.5	6071.8	6426.1	9634.1	6664.3	6721.2	6325.0	11638.9	8194.1	5541.1
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2166.7	1945.2	2206.1	1887.8	3292.9	2333.2	2768.5	2559.4	2327.6	1610.7	1511.6
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AY438103.1 gg_id:155955 Rhizobium sp. str. EGY AY4381
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GQ444136.1 gg_id:587424 Agrobacterium tumefaciens str. VKLR 01 GQ444
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AM157353.1 gg_id:142761 Agrobacterium tumefaciens AM157
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EF025327.1 gg_id:184622 Agrobacterium tumefaciens str. SREPS2 EF0253
DQ383276.2 gg_id:217367 Agrobacterium tumefaciens str. 7406 DQ383
DQ288946.1 gg_id:144288 Agrobacterium tumefaciens TG32 DQ288
GQ258493.1 gg_id:561134 Rhizobium galegae str. Ca2 GQ258
GQ169812.1 gg_id:577612 Agrobacterium tumefaciens str. B986 GQ169
EU295451.1 gg_id:242798 Agrobacterium sp. str. LKXJ-2 EU2954
DQ648579.1 gg_id:161239 Rhizobium undicola str. Liujia-81 DQ648
FN640463.1 gg_id:514145 Agrobacterium sp. str. ZX09 FN6404
DQ009494.1 gg_id:127447 Agrobacterium tumefaciens str. CCBAU 81181 DQ009
AB368996.1 gg_id:549668 and microbial oils produced Asia petroleum crude oil (Arabian Extra light) clone PT-A AB3689
AY353708.1 gg_id:92988 Azotobacter chroococcum str. DSM2286 AY3537
EF620435.1 gg_id:241441 Agrobacterium tumefaciens str. ISSDS-381 EF6204
EU256457.1 gg_id:254367 Agrobacterium tumefaciens str. CCBAU 85023 EU2564
EF102818.1 gg_id:253586 Agrobacterium tumefaciens str. G-1-22 EF1028
AY626383.1 gg_id:99992 Agrobacterium tumefaciens str. ICMP 369 AY6263
AF422644.1 gg_id:26211 TCE-sediment clone d035 AF4226
AJ295683.1 gg_id:26338 Agrobacterium tumefaciens str. IrT-JG-6 AJ2956
EU155875.1 gg_id:244531 Agrobacterium tumefaciens str. D6 EU1558
X73041.1 gg_id:5266 Blastobacter aggregatus str. IFAM 1003 X73041
GQ267695.1 gg_id:562519 Agrobacterium tumefaciens str. CCNWSX539 GQ267
FJ444745.1 gg_id:561714 Cotton Rhizosphere cotton rhizosphere clone 4y-57 FJ4447
AY576874.1 gg_id:101430 Agrobacterium tumefaciens str. BY6 AY5768
AB535700.1 gg_id:545894 Agrobacterium tumefaciens str. Pl.2-1 AB5357
EU834271.1 gg_id:315015 Agrobacterium tumefaciens str. DS54 EU8342
AJ306769.1 gg_id:66930 DCP-dechlorinating consortium clone SHA-91 AJ3067
DQ860031.1 gg_id:250206 anchovy intestinal microflora clone F1Y DQ860
AY048887.1 gg_id:33043 rhizosphere clone Q3-24C12 AY0488
AF239848.2 gg_id:47953 Bradyrhizobium japonicum str. PRY65 AF2398
DQ288890.1 gg_id:144720 Ensifer adhaerens DQ288
EU373406.1 gg_id:261377 Agrobacterium tumefaciens str. TPR09 EU3734
AY626382.1 gg_id:99841 Agrobacterium larrymoorei str. ICMP 15237 AY6263
AY568505.2 gg_id:107283 Agrobacterium tumefaciens str. C- AY5685
AJ389905.1 gg_id:34745 Agrobacterium tumefaciens str. Mushin6 AJ3899

461.4	3212.4	3478.4	3514.1	4873.7	4256.9	4049.1	4965.8	4070.1	6921.9	2423.4
6237.5	5814.5	5651.1	5702.8	6876.9	8549.9	6383.6	7141.0	6372.4	11410.5	4599.3
75.3	236.5	324.9	245.3	586.8	502.1	283.7	989.3	257.9	643.9	265.3
4896.8	5310.8	6282.5	6034.8	6188.0	5240.0	6398.0	5384.9	5821.6	5848.6	6312.2
1237.0	2180.2	3124.3	2816.1	4221.5	4578.2	3445.3	4437.1	1821.3	6735.1	1943.7
426.2	438.1	581.7	462.6	1144.0	881.4	422.2	744.5	322.4	1046.0	282.3
250.6	574.5	881.7	751.8	1273.8	1446.1	701.1	1140.2	687.7	1448.6	499.2
1318.8	3205.0	3372.5	3316.6	4916.6	4156.2	4019.2	4771.6	3879.9	6904.3	2393.5
27226.9	4072.8	3844.4	4689.0	6052.9	4927.0	4486.1	5540.3	4280.7	4707.5	3137.6
1835.7	2694.8	2882.0	3122.5	3613.5	3615.2	3916.5	3946.7	3806.8	5624.4	2408.8
129.7	1678.4	2312.0	1949.5	2378.5	2405.3	1652.8	2800.1	1692.5	7047.0	1583.1
4826.4	5250.2	5814.8	6014.6	7019.2	7134.4	7044.8	7027.0	6704.1	9980.0	5358.8
1364.6	3138.6	3599.0	3827.4	4318.3	4272.0	4268.2	4847.7	4607.4	6609.6	2809.8
1378.0	4158.3	4637.5	4572.6	6856.6	5858.5	5449.5	6433.6	4758.3	9531.0	3143.4
5414.1	5334.3	5751.4	5874.9	9899.2	6682.7	7247.9	7271.8	6744.7	9631.1	4837.0
1669.1	2874.5	3184.8	3372.7	4531.4	4159.0	3554.4	4355.0	3308.9	6123.9	2991.4
1761.8	3547.9	3920.2	3730.4	5734.6	5744.9	4023.2	4988.9	3440.7	7075.6	2740.8
11244.8	5877.5	5370.5	5493.8	8159.4	7420.9	5878.4	5660.4	7379.6	6776.4	5416.7
12174.2	4900.7	5315.2	5479.7	7475.5	7748.2	5625.5	6258.4	5888.2	7943.3	4877.5
3211.8	2910.8	4122.2	3891.0	4982.3	4575.2	4315.2	5522.6	3494.6	8729.8	2946.8
3861.9	3294.9	3791.0	3507.7	5470.5	5050.4	4523.4	4302.4	3086.1	6556.2	3106.7
2394.8	4118.7	4300.8	4314.0	6808.8	6638.1	4915.8	5395.8	4222.5	6757.4	3267.4
1397.6	3628.7	4371.7	4300.3	6081.5	6149.5	4761.4	5455.0	4057.2	7563.9	3364.8
15879.1	4230.7	4001.0	4836.1	5028.0	5018.7	4849.7	5376.9	4204.7	3668.3	4146.0
2640.4	2126.9	2772.8	2335.7	2989.3	3454.9	3468.7	5348.0	2339.7	7658.8	2241.8
575.7	3116.7	3268.7	3366.6	4713.9	4466.9	3712.8	4178.8	3330.6	5481.5	2539.2
12856.4	3938.8	3244.9	3233.0	4222.4	4095.0	4288.3	4494.8	3236.1	4076.3	2546.8
2135.1	5214.8	5626.0	5496.4	7765.0	7494.2	6293.8	7098.6	5396.3	9070.2	4395.8
5305.4	4339.8	4915.9	4602.7	5902.2	4538.0	5098.7	4578.3	4626.4	5305.2	4822.1
249.2	2804.0	3915.3	3739.3	5249.1	5223.3	4258.5	5064.9	3426.9	7731.4	2774.9
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3650.9	2729.9	3255.0	3075.5	5212.3	4168.3	3909.4	3923.7	2509.8	6207.4	2122.9
471.3	2927.2	3209.5	3003.7	3892.8	3647.8	3612.0	5008.1	2771.1	4711.1	2983.3
1349.5	2978.8	3640.8	3443.9	4044.8	3884.9	3850.6	4641.3	3495.8	6532.3	3179.8
9985.5	5094.3	5186.3	5478.4	7526.9	6645.3	6896.2	7568.1	4766.5	7371.2	4738.7
21686.8	8125.9	7542.2	8248.0	9463.0	8705.6	9479.9	8005.0	10217.9	10614.6	8745.6
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10073.2	8135.9	4701.0
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7127.0	6990.5	4833.8
8570.3	6348.4	3902.9
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8009.2	5235.7	3272.1
8412.2	4840.4	2893.2
5629.8	6147.0	4465.2
7038.0	3614.7	1606.7
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AB362777.1 gg_id:244116 Agrobacterium sp. str. YT0023
D13294.1 gg_id:5417 Agrobacterium tumefaciens str. IAM 14141
AY826796.1 gg_id:111301 Agrobacterium vitis str. PHX1
AB508898.1 gg_id:587039 Agrobacterium sp. str. TSH97
EU221403.1 gg_id:255931 Agrobacterium tumefaciens str. H2P4
GU233958.1 gg_id:584818 Agrobacterium tumefaciens str. HM-1
EU373439.1 gg_id:269871 Agrobacterium tumefaciens str. YRR11
AY682683.2 gg_id:142056 Microbial biofilms corroding systems heating system clone 62
DQ357728.1 gg_id:580478 Agrobacterium sp. ULV1
AY221180.1 gg_id:79849 Agrobacterium tumefaciens EBRI 20
EU618037.1 gg_id:279343 Rhizobium sp. str. CCBAU 65813
FM209485.1 gg_id:323633 Agrobacterium tumefaciens str. OLJ36
L22533.1 gg_id:199880 Candidatus Liberibacter africanus str. Nelspruit
AM181747.1 gg_id:161523 Sinorhizobium kostiense str. LMG 19225
AY034028.1 gg_id:43724 Sinorhizobium kummerowiae str. CCBAU 71714
X68390.2 gg_id:5210 Sinorhizobium saheli str. LMG 7837
AJ295073.1 gg_id:25282 Sinorhizobium terangae str. ORS1244 (LMG 15317)
AF250353.1 gg_id:20311 Sinorhizobium xinjiangense str. Rx22
AF250354.1 gg_id:52806 Sinorhizobium xinjiangense str. CCBAU110
FJ418688.1 gg_id:366662 Sinorhizobium fredii str. CCBAU 21119
AF250377.1 gg_id:39113 Sinorhizobium xinjiangense str. CCBAU 830844
AF452129.1 gg_id:69312 Ensifer adhaerens str. LMG 20571
EU221356.1 gg_id:249920 Ensifer adhaerens str. J2S2
DQ786803.1 gg_id:169278 Sinorhizobium fredii str. SjzE4
EF437258.1 gg_id:254285 Sinorhizobium sp. str. RH18
FJ418687.1 gg_id:359351 Sinorhizobium fredii str. CCBAU 21111
EU301688.1 gg_id:235385 Ensifer adhaerens str. Y12B
AB433352.1 gg_id:272085 Sinorhizobium fredii str. USDA 194
AB433350.1 gg_id:265416 Sinorhizobium fredii str. USDA 192
EU930422.1 gg_id:351757 Sinorhizobium fredii str. 15067
FJ405371.1 gg_id:360590 Ensifer mexicanus str. CAF249
EF506205.1 gg_id:225990 Sinorhizobium fredii S24
EU139306.1 gg_id:235960 Sinorhizobium fredii str. CCBAU 43300
DQ786804.1 gg_id:163644 Sinorhizobium fredii str. SjzZ4
DQ411930.1 gg_id:193675 Ensifer mexicanum str. ITTG-R7
EU410949.1 gg_id:262494 Sinorhizobium xinjiangense str. CCNWGS0023-2
D12796.1 gg_id:5260 Sinorhizobium xinjiangense str. IAM 14142
D14516.1 gg_id:5217 Sinorhizobium fredii str. ATCC35423
DQ859043.1 gg_id:204451 Sinorhizobium sp. str. ORS 3411
EF592609.1 gg_id:232106 Kaistia soli str. 5YN9-8

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AJ2950
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AB4333
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FJ4053
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EU1393
DQ786
DQ411
EU4109
D12796
D14516
DQ859
EF5926

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471.2	2636.3	3215.1	3210.9	4938.3	4597.8	3898.0	4464.2	2931.3	7025.4	2313.0
18698.4	6415.9	6271.8	6426.1	6302.0	6801.3	5538.1	7353.7	8596.1	8529.1	8857.7
2528.2	3042.9	3905.5	3420.6	4141.3	3566.5	3890.0	6527.7	3647.3	11112.1	3248.7
2496.1	3890.8	4131.4	4062.7	6474.7	5874.6	4670.6	5428.8	3576.2	7798.8	3030.0
10051.0	2786.3	2526.0	2404.7	3350.1	3449.0	2523.4	2855.3	3475.9	4106.1	1757.3
461.5	2607.1	3150.0	3198.4	5041.1	4264.7	3454.2	4395.9	2773.4	7103.5	2324.7
1475.8	2424.3	3005.5	2690.4	3647.7	3167.4	3605.6	5112.9	2930.2	7220.1	2733.8
13580.4	6493.4	6431.8	6547.9	6264.2	6184.9	6385.7	5974.1	7164.8	7878.0	9096.1
2229.6	2417.3	2564.1	2646.4	3902.6	3737.7	2841.8	3481.6	2386.5	4212.1	1898.4
318.8	1008.3	1378.7	1158.8	3011.1	1883.1	1329.1	1813.4	755.8	2899.4	785.6
1558.0	3517.7	4143.2	4080.1	6238.5	6071.7	4364.5	5149.0	3431.6	6931.2	3113.9
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6004.1	6288.0	5651.8	6305.6	8526.0	6829.6	7317.2	7317.8	6064.4	6307.3	5621.1
11480.9	6285.5	6995.3	6991.5	6892.2	6533.6	7324.9	6718.9	6031.5	6082.8	7520.1
3201.3	3560.1	3510.4	2859.7	4989.1	3562.9	4595.1	3917.0	2274.0	4565.3	2377.8
1555.8	2693.5	2503.8	2250.8	3828.4	2537.1	2980.7	2855.6	2237.0	3389.5	1665.4
10272.1	6164.8	5759.0	5864.5	7570.0	6553.2	7625.1	7007.3	5628.6	7466.8	4634.2
20502.1	6341.8	6107.0	6588.4	7745.7	6873.8	7357.9	7274.8	6494.5	7626.6	6561.7
13666.8	6746.8	5890.7	5956.3	7683.2	6848.4	6779.6	6997.2	6742.9	7178.4	5359.6
6404.6	3896.4	3860.6	3363.2	4417.9	3822.8	4108.0	3867.1	3604.1	4143.0	2928.4
23265.9	5338.1	5068.2	5191.8	6482.0	5348.4	6497.4	5555.2	4812.0	4269.7	4363.9
37975.8	4208.4	4308.2	4319.7	7214.1	4718.0	4894.1	4499.0	5470.1	5096.0	4557.7
10711.0	5456.6	5140.7	5200.1	7072.1	5808.0	6430.7	6172.2	5261.3	6342.0	4437.1
9647.1	3564.0	3368.3	3270.8	5981.6	3672.9	4039.9	3737.5	2814.7	2768.5	1539.9
13978.8	6188.9	5344.3	5473.5	7129.1	6211.2	6284.2	6207.6	6012.7	5782.1	4904.7
19147.7	5215.0	5090.9	6329.8	4908.1	5215.6	5828.6	4812.5	7768.4	6349.7	7746.8
18422.4	4596.7	4507.6	4161.9	7232.6	4897.4	4650.7	5076.2	3534.4	5499.8	2933.9
10756.1	5322.6	5012.3	5190.9	6561.3	5698.6	6326.4	6057.6	5142.3	6187.2	4387.3
11592.1	5282.6	4952.1	5161.2	6461.7	5629.0	6251.1	5933.2	5158.4	6070.7	4621.6
980.4	1964.8	2690.6	2581.4	3467.5	2824.0	2364.3	3618.5	2274.1	4720.0	1597.9
21257.8	5540.8	5356.8	5697.6	6190.4	5939.1	5498.2	6243.7	4384.9	5203.2	4888.8
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16186.5	6160.3	6179.8	6590.9	7437.5	6767.5	7560.1	6890.8	7126.0	7251.3	5468.1
18513.3	6038.4	5606.1	5985.2	9489.1	6150.3	6900.0	6775.9	5019.6	4561.1	3435.2
10181.2	5372.1	4886.3	4930.2	6371.7	5570.8	5760.3	5847.8	5153.1	5682.4	4060.6
12353.2	5255.0	4920.6	5052.4	6593.6	5588.1	6165.5	5866.6	5068.6	5987.6	4219.6
11993.2	5812.9	5467.0	5567.4	7147.7	6225.4	6660.9	6656.2	5798.9	7383.9	4674.5
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2579.0	2428.3	2494.5	3261.6	3959.0	3365.7	3690.0	3934.3	1923.0	1923.9	1470.9

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7917.6	5755.2	3375.5
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7524.6	4455.2	2209.0
5545.5	3525.0	1660.3
6373.4	6808.1	5589.2
4659.5	3243.6	1911.1
3710.3	1766.1	822.4
8150.0	4994.2	2955.6
8872.1	9026.0	9081.0
9417.2	7922.4	7213.1
6511.0	6428.9	7090.2
5578.4	3620.9	4138.8
3924.7	3332.1	2776.7
8463.4	6459.2	6663.2
7876.1	6511.6	7044.4
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5811.7	5448.6	6156.4
4955.1	5243.0	5919.0
7610.0	6024.0	6189.6
4835.0	4666.4	4630.3
7198.9	5816.2	6163.3
5077.7	7023.6	4895.4
6748.9	5095.1	6569.1
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7028.0	5688.6	6036.8
4698.8	3130.6	2303.7
6770.8	6278.8	5547.0
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g__Kaistia
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g__Ochrobactrum
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AM409365.1 gg_id:174460 Kaistia sp. str. B6-12 AM409
FJ542971.1 gg_id:527906 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone B FJ5429
AM409364.1 gg_id:180502 Kaistia sp. str. B6-8 AM409
AY394871.1 gg_id:95247 Rhizobium sp. str. EPR 13 AY3948
DQ768630.1 gg_id:238108 Martelella mediterranea MARC4N DQ768
EF207562.1 gg_id:215523 mangrove system sediment EF2075
EU258744.1 gg_id:235404 Mycoplana peli str. AN419 EU2587
DQ419569.1 gg_id:153696 Rhizobium sp. str. -1 DQ419
EU256384.1 gg_id:245182 Sinorhizobium borbori str. DN316-1 EU2563
GU433460.1 gg_id:521715 Rhizobium multihospitium str. CCBAU 31043 GU433
AY221178.1 gg_id:80113 Rhizobium tropici EBRI 32 AY2211
AY221176.1 gg_id:79981 Rhizobium etli EBRI 21 AY2211
AY221177.1 gg_id:80442 Rhizobium etli EBRI 26 AY2211
U89820.1 gg_id:5300 Rhizobium mongolense str. USDA 1877 U89820
AY117636.1 gg_id:63517 Rhizobium etli str. PRF164 AY1176
AF511497.1 gg_id:87964 Rhizobium sp. str. Gls-3 AF5114
AF025853.1 gg_id:5454 Rhizobium galegae str. 59A2 AF0258
AY509213.1 gg_id:107491 Rhizobium galegae str. S163 AY5092
DQ267108.1 gg_id:143997 Rhizobium sp. str. CCBAU 45111-1 DQ267
AY775170.1 gg_id:107864 Rhizobium sp. str. CCBAU 23084 AY7751
EU256413.1 gg_id:248308 Rhizobium giardinii str. CCBAU 85014 EU2564
FJ445210.1 gg_id:547364 Rhizobium sp. str. CCNWGS0271 FJ4452
EU399693.1 gg_id:271840 Rhizobium giardinii str. CCBAU 01209 EU3996
U89826.1 gg_id:5357 Rhizobium leguminosarum bv. viciae str. USDA 2434 bv. U89826
FJ025091.1 gg_id:331780 Rhizobium leguminosarum str. SEMIA 3025 FJ0250
U29386.1 gg_id:5334 Rhizobium leguminosarum bv. viciae str. USDA 2370; ATCC 10004; SEMIA 032 U29386
FJ025089.1 gg_id:352984 Rhizobium leguminosarum str. SEMIA 388 FJ0250
DQ406712.1 gg_id:154460 Rhizobium leguminosarum str. RP422 DQ406
FJ449665.1 gg_id:551782 Rhizobium leguminosarum CCNWSX0855 FJ4496
AY491062.1 gg_id:112424 Rhizobium leguminosarum str. ICMP 14642 AY4910
EF525223.1 gg_id:224132 Rhizobium leguminosarum str. PB166 EF5252
FJ025094.1 gg_id:328736 Rhizobium leguminosarum str. SEMIA 2082 FJ0250
AY904729.1 gg_id:112447 Rhizobium leguminosarum str. SEMIA 222 AY9047
DQ835293.2 gg_id:171581 Rhizobium leguminosarum bv. viciae str. CCBAU 03321 DQ835
AY509900.1 gg_id:112446 Rhizobium leguminosarum str. ATCC 14480 AY5099
U89831.1 gg_id:5335 Rhizobium leguminosarum bv. viciae str. USDA 2508 U89831
AY904742.1 gg_id:112445 Rhizobium leguminosarum str. SEMIA 3007 AY9047
EU256416.1 gg_id:257453 Rhizobium leguminosarum str. CCBAU 85142 EU2564
EU637927.1 gg_id:548867 Rhizobium leguminosarum bv. viciae str. XtP1 EU6379
DQ989228.1 gg_id:186910 Rhizobium leguminosarum str. CCBAU 73374 DQ989
EU256418.1 gg_id:251645 Rhizobium leguminosarum str. CCBAU 85010 EU2564

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1881.0	1794.0	1552.3	1790.1	3303.6	2022.7	2928.7	2851.0	1107.5	1107.4	1075.1
2335.3	3152.2	3363.9	3678.3	5088.3	3795.1	4694.7	4987.7	2870.1	2908.5	5204.7
1949.1	2179.7	2076.5	2131.0	3191.1	2435.7	2763.0	2749.3	1484.3	2258.1	1234.9
11157.5	5308.8	4856.5	4747.9	5474.9	4897.2	5550.4	5248.1	5648.3	5795.3	5381.3
644.6	1294.4	1714.1	1782.4	2063.3	1752.2	2159.8	2495.6	1495.8	2112.9	1227.7
5087.6	2437.4	3168.7	3079.0	3683.9	2955.1	3026.3	3921.7	2666.1	3448.4	2061.1
6781.5	6214.8	5567.5	6267.8	7494.7	6420.0	7772.7	6904.6	12305.0	8907.9	5933.4
19022.6	3644.9	3886.7	4246.3	5518.8	4086.0	4630.2	4477.8	3534.6	3541.4	2750.4
26228.0	12132.9	11525.6	12625.6	15084.0	12977.0	14086.9	12475.6	15835.8	14990.2	13355.5
19975.9	9778.0	8741.1	8437.2	11702.2	9751.0	10723.9	9263.7	13263.9	11606.0	11924.6
16915.6	6301.3	5318.7	5215.5	5642.9	7127.0	5174.3	6140.9	6421.1	8486.3	5011.8
2517.0	4439.4	4093.7	4702.0	6432.6	4567.9	5799.8	5490.5	7595.7	5869.2	4313.6
5078.8	5768.4	5245.3	5650.2	7014.3	6248.8	6119.9	6902.3	8773.9	8121.4	4940.9
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215.8	1375.1	2227.0	1758.3	2522.9	2017.8	1851.4	2806.7	1545.2	4488.4	1187.9
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361.0	1571.2	2529.5	2528.3	3375.9	2119.4	2709.2	2576.8	1390.0	2448.3	1242.8
12486.9	5653.7	6283.4	7025.7	7295.9	5983.7	7717.1	6147.9	6673.2	7406.1	7209.0
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2344.7	2831.4	3039.2	3095.1	4170.3	3495.8	3518.5	3787.6	3388.9	5140.1	2265.4
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1837.7	1616.8	1581.6	1487.8	1909.1	1640.4	2047.9	1932.0	1121.8	1286.0	1029.0
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1100.8	1924.0	2537.9	2156.4	2317.1	2331.3	1695.1	2683.8	1487.9	3982.9	1360.5
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17545.2	5235.1	5354.0	5396.3	5699.5	5159.0	6056.8	6092.1	5880.0	5580.9	4639.3
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8426.7	5525.2	4348.5
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1042.6	1913.4	2246.1	1977.7	2090.8	2331.4	1708.1	2421.5	1573.1	3907.8	1616.4
2307.3	2105.2	2576.6	2793.5	3507.5	3647.6	3864.3	3198.1	3751.9	2754.1	2757.0
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783.4	1274.7	1339.6	1325.2	1705.9	1419.0	1275.4	1528.2	1114.8	2399.9	1077.0
361.1	1976.2	2989.6	2163.8	2274.2	2196.9	2585.5	3120.9	2129.7	3715.0	1934.1
10377.0	4829.0	4121.6	5635.4	6536.9	5087.3	8008.0	5738.7	5805.4	8276.1	6663.0
13885.6	5454.1	5476.1	5980.5	6946.1	6517.2	7771.8	6685.0	6197.5	8692.1	5677.3
13790.6	5368.8	5395.3	6154.4	6017.2	5993.5	7817.0	6448.8	6894.5	6402.1	8440.7
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4275.0	1868.6	2221.7	2545.6	2468.1	2428.2	4057.0	3276.9	2352.4	4550.8	2854.7
10452.5	3156.0	3095.7	3783.4	4473.0	3606.5	5863.8	4129.0	4036.3	5675.1	3878.2
16968.8	5126.1	5157.5	5826.4	6746.7	5461.8	8942.4	6006.7	6432.5	7456.8	6238.9
3804.3	3533.6	4215.2	4058.1	4594.3	4944.2	5080.6	5230.5	3923.0	7153.7	3408.4
14571.4	5513.0	6213.7	7611.0	7157.1	6528.6	10349.0	6772.9	7376.5	7399.3	8687.7
4888.4	3722.9	4234.7	5120.3	4002.5	4113.5	4850.5	4699.0	5043.4	8051.5	5152.3
911.8	2064.9	2028.0	1914.9	2886.1	2344.8	2517.0	2597.6	1901.8	2961.8	1227.8
8766.1	4889.3	5274.4	5506.0	5009.8	4826.2	9510.9	5323.7	6753.2	8788.9	9232.3
12749.7	4880.2	3909.3	3929.9	4748.1	5230.3	6630.7	5180.1	4577.2	5152.7	4539.7
752.5	1959.2	2254.5	2671.8	3291.5	2975.9	4340.6	3243.0	2143.0	4485.4	1712.8
3855.6	2796.7	2620.6	2914.1	3655.6	3872.4	3809.9	3970.7	3091.5	6120.7	2608.1
6630.1	6061.2	6039.0	5815.8	7569.4	7723.5	5917.0	7693.1	6376.0	9559.3	4785.9
1898.7	4471.5	5722.1	5161.0	6723.6	5969.4	5842.4	7335.4	5219.6	10125.7	3678.1
19312.3	2598.3	2531.6	2233.3	3840.5	2759.9	2943.1	2984.7	2599.4	3997.4	1924.5
6652.3	3661.0	4301.3	3737.4	5822.1	4564.9	4033.0	4726.5	3978.0	7648.2	3288.8
723.5	2921.8	3250.2	3139.7	4768.5	3597.5	3779.1	4688.0	3662.8	5686.2	2655.3
2553.3	2182.6	2609.0	2145.3	3583.0	2896.2	2781.6	2934.0	2588.6	4776.3	987.5

5457.8	5568.6	4741.9
6337.4	4998.1	3494.7
1843.5	1470.8	945.5
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7633.9	5925.5	3836.1
3677.9	3554.6	3202.5
1612.9	1576.9	1487.7
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4823.1	3271.9	2574.1
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2001.5	1713.8	1362.8
2674.1	2183.6	2037.7
3313.2	3114.6	2245.3
5354.4	3874.9	2897.5
4730.4	4111.8	3789.4
1982.6	1640.0	1316.8
2918.7	3171.0	2917.4
6760.5	6813.1	5459.0
7988.9	6457.4	5710.1
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5879.8	6534.5	6048.1
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7112.6	5825.2	5549.4
6315.7	4959.1	3486.6
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3011.6	2281.3	1738.8
5863.1	6074.1	4666.4
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9435.5	7161.2	4977.4
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AY509212.1 gg_id:107348 Rhizobium mongolense str. S110 AY5092
AF417561.1 gg_id:45894 Rhizobium gallicum str. DASA12024 AF4175
EU399924.1 gg_id:264788 Rhizobium tropici str. CAF333 EU3999
DQ422964.1 gg_id:155498 Sinorhizobium sp. str. Lv6.1Se DQ422
AB487888.1 gg_id:554002 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSSUR0 AB4878
EU420078.1 gg_id:563426 Agrobacterium rhizogenes str. Cy-0 EU4200
AY509210.1 gg_id:107049 Rhizobium etli str. S1 AY5092
GQ015299.1 gg_id:494367 Topographical and Temporal Human Skin Microbiome skin palm clone nbw766g05c1 GQ015
GQ015367.1 gg_id:494299 Topographical and Temporal Human Skin Microbiome skin palm clone nbw767e11c1 GQ015
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GU129569.1 gg_id:583148 Rhizobium giardinii str. Qtx-3 GU129
EU694389.1 gg_id:299472 Rhizobium huautlense str. MI-7 EU6943
U89817.1 gg_id:5320 Rhizobium mongolense str. USDA 1844 U89817
D14515.1 gg_id:5330 Rhizobium sp str. OK-50 D14515
AJ810381.1 gg_id:159130 Rhizobium genosp. AK CsB1B3 AJ8103
GQ287633.1 gg_id:587508 Rhizobium tropici str. Sap110 GQ287
EF540480.1 gg_id:219212 Rhizobium sp. 8_4V EF5404
EU399716.1 gg_id:268493 Rhizobium giardinii str. CCBAU 83011 EU3997
EU881929.1 gg_id:346116 Rhizobium sp. str. DJA1 EU8819
FJ025131.1 gg_id:334111 Rhizobium tropici str. SEMIA 4088 FJ0251
GQ397032.1 gg_id:574749 Functional unvegetated perhumid recently-deglaciated soils do not correlate shifts s GQ397
DQ815117.1 gg_id:166290 zebrafish digestive tract clone aab50c07 DQ815
X67226.2 gg_id:5448 Rhizobium galegae str. LMG 6214 X67226
EU335452.1 gg_id:243842 Changes microbial metabolic and along hydrogeochemically variable profile unsatura EU3354
EU399916.1 gg_id:269266 Rhizobium tropici str. CAF226 EU3999
FJ405384.1 gg_id:358164 Rhizobium tropici str. CAF446 FJ4053
U89832.1 gg_id:5277 Rhizobium tropici str. CIAT 899; USDA 9030 U89832
EF515979.1 gg_id:225133 grassland soil clone FCPU446 EF5159
FJ821665.1 gg_id:562882 Rhizobium sp. str. M20 FJ8216
DQ406713.1 gg_id:154917 Rhizobium tropici str. RP261 DQ406
FJ405376.1 gg_id:369125 Rhizobium tropici str. CAF344 FJ4053
EU074168.1 gg_id:255982 Rhizobium galegae str. CCBAU 01393 EU0741
FJ405380.1 gg_id:370346 Rhizobium tropici str. CAF439 FJ4053
EU488741.1 gg_id:321329 Rhizobium tropici str. CFN 299 EU4887
FJ671671.1 gg_id:530568 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6716
FJ528271.1 gg_id:573223 Rhizobium sp. str. Cs217 FJ5282
U71078.2 gg_id:5393 Rhizobium hainanense str. I66 U71078
AJ863373.1 gg_id:120422 poplar tree microcosm rhizosphere flooded clone 17RHF35 AJ8633
EU488743.1 gg_id:339515 Rhizobium tropici str. H12 EU4887
EU399925.1 gg_id:273473 Rhizobium tropici str. CAF336 EU3999

688.8	3128.8	4353.8	4186.5	5987.5	4726.5	4396.6	6181.8	4288.6	9033.9	3036.0
6510.7	3832.5	3895.5	3940.5	3821.2	4125.4	3933.3	3805.0	4446.4	5110.2	3813.2
19611.1	6613.3	6641.7	7094.5	9376.9	7576.5	7158.2	8345.3	10865.4	9469.9	9163.2
4273.9	4744.7	5889.1	5510.7	7331.1	6272.4	6538.6	7694.2	5054.4	10370.3	3988.3
14820.1	4088.6	3658.8	3498.8	5990.2	5307.2	2017.3	4902.9	3432.3	5296.9	1704.4
5132.5	3182.5	3410.2	3139.9	4969.7	3638.3	4812.6	5612.6	3058.4	6837.6	2682.2
2482.5	1678.3	2156.4	2048.7	2252.5	2113.0	2737.5	2560.2	1641.3	2721.1	1336.0
1372.2	2705.8	2512.5	3103.2	4224.1	3324.1	3178.9	3432.1	2537.0	3860.0	1870.4
4188.7	4136.7	4426.6	3892.7	5017.6	3810.7	4306.9	6254.1	3266.4	4952.2	3077.4
10825.8	3019.1	3921.2	3191.3	6256.6	4054.4	3189.8	4796.6	3328.3	4868.8	1954.4
8940.0	4538.2	4869.5	4637.9	5105.9	4652.8	5369.4	4979.0	5682.0	5410.2	5100.6
379.8	980.1	801.3	1027.0	1535.5	934.7	1076.7	1101.7	705.8	1479.5	437.1
4713.7	5587.2	5130.8	4622.9	5756.8	7246.6	4583.8	6312.7	5283.1	9205.8	3380.0
1555.4	2691.5	3233.8	3052.7	6136.3	4081.3	5420.3	5292.2	3079.0	7579.3	2620.4
2438.9	2905.1	3474.0	3393.4	4947.1	3687.1	4219.8	5504.0	2923.4	5628.2	2361.3
247.7	1386.2	1855.4	1407.7	2080.5	1084.6	1494.2	1866.4	1171.7	1565.3	868.6
19793.1	5447.9	4678.0	4978.0	6160.9	5714.7	6685.3	4936.0	5373.5	5250.7	4895.4
364.3	637.9	791.4	675.8	652.6	719.6	1419.3	917.7	887.9	398.1	618.9
3423.9	2989.6	3909.0	3599.7	6909.2	4614.9	5048.1	5371.3	2908.8	6845.9	2246.6
2265.0	2899.3	3432.7	3240.7	5596.0	4275.6	5057.1	5440.0	3064.7	6918.1	2417.9
5909.0	5738.7	6007.5	5741.1	7459.6	7246.6	6176.2	7978.2	5811.8	10490.4	4675.4
260.0	1989.8	2604.6	2553.3	3400.1	2729.2	3123.9	3856.1	2037.1	2978.6	1898.8
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3596.5	5318.1	5758.8	6044.5	8192.0	6660.1	7458.9	7901.0	4636.3	11414.8	5103.9
5958.1	2533.8	3362.8	2881.1	2963.6	2857.5	3357.7	3133.2	2283.7	3170.1	1948.9
1877.9	2899.7	2704.0	2710.9	3760.6	2613.0	2806.2	2990.9	3321.1	3285.7	2079.8
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119.2	329.3	552.0	466.6	720.5	402.1	437.9	701.9	338.7	884.2	244.8
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2357.7	4823.8	5853.1	5417.6	7213.6	6180.5	6095.3	7623.6	5519.3	10202.7	3866.2
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8737.2	8481.1	7181.1
9819.1	8256.0	5305.8
6829.7	4576.4	3890.7
6503.5	4297.8	3491.6
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6902.3	5168.1	3721.5
4438.9	6695.3	4177.7
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2180.4	2255.2	1422.3
5277.5	5495.6	5354.8
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7320.8	5979.5	4692.8
6624.8	4354.0	3514.3
9835.8	7309.8	5243.8
4972.9	3164.8	2271.7
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5518.3	4547.6	4180.1
6911.0	5710.1	3997.7
8819.0	7581.0	4799.1
9792.6	8338.2	6149.0
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3529.3	3359.1	2109.3
5732.6	3527.4	3385.4
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5452.4	4914.7	3920.5
7917.2	7381.3	8649.0
3674.9	3587.3	2287.0
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AF510387.1 gg_id:86899 Rhizobium sp. str. Phr-9 AF5103
AY688621.1 gg_id:132540 Rhizobium huautlense str. Se130 AY6886
FJ527681.1 gg_id:570278 Agrobacterium rhizogenes str. rif200811 FJ5276
EU256404.1 gg_id:243982 Rhizobium etli str. CCBAU 85039 EU2564
AF417565.1 gg_id:48790 Rhizobium leguminosarum str. DASA23052 AF4175
AY509217.1 gg_id:99135 Sinorhizobium fredii str. S150 AY5092
DQ490336.1 gg_id:157614 Representation heterotrophic isolates respective libraries recent Hawaiian (<300 yr DQ490
U38469.1 gg_id:5280 Rhizobium tropici str. USDA 2676 synonyms: CIAT 166 U38469
EF364372.1 gg_id:225279 Rhizobium sp. str. Alm-1 EF3643
AF025852.1 gg_id:5449 Rhizobium huautlense str. SO2 () AF0258
AB255067.1 gg_id:170340 corroded concrete clone IC-50 AB2550
EU344941.1 gg_id:262518 Hepialus gonggaensis guts equalized library larval gut clone Hg5-31 EU3449
GU214130.1 gg_id:586800 and biota slimes Canadian paper mills slime mill taken wet section around papermal GU214
AY064414.2 gg_id:75987 Rhizobium sp. str. DCP1 AY0644
FJ405378.1 gg_id:369642 Rhizobium tropici str. CAF436 FJ4053
FJ154086.1 gg_id:338916 Rhizobium giardinii str. CCNW0174 FJ1540
DQ814224.1 gg_id:162443 zebrafish digestive tract clone aab65f01 DQ814
AF364068.1 gg_id:77604 Rhizobium indigoferae str. CCBAU 71042 AF3640
AY166841.1 gg_id:76567 Rhizobium tropici str. UPRM8033 AY1668
DQ337581.1 gg_id:149175 Rhizobium sp. BBTR4 DQ337
AF417564.1 gg_id:17261 Rhizobium leguminosarum str. DASA23046 AF4175
EU618036.1 gg_id:278997 Rhizobium sp. str. CCBAU 65810 EU6180
DQ337571.1 gg_id:149885 Rhizobium sp. CHNTR26 DQ337
DQ814410.1 gg_id:165081 zebrafish digestive tract clone aab68c07 DQ814
AJ864848.1 gg_id:131846 Rhizobium sp. J34 AJ8648
AY626396.1 gg_id:105525 Agrobacterium vitis str. ICMP 5960 AY6263
EU488749.1 gg_id:336323 Rhizobium tropici str. 233 EU4887
DQ532253.1 gg_id:166577 Geographical Variation Microbial Burden and Spacecraft Assembly Johnson Space Ce DQ532
FJ405385.1 gg_id:366415 Agrobacterium rhizogenes str. CAF448 FJ4053
EU556969.3 gg_id:271487 Rhizobium sp. str. SL-1 EU5569
EF364377.1 gg_id:223771 Rhizobium sp. str. Alm-6 EF3643
GQ118964.1 gg_id:443148 Rhizobium tropici str. BKBLV5 GQ118
FJ675259.1 gg_id:513708 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6752
FM209489.1 gg_id:310821 Agrobacterium rhizogenes str. TS54 FM209
EU133607.1 gg_id:240333 tallgrass prarie soil clone FFCH12734 EU1336
AY117624.1 gg_id:63521 Rhizobium tropici str. PRF93 AY1176
AM922184.1 gg_id:248062 Rhizobium sp. Sulf-536 AM922
CU927666.1 gg_id:555946 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU927
DQ100062.1 gg_id:132779 Rhizobium sp. str. CCBAU 43060 DQ100
FJ444645.1 gg_id:577522 Cotton Rhizosphere cotton rhizosphere clone 2h-14 FJ4446

22634.0	10237.7	8960.6	9738.8	9083.1	8699.0	9683.7	9592.1	11393.3	12213.9	11482.6
4019.2	4908.7	4941.9	4447.2	7052.1	5439.2	5748.9	5616.6	6624.5	7702.1	4351.1
208.5	1789.8	2813.0	2093.3	4056.5	2802.6	3224.2	3271.5	1637.0	5170.9	1327.2
4163.1	4569.3	5534.5	5180.0	6107.8	6157.8	5114.8	7232.2	5511.5	9689.2	3780.3
3359.8	2825.0	2997.4	3114.7	4340.8	3445.2	3426.9	3969.8	3767.1	4044.0	2425.7
5406.0	6571.0	6357.1	6453.3	8321.8	8123.5	6500.0	8208.9	8120.5	10804.2	5393.9
19732.7	5830.5	6070.0	6046.2	6470.3	5878.0	6552.1	6423.7	7410.9	6673.5	7167.4
75.7	1835.2	2883.9	2525.2	4316.5	2782.9	2341.3	3620.9	1984.4	5762.6	1345.9
4405.7	5326.5	6097.2	5870.6	7402.9	6517.2	6445.0	8100.0	6092.6	10524.2	4729.0
127.3	1666.8	2521.2	1981.3	3641.4	2825.2	2676.3	3427.9	1962.5	4593.9	1396.3
104.6	1273.3	2571.2	1361.3	1952.2	1988.3	1283.1	2786.7	1741.6	2922.6	1163.2
1109.8	3623.4	3615.5	4540.2	5554.7	4003.4	5517.0	4770.4	4616.3	4540.0	3098.2
2284.1	2976.4	3101.6	2913.2	3273.5	3233.4	2606.0	3949.3	4684.7	3605.5	2882.2
2462.2	2578.7	3009.7	2699.5	4715.5	3483.1	3402.9	3754.9	3069.7	5915.3	2095.9
15086.6	8385.1	7512.1	8799.5	10331.4	9348.8	8282.4	8570.6	8560.7	8104.5	6740.6
27980.8	8360.1	8309.9	8209.1	9364.9	8896.8	9068.8	8289.1	11496.8	10624.5	10763.3
7516.3	3826.7	4530.0	4831.3	7284.4	4972.4	6412.5	5259.6	4108.5	7823.7	4211.9
18126.4	4196.0	4600.7	4687.2	5041.2	4234.1	4695.9	6015.3	4615.8	6403.2	3979.3
1554.0	3002.0	3141.5	3742.3	3340.9	3250.8	3671.3	4025.9	2680.9	4634.3	2256.1
7735.6	5649.0	5650.1	6188.7	8170.3	6683.6	7056.7	7857.2	6227.7	9448.3	5661.9
256.5	2393.9	1711.7	1854.0	3008.5	2161.0	1657.9	2228.3	1536.7	2504.1	1275.1
19895.3	6194.1	7100.4	7245.0	7261.8	6794.6	6497.7	7176.7	8597.1	8956.6	7412.6
573.9	2571.3	2362.0	2294.6	3640.0	3185.3	3747.6	3605.8	1580.8	3516.2	1572.0
2794.2	2129.0	2062.3	2222.7	1953.6	2248.1	3512.6	2767.0	2903.9	3890.5	1525.2
7383.5	5054.8	5654.7	5116.4	5998.4	4809.6	5451.3	8194.7	5888.3	11136.3	4485.8
4560.5	4337.2	4416.8	4894.9	6201.3	4917.0	6072.3	6193.0	4999.2	6618.1	3501.3
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1640.4	1916.3	2582.0	2354.5	2419.8	2120.3	2535.2	2814.8	1346.7	4041.5	1519.4
4730.6	3374.2	3082.0	3321.0	4226.9	3588.4	3833.7	5145.9	2148.4	2824.2	3224.3
2091.3	4823.9	5790.3	5380.0	6750.8	6142.6	6160.4	7458.7	5351.1	10196.8	3877.6
1549.7	4438.0	4809.1	4532.4	6017.1	5306.2	4748.8	5111.9	5182.8	7241.6	3736.2
2383.7	2741.2	3353.9	2759.4	5364.3	3618.2	3480.6	4425.3	2773.3	4871.2	2370.3
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4128.9	2028.7	2267.6	2206.7	2607.2	2595.5	2577.6	2696.5	2294.2	3884.1	2069.6
12114.3	7178.3	7580.5	7591.2	9309.4	8578.9	8053.1	9062.4	8299.4	10541.8	6613.6
1421.4	4462.1	5270.5	5035.1	6995.2	5566.6	6539.4	5810.6	4885.3	7719.3	4302.0
3606.7	5021.2	5995.3	5559.2	7045.8	6328.0	6477.1	7598.0	5654.8	10465.7	4056.1
164.0	1296.8	1791.7	1543.9	1837.0	1430.6	1714.4	2496.0	1235.1	3764.1	994.4
1751.1	3283.9	4046.6	3770.5	5346.4	5126.3	4046.8	5472.7	2930.8	6300.4	2357.4
3398.2	2797.8	3023.1	3065.4	4777.1	3184.8	3944.4	3632.7	3533.9	3327.4	2804.6
11680.7	5202.0	4502.2	4918.8	5579.9	5615.6	5650.9	5273.4	5448.4	6542.1	4790.9

9528.4	10164.7	8828.3
7091.6	6296.9	5058.0
5087.6	3400.9	2154.1
8658.9	6580.9	4161.0
4834.3	3485.7	2880.0
9833.0	7476.4	5294.0
6172.1	7270.9	5260.5
6023.9	2622.8	1798.7
9998.2	7798.4	5158.0
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7118.7	6332.4	4752.5
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3409.1	3700.9	2642.3
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8675.7	5956.2	4114.9
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4492.9	3896.1	3386.3
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EU344911.1 gg_id:267554 Hepialus gonggaensis guts equalized library larval gut clone Hg5-01 EU3449
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AM697248.1 gg_id:221087 sequencing libraries indoor dust clone BF0001C089 AM697
Z94803.1 gg_id:5364 Rhizobium genosp. R str. BDV5365 Z94803
GQ181047.1 gg_id:511579 Rhizobium lusitanum str. BLN7 GQ181
EF157275.1 gg_id:243829 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon EF1572
AY034026.1 gg_id:31634 Rhizobium loessense str. CCBAU 7190B AY0340
AY117667.1 gg_id:63509 Rhizobium tropici str. PRF77 AY1176
EU399920.1 gg_id:264590 Rhizobium tropici str. CAF279 EU3999
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EU488756.1 gg_id:313755 Rhizobium tropici str. H52 EU4887
FJ025129.1 gg_id:315875 Rhizobium sp. str. SEMIA 6411 FJ0251
AY064412.2 gg_id:76783 Rhizobium sp. str. DCP2 AY0644
AB233492.1 gg_id:205713 Amorphomonas oryzae str. B26 AB2334
EU867317.1 gg_id:586260 Rhizobium sp. str. CCGE2052 EU8673
U29387.1 gg_id:5389 Rhizobium sp str. RCR 3618D; USDA 2947 U29387
EU256433.1 gg_id:255837 Rhizobium cellulosilyticus str. CCBAU 85045 EU2564
DQ310471.1 gg_id:199327 Rhizobium sp. 28/2 DQ310
DQ984537.1 gg_id:256496 FD oil-contaminated soil clone FD_52 DQ984
AF417562.1 gg_id:24266 Rhizobium leguminosarum str. DASA23002 AF4175
AF510386.1 gg_id:87585 Rhizobium sp. str. vgs-11 AF5103
AB233494.1 gg_id:212299 Amorphomonas oryzae str. B47 AB2334
AF417563.1 gg_id:47187 Rhizobium leguminosarum str. DASA23111 AF4175
EU410948.1 gg_id:267876 Rhizobium giardinii str. CCNWGS0022 EU4109
AY117623.1 gg_id:63522 Rhizobium tropici str. PRF34 AY1176
FJ405382.1 gg_id:361567 Rhizobium tropici str. CAF443 FJ4053
Z79620.1 gg_id:5452 Rhizobium galegae str. NBIMTC 2246 Z79620
AY904747.1 gg_id:111491 Agrobacterium rhizogenes str. SEMIA 6070 AY9047
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EU600086.1 gg_id:276672 Pueraria montana var. lobata EU6000
AM697022.1 gg_id:217449 sequencing libraries indoor dust clone BF0001B048 AM697
EF522124.1 gg_id:220384 Agrobacterium rhizogenes str. CU10 EF5221
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FJ405375.1 gg_id:359783 Rhizobium tropici str. CAF341 FJ4053
EU488750.1 gg_id:322227 Rhizobium giardinii str. H152 EU4887
AF510382.1 gg_id:87256 Rhizobium sp. str. Kusp-1 AF5103
EU399714.1 gg_id:274169 Rhizobium tropici str. CCBAU 83795 EU3997

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313.3	3079.9	2103.7	1953.7	3289.5	2044.8	1711.1	1856.6	1561.7	2410.5	1171.0
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7959.8	9301.3	7595.5
2830.2	2489.7	1567.2
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2770.9	2294.2	1197.3
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EU584258.1 gg_id:352865 Rhizobium sp. str. ORS 3441 EU584
AY316683.1 gg_id:200464 Reichenowia parasiticae AY316
EF173321.1 gg_id:192524 Sinorhizobium sp. MKI7 EF1733
FJ517717.1 gg_id:560086 Disturbing epithelial homeostasis metazoan Hydra leads drastic changes microbiota e FJ5177
EU399935.1 gg_id:260090 Rhizobium tropici str. CAF438 EU399
D12788.1 gg_id:5289 Agrobacterium rhizogenes str. IAM 13570 D12788
EU399919.1 gg_id:276979 Rhizopus oryzae str. CAF276 EU399
DQ304797.1 gg_id:154037 studies on and nifH Lasiurus sindicus Sewan grass Thar Desert India root clone C6 DQ304
AB187585.1 gg_id:104322 Granulella daejeonensis str. Ch06 AB187
EU723213.1 gg_id:334997 Shinella sp. str. NP526a EU723
FJ598327.1 gg_id:566021 Shinella sp. str. 2-9 FJ5983
EU346730.1 gg_id:267822 Shinella zoogloeoides str. BC026 EU346
AF502218.1 gg_id:55816 EBPR sludge lab scale clone HP1B02 AF502
GQ009804.1 gg_id:499861 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw77 GQ009
DQ898296.1 gg_id:173668 Rhizobium sp. str. MTR-3A DQ898
EU104300.1 gg_id:345964 Evidence Comamonadaceae determinants settling performance activated sludge clo EU104
AB285481.1 gg_id:232448 Sulfolanivorax yambarensis str. MS4 AB285
FJ154090.1 gg_id:351849 Shinella kummerowiae str. CCNWGS0228 FJ1540
EF437254.1 gg_id:249079 Rhizobium sp. str. RZ6 EF4372
FN436071.1 gg_id:573545 Molekularbiologische Charakterisierung der bakteriellen Populationsdynamik eines t FN436
FN555404.1 gg_id:511375 Sinorhizobium sp. I-Bh25-4 FN555
D14255.1 gg_id:5205 Zoogloea ramigera str. IAM12669 D14255
DQ984584.1 gg_id:256527 Mt. Nan-Jen litterfall clone IYF06 DQ984
DQ096644.1 gg_id:132981 Rhizobium sp. PIP4 str. PIP4; JCM 12219 DQ096
EU888002.1 gg_id:349041 Microbial structure hydrolytic stage two-stage anaerobic digestion grass silage leach EU888
DQ814239.1 gg_id:162359 zebrafish digestive tract clone aab65g10 DQ814
X74915.1 gg_id:5207 Shinella zoogloeoides str. ATCC 19623 X74915
AM181744.1 gg_id:160209 Sinorhizobium arboris str. LMG 14919 AM181
D14509.1 gg_id:5245 Sinorhizobium meliloti str. IAM12611 D14509
EU379945.1 gg_id:270061 Sinorhizobium meliloti str. CCBAU 83856 EU379
EF531326.1 gg_id:278035 Sinorhizobium meliloti str. AC-1 EF5313
GU433464.1 gg_id:517976 Sinorhizobium meliloti str. CCBAU 65887 GU433
EU256454.1 gg_id:253057 Sinorhizobium meliloti str. CCBAU 85101 EU256
EF634450.1 gg_id:278262 Sinorhizobium meliloti str. PP3 EF6344
DQ989230.1 gg_id:176599 Sinorhizobium meliloti str. CCBAU 81180 DQ989
AY904726.1 gg_id:111921 Sinorhizobium meliloti str. SEMIA 103 AY904
AM946566.1 gg_id:325210 Ensifer maghrebium str. ORS 1410 AM946
EU625296.1 gg_id:278661 Sinorhizobium meliloti str. 27 EU625
FJ025127.1 gg_id:351945 Sinorhizobium meliloti str. SEMIA 6162 FJ0251
EU545511.1 gg_id:342747 Sinorhizobium meliloti EU545

16377.8	6450.3	6645.1	6426.4	7655.8	6572.3	7131.8	6753.2	8150.3	9391.8	6821.5
815.1	1754.8	2019.4	2212.0	2793.4	2026.7	1819.1	3222.4	1980.1	2455.2	1459.2
16540.9	6936.2	6765.4	7022.1	9296.5	7443.5	9254.7	8209.3	6056.4	7778.8	5439.6
541.3	1528.5	1997.7	1983.3	2555.8	2156.2	1700.5	3204.6	2018.0	2816.3	1242.6
1524.1	4866.7	4738.2	5015.0	6405.9	5284.9	6161.2	6261.5	4938.9	5230.4	3405.2
2630.9	4703.4	5371.3	5258.6	7096.9	6108.9	6207.0	7553.3	5161.9	11048.4	3837.4
6146.0	6234.9	6664.4	6958.7	8374.4	7104.4	7567.6	8513.2	8044.2	10702.9	6155.2
2861.4	5183.3	6261.1	5905.8	7677.4	6645.2	6747.1	8268.1	6497.3	11788.8	4533.6
10017.7	5976.7	7354.6	7520.3	9376.2	7136.7	5985.6	9813.7	7276.6	8570.2	8120.8
4278.6	4771.4	4689.5	5265.7	6592.4	4811.2	6046.6	6736.6	5834.0	5093.9	4079.3
1443.5	2264.4	2307.3	2625.1	3651.5	2483.2	2528.5	3608.6	2004.7	2349.5	1644.7
246.6	1140.4	788.0	756.9	1598.3	1180.2	1239.0	1214.6	551.0	916.8	548.4
1185.1	1570.7	1778.1	1833.2	3105.1	1895.6	1982.1	2692.2	1515.3	1692.8	1094.4
15271.2	8064.1	8039.3	8293.1	9620.2	9044.3	9220.5	8390.7	12445.5	10777.0	9297.5
1830.6	3639.7	3411.1	4013.1	5173.7	4114.0	4740.6	5938.8	6462.5	4508.0	3740.8
921.9	3732.9	2836.8	3769.7	3710.3	3442.3	3305.1	3565.5	2590.5	3447.6	1826.1
598.3	1590.1	1830.8	2195.8	2646.8	1975.6	1997.8	3379.3	2579.6	2624.7	1478.3
7622.7	5914.5	5983.5	6576.3	8008.9	6245.8	7455.2	7668.4	7406.4	6464.6	5208.3
21873.6	6980.5	7665.7	8857.8	11166.3	7664.5	10082.4	8812.1	9436.9	9895.2	7422.3
44.6	956.7	1638.5	1401.4	2421.0	2470.0	2263.6	3229.6	1042.1	3463.2	1054.9
828.7	2915.4	3897.5	3766.1	5218.3	3988.2	5262.6	5090.0	2510.5	3821.0	3006.4
5811.0	2690.4	2389.3	2553.1	4169.6	2942.2	3414.3	3139.2	2029.4	1678.4	1488.4
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119.6	2315.7	3305.6	3248.2	4820.4	3430.2	3480.5	6029.4	2099.2	4705.4	4238.3
5891.4	3956.2	4219.1	4501.6	5602.6	4258.3	5515.1	6168.4	5716.6	5798.1	3513.0
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115.0	779.4	1012.3	808.4	1901.9	1182.7	1114.2	1972.7	911.0	1491.1	644.9
11569.7	3059.7	3158.5	3125.7	8726.9	4429.8	4866.2	4329.0	2532.3	2961.6	1037.6
4218.7	2946.3	3227.2	2993.1	6290.3	4227.1	4738.5	4561.9	2936.0	4434.1	2553.9
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78.8	1153.6	1176.4	1743.4	1474.0	1286.4	1156.6	1647.1	731.7	1635.9	647.5
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21343.3	5608.2	5495.6	5777.9	7713.9	5910.6	7056.9	5856.8	7322.3	6650.8	6709.7
5762.0	3822.4	3695.6	3861.9	8943.5	5162.8	6901.7	5129.2	2943.2	3953.2	2801.1
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8380.3	4426.0	5020.2	4964.3	7887.7	5720.0	6020.8	6406.0	5219.5	6664.7	4273.3
3232.4	3734.9	4360.5	4296.0	7435.4	4575.5	6882.2	6097.3	2847.9	4955.7	2724.7
11022.6	4378.0	4313.0	5192.5	7517.3	5545.7	6744.5	5569.6	4760.1	4324.0	5905.7

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AB535696.1 gg_id:557105 Sinorhizobium medicae str. Cl.3-2 AB5356
EU379949.1 gg_id:261990 Sinorhizobium meliloti str. CCBAU 83575 EU3799
AY904727.1 gg_id:111751 Sinorhizobium meliloti str. SEMIA 134 AY9047
EU256452.1 gg_id:244861 Sinorhizobium meliloti str. CCBAU 85092 EU2564
AF533685.1 gg_id:61015 Sinorhizobium meliloti str. WSM1702 AF5336
AM946567.1 gg_id:343932 Ensifer xericitae str. ORS 1401 AM946
GU129566.1 gg_id:594144 Sinorhizobium meliloti str. Qtx-8-1 GU129
AB535703.1 gg_id:545858 Sinorhizobium medicae str. Pl.4-2 AB5357
AB015420.1 gg_id:34931 Sinorhizobium indiaensis str. Ra-3 AB0154
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EF070136.1 gg_id:182386 Sinorhizobium meliloti str. CCBAU 05137 EF0701
AB017203.1 gg_id:50238 Prosthecomicrobium pneumaticum str. MBIC3489 AB017
EU488283.1 gg_id:551681 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU488
FJ793198.1 gg_id:564313 Rhizobium sp. str. CAAS-2R FJ7931
CU920781.1 gg_id:563220 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU920
EU488449.1 gg_id:570051 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU4884
EU488300.1 gg_id:559383 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU4883
EU488378.1 gg_id:565999 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU4883
EU488368.1 gg_id:542279 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU4883
EU488131.1 gg_id:534712 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU4881
AB232339.2 gg_id:155467 Bartonella sp. str. TFC2 AB2323
EU488467.1 gg_id:553301 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU4884
EF540509.1 gg_id:219954 Rhizobium sp. 4_C16_39 EF5405
EF516927.1 gg_id:218154 grassland soil clone FCPP541 EF5169
EU488260.1 gg_id:547565 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU488
AY133103.1 gg_id:56163 TCE-contaminated site clone ccspost2147 AY1331
EU488463.1 gg_id:571469 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU4884
EU488371.1 gg_id:534308 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU4883
EU817493.1 gg_id:326733 Rhizobium sp. str. XJ-L72 EU8174
EF090606.1 gg_id:197918 Agrobacterium sp. str. Mei-QS6 EF0906
EU488459.1 gg_id:565076 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU4884
EU488190.1 gg_id:543717 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU4881
EU488204.1 gg_id:553575 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU488
NZ_AAUW01000023.1 gg_id:175858 Stappia aggregata str. IAM 12614 NZ_AA
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23757.4	7542.7	7481.2	7770.6	12248.0	8320.1	11732.8	8953.8	6368.3	6445.1	5807.5
12798.1	6825.8	6600.1	6838.4	10010.8	7939.2	8268.2	8080.7	7266.2	8146.0	6051.4
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725.1	1390.8	1488.1	2086.9	2871.6	1504.4	1895.5	2205.1	1392.1	1116.8	927.3
3782.5	2913.9	2949.5	2807.6	7408.6	4035.0	5185.1	4114.2	2363.3	3115.9	1917.1
12649.7	5886.8	5504.0	5649.9	9184.0	6597.0	8208.4	6708.4	4780.3	6090.6	4326.2
4952.4	1161.2	1343.9	1197.4	2326.9	1492.2	1937.2	1618.8	794.9	1111.3	847.0
7981.3	3102.2	2590.3	3678.6	4703.1	3605.4	4750.9	3762.1	3206.7	3671.8	5596.7
26921.9	3611.7	3757.9	3247.3	3416.1	3978.5	2852.2	4773.8	4551.9	5247.3	3584.4
353.5	1235.5	926.6	824.3	1575.1	1560.9	1100.0	1111.2	629.7	998.0	511.0
12678.4	5200.8	5267.4	5237.4	7996.5	6099.8	6216.1	6569.0	5110.3	6575.2	4486.2
3207.2	4251.3	4727.1	4708.5	7408.2	5516.1	5513.5	6444.2	5052.3	6815.0	3961.2
4687.8	4041.8	4198.4	3916.9	6577.2	4991.7	4736.6	5574.5	3817.5	5612.1	3134.6
196.4	798.7	870.6	947.2	1665.5	1139.4	1522.1	1039.5	614.7	807.6	369.0
20383.0	5757.1	6329.9	6385.7	6782.0	6972.4	6612.9	6405.0	8584.8	8446.2	8558.5
2881.5	2915.7	3027.6	3012.2	4542.7	3740.6	4455.8	4434.8	2686.9	5126.3	2199.2
12354.8	1914.3	2568.2	2697.2	4489.7	2702.9	1404.7	2750.7	2089.3	2968.4	805.3
11831.8	4991.1	5778.0	5805.7	6445.1	6086.0	6004.1	6512.1	6497.9	5032.3	5495.7
5639.6	4447.1	4209.7	4519.1	5210.2	5130.9	4523.5	4838.4	4452.4	4735.5	5505.1
4735.6	5297.3	5580.5	5658.1	6706.7	5826.9	5477.5	5640.4	4934.9	5787.4	5115.0
3530.5	3056.7	3211.1	3516.3	6680.8	5007.3	4755.9	5406.4	2391.5	5823.1	2551.7
6469.0	3622.8	3439.9	3630.3	5802.5	4593.4	4948.6	5299.6	3167.6	4728.2	2718.9
4641.0	4002.1	4037.1	3697.1	9006.9	5460.9	6433.3	5252.9	3133.7	4429.9	2599.9
22238.7	4848.9	5022.6	5193.7	5268.6	5063.0	5733.5	5513.7	6827.2	6515.3	5394.9
1459.9	1295.9	1550.5	1695.2	2661.2	2702.3	2180.8	3477.9	1110.0	4306.3	1109.2
222.2	2132.3	2875.7	2822.9	2891.8	2849.7	2642.9	3823.5	2110.5	4398.7	2170.3
17119.0	5034.4	5375.1	5832.2	6079.5	5707.2	6027.9	6281.2	6259.3	5634.1	4532.9
17349.2	6330.6	6506.5	6966.1	8137.1	7056.7	8047.0	7752.9	9336.8	7605.3	8572.1
7625.0	5352.5	5289.7	5342.2	4794.8	5373.2	5251.7	5411.3	5694.3	4330.6	6525.5
13688.9	7188.9	7493.1	7887.4	8468.2	7990.7	8448.7	7780.0	9629.8	9935.1	10317.4
2303.7	2970.9	3511.8	3482.1	7151.2	4654.2	5422.3	4994.4	3119.1	7649.2	2511.9
8759.6	5689.5	5861.5	6242.8	8003.0	6896.4	6341.9	7672.5	7083.9	8917.0	5677.1
9163.6	6041.8	6352.1	6215.9	6526.5	6264.6	6206.6	6728.9	8029.7	9039.2	5811.3
13244.2	6102.8	6129.3	6475.3	6601.2	6408.8	6121.6	6198.4	7507.8	7997.6	8107.1
12362.9	5561.3	5593.7	6344.4	8689.7	7200.9	7380.2	7741.4	6521.9	8075.3	6564.9
1174.0	1676.9	1536.7	1741.2	2610.0	2571.1	1534.5	2599.9	1714.7	2245.5	1789.6
2134.7	4325.5	3476.0	3733.1	5729.6	4756.9	5011.4	4069.5	2676.9	2747.1	2474.8
544.3	1523.7	1458.6	1382.8	2353.2	2721.5	1667.0	1927.5	1084.2	1759.6	869.7

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6903.3	4825.1	4144.7
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10657.1	7488.9	9359.5
9560.8	8169.5	7009.9
6191.2	4823.7	4031.1
2444.0	1761.3	1426.7
5362.3	3671.0	3015.3
8132.2	6590.9	6868.5
1806.1	2952.5	1794.9
4008.0	4192.0	3574.0
4700.6	4815.4	4037.7
1175.3	1230.1	1015.7
8390.1	6488.9	5384.9
8701.4	6356.7	4563.9
7215.8	5233.1	3971.9
1123.9	1478.1	1516.4
7161.8	8030.4	5171.4
5897.0	4856.9	3546.6
4967.4	3080.5	2637.8
6596.0	8037.4	5923.5
5670.0	5109.3	3267.5
6933.1	6068.6	5064.9
6845.4	4553.0	2299.0
5682.2	4764.5	2792.9
7414.3	5216.9	4257.6
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4523.3	2414.9	1160.7
4186.2	3726.2	3711.0
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9078.8	6823.8	5564.4
7179.9	7259.3	4963.4
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8489.1	6981.7	5382.0
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s__Afifella marina	60542
s__Afifella marina	60815
s__unclassified	60973
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s__Rhodobium orientis	59356
s__unclassified	58949
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EU841534.1 gg_id:340002 Pannonibacter phragmitetus str. 224 EU841
EF608175.3 gg_id:535229 Pannonibacter sp. str. HT23 EF6081
AM990762.1 gg_id:279133 Pseudovibrio sp. MOLA 539 AM990
FJ169215.1 gg_id:342767 microbial and polyketide biosynthetic potential palmerolide-producing tunicate Synoi FJ1692
FJ169195.1 gg_id:321382 microbial and polyketide biosynthetic potential palmerolide-producing tunicate Synoi FJ1691
EU726271.1 gg_id:342195 Stappia sp. str. B106 EU726
EU581698.1 gg_id:275806 Rhodobacteraceae sp. MEBiC05064T marine sponge Geomun-Island South Korea EU581
DQ985041.1 gg_id:193166 Halomonas sp. str. JL1044 DQ985
EF101502.1 gg_id:194356 Stappia meyerae str. GA15 EF1015
EU167953.1 gg_id:269625 Stappia sp. str. 16-23 EU167
AY162083.1 gg_id:135498 Cultivating Sargasso Sea clone GMD37F4 AY162
FJ202909.1 gg_id:325677 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2029
AY628423.1 gg_id:99161 Stappia marina str. mano18 AY6284
D85832.1 gg_id:111501 Roseibium denhamense str. OCh 254 D8583
AY588950.1 gg_id:122223 Pacific Ocean deep sea sediment clone DE6.8 AY588
EU168019.1 gg_id:269506 Stappia sp. str. 23-28 EU168
EU999013.1 gg_id:304551 Predominance Methanolobus and Methanoculleus spp. Archaeal Saline Gas Field Foı EU999
DQ270709.1 gg_id:144694 Halomonas sp. B-3046 DQ270
GU199002.1 gg_id:593115 Mycoplana sp. str. G110 GU199
GU322907.1 gg_id:524664 Labrenzia sp. str. YC6927 GU322
EF101504.1 gg_id:185052 Stappia conradae str. MIO EF1015
DQ660386.1 gg_id:161779 Pseudovibrio sp. str. SPO723 DQ660
AJ889009.1 gg_id:139632 Stappia alba str. 5OM9 AJ8890
DQ416561.1 gg_id:151808 s1cb71 DQ416
DQ985044.1 gg_id:196145 Rhodopseudomonas sp. str. JL1015 DQ985
AM696707.1 gg_id:224191 Rhodobium marinum str. JA211 AM696
GU370102.1 gg_id:521541 Rhodopseudomonas sp. str. P530(9) GU370
EU445271.1 gg_id:272585 Rhodobium pfennigii str. AR 2102 EU445
AM180706.1 gg_id:161325 Rhodobium gokurnum str. JA 173 AM180
DQ532207.1 gg_id:166078 Geographical Variation Microbial Burden and Spacecraft Assembly Johnson Space Ce DQ532
AB374392.1 gg_id:269733 sequences Weissenstein (white rock) / few millimeters be surface rock called 'Weiss AB3743
AB257630.1 gg_id:273081 Microbial few millimeters be surface dolomite rock 'Val Piora' Alps 1965 meters abov AB2576
EU133571.1 gg_id:245274 tallgrass prarie soil clone FFCH4802 EU1335
FJ152795.1 gg_id:310212 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX5A_ FJ1527
DQ451507.1 gg_id:156833 forest soil clone FAC68 DQ451
AY862042.1 gg_id:112593 Washburn Spring 1 community clone WB1B012 AY8620
GQ093827.1 gg_id:452509 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ093
FJ152772.1 gg_id:315470 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX5A_ FJ1527
AF050531.1 gg_id:4714 contaminated aquifer clone WCHB1-55 AF0505
GQ402732.1 gg_id:538998 Accessing microbial biodiversity and metabolic potential tropical -based approach pe GQ402
EU104345.1 gg_id:338628 Evidence Comamonadaceae determinants settling performance activated sludge clo EU1043

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7236.4	2168.9	1316.3	1395.2	2651.3	2478.5	2160.8	1909.9	1323.8	1704.6	863.8
268.6	159.9	227.0	225.4	456.8	209.8	269.3	447.3	114.8	192.7	143.5
15060.0	7676.4	8253.3	8756.4	10516.2	8512.4	9666.5	8996.0	11220.6	9723.4	8128.0
18918.7	6946.1	6367.2	6716.2	10787.9	8033.8	7277.1	7592.6	6878.9	9241.4	5813.8
6892.0	3774.0	3436.8	4552.9	4335.9	4419.7	4163.5	4032.7	6310.4	2532.1	3744.1
1631.9	1949.7	1644.7	1656.8	2350.0	1900.1	2157.0	1997.9	1092.5	1194.5	1155.5
1523.8	2964.4	2852.4	3073.1	4021.5	4412.1	4083.7	3807.7	3892.0	2267.3	2430.2
14265.5	6728.5	5694.7	5540.9	7887.4	7282.9	6253.7	6457.6	6278.4	7389.9	4007.6
4362.0	3929.1	4204.8	4577.2	5218.1	4509.2	4833.2	4778.5	4598.9	4479.6	3455.3
783.7	1269.4	1458.0	1463.6	2096.2	1756.1	1656.8	2452.3	1135.9	1339.5	1301.6
62.8	272.6	275.9	224.3	356.3	289.5	264.6	626.9	1409.8	52.5	200.2
1359.6	1567.1	1634.2	1232.7	1539.7	1878.6	1391.3	1994.9	636.0	636.6	1119.6
4880.6	2939.6	2521.4	2057.5	2627.3	2699.2	2221.1	2605.7	1952.2	1294.8	1957.9
124.0	820.9	816.9	695.8	1200.0	1318.1	834.9	1196.3	423.0	472.9	409.4
5299.8	1593.4	2057.1	1899.2	2566.6	2139.2	1725.2	2100.9	1605.3	2174.5	1331.2
4334.4	4631.6	3576.3	4331.3	6530.8	5246.8	5360.3	4820.5	6353.8	3347.5	3644.5
196.2	838.9	1597.0	1790.5	1747.5	1749.3	2412.9	1210.2	2225.2	1464.4	1741.9
844.2	1486.8	1487.7	1234.2	1809.7	2957.1	1145.7	1758.7	676.4	1053.1	611.9
29844.3	9506.0	8062.0	8851.0	9766.8	8594.6	10463.8	7781.3	13075.0	9656.9	12015.7
8601.8	4353.8	4433.3	4407.2	4482.5	4722.3	4139.8	4872.9	4435.8	4425.6	3544.3
687.1	1682.8	2513.7	2666.3	2268.9	3121.9	1939.2	2975.5	2073.9	4110.1	1924.2
2825.7	1427.7	1524.3	1616.6	2117.5	2242.1	1561.7	2332.3	1705.2	1754.2	1231.8
757.9	1800.5	2034.1	2001.9	3225.9	2527.6	2129.0	3152.9	2407.4	2966.1	853.1
436.2	1237.8	1526.7	1712.1	2326.5	1497.0	1820.9	2154.9	1087.3	820.5	1063.7
2265.2	1318.2	1463.2	1458.6	1501.1	1307.2	1759.8	1687.0	1231.4	600.7	1484.4
2531.0	2094.7	2284.7	2291.5	3487.5	3261.8	3085.4	3099.0	2071.2	2507.6	2239.1
3043.0	1120.5	1534.5	1589.5	2707.7	1579.6	2565.2	2067.9	771.4	577.4	652.7
5046.0	2143.4	3038.3	2823.9	3728.6	3802.9	3361.0	2561.7	2230.2	1833.7	1456.5
219.1	1254.4	1276.9	1445.1	2704.9	1755.5	1832.8	1914.0	973.3	737.9	1052.4
18740.5	8979.9	8083.9	8306.4	11481.7	9336.4	10396.1	8577.4	8788.9	7454.9	7363.0
4484.4	4860.5	5633.0	7109.4	5387.0	4404.5	5908.4	6428.2	4125.0	3107.1	5097.5
14147.6	4285.7	4423.6	4876.1	6279.2	4818.1	5659.6	5024.5	4768.9	3270.5	3861.8
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10230.6	5613.1	4939.6	5081.1	5659.6	5240.2	7117.2	5153.6	7964.5	5546.5	6023.6
19901.8	8386.3	7277.4	7229.0	10764.5	7625.8	9481.8	7318.2	7203.3	4672.9	5655.8
13430.1	5845.4	5578.6	6061.6	6859.1	5798.2	6755.4	6784.8	3857.3	3276.6	4643.7
2393.7	3649.0	3514.9	3511.8	4874.6	4001.3	4975.7	4331.2	2344.6	2099.1	2483.9
8991.6	7693.5	6543.3	7163.0	9742.6	7925.2	9889.7	7652.2	6467.5	5312.4	7500.5
4195.0	3609.7	2491.7	2447.1	4465.2	3915.1	4157.2	3319.2	3326.7	2015.1	1730.7
23328.1	8053.4	5989.9	5882.8	7436.8	6808.9	7487.6	5944.7	7232.0	6411.5	7339.0

8236.5	7213.6	7268.0
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7191.3	6555.4	5943.5
4480.3	3273.2	4016.3
2510.5	1563.0	1980.2
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7919.9	7546.4	7154.2
5567.9	5365.4	5043.8
2793.7	1581.5	1524.1
151.3	143.4	98.0
2406.2	1879.3	1464.4
2709.5	2915.1	2942.0
1016.6	772.2	749.5
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5501.0	4435.9	2918.6
1396.7	1529.4	1758.7
2221.6	1629.8	1233.5
8105.8	9421.3	8369.2
5127.5	4622.4	4676.3
3334.6	4046.0	2230.6
2740.0	1628.4	1872.4
3674.5	2833.2	1820.0
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1685.4	1895.2	2148.0
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2327.2	2297.0	3824.7
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2501.7	2305.7	2737.4
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EU887986.1 gg_id:304250 Microbial structure hydrolytic stage two-stage anaerobic digestion grass silage leach EU887
AF200695.1 gg_id:51286 13C- extracted 13C-methanol exposed soil clone UP2 proteobacterium AF200
EF516292.1 gg_id:222685 grassland soil clone FCPT613 EF5162
EF465533.1 gg_id:225699 Pseudoxanthobacter soli str. CC-CC4 EF4655
GQ263890.1 gg_id:510008 Structure Simulated Level Waste Site simulated level waste site clone WC2_141 GQ263
EU881257.1 gg_id:332410 (long-term grazing and burned annual) Karst region serious disturbance field soil clor EU881
DQ984620.1 gg_id:257087 YK oil-contaminated soil clone YK_31 DQ984
GQ262949.1 gg_id:538739 Structure Simulated Level Waste Site simulated level waste site clone F1_86X GQ262
AJ229208.1 gg_id:25697 anoxic bulk soil flooded rice microcosm clone BSV56 clone AJ2292
AM162440.1 gg_id:155413 and situ identification acidic sphagnum peat bog clone B83 AM162
U87772.1 gg_id:4760 Afipia genosp. 6 str. G8665 U8777
EF020321.1 gg_id:207430 aspen rhizosphere clone Elev_16S_1897 EF0203
X97077.1 gg_id:4765 peat bog clone TM19 X97077
FJ380167.1 gg_id:360221 ornithogenic Ross Sea region Antarctica AB1 soil clone 13/1/8F FJ3801
AF358012.1 gg_id:29077 peat soil microcosm clone LO13.2 AF358
DQ129631.1 gg_id:137916 microarray level air two cities Texas urban aerosol clone AKIW856 DQ129
DQ823159.1 gg_id:162179 Techniques Microbial Studies Oregon Caves National Monument Quad 3 off trail clo DQ823
GQ350414.1 gg_id:586170 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ350
EF516212.1 gg_id:225488 grassland soil clone FCPP499 EF5162
FJ152802.1 gg_id:308948 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX5A_ FJ1528
EU881153.1 gg_id:310925 Karst region primary forest soil clone KPF200711-196 EU881
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AM936498.1 gg_id:559544 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM936
EF019286.1 gg_id:209662 aspen rhizosphere clone Elev_16S_473 EF0192
GQ402711.1 gg_id:546022 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
DQ451452.1 gg_id:156829 forest soil clone FAC13 DQ451
GQ097820.1 gg_id:417366 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw397h0 GQ097
AM935446.1 gg_id:547229 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM935
FM253652.1 gg_id:332834 Rock gold mine unusually microbial biofilm clone D06-2 FM253
EU861875.1 gg_id:338761 effects chronic fertilization on alpine tundra microbial implications carbon and cyclin EU861
CU925666.1 gg_id:553033 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU925
CU926879.1 gg_id:567435 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU926
DQ813987.1 gg_id:162431 zebrafish digestive tract clone aab58b10 DQ813
AY913367.1 gg_id:137744 forest soil clone DUNssu160 (+7B) (OTU#170) AY9133
CU923391.1 gg_id:570766 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU923
GQ021391.1 gg_id:488276 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbu27 GQ021
FJ658644.1 gg_id:555885 Metalworking Fluids and Aerosols Metallurgy Plant metalworking aerosol clone Sum FJ6586
NR_025428.1 gg_id:548469 Chelatococcus asaccharovorans str. TE2 NR_02
GQ848214.1 gg_id:552413 and Archaeal Xiarinur Soda Lake Water-sediment Interface water-sediment interfac GQ848
FJ592562.1 gg_id:574090 Fumarole-supported islands biodiversity within hyperarid -elevation landscape on Pu FJ5925
AY792286.1 gg_id:124699 Humic Lake clone CrystalBog021H4 AY792

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30139.1	8838.1	6333.4	6620.0	9954.3	7997.4	8953.7	6996.4	6884.7	4829.9	4694.3
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FJ624896.1 gg_id:544990 Influence lead contamination on boreal pine forest soil clone HF_C_23 FJ6248
GQ065523.1 gg_id:452998 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw89d08(GQ065
AY212626.1 gg_id:106732 water 20 m upstream manure clone 175up AY212(
FM253660.1 gg_id:338715 Rock gold mine unusually microbial biofilm clone E09-2 FM253
DQ660884.1 gg_id:254810 DongChuan copper pyrites PRC determined acid mine drainage (AMD) clone DCK-I-2 DQ660
AY921699.1 gg_id:113477 farm soil clone AKYG1801 AY921(
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AB240233.1 gg_id:144675 microbial structure rhizosphere Phragmites bulk soil reed bed reactor laboratory clo AB240
EU617827.1 gg_id:344447 Seasonal variation microbial Yel Sea sediment clone D13S-4 EU617
EF079080.1 gg_id:252325 seeps sulfur-rich neutral pH ecosystem ochre-colored flocculent iron seep ditch fresh EF079(
EU050753.1 gg_id:256661 libraries sediment Kings Bay Svalbard Arctic clone ss1_B_08_05 EU050
EF018669.1 gg_id:209579 aspen rhizosphere clone Amb_16S_956 EF018(
FM253680.1 gg_id:310692 Rock gold mine unusually microbial biofilm clone H07-2 FM253
AY921829.1 gg_id:114266 farm soil clone AKYH1529 AY921
AM935046.1 gg_id:566962 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM935
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AY922106.1 gg_id:113801 farm soil clone AKYH1402 AY922
GQ263169.1 gg_id:511500 Structure Simulated Level Waste Site simulated level waste site clone F3_121X GQ263
GU118725.1 gg_id:567929 Threatened Corals Provide Microbial Habitats clone Mfra_B11 GU118
GQ008167.1 gg_id:501498 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ008
DQ378213.1 gg_id:154041 oil-polluted soil clone F51_Pitesti DQ378
GQ263279.1 gg_id:534132 Structure Simulated Level Waste Site simulated level waste site clone FW1_a25 GQ263
DQ230971.1 gg_id:141437 subsurface water clone DR938CH110701SACH95 DQ230
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GQ263601.1 gg_id:589565 Structure Simulated Level Waste Site simulated level waste site clone FW3_155C GQ263
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FJ998414.1 gg_id:390344 Amorphus sp. str. YIM D10 FJ9984
FJ477551.1 gg_id:509105 gut symbionts are tightly linked herbivory ants whole extracted single ant clone 83f FJ4775
FJ416098.1 gg_id:368583 sediments sediment station NEC5 Northern Bering Sea clone 061M64 FJ4160
FJ430076.1 gg_id:360023 Rhizobium sp. str. CCNWGS114 FJ4300
DQ454123.3 gg_id:229692 Rhizobium sp. str. J3-A127 DQ454
EF580937.1 gg_id:277780 Survey Microbial Freshwater Calcareous Mats freshwater calcareous mat clone CM4 EF5809
DQ113411.1 gg_id:143364 microflora ants genus Bartonella Tetraponera attenuata RT13 clone DQ113
GU118131.1 gg_id:535654 Threatened Corals Provide Microbial Habitats clone Apal_F11 GU118
FJ477662.1 gg_id:591010 gut symbionts are tightly linked herbivory ants whole extracted single ant clone UAB- FJ4776
EU056822.1 gg_id:354679 Rhizobium oryzae str. Alt 501 EU056
DQ269119.1 gg_id:197574 marine macro-alga surface clone DPC247 DQ269
GQ199732.1 gg_id:591717 Mycoplana sp. str. 210_30 GQ199

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8342.5	6575.9	5468.8	5509.3	7893.6	6028.0	8065.3	5787.5	5167.0	3277.5	3707.0
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4502.0	5791.4	3534.2	3240.1	7816.9	4866.1	7231.8	4752.2	3068.1	1538.5	1645.0
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334.4	1747.7	1282.2	1225.2	2928.9	1989.4	2620.6	1792.3	711.9	856.2	596.3
14883.9	6436.9	5771.4	6756.6	6876.3	6500.8	8122.6	5669.7	5842.5	3879.6	5176.6
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FJ202935.1 gg_id:348688 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2029
FJ230932.1 gg_id:323791 under Level Antibiotic Selection Pressures river water clone F30 FJ2309
EU290679.1 gg_id:254474 microbial structure biogeochemical contrasting shelf sediments Namibian upwelling EU290
EF125460.1 gg_id:176046 mangrove soil clone MSB-2G6 EF1254
EU022307.1 gg_id:256730 Mycoplana dimorpha str. DSM 7138 EU0223
AB476277.1 gg_id:567915 Compositional and functional transition epibiotic microbial hydrothermal vent galath AB476
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GU118008.1 gg_id:558255 Threatened Corals Provide Microbial Habitats clone Acer_O09 GU118
AM403234.1 gg_id:165611 Nitrate-reducing and Denitrifying Marine Aqua Biofilter marine aqua AM403
AJ318143.1 gg_id:46411 Waste-gas biofilter clone BIhii25 AJ3181
GQ093939.1 gg_id:462605 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ093
GQ033083.1 gg_id:432897 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ033
EF363715.1 gg_id:215874 Rhizobium soli str. DS-42 EF3637
GU118128.1 gg_id:548423 Threatened Corals Provide Microbial Habitats clone Apal_H04 GU118
GU118281.1 gg_id:563202 Threatened Corals Provide Microbial Habitats clone Dstr_J12 GU118
EU491593.1 gg_id:273684 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR4C EU491
AF423220.1 gg_id:51992 soil clone 1315-2 AF4232
FJ712592.1 gg_id:517638 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) k FJ7125
AY642558.1 gg_id:155596 and carbonate precipitation giant microbialites ly alkaline Lake Van Turkey microbiali AY6425
GQ054602.1 gg_id:405655 Topographical and Temporal Human Skin Microbiome skin back clone nbw1092d01c GQ054
DQ917801.1 gg_id:217617 Microbial profiles bleached and wild-type Muricea elongata Mesorhizobium clone BI DQ917
AJ294417.1 gg_id:22665 Rhizobium sp. str. TCK AJ2944
EU246825.1 gg_id:240545 polyphasic description Pocillopora meandrina Palmyra Atoll Calcinus obscurus abdon EU2468
EF532794.1 gg_id:221752 Mycoplana caeni str. K107 EF5327
GU369925.1 gg_id:525633 and mats vents Arc white microbial film on pebble aphotic zone shal hydrothermal v GU369
AM930452.1 gg_id:259822 involved Tripneustes gratilla (Echinoidea) cloning and FISH host body wall lesions cl AM930
EF649779.1 gg_id:244917 Rhizobium sp. str. J3-AN59 EF6497
DQ330994.1 gg_id:159335 Guerrero Negro hypersaline microbial mat clone 09D2Z18 DQ330
CU920079.1 gg_id:535750 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU920
AM697186.1 gg_id:223514 sequencing libraries indoor dust clone BF0001C027 AM697
GQ093897.1 gg_id:466355 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ093
FJ425633.1 gg_id:365493 communnities healthy and diseased colonies Caribbean coral Montastrea faveolata cl FJ4256
EU528264.1 gg_id:286797 Seasonal Dynamics Mudflat Mouth Major Kentucky Lake Reservoir Tributary sedime EU528
GQ365715.1 gg_id:548464 Hoeflea sp. str. AY-2 GQ365
DQ289935.1 gg_id:167459 Microbial Carbon and Nitrogen Cycling Sediments South Atlantic Bight Permeable Sh DQ289
FJ193930.1 gg_id:340714 Genetic inventory 'KSC-Astrotek' spacecraft assembly clean room during DAWN missi FJ1939
FJ203409.1 gg_id:331011 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h FJ2034
AF359524.1 gg_id:38898 Alexandrium lusitanicum NEPCC 253 AF3595
U78037.1 gg_id:5136 Ophiactis balli symbiont U7803
EU753666.1 gg_id:306406 modern freshwater stromatolites Ruidera Pools Natural Park Spain dry stromatolite EU753

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37.7	404.1	281.3	118.6	344.4	317.3	380.5	441.8	151.2	217.3	92.0
348.7	1730.7	2203.0	2164.7	2900.4	2562.0	2742.1	3642.6	2736.9	3276.2	1867.2
14072.9	5164.9	5144.9	5462.7	5890.9	5149.5	5320.7	5152.6	4346.5	4909.7	4474.7
19855.4	7915.3	7601.9	8310.7	10332.8	8569.5	9066.3	9214.0	11780.5	10107.9	7661.2
5275.5	2498.3	2716.2	2410.8	5481.7	3123.7	3934.9	3417.5	1546.1	1921.6	1129.5
3456.9	1525.7	1297.7	1368.9	2901.8	801.9	2004.8	1922.0	1189.1	1105.0	917.5
6735.7	6537.1	6101.8	6631.1	8185.9	6473.0	6865.7	6577.2	6333.4	6880.5	4623.5
2014.4	3092.2	3974.7	4057.8	3365.8	3673.1	3625.3	3625.5	4384.7	3934.3	3194.0
62.7	333.5	539.8	455.1	551.5	517.4	835.2	1306.0	449.1	1746.8	384.3
44.1	197.5	324.5	294.3	748.7	445.7	537.9	492.6	155.2	217.7	124.8
11286.6	5003.0	5141.8	4992.9	8224.4	5649.2	6990.6	4874.4	7403.3	5947.3	6484.7
1355.2	1880.4	2013.0	2421.3	2836.1	2006.5	3255.9	2922.4	2649.2	1517.7	1552.0
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3434.8	2079.4	2312.2	2302.6	5520.3	2650.1	3510.7	3537.0	1582.3	1468.7	1548.4
6282.1	3890.7	4809.1	5308.4	5773.9	4778.1	6203.5	5382.1	5988.5	4324.8	4370.3
237.0	721.4	697.9	851.4	1842.5	1089.6	1523.3	1408.9	457.8	394.5	491.4
556.2	1419.0	1606.3	1618.1	2137.8	1727.6	2264.0	2129.5	1305.4	2408.3	994.6
7935.1	5563.1	5915.7	6174.2	9038.0	6196.8	7040.2	6791.8	5781.2	4658.0	4815.2
3158.2	1842.4	1827.5	2008.3	2638.0	2378.4	2687.8	2990.7	1333.4	1953.6	1098.7
8516.0	4835.2	5303.2	6028.2	6918.6	5334.8	5424.8	7580.9	7975.7	5671.9	6846.2
946.4	3183.8	2392.0	2419.4	3467.1	2721.6	3870.5	2781.2	2062.4	1757.3	1957.8
297.4	2800.1	2989.8	3432.5	4107.0	3025.5	3540.5	4940.2	3852.7	3178.1	3301.1
7433.9	4437.3	4640.8	4769.2	8259.8	5699.9	6536.9	6761.4	4478.4	6095.7	3472.1
441.1	1167.5	1353.7	1413.1	2124.1	1691.6	1778.3	2036.9	1430.7	1264.6	715.8
2247.2	6331.6	5898.2	6003.9	8631.7	6869.5	7270.1	7058.9	6727.5	7443.3	4941.3
11033.3	7119.7	6943.9	7670.8	8873.7	8182.1	8190.8	7827.4	8603.2	9430.1	7280.9
298.2	3058.8	3546.4	3881.9	5460.1	4019.9	3893.7	5483.8	3038.5	4281.3	3927.1
39.4	264.5	262.7	197.9	366.5	330.3	173.6	398.8	141.7	359.2	110.4
17311.5	6836.0	6590.9	7126.4	10245.3	7501.2	9584.6	7445.2	7639.8	7499.4	6096.2
7667.7	8651.3	4563.9	4657.4	9705.7	5734.8	4333.0	5861.9	4315.9	6620.4	3200.9
3697.9	4995.3	4913.0	4951.5	8720.2	6328.8	7197.4	6264.9	4732.9	6105.9	3436.2
2980.2	3599.0	4309.2	3879.3	4603.9	3637.3	4288.6	4785.4	4567.3	4098.0	3317.1
5504.1	6391.1	5633.7	5924.2	5241.3	5991.0	6157.7	5325.7	7374.4	5587.8	5947.8
4803.7	7586.4	6613.3	6956.7	9018.5	9459.7	8459.0	8727.0	6652.9	7471.2	7324.0
8641.5	2077.0	2246.9	2204.8	4393.5	2424.8	4007.8	3261.4	1623.3	1627.6	1402.3
2337.6	3493.5	3270.8	3099.3	5165.6	3883.1	4623.8	4303.7	3094.1	3591.7	2436.5
2104.6	2090.5	2475.0	2442.9	4078.3	2337.5	3063.9	2856.1	2394.6	1830.2	1484.1
1264.2	3332.7	4034.9	3706.4	5142.0	3893.1	3593.7	4167.1	3320.5	4251.6	2970.3
39.4	25.7	25.1	33.8	70.2	46.6	30.4	34.7	23.9	24.1	25.3
8362.5	5499.0	5105.3	5391.7	6642.9	6497.5	6412.8	6798.2	9119.9	8414.4	4782.1

6332.6	7273.1	6616.2
388.1	255.2	116.9
4718.2	2779.4	1164.1
5870.3	5905.1	5516.8
10732.2	10289.9	8584.8
4648.6	2617.1	3721.2
2102.9	1652.4	1654.0
8520.8	8437.6	6555.7
3884.7	4469.8	4794.8
1299.9	851.6	254.4
810.4	503.3	358.6
5038.8	7101.2	4039.6
3163.0	2068.1	1522.8
6076.5	4426.7	3950.2
4278.5	3453.9	3087.9
6084.5	5404.2	4786.8
1203.9	1284.8	1267.8
2760.9	2439.4	2723.3
7982.1	6845.5	7037.3
3205.2	2518.1	2254.1
7982.6	6640.1	5544.6
3625.9	3401.5	3826.5
4861.0	4328.0	4480.8
8044.7	7046.1	5998.2
2458.3	2298.3	2368.3
8752.6	7755.0	7942.1
8619.3	8877.9	6942.9
5371.9	4730.7	4291.1
508.5	560.1	208.7
8530.6	9424.4	7788.4
6488.3	5294.1	4437.7
7649.7	6927.9	5637.7
4926.8	4828.5	4850.2
5361.3	6005.7	5463.6
9775.0	7196.1	4923.5
3916.1	3062.9	2686.7
5371.6	4296.8	5226.1
3468.0	4156.7	2866.7
4613.9	5117.8	3458.8
84.6	45.4	21.8
6471.4	6682.6	5424.9

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g__sfA
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g__sfB
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g__Azorhizobium
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s__Xanthobacter flavus	59876
s__Hirschia baltica	60559
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s__Hyphomonas jannaschiana	60685
s__Hyphomonas neptunium	60263
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AF003376.1 gg_id:5163 Rhizobium sp. str. SH2672	AF0033
DQ103630.1 gg_id:132060 hypersaline endoevaporitic microbial mat clone E2aG02	DQ103
DQ103632.1 gg_id:150577 hypersaline endoevaporitic microbial mat clone E6aD10	DQ103
DQ103628.1 gg_id:150589 hypersaline endoevaporitic microbial mat clone E2aB07	DQ103
AF004845.1 gg_id:4722 Methylorhabdus multivorans str. DM13	AF0048
AY056830.1 gg_id:17276 Ancylobacter rudongensis str. AS1.1761	AY0568
X94200.1 gg_id:4704 Azorhizobium caulinodans str. ORS 571	X94200
AY904784.1 gg_id:111946 Azorhizobium sp. str. SEMIA 6402	AY9047
EU876663.1 gg_id:317195 Azorhizobium sp. str. pcnb-3	EU8766
AB236172.1 gg_id:148902 Labrys methylaminiphilus str. DSM16812	AB2361
FJ707292.1 gg_id:572030 Labrys wisconsinensis str. SRNK-1	FJ7072
AB236169.1 gg_id:147634 Labrys okinawaensis str. MAFF210191	AB2361
FJ478661.1 gg_id:543156 species richness estimates obtained nearly and simulated pyrosequencing-generated	FJ4786
EF019390.1 gg_id:209096 aspen rhizosphere clone Elev_16S_622	EF0193
AJ535707.1 gg_id:105233 Labrys monachus str. VKM-B1479	AJ5357
EF516667.1 gg_id:218772 grassland soil clone FCPT638	EF5166
AB236170.1 gg_id:149143 Labrys miyagiensis str. G24103	AB2361
EF516470.1 gg_id:224138 grassland soil clone FCPO739	EF5164
AB271044.1 gg_id:166471 Labrys ginsengisoli str. Gsoil 106	AB2710
DQ986319.1 gg_id:174214 Thiobacillus sp. str. S1	DQ986
GQ046109.1 gg_id:464010 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw	GQ046
AJ535709.1 gg_id:105545 Angulomicrobium amanitiforme str. NCIMB 1785	AJ5357
FJ588700.1 gg_id:541172 Starkeya sp. str. pcnb4	FJ5887
X94198.1 gg_id:4663 Xanthobacter agilis str. SA35	X94198
X99469.1 gg_id:4700 Xanthobacter tagetidis str. TagT2C	X99469
EF540453.1 gg_id:221589 Ancylobacter sp. b1M	EF5404
AM778407.1 gg_id:236974 Ancylobacter oxalaticus NS05	AM778
EU289458.1 gg_id:239819 metagenomic approach biosynthesis ansamycin endophytes or symbionts enriched s	EU2894
AJ306541.1 gg_id:68682 Xanthobacter sp. str. INA43/2-2 (DSM 11820) sewage sludge INA43/2-2	AJ3065
DQ533878.1 gg_id:231483 Xanthobacter flavus str. WM2814	DQ533
X94201.1 gg_id:4654 Xanthobacter autotrophicus str. 7c	X94201
X94202.1 gg_id:4673 Xanthobacter flavus str. H4-14	X94202
AF399969.1 gg_id:62751 Xanthobacter aminoxidans str. 14a	AF3999
AJ421782.1 gg_id:43442 Hirschia baltica str. DSM 5838T	AJ4217
FM202386.1 gg_id:570096 Hirschia sp. str. GSW-2	FM202
AJ227814.1 gg_id:5865 Hyphomonas jannaschiana str. ATCC 33883 (T)	AJ2278
CP000158.1 gg_id:162510 Hyphomonas neptunium str. ATCC 15444	CP0001
AF082795.1 gg_id:5870 Hyphomonas rosenbergii str. VP-6	AF0827
EF540362.1 gg_id:217590 oil-shale semi-coke solid waste clone 07B_MJK	EF5403
NR_024937.1 gg_id:543637 Hyphomonas adhaerens str. MHS-3; ATCC 43965	NR_024

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10816.8	3890.8	4782.2	4306.5	6340.5	4729.8	6853.0	4971.8	5293.8	5024.4	3773.6
5060.0	3631.9	3933.5	3670.3	4945.7	3746.1	5639.1	3862.5	3816.6	2638.3	3446.3
114.9	162.2	103.2	97.0	121.7	123.4	130.8	190.4	64.2	37.2	80.6
7440.3	3998.3	4820.6	5473.8	4751.0	4487.6	5013.0	5409.7	3921.0	1493.2	3719.5
15250.6	4829.1	4391.4	5275.7	5486.6	4760.9	5586.0	5117.8	5685.1	4555.6	3936.7
221.7	1781.3	1299.0	1244.2	2901.6	1935.0	2690.7	1896.8	736.9	811.1	549.8
902.3	2065.6	1695.4	1569.9	1921.7	1970.8	1982.3	2308.3	724.9	622.1	704.5
5386.6	4670.3	4035.7	4351.3	6058.3	5027.9	5612.7	4911.4	3237.1	4619.4	2718.3
1512.2	976.5	1299.3	1140.1	1886.4	1297.7	1707.2	2056.7	766.6	549.6	542.4
1800.5	2472.7	2616.3	3099.3	3234.2	2893.3	3077.6	3715.5	2543.7	1842.1	2072.2
1383.4	1671.5	1267.5	1024.3	2888.0	1835.1	2593.6	1485.9	982.6	431.2	441.0
1564.5	4518.2	5012.2	5036.1	5809.7	5416.0	6098.6	5999.9	4085.7	5321.2	3931.2
4600.6	1990.8	1546.3	1481.5	2617.1	2685.3	2870.4	2108.9	1993.0	687.2	672.8
339.6	1295.4	944.7	1273.5	2661.6	1561.6	2826.5	1723.5	1207.2	574.3	491.3
4206.5	1692.9	1698.6	1610.8	2502.5	1750.1	2393.7	1972.9	819.4	1881.1	824.1
207.7	1927.4	2068.7	2143.0	2923.2	2082.0	2498.4	2459.4	1453.5	1182.2	1088.8
11284.9	4601.8	4158.4	4745.7	7103.6	5123.6	7236.9	5279.1	3606.6	5035.7	3208.2
79.8	455.7	468.8	441.4	1015.9	575.1	1509.3	916.3	317.1	216.2	194.6
1976.3	2359.6	2363.6	2624.3	2884.3	2867.6	2780.1	3024.9	1652.7	4263.5	2298.4
1741.4	1345.5	1350.0	1959.3	1529.3	1018.7	1516.2	1968.3	887.6	504.7	551.7
19096.1	8486.2	7061.9	8025.4	10821.7	8982.6	9608.9	7921.3	8701.0	7539.4	9217.9
5660.9	2430.6	2081.4	2502.3	2862.6	2356.2	2558.3	878.1	2033.2	1678.3	3249.0
13482.0	4283.0	3942.1	4287.4	5675.7	4207.1	5940.9	4661.6	3244.9	2632.5	3910.1
204.3	434.6	528.7	464.3	765.4	585.5	309.5	1078.0	326.9	287.1	348.4
94.5	1511.6	1593.7	1783.6	1392.5	1390.3	1281.3	1894.8	1008.1	671.9	778.4
10953.4	8353.5	6063.8	6341.9	8871.5	7454.0	8472.0	6656.7	5204.0	5630.6	4525.3
2395.8	2636.1	1921.5	1694.3	2606.7	2052.8	2435.4	2756.0	1202.7	1218.0	1132.0
329.1	4459.0	4380.7	3803.7	4145.3	4373.3	4231.0	4707.9	3510.0	3320.0	2503.1
11697.8	6941.6	6302.7	6161.2	8028.2	7166.3	7514.0	7540.2	6741.0	5012.5	5268.6
3875.8	4445.7	4041.4	4591.1	5135.3	5021.6	4955.7	4685.0	5114.5	3370.7	3567.6
131.0	1964.6	1915.4	1663.6	2465.0	1944.7	2541.1	2772.2	1198.9	935.2	932.4
501.7	3430.4	3094.2	3429.1	4079.3	3770.3	3711.0	3968.9	4633.9	2457.8	2145.2
4563.7	3866.7	3532.8	4064.8	4398.5	3955.3	4059.0	3472.3	4718.8	2616.5	3799.3
1079.5	4627.6	4264.8	5328.3	4804.2	6036.6	4262.9	4946.0	3589.3	2872.0	3897.9
375.0	2584.5	2212.2	2311.9	3090.9	2783.3	2283.8	3380.8	1960.0	1521.2	1630.8
891.1	2313.2	2252.9	2864.4	3084.6	2313.4	3406.5	3140.3	2083.0	830.0	1610.3
175.0	567.6	1325.3	1301.3	835.1	690.8	1103.4	2230.7	932.0	289.2	566.1
8224.1	4711.7	4380.2	4718.4	4879.6	4280.0	5437.5	4776.7	4453.0	3460.5	4806.2
229.2	1128.2	1885.0	1869.2	1304.1	1131.9	1509.0	2859.5	1658.2	795.6	838.4
9121.8	6182.4	6376.4	7058.3	6539.2	5408.6	7307.8	6038.7	7653.5	5389.0	7634.8

7689.8	6287.0	4769.5
5645.3	5927.8	6478.9
4251.8	3517.1	4472.6
95.3	164.3	508.1
5308.3	5084.2	5542.2
5500.4	5634.2	5462.1
2569.0	1459.4	1032.9
2467.5	1562.9	1812.8
5359.2	5301.7	4646.9
2777.4	1478.1	2529.5
3903.3	3386.9	2960.7
1995.1	1889.8	3485.3
5696.1	6176.8	7206.9
2382.1	2348.7	3517.2
1979.3	1753.9	2825.2
2309.1	2362.5	2666.0
2302.1	2702.0	2910.4
6027.3	6235.0	6918.3
1028.3	810.9	748.3
3045.3	4379.2	4460.0
2278.2	1619.9	1242.7
8663.6	8549.9	8133.4
3007.7	3521.3	2562.6
5406.4	4798.3	4583.5
1015.5	1593.2	582.5
2003.8	1335.0	1585.8
8000.3	6271.8	7195.2
3110.2	2226.7	1483.7
4983.5	4931.3	5086.1
7504.0	7350.4	7194.7
4937.5	4358.0	4448.8
2798.1	2374.7	3259.0
4433.5	3486.2	3252.6
4044.3	3802.5	2828.6
5035.9	4111.5	3008.2
3093.7	2724.8	2336.1
3557.8	3259.0	3350.6
2456.6	1641.3	688.6
4855.1	5112.8	4048.1
3214.9	2035.1	1025.3
6264.3	6986.3	6319.5

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DQ396058.1 gg_id:151886 deep-sea octacoral clone ctg_NISA280 DQ396
DQ160243.2 gg_id:139361 Hyphomonas taiwanensis str. HYP1 DQ160
NR_024938.1 gg_id:572877 Hyphomonas johnsonii str. MHS-2; ATCC 43964 NR_02
AF082797.1 gg_id:5859 Hyphomonas oceanitis str. SCH-89 AF082
AJ007807.1 gg_id:5841 Maricaulis maris str. ACM 5106 (T) AJ0078
EU528177.1 gg_id:286163 Seasonal Dynamics Mudflat Mouth Major Kentucky Lake Reservoir Tributary sedime EU528
AJ301667.1 gg_id:26948 Maricaulis virginensis str. VC 5 AJ3016
DQ768642.1 gg_id:245137 Maricaulis virginensis MARC4M DQ768
FJ797347.1 gg_id:567500 Arenicola marina bioturbated mesocosm marine sediment clone 20 FJ7973
AY162105.1 gg_id:135262 Cultivating Sargasso Sea clone GMD21C01 AY162
NR_025323.1 gg_id:545614 Maricaulis parjimensis str. MCS 25; DSM 16078 NR_02
AJ309862.1 gg_id:40525 Oceanicaulis alexandrii str. C116-18 AJ3098
DQ644012.1 gg_id:236476 Production cyanobacterial toxin Microcystin disease corals black band diseased (BB DQ644
AY701470.1 gg_id:108547 dinoflagellate symbiont clone GCDE08_V AY701
AJ227811.1 gg_id:5847 Caulobacter sp. str. MCS33 AJ2278
GQ441337.1 gg_id:593605 and dynamic mat present vs. active nitrogen-fixing microorganisms marine microbia GQ441
FJ152756.1 gg_id:347767 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX5A_ FJ1527
DQ395426.1 gg_id:154213 deep-sea octacoral clone ctg_CGOAB48 DQ395
FJ203305.1 gg_id:307703 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c FJ2033
AB286621.1 gg_id:209532 Reducing production and domination comamonadaceae reducing oxygen supply was AB286
AF359547.1 gg_id:18991 Scrippsiella trochoidea NEPCC 15 AF3595
AY942774.1 gg_id:148699 but species richness marine sponge Cymbastela concentrica clone Cc118 AY9427
FJ497641.1 gg_id:542217 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun FJ4976
EU881181.1 gg_id:303607 Karst region natural restoration land soil clone KNR200711-027 EU881
AF234756.1 gg_id:18609 sludge clone S36 AF2347
GU118388.1 gg_id:538371 Threatened Corals Provide Microbial Habitats clone Gven_P10 GU118
EU196330.1 gg_id:244514 Investigation heterotrophic and autotrophic microbial perennial springs cold saline (EU196
EU245307.1 gg_id:241958 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-H5-G02 EU245
DQ376579.1 gg_id:150962 Microbial ecology removing phosphate wastewater EBPR process aerobic sequencin DQ376
AB294313.1 gg_id:205348 Microbial structure deep coal seem groundwater stream clone SWB02 AB2943
AY654758.1 gg_id:105062 Oculina mucus isolate 111 AY6547
AM990862.1 gg_id:278552 Caulobacter sp. MOLA 88 AM990
FM242321.1 gg_id:337659 sequences sediment clone 83 T9d-oil FM242
AJ578477.1 gg_id:102289 Woodsholea maritima str. CM251 AJ5784
AB286463.1 gg_id:208631 Reducing production and domination comamonadaceae reducing oxygen supply was AB286
EF495229.1 gg_id:222908 Croceitomaculum antarcticum str. IMCC3195 EF4952
AJ617875.1 gg_id:110283 oxic-anoxic interphase flooded paddy soil clone D14429 AJ6178
FM242450.1 gg_id:332051 sequences sediment clone 21 T12d+oil FM242
EU665092.1 gg_id:571737 Soil are Changed Agricultural Practices agricultural soil clone Plot22-2G04 EU665
GQ500759.1 gg_id:590926 Surveys Biofilms and Sediments Mammoth Cave Karst Aquifers Bio-Sep beads conta GQ500
FJ826144.1 gg_id:514038 Succession during spring Sea filtered surface sea water decay period after diatom blo FJ8261

4125.8	2603.0	3046.5	3779.3	2948.2	2562.9	3579.7	4305.8	3568.9	2435.1	2435.3
4132.9	3674.7	3337.5	3397.7	3916.0	3656.7	4207.8	4259.2	3258.2	2476.7	2445.0
286.7	4371.8	4014.8	4591.2	6145.9	4604.9	4776.4	4729.7	3850.2	2894.4	2668.8
1227.2	912.0	1301.1	1593.7	1310.2	710.1	1643.7	2187.8	1056.8	531.3	788.5
13126.7	6443.0	5742.5	6727.5	7753.9	5093.9	5284.6	6599.8	11994.1	6451.4	9429.2
2272.7	5297.7	4980.9	5482.5	6295.4	4534.3	5165.1	6045.7	7574.3	6170.0	5847.9
2519.0	4599.3	4350.8	4562.6	5087.2	4256.3	4450.9	5145.4	4036.1	3313.1	3887.1
20452.4	8642.5	7369.8	7875.9	7660.9	6580.0	7485.3	8638.2	11238.7	7503.0	9577.5
11017.3	6684.8	6685.9	7820.1	9663.4	7130.6	8617.6	7133.8	8033.9	6104.6	6557.6
8508.8	5763.1	5925.3	6811.2	7460.8	4954.1	5311.6	7429.0	7025.8	4614.1	6332.6
951.1	2831.5	2801.9	3022.7	3406.8	2618.5	2454.6	3600.5	1730.4	687.7	1773.4
4025.1	4275.2	3894.7	3990.3	5623.6	4293.3	4947.0	4381.8	3427.4	3934.4	3106.2
8718.7	4717.9	4685.5	4896.7	6054.3	5014.4	5226.1	5280.6	4785.5	4252.8	3802.3
6420.9	6481.2	6572.3	7107.1	7334.9	6671.2	7502.9	7416.8	6562.6	6093.3	6553.8
55.3	1757.1	1561.2	2036.8	3289.2	2164.2	2078.7	2764.4	1954.3	1518.9	1352.9
8039.9	6101.3	5078.2	6095.8	6547.4	5853.4	7051.6	6283.2	5795.9	5667.6	5181.8
9998.1	6383.7	6021.0	6725.2	9507.2	6621.8	9169.8	7310.5	5907.8	5759.5	5346.9
55.9	80.5	126.6	168.3	153.0	96.8	110.6	117.0	73.0	67.9	62.3
9913.5	4012.5	3479.1	4057.9	3810.4	3840.0	4392.6	3679.5	7638.2	2937.8	4894.7
97.8	469.9	463.0	729.6	3124.5	676.3	2042.8	858.9	1584.3	122.8	233.9
7865.2	1628.1	1594.8	1859.0	2126.3	1740.8	1895.4	2060.8	2276.8	1931.8	1564.2
397.7	1932.7	1879.2	2313.7	2366.8	2453.8	2300.3	2783.1	2313.0	2067.4	1968.1
11226.7	8447.9	8221.8	8606.1	9682.1	7780.3	10198.9	7607.3	9967.1	7660.2	7801.9
2260.1	4315.9	3336.1	2925.2	5786.3	5198.0	4769.2	3494.5	1316.3	1022.3	2056.9
7634.8	3454.9	3363.0	3931.9	7554.7	4154.7	6436.5	5214.1	3475.2	2152.1	2930.4
6158.5	2371.7	2348.2	2911.7	2482.1	2673.4	3274.6	3787.2	3668.5	1930.5	2125.1
4116.2	1452.0	1591.5	2030.4	2473.7	2125.5	1970.1	2246.0	3016.5	1836.8	1151.0
3984.4	2038.2	2170.9	2099.0	2675.1	2056.0	2748.7	2129.9	1529.0	1017.8	1355.8
979.5	1664.8	1521.6	1410.1	1771.1	1635.8	2491.2	2274.1	1163.8	493.8	693.5
1664.3	2385.0	2535.4	3878.2	3573.6	2713.8	3171.0	2990.6	2239.7	1819.0	1397.7
58.3	812.1	805.5	893.3	1029.2	838.4	1075.2	1346.6	663.9	482.1	661.5
7052.4	2169.6	2062.7	2690.3	2545.2	2580.6	2190.9	3243.0	2544.2	2599.1	1407.8
737.0	2427.1	2049.4	2232.2	3532.5	2261.7	2478.3	2510.4	1436.2	1133.4	1437.9
544.8	1990.2	2203.3	2254.7	2628.1	2581.3	2787.4	2576.2	2068.3	1025.0	1356.0
37.6	556.9	893.7	1124.3	1784.7	1280.5	1098.4	1298.7	803.3	147.8	277.2
38.7	89.6	115.4	110.9	173.8	146.6	47.5	144.3	69.8	41.7	53.7
38.9	783.3	1463.7	1452.7	4518.7	1716.8	4514.0	2989.5	1031.9	283.4	644.4
727.2	1381.6	1689.8	1551.7	2156.3	2030.9	1469.4	2396.2	1506.0	1224.0	763.1
237.9	1222.4	1452.6	1193.4	2136.4	1711.8	1927.7	1554.3	913.6	428.9	579.7
8117.7	4574.6	3657.6	3392.1	6437.2	6183.0	6107.6	4835.3	2668.2	2529.7	3018.0
955.0	1135.4	1455.2	1751.1	1554.8	1284.7	1501.7	1440.9	930.3	669.3	1093.3

4641.6	3992.9	3077.9
4634.7	3788.2	3737.4
5101.9	3782.2	4260.7
2361.2	2080.6	1979.6
5541.8	7673.4	5308.7
6552.1	5827.0	5988.6
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7499.8	8771.4	5959.5
9228.2	7131.3	7441.4
6866.0	7309.8	5828.1
3338.3	3529.7	2512.5
4732.8	4950.5	4452.9
5961.0	5617.0	5420.9
7213.0	7476.6	6876.1
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6847.6	6533.6	6181.7
8907.2	6668.0	7708.5
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3141.9	5733.8	3124.4
1527.7	990.9	1382.4
2461.3	2214.7	1943.9
2257.6	3063.9	1432.5
8314.7	8386.8	8884.4
3404.5	2642.2	4080.4
6602.1	3624.7	5906.6
4209.2	3868.8	3241.5
2887.5	1777.0	1976.9
2735.8	2999.9	1814.4
2391.5	1479.0	1226.1
4234.7	2647.5	2616.2
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3333.4	2320.1	2111.9
3529.5	2691.2	2692.7
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4545.1	581.3	96.9
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AY921760.1 gg_id:112748 farm soil clone AKYH1490 AY921
FJ516864.1 gg_id:565583 semiarid 'Tablas de Daimiel National Park' wetland (Central Spain) unravelled lower s FJ5168
GU444088.1 gg_id:530619 Effects amendments on fertility and microbial structure cucumber Cucumis sativus L GU444
EU491552.1 gg_id:263491 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR4C EU491
EU236280.1 gg_id:296183 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg5aCo7 EU236
EU236341.1 gg_id:298881 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg5a2G5 EU236
EU104323.1 gg_id:309713 Evidence Comamonadaceae determinants settling performance activated sludge clo EU104
GQ441341.1 gg_id:581650 and dynamic mat present vs. active nitrogen-fixing microorganisms marine microbia GQ441
NR_026060.1 gg_id:570345 Amaricoccus tamworthensis str. Ben103; ACM 5097 NR_02
U88042.1 gg_id:5811 Amaricoccus macauensis str. Ben104 U8804
DQ130031.1 gg_id:151324 microbial biota normal forearm human skin clone GL97 DQ130
NR_029203.1 gg_id:580499 Amaricoccus veronensis str. Ben102; ACM 5098 NR_02
FJ152897.1 gg_id:336456 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX4CI FJ1528
DQ346506.1 gg_id:154801 during composting libraries compost clone 2B22 DQ346
FJ152955.1 gg_id:323451 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX4CI FJ1529
EF489005.1 gg_id:245310 Antarctobacter sp. str. TG22 EF489
EU053204.1 gg_id:246019 Catellibacterium terrae str. QMT-4 EU053
NC_009952.1 gg_id:250733 Dinoroseobacter shibae str. DFL 12 NC_00
FJ202183.1 gg_id:343990 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2021
DQ289933.1 gg_id:167723 Microbial Carbon and Nitrogen Cycling Sediments South Atlantic Bight Permeable Sh DQ289
AF452106.1 gg_id:62868 Rhodobacter massiliensis str. Framboise AF452
DQ342310.1 gg_id:205946 Haematobacter massiliensis str. H2443 DQ342
AJ534225.1 gg_id:75300 Jannaschia helgolandensis HEL-43 AJ5342
AM990650.1 gg_id:278279 culturable oligotrophic ocean (South Pacific Gyre) sea water AM990
AJ748747.1 gg_id:110922 Jannaschia rubra str. 4SM3 AJ7487
AY906862.1 gg_id:112620 Jannaschia sp. str. CL-SP26 AY906
EF202612.1 gg_id:200932 Jannaschia donghaensis str. DSW-17 EF2026
DQ643999.1 gg_id:159971 Jannaschia pohangensis DQ643
EU034641.1 gg_id:253055 Ketogulonicigenium vulgare str. VC-2-2 EU034
DQ915605.1 gg_id:320216 Ketogulonicigenium robustum str. NRRL B-12627 DQ915
AF136849.1 gg_id:135903 Ketogulonicigenium vulgare str. DSM 4025 AF1368
AY005463.1 gg_id:45273 Leisingera methylohalidivorans str. MB2 AY0054
AJ582229.1 gg_id:93357 Loktanella salsilacus str. LMG 22002 AJ5822
DQ533555.1 gg_id:163668 Loktanella tamlensis str. SSW-27 DQ533
FJ172067.1 gg_id:327793 Microbial athalassohaline Tirez lagoon (Spain) water clone MJZ2 FJ1720
AJ582227.1 gg_id:94079 Loktanella vestfoldensis str. LMG 22006 AJ5822
AY576770.1 gg_id:138842 Ruegeria sp. str. 3X/A02/236 AY5767
AF173971.1 gg_id:73505 Roseobacter sp. str. KT1117 AF1739
FJ172062.1 gg_id:354977 Microbial athalassohaline Tirez lagoon (Spain) water clone MJW2 FJ1720
EF659438.1 gg_id:246665 within Poole Harbour seawater clone PH-F10 EF6594
AM691092.1 gg_id:220404 Rhodobacteraceae clone EG3 AM691

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3998.9	4845.4	4331.3	5130.9	7105.3	6090.7	5740.1	5736.0	4272.8	2824.4	3160.5
6071.2	6184.2	6445.4	7104.0	7111.5	6251.3	7256.2	7415.7	6617.9	6709.8	5057.6
704.5	1501.7	1801.2	1750.9	2175.4	1501.6	2318.6	2100.9	1206.2	1576.7	1125.1
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4235.0	3270.8	2995.3	3263.5	4678.0	4044.8	4158.2	3501.0	4368.0	2546.6	2499.8
1131.3	3950.9	4199.1	4154.5	5612.4	5943.0	5236.7	5723.7	4179.1	3311.9	2961.7
6777.3	6832.4	6407.1	6901.3	9669.2	8315.7	8761.8	7326.7	9774.5	7743.7	6427.2
308.4	1926.4	1940.6	1819.6	2806.1	3297.4	2211.9	2585.9	1950.1	1440.7	1339.0
22786.5	10023.4	9207.7	9865.4	12112.6	10757.5	11218.1	9961.5	13402.1	10414.2	10014.6
66.0	367.1	389.3	372.0	432.7	419.4	538.9	504.8	228.8	100.0	184.3
1409.2	3269.9	2982.7	2825.7	4675.5	5280.8	3393.2	4498.1	2613.4	2888.1	2759.3
4029.6	3781.8	3379.9	3630.0	5586.8	3846.1	3634.9	4185.1	5404.3	1901.5	2966.2
16138.9	9013.1	8226.9	8264.3	9666.3	8982.2	10801.6	8185.2	9725.9	8501.9	7964.4
19886.2	8745.7	8319.4	8508.8	8250.3	7546.4	8820.9	7800.1	10675.6	8740.8	12572.0
1085.3	2632.8	3002.0	3310.3	2875.4	3113.0	3100.4	2529.7	2755.5	1943.8	1848.7
789.0	1843.3	1544.6	1744.0	1774.9	1032.2	2017.3	2414.1	1264.0	1995.1	1026.0
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8515.4	4163.4	3985.6	4786.5	6309.3	4446.5	5682.1	5373.1	4092.1	4281.3	4284.8
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1086.2	5569.8	2622.8	2589.3	3022.2	3038.1	2199.4	2557.8	1912.2	1752.0	1648.9
749.6	407.4	630.4	631.9	693.7	355.3	436.3	602.2	277.9	212.4	292.5
2356.7	5128.3	2634.2	2935.8	3228.5	3468.3	2782.0	3296.2	1946.9	2423.0	2063.7
544.0	1244.7	1154.3	1279.3	1641.9	2266.1	1341.3	3171.1	967.0	775.2	1708.1
442.2	2335.3	2311.0	2078.4	2461.5	2919.3	1965.5	2695.2	1949.8	1753.1	1472.4
359.8	219.0	667.0	519.1	768.7	473.4	580.4	543.3	348.0	447.0	411.0
6199.0	2324.2	2255.1	2380.3	3190.9	2491.4	2460.3	2829.0	2936.9	1945.0	1441.8
2594.4	2566.1	2891.6	3183.2	2866.1	2260.6	2934.1	3828.1	2257.6	1390.4	2914.3
1909.7	979.7	1124.2	1209.5	1165.1	880.0	956.9	1377.2	1076.5	539.8	608.0
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2012.4	3120.8	2572.7	3037.6	3602.6	3182.1	3255.6	3710.9	2386.0	1966.3	2202.0
165.6	1246.5	1318.3	1340.0	1941.6	1099.6	1054.6	2062.8	1325.6	481.9	1309.4
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3620.1	3307.3	3205.0	3730.6	4599.6	3415.2	3783.0	4426.7	3205.1	3872.8	4268.9
583.4	2442.3	2430.8	3239.1	3646.4	2932.2	3854.9	3858.9	2295.1	1178.6	2499.1

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FJ152873.1 gg_id:328838 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX4CI FJ1528
FJ716887.1 gg_id:510302 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United Kingc FJ7168
DQ397336.1 gg_id:153999 Thalassobius sp. str. UST050418-052 DQ397
GU061095.1 gg_id:592005 Evaluation culturing methods cultivate previously Yel Sea intertidal beach clone TFS- GU061
DQ344498.1 gg_id:145649 Loktanella koreensis str. GA2-M3 DQ344
AY167339.1 gg_id:81378 Roseobacter sp. str. ARK9990 AY1673
FJ203462.1 gg_id:307704 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h FJ2034
AJ505788.2 gg_id:61250 coastal sediment clone AJ5057
FJ889546.1 gg_id:563888 Phaeobacter sp. str. ZS356 FJ8895
AY654808.1 gg_id:103608 Oculina mucus isolate 78 AY6548
AY654838.1 gg_id:100870 Oculina mucus isolate 40 AY6548
AF170751.1 gg_id:5658 Roseobacter sp. str. QSSC9-8 AF1707
DQ514326.1 gg_id:161345 Maribius bermudensis str. B5-6 DQ514
AY162102.1 gg_id:135261 Cultivating Sargasso Sea clone GMD21D01 AY1621
X78313.1 gg_id:5670 Ruegeria algicola str. ATCC 51441ML4 X78313
AB491842.1 gg_id:557828 affiliation (Litopenaeus vannamei) Banyuwangi East Java microbial flocs floating brac AB4918
AJ633967.1 gg_id:114827 host's accessory nidamental gland clone T65ANG1 AJ6339
FJ716854.1 gg_id:541703 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United Kingc FJ7168
AJ295988.1 gg_id:26995 Ruegeria aff. gelatinovorans str. ch611 AJ2959
EU592330.1 gg_id:539299 Seasonal changes Salton Sea hypersaline water clone SSW55N EU5923
AY258078.1 gg_id:135688 Ruegeria sp. str. DG882 AY2580
AY344411.1 gg_id:91079 Lake Kauhako surface clone K2-S-32 AY3444
GU324080.1 gg_id:556772 Marivita sp. str. CB 1101 GU324
AY600300.1 gg_id:103542 Loktanella hongkongensis str. UST950701-009P AY6003
FN431787.1 gg_id:544367 Loktanella hongkongensis str. AMV3 AMV18 FN4317
AM983542.1 gg_id:537512 Loktanella pyoseonensis str. JJM85 AM983
EU143345.1 gg_id:252067 Loktanella sp. str. J20 EU1433
AM944522.1 gg_id:268667 Nautella italica str. R-28753 AM944
FJ202078.1 gg_id:310849 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2020
FJ202115.1 gg_id:343849 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2021
EU592375.1 gg_id:583983 Seasonal changes Salton Sea hypersaline water clone SSW89Au EU5923
EF092158.1 gg_id:267120 Persistent Axinella corrugata Roseobacter clone AC2_A2 EF0921
DQ675021.1 gg_id:162482 Pseudoruegeria aquimaris str. SW-255 DQ675
DQ917854.1 gg_id:219732 Microbial profiles bleached and wild-type Muricea elongata clone BME80 DQ917
FJ202604.1 gg_id:318096 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2026
FJ202395.1 gg_id:319436 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2023
DQ915613.1 gg_id:346324 Nereida ignava str. CECT5292 DQ915
DQ915614.1 gg_id:327289 Oceanibulbus indolifex str. DSM14862 DQ915
NR_027563.1 gg_id:544041 Oceanibulbus indolifex HEL-45 str. Hel-45; DSM 14862 NR_02
EU694388.1 gg_id:293008 Oceanibulbus indolifex str. D15 EU6943

38.6	1196.4	1303.3	936.0	3101.6	4919.8	2382.6	2280.3	853.2	688.5	884.1
9519.3	4134.3	3998.1	4640.7	4414.1	4207.7	5190.5	4471.3	4879.8	5543.0	5315.9
1176.0	3090.2	2911.6	2984.8	3653.0	4452.3	3583.2	3443.0	3100.5	1567.3	3056.0
91.7	347.2	647.7	647.9	487.3	467.8	822.1	705.2	204.6	98.4	384.6
195.9	1774.6	1435.5	1626.7	2082.5	3354.5	1268.4	1971.1	1765.3	1271.2	1316.2
776.7	2451.3	2651.3	2611.6	4070.9	3566.9	3903.9	3227.1	1781.4	1677.3	1500.6
1102.3	2646.9	2044.1	2254.0	3486.3	3011.3	2985.3	2982.2	3284.7	1827.7	1781.4
7260.2	2038.0	2359.0	2508.8	3045.8	2734.4	2354.4	3593.4	1923.6	1202.1	2731.0
26.5	21.7	37.5	38.3	42.1	55.9	52.3	59.6	32.7	20.4	24.3
125.1	977.1	1110.2	1326.1	1399.9	1088.0	1775.6	1801.0	529.4	837.1	737.2
9312.6	3776.9	3915.3	4601.4	4999.1	5211.3	5328.7	6504.6	4555.3	2841.3	3600.6
2258.8	1124.4	1393.1	1839.0	1103.7	1037.5	1245.8	2226.9	879.5	282.7	1183.5
42.1	98.4	174.9	184.7	131.3	81.2	106.6	171.0	55.9	37.8	57.8
8233.0	4173.6	4076.3	3927.8	5357.5	3981.8	4704.7	4236.0	4267.5	5070.9	3463.9
187.1	1079.6	801.5	1035.1	1378.3	1123.5	1475.2	1475.0	1467.3	648.4	971.1
298.3	5269.8	2795.8	3262.5	5575.1	4237.0	3441.6	4005.8	3517.4	3293.1	2171.1
319.8	2343.8	1922.6	2400.1	2121.2	2176.8	1670.6	2660.0	1605.6	2011.1	1351.2
92.7	1257.7	671.9	770.0	1221.3	996.7	1019.0	1419.5	756.9	699.9	522.0
454.4	1724.1	2104.9	1851.6	2055.8	2044.2	2255.4	2723.1	1134.9	3117.0	1435.1
7196.3	3137.5	2982.6	3042.4	3136.3	3756.3	3382.7	3375.8	3530.7	3000.1	2920.0
7128.9	1866.8	2710.5	2413.8	2451.1	2300.9	2851.7	2673.6	1283.8	1262.2	2239.8
58.5	1712.0	1782.0	2455.2	2484.1	2415.2	2662.5	2767.4	1326.1	1531.4	1904.5
186.8	2521.2	2661.0	2457.1	2668.4	2473.1	2866.5	2790.0	1446.6	1865.8	1829.7
7172.4	5711.9	5729.2	6228.3	6230.5	6369.8	5667.1	5900.2	7018.4	5787.5	7212.0
295.9	753.3	990.8	1155.0	1204.1	738.2	1134.6	1414.6	776.2	606.0	749.4
44.7	112.7	163.3	198.1	337.5	181.7	226.2	243.4	185.0	177.8	95.5
5638.1	1984.0	1812.1	2078.5	2248.4	1939.5	2258.2	2437.4	1437.8	1342.9	1125.3
7524.5	2037.9	1743.8	1431.5	2255.5	2400.6	1580.0	2046.2	1178.1	1361.0	1070.6
2113.1	3732.4	3307.8	3890.7	6080.8	4225.6	5232.8	5570.4	5745.2	2581.3	2943.1
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909.2	2420.9	1904.9	2815.1	3173.9	2988.6	3301.8	2963.2	1782.8	873.6	2420.3
109.6	237.9	226.8	281.0	250.6	297.4	315.6	419.3	167.2	152.7	254.2
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429.8	777.6	671.9	812.2	909.7	1185.9	910.3	1060.1	87.7	594.9	416.7
6808.5	3553.6	2941.4	3760.9	6025.5	4895.6	4076.3	3439.4	4068.5	2843.0	3639.4
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66.1	374.7	400.8	361.2	376.1	260.0	424.4	265.0	48.7	162.1	268.9
44.5	30.1	25.0	28.2	36.6	31.2	36.1	29.4	19.3	16.1	29.4
1591.1	1829.8	1985.8	2160.4	2919.9	2235.2	2836.5	2420.0	1664.1	1119.5	2341.2
1586.1	1820.1	1836.5	1932.9	2935.6	2127.2	2548.7	2297.8	1566.6	1034.1	2303.5
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4411.6	2768.4	1805.1
423.1	576.6	619.3
2053.7	1585.7	1803.4
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3440.2	2625.8	1741.8
3315.0	3707.1	2748.3
58.7	34.4	64.3
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1302.2	1347.8	1290.9
134.2	258.9	97.4
4737.1	5045.3	4582.9
1596.6	1320.5	970.0
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NZ_AAMO01000005.1 gg_id:146037 Oceanicola batsensis str. HTCC2597	NZ_AA
DQ915616.1 gg_id:305517 Oceanicola granulosus str. KCTC12143	DQ915
GQ250665.1 gg_id:544324 bulk sea water column Gulf Mexico clone GOM_WB10-7	GQ250
AB166982.1 gg_id:101280 Roseobacter sp. str. NT N37	AB166
FJ230846.1 gg_id:341497 marine str. SD7	FJ2308
FJ196062.1 gg_id:310847 Octadecabacter sp. str. ZS6-9	FJ1960
AB180384.1 gg_id:109216 Octadecabacter sp. str. No. 49	AB180
AF030437.1 gg_id:5737 Methylarcula terricola str. h37; VKM B-2160	AF0304
AF030436.1 gg_id:5762 Methylarcula terricola str. h1; VKM B-2159	AF0304
DQ402044.1 gg_id:150822 Paracoccus alcaliphilus str. mku-E2	DQ402
DQ469585.1 gg_id:158059 Paracoccus alcaliphilus str. Sty2-VH	DQ469
D32240.1 gg_id:5761 Paracoccus aminovorans str. JCM 7685	D3224
GQ497295.1 gg_id:552938 Paracoccus sp. str. KSL5401-001	GQ497
GU201846.1 gg_id:518236 Paracoccus aminophilus str. Zw-11	GU201
AY312056.1 gg_id:88947 Paracoccus sp. Ol18	AY312
AF376134.1 gg_id:24018 Paracoccus sp. str. T231	AF376
FM207553.1 gg_id:348847 Paracoccus denitrificans E4	FM207
FJ381982.1 gg_id:582190 Potentially pathogenic and air stem cell transplant winter hospital shower water BMT	FJ3819
EF070124.1 gg_id:190880 Paracoccus sp. TRP	EF0701
DQ539490.1 gg_id:169913 Paracoccus sp. SBRD2	DQ539
DQ270723.1 gg_id:142241 Pseudomonas sp. B-1015	DQ270
AF139992.1 gg_id:5771 Paracoccus marcusii str. ML-003	AF139
AJ582185.1 gg_id:93958 soil near uranium mill tailings clone Gitt-GS-149	AJ5821
AY014175.1 gg_id:47316 Paracoccus solventivorans str. ATCC 700252	AY014
FJ950555.1 gg_id:410450 Paracoccus versutus str. c75	FJ9505
EU434343.1 gg_id:275527 Paracoccus versutus str. a266	EU4343
DQ512861.1 gg_id:159464 Paracoccus sp. str. LW36	DQ512
AY004210.1 gg_id:28386 Paracoccus versutus str. kps	AY0042
EU434456.1 gg_id:276317 Paracoccus versutus str. a234	EU4344
FM872636.1 gg_id:369875 occupant source house floor dust clone FA04D10	FM872
AY014179.1 gg_id:46743 Paracoccus yeei str. G3060	AY014
GU108563.1 gg_id:545865 active chemolithoautotrophic prokaryotes sulfidic zone Black pelagic redoxcline dete	GU108
FJ713782.2 gg_id:571011 Paracoccus sp. str. DEH99	FJ7137
AB275604.1 gg_id:212709 Paracoccus kamogawaensis str. YSFL3	AB2756
AJ864466.1 gg_id:109475 Paracoccus pantotrophus str. JT001	AJ8644
GQ250442.1 gg_id:577514 Paracoccus sp. str. MJ17	GQ250
AB025189.1 gg_id:5770 Paracoccus sp. str. MBIC4018 HI7	AB025
DQ923133.1 gg_id:180344 Paracoccus halotolerans str. YIM 90738	DQ923
D32238.1 gg_id:5766 Paracoccus alcaliphilus str. JCM 7364	D32238
DQ108402.1 gg_id:137632 Paracoccus sp. Tibet-S9a3	DQ108
FJ842690.1 gg_id:576262 Paracoccus sp. str. NII-0918	FJ8426

588.3	765.7	894.7	1136.0	857.9	765.4	1047.4	1528.5	448.4	257.1	798.2
94.9	817.6	891.9	1009.6	958.5	776.1	1217.3	1403.7	480.6	802.6	590.4
681.1	1202.2	1349.6	1654.7	1326.0	1614.9	1459.8	2579.0	1631.5	467.2	1097.9
152.8	1295.4	1726.4	2181.2	1217.1	1319.0	1508.6	2203.8	649.9	280.7	1846.5
493.7	413.2	508.7	603.7	454.9	708.4	335.4	851.3	226.0	189.7	186.6
4436.0	3696.9	3144.9	3389.8	3116.9	4312.9	3710.3	7049.6	2854.2	2740.5	5758.4
373.2	2255.1	2277.1	2392.7	2553.7	3628.0	2911.3	4983.1	1930.7	2724.0	2741.2
95.5	297.9	229.7	199.5	368.5	284.3	284.5	431.8	175.1	173.1	178.6
41.8	50.3	53.0	53.3	67.9	77.9	65.4	67.2	48.7	60.9	51.8
57.9	557.4	731.1	736.9	359.8	498.9	374.2	553.1	216.5	113.2	245.4
4054.6	5168.1	5501.6	5667.1	6556.7	5917.1	5930.5	6214.3	8609.9	5792.7	5406.7
241.4	4234.1	3185.5	3593.5	6027.3	4634.1	5234.8	5121.4	3123.0	3783.5	3155.5
64.0	5105.7	3150.1	4103.5	5260.2	5985.1	5388.1	5709.8	2775.1	4418.6	4309.1
134.5	2645.2	1871.2	2979.6	2641.4	2718.8	2593.7	3665.7	2228.0	2038.8	1709.8
189.5	1757.5	1693.7	2309.8	2615.9	4661.6	2228.1	3106.2	1370.1	1615.5	1641.8
7969.1	4669.7	4552.0	4143.4	5724.0	7363.7	5624.1	5532.4	3663.4	3759.9	4144.9
219.0	5321.6	3512.2	4111.4	6768.8	6207.6	6413.1	5699.3	3056.8	4169.0	4376.9
255.6	4345.8	3084.9	3459.8	4970.5	3825.6	5421.8	5108.5	3915.6	3445.0	3791.1
430.4	5043.2	3857.9	3929.6	5390.4	4533.2	5462.7	5005.2	3820.3	3518.5	2911.8
9514.1	5825.6	5476.4	5602.1	5871.3	5483.2	5812.3	5610.8	7333.5	5258.5	6658.5
4511.1	6585.8	5293.4	5693.7	8193.6	6435.4	6710.6	6929.4	6185.7	4934.0	5174.7
5247.9	5127.8	4778.8	4673.8	5406.6	5294.5	5238.7	4927.5	6220.8	4258.6	5143.1
18981.5	6391.3	6137.6	7259.7	9012.3	6544.9	8157.2	7407.6	6729.5	5370.3	6587.6
3588.0	6730.2	5650.3	6330.5	7489.5	6899.1	7211.5	6600.7	9054.4	7141.6	5800.8
16956.8	6420.4	4444.5	4897.7	5385.3	6063.6	5370.1	5619.3	5569.0	5321.0	8456.1
17066.3	6050.6	5384.9	5917.8	5923.2	7161.6	6653.6	5638.1	7825.0	7459.1	8309.4
90.4	1794.8	1353.9	1717.4	2178.6	2879.5	2098.9	2731.7	952.4	1612.1	1367.8
168.7	1852.4	1170.3	1176.8	2088.8	3006.4	1747.5	2733.1	2071.2	1793.2	1400.0
826.1	2652.5	2153.4	2274.2	3138.6	4982.0	3042.8	3860.2	2866.0	1986.4	2314.0
854.8	4302.2	4406.6	4160.8	4869.9	4221.6	5106.9	5569.2	5148.2	3254.6	2607.8
4922.7	1248.5	2415.3	1814.9	1662.6	712.8	2464.5	2259.0	1750.0	1267.8	1760.0
9407.2	5148.7	4998.5	5547.0	8028.8	6718.2	7028.1	6227.6	9674.5	4058.4	5725.7
1337.9	2208.3	1555.6	1932.0	2090.4	2966.7	1763.0	2471.0	2895.6	1423.4	1911.3
3897.1	2451.3	2745.0	3024.1	3437.6	2802.1	3118.5	3389.8	3403.8	1430.7	3476.3
441.0	3182.5	1965.0	2105.1	2943.1	3216.9	3363.1	3078.7	2495.2	2141.4	2494.3
1908.4	3361.4	3182.0	3218.9	5148.4	5263.0	4177.5	4153.3	2244.2	2136.0	2183.6
124.0	1548.1	1071.6	1459.4	1504.9	1210.4	1619.8	1743.6	1267.8	889.9	876.8
2957.0	2901.1	2306.7	2656.9	3164.5	2883.2	2732.1	3023.3	3159.9	1277.7	2063.5
6746.2	6471.1	4625.5	4805.9	6325.2	6193.7	5824.4	6058.4	5864.9	3953.4	3947.2
523.4	2858.8	3436.0	4220.9	3324.3	2856.3	3231.3	4943.7	4332.0	1871.8	3910.8
155.9	2548.7	1900.4	2133.1	3587.7	2432.1	2831.1	2929.0	1730.4	1694.7	1198.4

841.3	948.1	793.5
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2200.8	1740.4	1326.7
1318.2	1383.2	1151.5
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7033.4	5668.9	5799.9
4756.6	4117.9	3831.6
268.5	351.1	230.6
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420.9	442.0	403.4
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5210.5	3890.9	3917.1
5525.7	3085.1	1665.8
3697.8	2725.5	1412.5
3419.7	1730.6	685.0
5363.8	4304.5	4579.3
5960.5	3938.5	3709.5
4091.9	3282.6	2054.0
4139.9	4066.7	4276.3
5592.1	6265.7	5665.6
7337.1	4918.5	2962.5
4614.8	4304.2	3850.9
7466.1	7405.4	6004.9
6774.6	6337.3	5232.9
5323.1	6041.8	4803.7
5368.6	4845.1	4901.8
2714.9	2059.2	1129.6
1980.3	1164.5	676.4
3041.1	1680.5	1311.0
5199.9	4097.5	3099.9
2414.6	2296.1	1608.2
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EU341164.1 gg_id:238449 Evaluation Rapid Technologies Estimate Microbial Burden and Commercial Airline Ca EU341
AY626831.1 gg_id:103986 Paracoccus sp. str. QD5-2-1 AY6268
AM697590.1 gg_id:225243 sequencing libraries indoor dust clone BF0002D101 AM697
DQ423482.1 gg_id:155546 Paracoccus sp. str. HN-182 DQ423
EU196530.1 gg_id:241681 Paracoccus sp. Ol18 EU1965
FJ670987.1 gg_id:527854 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6709
FJ675504.1 gg_id:532336 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6755
AM231051.1 gg_id:159385 Paracoccus sp. str. R-24342 AM231
AJ864463.1 gg_id:109472 Paracoccus thiocyanatus str. SST AJ8644
FJ675534.1 gg_id:519944 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6755
AY573045.1 gg_id:106521 Paracoccus sp. str. ARCTIC-P17 AY5730
AJ534231.1 gg_id:202277 Methylarcula sp. HEL-8 AJ5342
AB255110.1 gg_id:172587 corroded concrete clone SC-148 AB2551
FM874023.1 gg_id:370368 occupant source house mattress dust clone MB05C10 FM874
DQ116009.1 gg_id:130794 bovine teat canal clone D-64 DQ116
DQ337586.1 gg_id:150080 Paracoccus sp. BBTR62 DQ337
FJ774966.1 gg_id:559136 Symbionts Brown Planthopper (Homoptera: Delphacidae) symbiont Nilaparvata luger FJ7749
EU368762.1 gg_id:267622 Paracoccus sp. str. B61 Ydz-zz EU3687
DQ129626.1 gg_id:138528 microarray level air two cities Texas urban aerosol clone AKIW1050 DQ129
GQ129980.1 gg_id:370584 Genetic inventory 'JPL-SAF' during MSL mission spacecraft assembly clean room floc GQ129
DQ532252.1 gg_id:165945 Geographical Variation Microbial Burden and Spacecraft Assembly Johnson Space Ce DQ532
D32239.1 gg_id:5758 Paracoccus aminophilus str. JCM 7686 D32239
AB264130.1 gg_id:165184 Paracoccus sp. str. TDMA-10 AB2641
GQ260189.1 gg_id:588165 Paracoccus sp. str. 22-5 GQ260
D32241.1 gg_id:5779 Paracoccus kocurii str. JCM 7684 D32241
AM900779.1 gg_id:235419 Paracoccus sp. PA216 AM900
AY167832.1 gg_id:77519 Paracoccus sp. str. SAFR-029 AY1678
AB264129.1 gg_id:164471 Paracoccus sp. str. TDMA-8 AB2641
AM990798.1 gg_id:279292 Paracoccus sp. MOLA 22 AM990
EF157164.1 gg_id:237879 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon EF1571
FJ267566.1 gg_id:323776 Paracoccus sp. str. II_Gauze_W_10_18 FJ2675
FJ658279.1 gg_id:570280 Metalworking Fluids and Aerosols Metallurgy Plant metalworking aerosol clone Winte FJ6582
AB098589.1 gg_id:78216 Paracoccus sp. str. TUT1021 AB0985
AB185957.1 gg_id:265461 Paracoccus marinus str. KKL-A5 AB1859
DQ856507.1 gg_id:243813 intestinal microflora Chinese mitten crab (Eriocheir sinensis) clone C1I DQ856
GQ452286.1 gg_id:582083 Paracoccus sp. str. MU2A-22 GQ452
AJ580352.1 gg_id:107767 Paracoccus sp. BOG6 AJ5803
AB012914.1 gg_id:5765 Paracoccus sp. str. MBIC3345 Y4 AB0129
AM084041.1 gg_id:139889 Paracoccus sp. str. R-24616 AM084
AB024613.1 gg_id:5740 Paracoccus sp. str. MBIC1145 AB0246
FJ210812.1 gg_id:323743 Paracoccus sp. str. QDHT-17 FJ2108

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860.9	2005.1	2194.7	2269.7	3105.7	4818.8	2812.8	2719.8	1303.9	1757.5	1315.1
1819.2	2913.0	3769.2	3235.0	3500.3	3719.2	3200.8	4125.6	3740.1	3159.1	2507.8
138.3	1209.9	756.8	791.3	1245.5	1683.9	1127.5	1498.8	645.1	560.0	544.9
2848.5	6041.5	5353.8	5676.8	7755.0	7865.6	6011.5	7278.7	5757.6	4620.7	4671.0
9618.3	8911.0	7145.5	7790.6	8596.2	7105.9	8965.8	8224.9	9698.3	8331.3	8461.2
644.0	3429.1	2447.2	2793.6	4169.2	6605.9	4137.2	4402.4	1898.3	2555.0	2609.9
54.0	642.7	705.0	1110.0	1175.2	1054.2	1233.7	1451.3	960.8	418.5	453.2
6702.9	3899.5	3391.2	4122.5	3775.5	3863.8	4048.6	4185.7	4578.1	3258.3	3260.3
505.2	1016.3	1126.7	1043.8	855.1	792.0	904.5	1052.7	873.2	418.9	806.4
10010.8	4236.8	4198.3	4215.2	3894.2	3653.2	3935.8	4085.4	6205.5	3538.7	4145.1
4070.3	5155.1	4192.4	4828.5	5917.1	4798.5	5402.0	5199.9	8340.4	3914.6	4246.8
13419.9	4975.4	3535.4	5327.8	5140.6	5150.3	5274.9	4970.0	6850.3	5599.4	6020.2
1310.7	5797.4	4541.3	4962.7	6136.0	8118.4	5460.1	6965.4	5989.4	5350.2	4242.5
1804.0	3489.9	3730.1	2678.1	3504.7	3346.0	3352.9	3502.9	2066.4	809.3	2769.8
1744.7	2205.7	2988.4	3220.7	2601.8	2409.8	2959.1	3492.6	1809.0	1005.1	2884.2
10608.9	5904.9	5370.1	6039.5	7486.8	5634.6	6937.5	5542.7	8284.1	5406.3	3378.5
83.9	1245.5	1201.0	1161.1	1749.0	1190.0	1525.0	2197.4	1429.3	1099.9	1215.4
9333.8	2564.2	2460.7	2957.3	3935.2	3233.1	3737.0	3223.0	2653.0	1629.1	2394.7
179.0	2421.4	2029.5	1996.3	2027.5	1596.7	2300.2	2473.8	2468.0	1253.8	1556.0
3972.7	5068.3	4648.0	4813.4	6909.6	4945.7	6543.7	5537.0	6894.0	3433.7	3362.3
2763.7	3068.3	2708.0	3410.4	4400.5	3612.7	3519.2	4098.2	3506.7	2123.8	1741.8
1101.6	4110.7	3568.6	3948.0	5291.7	4294.7	4814.9	3981.6	3435.8	3118.4	2487.8
5822.8	4052.1	3622.7	3834.0	4421.1	4200.2	4288.0	4270.6	2789.3	2036.8	2543.9
11951.1	10296.8	8603.0	9774.5	12430.4	12883.2	11868.7	10564.0	13112.9	9446.9	10659.2
1957.4	2504.0	1549.5	1947.3	3063.7	3831.6	2589.8	3698.0	1270.2	2794.2	2479.5
4008.3	5203.6	4876.0	5484.2	7325.6	6309.4	6788.5	5629.9	5957.9	3784.4	5283.7
110.4	3092.6	1984.7	2858.7	3075.8	1851.9	3976.8	3558.6	6651.9	2126.6	2170.9
253.5	3644.9	3056.1	3859.3	4301.2	4023.2	3946.4	4693.7	4227.7	1995.1	1837.8
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379.8	2381.0	2039.6	4149.2	3885.0	3485.9	4061.0	3610.3	3774.7	2208.9	1525.7
941.0	2647.9	1778.5	2131.2	2563.0	1977.3	2137.8	2444.5	1553.1	1680.9	1256.8
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76.4	4422.5	3344.7	3463.0	5216.5	5427.5	4627.7	5398.1	3527.4	4424.5	3570.1
29.7	2813.4	2466.8	2185.1	2352.4	2627.2	2866.7	3007.4	2204.7	1028.6	2813.0
291.2	3303.0	2157.8	2346.5	3329.5	2944.0	2845.5	4229.0	2834.6	3255.8	2138.6
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5510.1	4231.1	3994.5
5125.3	5760.1	5122.8
7150.9	4728.1	3581.3
3114.2	3113.9	3275.1
3822.1	2858.6	1943.9
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3087.2	3018.0	1538.0
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3059.8	1986.5	1577.1
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3394.5	2463.1	1661.2

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DQ178660.1 gg_id:138722 Salipiger bermudensis str. HTCC2601 DQ178
AY177712.2 gg_id:83687 Phaeobacter inhibens str. T5 AY177
AF365991.1 gg_id:111393 marine str. BB2AT3 AF365
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DQ514304.1 gg_id:161029 Roseobacter sp. str. BSs20188 DQ514
AJ633943.1 gg_id:114641 host's accessory nidamental gland clone 53ANG1 AJ6339
DQ915619.1 gg_id:311058 Phaeobacter gallaeciensis str. NBRC16654 DQ915
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FJ014973.1 gg_id:304780 Phaeobacter sp. str. M3-1.1 FJ0149
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DQ660384.1 gg_id:172912 Roseobacter sp. str. HJ105 DQ660
DQ906715.1 gg_id:163091 and marine microorganisms Antarctic sea water 20 m clone AntCL1C10 DQ906
FJ202414.1 gg_id:334773 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2024
AM884343.1 gg_id:275025 Ruegeria sp. str. SCS1 AM884
GQ348550.1 gg_id:533795 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ348
FJ203339.1 gg_id:314415 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c FJ2033
FJ202225.1 gg_id:350338 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2022
FJ716879.1 gg_id:554782 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United Kingc FJ7168
FJ203234.1 gg_id:305694 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c FJ2032
DQ811850.1 gg_id:172275 mangrove soil clone MSB-3ax5 DQ811
EU799430.1 gg_id:308804 It's all ranking aquatic Newport Harbour RI clone 1C227029 EU799
FJ203312.1 gg_id:327709 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c FJ2033
FJ664800.1 gg_id:554245 Quantitative dynamics cells plankton-fed microbial fuel cell clone plankton_D11 FJ6648
EU642854.1 gg_id:279275 Pseudoruegeria sp. JC2496 str. JC2496; IMSNU 14150 EU642
EU246829.1 gg_id:248590 polyphasic description Pocillopora meandrina Palmyra Atoll Calcinus obscurus abdon EU246
AF384204.1 gg_id:23935 Rhodobaca bogoriensis str. CL1 AF384
EF554833.1 gg_id:224271 Rhodobaca barguzinensis str. VKM B-2406 EF5548
AF513929.1 gg_id:62508 Rhodobacter group clone LA1-B42N AF513
AJ605746.2 gg_id:148330 Rhodobacter sp. str. EL-50 AJ6057
AF454295.1 gg_id:63841 hypersaline Mono Lake clone ML812M-6 AF454
AJ132383.1 gg_id:73883 Natronohydrobacter thiooxidans str. AHO 1 sediments ly alkaline soda lakes AJ1323
DQ659236.1 gg_id:170558 Roseinatronobacter monicus str. Ros35 DQ659
AB369166.1 gg_id:243619 Microbiological Assessment Circulation Mud Fluids During First Operation Drilling De AB369
DQ432310.1 gg_id:156883 prokaryotic alkaline hypersaline lakes Wadi Natrun Egypt Lake Hamra sediment clon DQ432
AF454292.1 gg_id:63844 hypersaline Mono Lake clone ML602M-13 AF454
DQ432219.1 gg_id:156640 prokaryotic alkaline hypersaline lakes Wadi Natrun Egypt Lake UmRisha sediment cl DQ432
DQ432393.1 gg_id:156929 prokaryotic alkaline hypersaline lakes Wadi Natrun Egypt Lake Hamra water clone W DQ432

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333.7	1201.5	1172.2	1365.3	2191.7	1665.1	1881.1	1898.7	1427.1	1506.9	904.6
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90.2	1040.6	906.9	925.9	1605.3	1104.7	1321.6	1349.2	804.9	1213.0	585.4
9366.1	4018.9	5727.3	5981.0	6277.2	5459.9	5842.0	5202.5	7215.8	4656.3	5556.7
472.1	1819.3	1298.3	1616.8	1960.3	1127.1	1723.5	2330.9	1179.2	1399.3	1047.5
231.4	3281.5	2929.1	3223.4	5879.0	4128.4	5099.2	4902.5	4827.4	2664.0	2886.5
36.4	450.0	197.3	224.2	253.4	219.8	255.7	488.5	137.0	140.6	124.5
3237.5	4781.9	4050.8	4237.0	6057.3	5586.5	5175.1	4908.7	4834.8	5391.6	3440.7
13690.3	5036.8	4693.5	5227.6	5589.8	5942.9	5437.7	5812.5	6772.0	6418.5	5781.7
105.4	1322.4	905.9	796.1	1673.3	1178.1	1170.9	1259.3	644.0	786.8	505.1
2041.8	4021.2	3434.2	4888.1	3530.8	4890.4	4568.4	5174.3	2209.5	1585.9	4797.5
7769.9	4244.6	4261.9	4995.0	5112.7	5471.0	5358.8	4994.4	4875.5	4187.4	4589.5
174.5	664.2	744.0	917.2	1385.4	989.3	1128.1	1337.7	611.6	634.4	476.6
7464.3	5536.9	5237.4	7327.5	6944.0	6533.9	7383.1	6372.4	6663.1	6884.6	5450.7
98.0	342.8	368.5	473.7	308.0	342.5	399.0	642.7	265.1	93.6	462.3
1959.0	3533.1	3703.9	4236.9	5044.6	3804.8	4437.1	4274.9	4222.4	2139.0	3198.5
1801.7	2905.0	3195.6	3320.3	4072.5	5496.2	4577.7	3918.8	3680.8	4990.3	3002.9
10618.7	4085.4	2676.3	2626.2	2994.5	3512.4	3202.2	3101.8	4286.4	3405.3	2713.8
968.5	2626.1	3567.0	3299.7	3467.8	3130.9	3030.8	4038.4	2668.9	2317.2	3547.5
972.8	1474.1	1636.8	1889.0	1859.4	1944.1	1854.0	2057.2	1816.1	2348.5	1190.5
231.8	2792.8	2318.1	2458.1	2989.1	2664.2	3037.1	3156.6	2410.9	3521.6	2660.0
82.5	963.3	693.6	1069.6	1168.4	911.6	1235.3	1875.5	1167.6	480.7	768.7
1391.0	2942.6	2762.9	3332.8	3639.2	3554.1	4050.3	3386.8	3248.8	3596.7	2540.8
114.3	2052.5	997.3	1310.2	1346.2	2321.5	1350.6	1553.0	1843.3	1061.3	1013.2
61.6	363.4	660.8	785.3	575.2	788.6	323.3	715.1	545.1	113.4	365.7
192.8	1772.3	1924.1	2549.6	2445.0	3028.2	1917.3	2763.1	2242.7	396.8	1243.0
4398.9	3067.9	2589.9	2591.4	3658.2	4218.1	3798.5	4489.7	3037.1	2706.1	2375.8
981.4	3156.8	2525.4	2625.3	2863.7	3943.3	2403.6	5261.2	4036.9	2394.9	3354.9
14239.8	2286.8	2007.4	2001.5	2428.2	3818.4	1721.7	3290.5	2865.0	1601.7	1898.0
38.2	2550.5	1816.5	2182.9	2697.2	2201.1	3869.1	3219.7	5140.0	1444.7	1782.4
7205.3	6677.9	5664.9	6043.9	7264.7	8108.1	6440.7	7503.6	7595.3	4468.0	5974.2
30021.7	8378.4	8836.1	8635.7	8533.2	11562.5	8555.9	8642.2	12684.0	10392.1	11524.7
98.8	534.2	497.8	542.5	720.8	482.2	871.3	1431.5	1574.7	706.2	641.9
669.0	2190.3	1541.5	1971.3	2626.3	1744.4	2856.4	2675.1	3482.5	1024.1	1818.1
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514.7	2002.8	1870.1	1848.3	2569.0	1601.0	2238.2	3866.2	1455.5	2125.7	2234.9
21624.7	6720.1	6319.1	6003.4	6134.8	10795.9	6352.0	7541.3	9282.0	5040.8	7602.4
5782.8	7945.8	5588.0	5859.2	8672.9	10358.1	8186.5	8493.7	5896.7	7216.6	6407.8
2319.8	1708.1	2075.8	1908.1	1973.8	1643.8	1983.7	2565.1	1897.7	595.3	1475.8

6095.1	5736.8	5651.7
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1817.9	2466.8	1405.9
1647.5	1545.8	1097.2
1537.7	1449.4	1065.9
6678.7	6375.4	4603.6
2937.0	1525.7	576.9
4813.4	3296.2	1629.8
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5608.3	6356.4	4344.9
1473.8	1144.3	927.2
4127.7	3693.0	3195.6
6254.1	5262.2	4745.8
1402.6	1436.6	566.8
6650.2	7038.3	5376.6
449.3	474.0	890.4
4623.5	4822.0	4851.7
3345.1	4229.5	2982.3
3136.3	3899.1	2764.9
3257.5	3387.0	4436.1
2269.6	2316.7	2074.9
3215.6	2927.9	2582.5
1630.2	955.7	671.7
3401.1	3560.0	2601.0
1502.3	977.0	379.9
1209.0	754.7	282.1
3944.3	2326.4	2134.0
4049.2	2981.6	2614.6
3456.0	2958.5	1628.9
2345.9	1983.8	1991.1
3138.4	2049.5	1261.6
7809.0	6703.9	5758.5
8349.0	9222.7	8014.6
724.2	1317.2	412.3
2417.0	2005.4	2051.7
2686.4	1859.9	2500.9
2636.6	1844.5	1655.9
6891.0	5877.4	5156.6
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DQ659237.1 gg_id:173742 Roseinatronobacter monicus str. Ros10 DQ659
FJ153015.1 gg_id:332691 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX4CI FJ1530
CP000663.1 gg_id:219103 Rhodobacter sphaeroides str. ATCC 17025 CP000
D16427.1 gg_id:5815 Rhodobacter capsulatus str. C5 D1642
GU370088.1 gg_id:514578 Rhodobacter sphaeroides str. P230(6) GU370
GU370084.1 gg_id:532163 Rhodobacter sphaeroides str. P230(1) GU370
GU455302.1 gg_id:522935 Understanding short-chain fatty acids accumulation enhanced alkaline digestion: kir GU455
AF280854.1 gg_id:49391 bioreactor clone mle1-20 AF280
GU086365.1 gg_id:560393 Pseudorhodobacter sp. str. HDW-19 GU086
FN428770.1 gg_id:543416 Looking India metagenomic approach Mahananda river water clone MRM1024 FN428
EU703461.1 gg_id:377032 lakes on Eastern Tin Plateau freshwater lake altitude 4279 masl clone XZZLH1 EU703
AB355088.1 gg_id:240664 Monitoring and archaeal two heavy polluted areas lake Egypt based on sediment Ma AB355
AY212706.1 gg_id:102583 water 10 m downstream manure clone 257ds10 AY212
EU580696.1 gg_id:268039 Rhodobacter sp. str. NP25b EU580
GQ500826.1 gg_id:587231 Surveys Biofilms and Sediments Mammoth Cave Karst Aquifers Bio-Sep beads conta GQ500
DQ815272.1 gg_id:169528 zebrafish digestive tract clone aab52e09 DQ815
EU104326.1 gg_id:321409 Evidence Comamonadaceae determinants settling performance activated sludge clo EU104
GU257946.1 gg_id:566382 Rhodobacter changlensis str. HXG-D9 GU257
DQ342322.1 gg_id:214765 Rhodobacter blasticus str. ATCC 33485; KC2138 DQ342
AB077986.1 gg_id:67721 Rhodobacter gluconicum AB077
DQ676414.1 gg_id:225039 Archaeal and plankton freshwater pond suboxic freshwater-pond sediment clone M DQ676
AM690348.2 gg_id:225526 Rhodobacter katedanii str. JA234 AM690
EU652478.1 gg_id:277835 Catellibacterium sp. str. JPB-2.07 EU652
GU454898.1 gg_id:520640 Understanding short-chain fatty acids accumulation enhanced alkaline digestion: kir GU454
EF192900.1 gg_id:201726 sediments temperate artificial lake Rapel reservoir sediment clone Rap2_6C EF1929
AF234745.1 gg_id:35565 sludge clone A26 AF2347
FJ382199.1 gg_id:512277 Potentially pathogenic and air stem cell transplant summer hospital shower water BN FJ3821
AF035433.1 gg_id:5793 Rhodobacter apigmentum AF0354
EU464681.1 gg_id:301082 Hartmann's mountain zebra feces clone AFZEB_aaj69a12 EU4646
AY957924.1 gg_id:114895 drinking water biofilm clone B3NR69D9 AY9579
DQ337005.1 gg_id:147896 subsurface water clone EV818CFSSAHH73 DQ337
EU979475.1 gg_id:307279 Rhodobacter sp. str. CR07-8 EU9794
AB122032.1 gg_id:98295 Rhodobacter sp. str. Jip03 AB1220
D16429.1 gg_id:5800 Rhodobacter blasticus str. ATCC33485 D16429
AF368183.1 gg_id:58379 non-EBPR sludge clone SBRT155 AF3681
FJ196030.1 gg_id:333434 Rhodobacter sp. str. ZS3-33 FJ1960
AM696303.1 gg_id:217363 Rhodovulum marinum str. JA219 AM696
D16420.1 gg_id:5840 Rhodovulum sp str. MB260 D16420
U55277.1 gg_id:5835 Rhodovulum sulfidophilum str. W-1S=FERM P-15320 U55277
GU370080.1 gg_id:519755 Rhodovulum sulfidophilum str. P210(4) GU370
EU770422.1 gg_id:306266 Rhodovulum sulfidophilum str. sy59 EU7704

8725.7	2601.5	1849.9	2299.2	4121.4	3845.5	2768.9	3218.0	1823.9	1408.6	1349.3
529.6	1466.0	1411.3	1575.5	1951.5	1592.3	1345.7	2511.7	1400.2	1401.9	1083.7
478.7	4720.9	3400.3	3839.9	4501.8	5205.9	4718.7	5639.8	4229.2	3675.3	3804.1
97.5	1991.2	1444.1	1538.1	1958.9	3015.5	2050.7	3039.4	951.6	1454.0	1548.4
3897.1	7360.6	4566.4	5080.4	8185.2	7807.9	6814.3	7126.2	4531.0	5409.5	5368.1
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7080.8	8056.2	6525.3	7470.2	9779.6	7195.7	9685.4	8722.8	7237.8	7623.2	7539.7
3059.7	4533.5	2986.8	3130.7	4387.5	5377.3	4165.8	4500.1	3953.0	3636.4	3061.2
12320.3	6518.3	5190.0	5256.5	6980.3	11614.8	6250.0	7023.4	6939.8	4475.4	5523.8
2224.6	4979.2	3641.4	3687.0	4967.8	4075.5	4970.2	4934.7	3365.8	2274.7	3280.5
43.5	1804.9	1547.9	1596.7	2484.8	4136.5	2061.5	2619.5	1403.1	1120.2	1392.3
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6701.0	6200.8	5338.5	6443.4	8236.8	5496.2	8814.6	7089.8	6834.2	7065.4	6657.5
1699.9	3902.5	2925.4	2927.3	4360.1	3815.4	4439.6	4251.6	2636.0	2243.4	2381.4
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2689.7	4668.2	3694.4	4175.1	5942.7	6437.6	4931.5	5155.9	4317.4	3140.8	3662.5
330.9	4413.6	3196.0	3482.5	4006.7	3477.0	4796.5	4536.4	2060.6	2627.3	2792.1
604.2	8308.8	5509.4	5560.2	9406.4	9897.6	7875.2	8785.5	6645.3	7960.6	6473.0
1674.0	6758.6	4334.3	4434.6	7870.7	7050.3	7188.0	6911.5	3895.6	5283.2	4204.9
528.9	5537.1	4345.3	5088.4	7422.0	6291.9	6527.1	6168.4	4222.2	3891.0	3856.0
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AM696304.1 gg_id:220300 Rhodovulum marinum str. JA242 AM696
AM748927.1 gg_id:256512 Rhodovulum kholense str. JA297 AM748
AM921780.1 gg_id:291146 Rhodovulum puniceilacus str. JA322 AM921
NR_025222.1 gg_id:555568 Albidovulum inexpectatum str. FRR-10 NR_02
AB079635.2 gg_id:62339 Rhodovulum strictum str. JCM 9221 AB079
NR_025608.1 gg_id:568416 Roseisalinus antarcticus str. EL-88; DSM 11466 NR_02
FJ593905.2 gg_id:592117 Roseivivax sp. str. sw-2 FJ5939
FJ897782.1 gg_id:543161 Roseivivax sp. str. BH87090 FJ8977
AB166989.1 gg_id:102398 Roseivivax sp. str. NT N51 AB166
GQ243710.1 gg_id:578525 consortia immobilizing nitrifying bioreactors designed penaeid and non-penaeid larv GQ243
EF512126.1 gg_id:220146 Roseobacter denitrificans str. CSQ-3 EF5121
NC_008209.1 gg_id:163757 Roseobacter denitrificans str. OCh 114 NC_00
GQ249575.1 gg_id:513025 Microbial anaerobic sediments Bay Cadiz (Spain) marine sediment: 12-14 cm layer cl GQ249
AY654757.1 gg_id:104921 Oculina mucus isolate 112 AY654
AY177714.1 gg_id:83398 Rhodobacteraceae T11 AY177
DQ446103.2 gg_id:164817 Surface Mucopolysaccharide Layer and Band Microbial Mat Black Band-Diseased Sid DQ446
AJ844283.1 gg_id:160252 Rubellimicrobium thermophilum str. E-R2A-8a AJ8442
FM874293.1 gg_id:360432 occupant source house mattress dust clone MC04B03 FM874
EU338486.1 gg_id:242423 Pararubellimicrobium aerilata str. 5715S-9 EU338
EF547368.1 gg_id:218626 Rubellimicrobium sp. str. MSL 20 EF5473
DQ532142.1 gg_id:167156 Geographical Variation Microbial Burden and Spacecraft Assembly Jet Propulsion Lal DQ532
DQ532274.1 gg_id:172438 Geographical Variation Microbial Burden and Spacecraft Assembly Johnson Space Ce DQ532
EF682991.1 gg_id:243852 Eastern Mediterranean atmosphere clone F13_3E_FL EF6829
AJ968649.1 gg_id:144280 Ruegeria atlantica str. N5III AJ9686
DQ915630.1 gg_id:330249 Silicibacter lacuscaerulensis str. DSM11314 DQ915
DQ915631.1 gg_id:306399 Silicibacter pomeroyi str. DSM15171 DQ915
EF092256.1 gg_id:264007 Persistent Axinella corrugata Roseobacter clone MAx29_D12 EF0922
AM709700.1 gg_id:254802 symbiotic Ruegeria strains cuttlefish Sepia officinalis egg yolk clone B4SOVto5 AM709
AM709703.1 gg_id:254660 symbiotic Ruegeria strains cuttlefish Sepia officinalis shell sacs clone 2SOSC91 AM709
AM930441.1 gg_id:268418 involved Tripneustes gratilla (Echinoidea) cloning and FISH host body wall lesions cl AM930
GU118794.1 gg_id:533437 Threatened Corals Provide Microbial Habitats clone Mfra_N19 GU118
FJ203171.1 gg_id:354074 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c FJ2031
GU118756.1 gg_id:593469 Threatened Corals Provide Microbial Habitats clone Mfra_C19 GU118
FJ203011.1 gg_id:350278 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c FJ2030
AM709701.1 gg_id:248371 symbiotic Ruegeria strains cuttlefish Sepia officinalis embryo clone B4SOEmb23 AM709
FJ403069.1 gg_id:357398 Disease- changes healthy and diseased colonies Caribbean coral Montastrea faveolat FJ4030
AJ633996.1 gg_id:114809 host's egg clone IEGG2 AJ6339
DQ357745.1 gg_id:149148 Marine Hatchery: Balance Between Pathogenic and Potentially Probiotic Strains mo DQ357
FJ716889.1 gg_id:549008 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United King FJ7168
EF629830.1 gg_id:274739 Changes marine Mycale laxissima on transfer aqua sponge tissue EF6298

400.1	2444.2	643.2	686.3	1424.5	2575.9	943.3	1783.7	307.1	1194.7	1006.6
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6887.1	4387.9	3545.1	3711.0	7305.2	6042.4	5060.5	4792.1	2331.6	2252.8	2761.4
12989.8	3814.3	3541.6	3320.3	5640.3	4606.6	5827.3	4384.1	3925.4	2504.4	2667.6
1651.7	3954.7	4672.6	6156.2	4712.9	3545.8	4954.4	4841.8	2953.3	2291.8	1942.9
1788.0	2997.6	1315.9	1630.6	2035.2	3649.2	1920.4	1992.1	1539.0	1526.1	1838.7
937.2	3021.9	2885.7	3542.1	3393.3	3366.2	3793.9	3656.2	3358.2	2249.7	2459.9
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10002.0	3203.5	3281.6	3660.3	5375.9	4049.2	5139.9	4237.6	3425.6	1932.3	2523.3
15132.0	4958.7	5560.6	5591.8	7236.5	5859.8	8303.8	5863.8	7216.5	5145.4	4235.9
226.0	823.4	649.9	798.9	806.1	1287.7	855.3	1439.0	874.0	418.4	457.9
1185.3	1815.2	1746.6	2468.3	1666.6	2563.9	2109.5	1988.8	2048.1	870.1	1932.0
218.7	778.8	1034.1	1139.3	1057.3	838.6	1120.4	942.0	539.8	654.8	600.4
17030.6	9232.8	7364.5	8238.6	9510.5	8902.9	8987.1	9310.5	9898.7	7368.8	7187.2
43.2	980.2	355.6	355.2	436.1	588.8	446.4	474.1	158.7	231.0	157.9
53.2	1409.9	438.0	346.3	1107.6	706.0	726.9	985.6	488.3	424.2	426.2
81.8	239.7	435.7	582.5	131.2	262.6	146.8	213.8	92.5	59.0	200.7
5180.2	3247.3	2024.4	2713.3	3061.6	4441.8	3107.0	3859.7	3562.6	1546.2	2118.2
3203.6	5566.3	5973.3	6163.4	7002.3	7179.9	7688.4	6838.6	7091.2	5880.9	5761.1
8207.1	7773.3	6717.4	7429.8	8519.5	7772.8	8692.7	7853.4	6867.0	6952.0	6588.8
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19834.7	5929.6	5837.9	6566.4	6986.2	6315.4	7395.9	6584.2	7361.9	6357.5	6938.3
14921.0	4869.1	3904.3	4456.5	4467.7	4718.3	5392.7	4778.9	6293.0	6108.7	4089.4
170.9	2639.7	2182.9	2373.0	3948.4	4832.2	3042.4	3525.7	2080.2	1895.3	2131.6
225.1	1599.7	1831.4	2082.1	1984.3	1943.5	2200.7	2567.5	1458.3	1331.9	1946.7
114.1	738.9	705.2	781.2	1177.0	916.7	938.9	1228.5	724.6	539.4	511.4
142.9	655.4	1017.5	1131.0	792.4	761.6	979.6	1380.1	1638.3	353.2	650.3
143.9	1397.1	1237.5	1424.7	1718.8	2049.7	1399.9	1848.7	1354.6	899.8	1166.1
137.8	2009.3	1786.9	1897.9	2813.6	3453.9	2203.3	2533.3	1678.4	1291.1	1583.3
1641.5	1751.8	2121.4	2211.3	2582.0	3725.3	2400.8	2828.5	1451.9	1213.2	1672.9
1291.8	3338.6	2877.6	2758.9	3202.8	2910.8	3319.6	3849.8	2408.5	3721.3	2299.9
25350.3	10073.9	8003.7	8849.9	9255.3	8560.6	9088.0	7638.2	10925.9	9370.9	9084.6
417.4	2410.3	2053.9	2064.8	2287.5	2153.2	2719.5	3006.3	1313.9	2781.8	1797.8
14676.5	4296.3	4762.3	4626.6	5229.9	4544.0	4913.9	4454.6	5260.2	3322.5	3954.6
143.2	2033.0	1694.6	1917.1	2997.1	3534.1	2326.4	2646.9	1769.9	1419.9	1693.3
22777.3	7150.0	7469.6	7118.9	7574.3	7155.7	7926.9	6670.3	10975.2	8293.9	9776.6
997.1	2994.8	3310.7	3300.5	4136.5	3067.9	3502.7	4356.8	2550.9	2596.6	2481.1
422.0	1548.4	1329.2	1401.8	1341.6	1864.8	1267.9	2022.8	525.6	671.8	883.5
26504.8	7692.3	7344.9	8143.0	8146.7	7348.0	6875.6	7032.9	10208.7	10743.5	10863.1
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1821.2	2100.2	1397.9
5098.9	4037.2	2844.3
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1269.9	2138.0	1456.1
762.9	1627.1	942.4
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7642.5	7488.9	7908.2
5596.4	5556.0	4445.0
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4208.3	5432.1	5321.2
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1959.0	1840.0	1482.8
1039.9	905.4	818.7
953.1	865.1	850.3
1661.7	1511.6	769.3
2480.2	1764.6	914.0
2314.5	2672.9	1399.8
3417.1	3813.5	3055.7
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D88526.1 gg_id:5714 Ruegeria atlantica str. IAM14463 D8852
FJ403081.1 gg_id:369403 Disease- changes healthy and diseased colonies Caribbean coral Montastrea faveolat FJ4030
EU195952.1 gg_id:251321 Roseobacter sp. str. P123 EU195
DQ917807.1 gg_id:220204 Microbial profiles bleached and wild-type Muricea elongata Oleiphilus clone BME10 DQ917
FJ203260.1 gg_id:346584 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c FJ2032
AM709702.1 gg_id:256402 symbiotic Ruegeria strains cuttlefish Sepia officinalis renal appendage clone B4SOAr AM709
FJ937894.1 gg_id:534136 Ruegeria sp. str. LS36 FJ9378
DQ917855.1 gg_id:223353 Microbial profiles bleached and wild-type Muricea elongata Ruegeria clone ME108 DQ917
GQ391987.1 gg_id:522785 Silicibacter sp. str. PaD1.36a GQ391
FJ203147.1 gg_id:315763 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c FJ2031
AM709704.1 gg_id:235710 symbiotic Ruegeria strains cuttlefish Sepia officinalis shell sacs clone B6SOSCV22_3 AM709
EU907925.1 gg_id:328931 Ruegeria sp. str. SKUK MB1010 EU907
U58356.1 gg_id:5685 Sagittula stellata U5835
AJ557871.1 gg_id:84036 Arctic deep sea Isolation common chemoorganotrophic oxygen-respiring polar current AJ5578
FJ425632.1 gg_id:362713 communnities healthy and diseased colonies Caribbean coral Montastrea faveolata S FJ4256
FJ203292.1 gg_id:321452 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c FJ2032
DQ915633.1 gg_id:351778 Sulfitobacter brevis str. DSM11443 DQ915
DQ915634.1 gg_id:345214 Sulfitobacter delicatus str. LMG20554 DQ915
AM990658.1 gg_id:278280 Sulfitobacter sp. MOLA 381 AM990
DQ357749.1 gg_id:146001 Sulfitobacter sp. G5-5b DQ357
DQ357751.1 gg_id:150184 Sulfitobacter sp. Cl-H6 DQ357
AF007254.2 gg_id:5638 Sulfitobacter sp. str. EE-36 AF007
NZ_AALV01000004.1 gg_id:149068 Sulfitobacter sp. str. EE-36 NZ_AA
AY794211.1 gg_id:109147 soil clone F457 AY794
GU061076.1 gg_id:592471 Evaluation culturing methods cultivate previously Yel Sea intertidal beach clone TFS- GU061
GU061073.1 gg_id:590614 Evaluation culturing methods cultivate previously Yel Sea intertidal beach clone TFS- GU061
GU061065.1 gg_id:544093 Evaluation culturing methods cultivate previously Yel Sea intertidal beach clone TFS- GU061
EU823295.1 gg_id:310853 Sulfitobacter sp. str. P64 EU823
AF007260.2 gg_id:5681 Sulfitobacter sp. str. GAI-37 AF007
AF173972.1 gg_id:71580 Roseobacter sp. str. KT0917 AF173
GU061114.1 gg_id:579705 Evaluation culturing methods cultivate previously Yel Sea intertidal beach clone YAF- GU061
GU061035.1 gg_id:537289 Evaluation culturing methods cultivate previously Yel Sea intertidal beach clone Mix GU061
AJ534237.1 gg_id:75228 Sulfitobacter sp. LM-16 AJ5342
GU061104.1 gg_id:592909 Evaluation culturing methods cultivate previously Yel Sea intertidal beach clone TFS- GU061
GU061041.1 gg_id:571091 Evaluation culturing methods cultivate previously Yel Sea intertidal beach clone Mix- GU061
AY162107.1 gg_id:135250 Cultivating Sargasso Sea clone GMD16F09 AY162
GU061096.1 gg_id:572670 Evaluation culturing methods cultivate previously Yel Sea intertidal beach clone TFS- GU061
AY771778.1 gg_id:144788 Arctic Sulfitobacter brevis clone SE96 AY771
EU919845.1 gg_id:315930 Kongsfjorden western Spitsbergen Svalbard ocean water clone s81 EU919
GU061088.1 gg_id:593911 Evaluation culturing methods cultivate previously Yel Sea intertidal beach clone TFS- GU061

17510.4	4121.7	4498.4	4383.8	4795.5	4015.9	4318.6	4413.5	4447.4	3279.2	4307.7
13054.2	5393.0	5323.2	6128.4	7279.3	6370.7	6525.8	6734.7	7077.7	7945.9	7695.5
3753.7	5466.2	6604.7	7082.2	5867.1	5850.4	6914.4	7053.2	4503.2	5281.1	6738.8
63.5	177.6	249.8	298.2	504.8	311.5	257.8	324.7	176.4	135.7	144.7
9939.6	4079.4	3908.8	4867.9	4317.0	4045.4	4511.0	4450.5	4133.4	3331.3	3865.1
1757.0	5701.4	4994.7	5621.2	7486.4	7236.8	7177.0	6239.8	6394.3	5405.0	5087.9
4207.5	2604.8	2640.6	2881.2	3332.3	3208.6	3059.8	3237.2	2726.1	3147.4	2794.5
85.5	1508.7	1857.7	2057.0	1962.5	2775.8	2028.1	2489.4	1017.5	1086.0	1350.4
6171.8	4388.9	4184.3	3844.2	4555.1	4895.8	4596.3	5036.7	5349.0	4327.0	3146.2
10553.3	3424.2	3615.5	3376.6	5642.0	5240.9	4413.6	4128.9	3987.2	2820.4	3351.5
279.6	598.3	680.7	914.1	968.0	692.6	771.3	1285.6	479.3	374.4	424.9
167.9	1542.6	1245.2	1565.4	1968.0	2870.4	1434.7	2191.5	1307.4	894.2	1183.1
11092.7	3971.8	3550.2	4124.8	3688.0	3774.2	4088.3	4102.2	3552.5	3179.1	4672.1
3874.0	3227.2	2642.1	2721.6	3534.1	4123.4	3331.9	3383.0	2965.3	1827.7	2476.4
281.9	1585.1	1374.4	1687.3	2802.6	2110.1	2415.5	2087.3	1492.8	1273.1	984.3
1664.2	1925.5	1746.5	1998.6	2121.7	1861.7	2127.4	2275.0	1832.2	1219.2	1804.1
2210.9	3636.4	2988.2	3440.4	3218.2	3379.7	3454.0	3436.8	2280.2	2712.8	2695.2
158.6	2141.2	2304.1	2878.1	2785.4	2893.3	2597.4	3042.0	2313.7	1010.9	1652.6
2649.5	2850.1	2411.3	2459.6	3531.8	2813.2	3283.5	3033.4	2300.3	1695.1	2717.0
11884.4	4021.7	3660.8	3984.1	5425.2	4281.3	4196.8	4220.8	3968.8	2989.5	2399.5
82.4	1138.3	1131.2	1417.8	1241.0	1547.9	1161.3	2127.7	767.6	562.7	704.7
90.4	1033.3	1100.9	1303.6	1057.0	1449.9	1068.3	1924.1	749.7	464.3	648.6
68.7	1291.5	1504.0	1988.0	1159.8	1779.4	1380.5	2656.7	801.3	515.7	1172.9
776.0	1850.4	1512.6	1952.7	1967.3	2247.1	1581.8	2784.2	1249.2	1065.4	1017.1
508.2	1373.5	1623.3	2320.5	1694.5	2130.6	1700.0	2390.6	1279.3	1159.1	1794.2
600.6	1382.5	1592.4	1755.2	2939.2	2660.8	1872.1	2019.8	1955.1	819.3	1135.0
278.7	2092.8	1276.2	1505.5	2393.4	2368.1	1569.3	2867.5	1673.4	1024.9	986.4
178.7	1186.1	1147.7	1311.5	1081.7	1189.5	1254.0	1502.2	705.6	615.1	1386.0
14735.5	6845.0	5106.8	6965.9	8997.1	7107.0	7081.7	6879.9	7226.1	5495.0	5781.3
417.4	993.6	637.0	575.9	686.0	748.3	887.5	420.4	583.0	450.6	334.2
245.3	2531.6	1783.4	1867.7	1665.0	2877.1	2251.7	3836.1	3622.5	5955.1	1345.2
2393.6	1951.0	1699.2	2040.1	2529.1	3767.2	1880.5	3526.3	2112.4	1293.1	1744.5
137.8	1254.7	1336.2	1227.0	1322.8	3346.8	1760.0	1928.4	1760.5	257.4	810.4
135.0	1298.8	1249.5	1523.8	1617.6	1754.6	1298.7	1835.6	717.0	689.0	735.1
1254.2	3299.1	2314.7	2742.0	2669.3	5325.7	2243.7	3139.7	2309.0	2206.5	2284.0
3706.7	2557.4	2176.2	2674.0	4438.3	2738.5	2757.7	2780.7	1983.3	1444.7	2418.2
122.4	1384.0	1404.8	1631.6	1708.2	2135.7	1979.5	2150.7	1824.0	804.5	853.3
81.1	396.2	220.0	244.0	740.8	292.7	381.5	566.9	337.0	192.6	138.7
122.3	2553.4	2732.3	3286.1	2714.9	3073.7	3025.5	3361.3	2156.8	1107.7	2270.4
657.8	868.4	1353.5	1574.1	873.3	689.3	736.9	2418.4	1651.4	364.2	957.3
90.5	651.8	610.4	497.8	849.2	1398.9	641.4	1248.4	940.0	830.3	497.8

4595.1	4531.9	4116.8
6703.4	7606.0	6190.5
6561.0	6477.5	6684.9
474.2	425.1	382.4
3902.5	4954.0	4146.6
6284.8	5257.7	3819.5
3279.3	3569.9	3016.8
2225.2	1815.8	1063.7
4729.3	5372.0	3467.8
4452.7	3462.4	2981.3
1063.8	976.9	590.2
1934.0	2042.1	1326.3
3437.8	4894.8	3329.5
2801.9	3018.7	2573.3
2411.0	2216.3	1424.6
2376.0	2481.2	1823.7
3503.1	3850.2	2863.1
4114.3	3224.6	2248.4
2904.2	3030.7	3098.4
4736.5	4673.7	3740.1
2252.1	2110.3	2622.3
2113.8	1960.4	2586.4
2378.5	2127.0	2913.3
2921.8	2889.9	3792.5
1851.4	2146.1	1723.6
2598.1	2163.0	1898.7
2403.5	2276.7	1438.0
1247.8	1336.4	1210.6
7125.5	5118.4	3274.8
961.4	907.3	617.7
2891.1	3162.8	2441.0
3497.4	3150.8	2190.2
2124.1	1984.2	1559.6
1843.9	2045.8	1275.3
3233.5	3037.7	1313.0
3167.3	2863.2	3096.4
2176.4	1113.8	1165.3
530.5	645.5	292.2
4018.3	3229.6	3190.9
814.8	1494.6	820.6
783.0	778.4	507.9

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g__Sulfitobacter
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s__unclassified	60718

DQ097527.1 gg_id:132683 Sulfitobacter litoralis str. iso1 DQ097
AJ534236.1 gg_id:76438 Sulfitobacter sp. LM-11 AJ5342
DQ659417.1 gg_id:166927 Roseobacter sp. str. SO3 DQ659
GU061005.1 gg_id:572128 Evaluation culturing methods cultivate previously Yel Sea intertidal beach clone SF7 GU061
AY690671.1 gg_id:107730 Sulfitobacter sp. str. GC02 AY6906
AB121782.1 gg_id:104397 Jannaschia cystaugens str. CFPB-A9 AB1217
DQ915638.1 gg_id:316408 Thalassobacter stenotrophicus str. CECT5294 DQ915
AB121783.1 gg_id:104544 Jannaschia cystaugens str. CFPB-A5 AB1217
AJ631302.1 gg_id:109582 Thalassobacter stenotrophicus str. CECT 5294 = 5SM22 AJ6313
DQ915639.1 gg_id:315323 Thalassobius gelatinovorus str. NBRC15761 DQ915
AJ878874.1 gg_id:142415 Thalassobius mediterraneus str. CECT 5383 = XSM19 AJ8788
FJ202550.1 gg_id:341164 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2025
AJ968650.1 gg_id:143564 Roseovarius pelophilus str. G5II AJ9686
AF114484.2 gg_id:5704 CVSP isolate str. CV919-312 AF1144
EU236364.1 gg_id:297563 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg91D8 EU2363
FJ203176.1 gg_id:337783 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c FJ2031
FJ203129.1 gg_id:341596 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c FJ2031
DQ376573.1 gg_id:152175 Microbial ecology removing phosphate wastewater EBPR process aerobic sequencin DQ376
EF540436.1 gg_id:220130 oil-shale semi-coke solid waste clone PK_V EF5404
DQ640665.1 gg_id:233567 full-scale EBPR sludge clone Skagenf58 DQ640
EU979473.1 gg_id:344892 Rhodobacter sp. str. CR07-5 EU9794
AM403212.1 gg_id:163121 Nitrate-reducing and Denitrifying Marine Aqua Biofilter marine aqua AM403
EF205262.1 gg_id:188150 Paracoccus sp. 'CJSPY1 (P-I)' str. CJSPY1 (P-I) EF2052
FJ872532.2 gg_id:593437 Rhodobacter sp. str. ZH15 FJ8725
AY656719.1 gg_id:99632 Thioclava pacifica str. TL2 AY6567
AM745438.1 gg_id:243786 Rhodobacter maris str. JA276 AM745
AY914074.1 gg_id:114095 Rhodobacter sp. R-8 AY9140
GQ355283.1 gg_id:593578 Thioclava sp. str. GT-5 GQ355
FJ542826.1 gg_id:530503 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone A FJ5428
AY172658.1 gg_id:77954 Rhodobacter sp. str. B-7005 AY1726
AM408117.1 gg_id:186127 Rhodobacter vinaykumarii str. JA123 AM408
EF061947.1 gg_id:193660 Xiamen China mangrove sediment clone XME33 EF0619
EU491911.1 gg_id:264288 Abundance and microbial life ocean crust deep seawater East Pacific Rise clone EPR4 EU4919
FJ202842.1 gg_id:306401 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2028
FJ497541.1 gg_id:586757 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun FJ4975
GU220746.1 gg_id:591725 Microbial mineralization and involved microbial Basin field temperature hydrotherm GU220
EU287008.1 gg_id:239638 Pacific arctic surface sediment clone B78-44 EU2870
FJ905620.1 gg_id:568278 s Tonga-Kermadec iron oxide chimney-like structure on Volcano 19 Tonga Arc clone V FJ9056
AF468367.2 gg_id:80906 Arctic sea ice ARK10115 AF4683
EF573178.1 gg_id:231130 Coco's Island site 23 marine clone S23_1277 EF5731
FJ905703.1 gg_id:552641 s Tonga-Kermadec iron oxide sediments Volcano 1 Tonga Arc clone V1F23b FJ9057

82.9	1225.9	1740.7	2389.2	772.9	1835.8	1374.3	4046.7	639.5	1188.0	1735.3
2144.2	3647.2	3055.9	3443.2	4533.9	4256.6	3796.6	4350.7	2724.0	3544.4	2392.5
103.7	1159.1	1211.8	1800.2	1273.9	1499.8	1933.0	2240.0	769.5	784.8	841.8
63.2	437.5	615.3	622.7	589.1	879.2	663.0	1270.3	195.9	809.7	239.3
634.1	1506.9	1942.2	2950.6	1934.9	1839.2	2888.2	2780.0	725.4	575.3	1394.7
9048.4	6120.5	5052.4	5572.0	6353.5	5558.8	5920.6	5660.4	5018.3	5397.1	5463.0
4933.4	2718.8	2551.5	2849.8	3442.1	3378.4	3296.5	2939.9	3404.5	2582.9	3020.4
562.5	1503.7	1137.9	1410.0	2089.2	1683.5	1552.9	1596.6	1183.5	956.6	988.5
8847.4	6716.6	5166.2	5756.8	6906.2	6820.3	6373.5	6104.3	6167.4	5243.7	5493.2
90.8	1235.8	1687.1	2007.4	898.5	1217.2	1396.0	1535.2	1323.9	169.1	1074.9
248.4	1133.3	1168.0	1369.3	1564.4	1294.1	1551.2	895.2	786.4	961.5	1355.4
17869.6	6077.7	6319.2	6737.6	5675.3	5239.0	6257.6	6935.6	8313.2	6908.4	9116.1
7479.4	3842.0	3501.5	4014.3	4544.5	4915.5	4512.9	4424.0	4368.1	3345.2	3099.6
244.2	2211.2	2036.4	1898.4	2901.4	2734.8	1905.0	2539.6	2496.3	1618.3	2459.6
265.8	2495.9	3111.2	3371.6	2644.3	3654.9	2762.9	3612.9	1981.7	1763.9	3042.1
112.5	343.5	290.7	361.5	20.2	341.3	365.2	736.5	430.6	227.4	261.2
136.4	2201.9	1473.1	1710.3	1162.9	1615.0	1674.0	1739.6	1157.6	947.1	1081.6
4389.7	5013.7	3543.2	3515.4	4518.2	7159.6	3065.6	3834.4	3772.2	3285.5	3009.1
156.0	2465.2	2504.5	3077.6	3943.4	4319.6	2718.8	3529.1	2367.1	1190.5	1636.4
3676.6	2833.0	3015.2	2842.3	3878.6	3935.3	3914.3	3523.1	1926.0	3491.8	2490.4
955.7	4523.8	3073.6	4622.5	6658.4	4842.3	4215.2	4980.4	4462.4	2868.7	2731.9
2514.7	2114.5	1724.3	1961.2	2570.4	2650.1	2808.9	2560.3	1317.7	1207.1	1227.4
503.5	3354.2	2756.1	3141.2	4601.4	5447.1	3526.3	4948.8	4837.6	2738.2	3008.0
853.6	2769.0	1823.7	2178.1	2581.1	3520.2	3415.7	3122.3	2258.9	1852.4	1762.5
8171.1	5428.5	2573.1	3283.3	3289.8	3197.4	3412.2	3220.9	4035.1	2423.0	3055.6
7071.3	5590.0	3898.1	4662.9	5612.6	7524.1	5527.0	6275.9	4819.0	5037.5	4073.5
11018.5	5958.7	5395.6	6140.6	6897.8	6736.6	6656.3	6858.6	7382.9	4729.4	6212.4
386.4	2372.4	2410.1	2631.7	2044.4	3287.1	2392.5	2690.2	2447.4	711.3	1588.5
724.4	3842.9	1847.4	2639.9	3556.6	3523.2	4143.8	3484.2	2164.5	2336.0	2132.2
7928.7	7781.3	6822.7	7801.3	8738.9	7769.6	8491.1	8147.7	8148.7	8979.1	8462.8
22841.4	5394.8	4591.9	5382.6	8266.6	5811.9	7186.4	5826.0	3430.1	3450.1	3175.9
994.3	2317.1	2264.3	2652.5	4400.1	3938.9	3512.3	3604.5	3882.3	2786.4	2014.8
9717.5	2944.6	2854.6	3297.2	3836.3	4274.5	3976.4	4623.2	3185.8	3020.7	2836.6
2221.0	4624.5	5766.9	4859.4	4775.7	4643.3	4369.7	4999.2	4520.5	4253.5	5703.5
2290.3	5017.1	4888.1	4584.5	5209.7	5028.9	5061.2	5174.2	4407.8	5200.7	4927.8
2485.3	4081.4	2166.9	2842.5	4698.9	3814.4	2674.3	3216.0	6699.5	2927.6	1834.2
117.5	1316.2	1025.3	1186.0	1762.9	1902.9	1029.1	1862.5	2352.7	664.9	1101.0
866.2	3007.1	2161.4	2649.1	5383.1	3386.5	3425.9	3572.2	5965.0	1801.3	1826.2
842.9	873.6	672.6	754.9	803.3	775.0	973.9	925.2	714.5	429.5	488.7
2493.2	3809.1	3500.2	3244.5	3639.7	4005.3	3822.5	3845.1	4774.2	2848.2	2943.3
2953.1	4859.2	4174.7	4514.7	4844.1	4975.4	5115.6	5602.0	3635.3	3726.2	3655.6

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5960.7	5884.6	5962.7
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2408.2	1633.5	1269.9
1592.8	1482.3	1748.9
6462.3	7467.7	7937.5
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3064.5	2634.2	2633.2
530.9	634.1	465.9
1334.1	994.3	1308.3
5217.3	4305.4	2975.2
3925.8	2684.4	1793.9
3902.3	3182.3	3035.5
5239.4	3951.3	3256.6
3179.4	2427.3	1520.1
4678.0	2579.7	1018.0
2811.1	2029.7	1291.8
3171.4	3369.3	2715.8
5969.9	5057.3	3105.9
6243.8	6094.8	4602.2
3597.3	3097.6	1888.5
4285.6	2943.8	1692.4
7382.3	8252.2	7305.2
6421.6	5346.3	7062.7
4130.0	4001.2	3023.1
4357.3	4391.8	3611.2
4467.9	5289.7	4125.2
4775.2	5509.1	4570.2
3155.2	3300.9	2024.5
1749.0	1525.9	1316.1
3878.0	2707.6	1537.4
858.9	1255.6	641.7
3252.1	3814.8	3652.6
4903.7	5716.5	3816.9

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