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AF417546.1 gg_id:68929 Bradyrhizobium japonicum str. DASA03066
GQ848213.1 gg_id:586303 and Archaeal Xiarinur Soda Lake Water-sediment Interface water-sediment interfac
AY904786.1 gg_id:111454 Bradyrhizobium japonicum str. SEMIA 6420
AM990460.1 gg_id:277676 Chelatococcus sp. str. TKE5A
L37584.1 gg_id:5189 Brucella canis
X13695.1 gg_id:5204 Brucella melitensis biovar Abortus str. 11-19
EU165529.1 gg_id:255878 Ochrobactrum sp. str. MI9.3
U70978.1 gg_id:5195 Ochrobactrum anthropi str. LMG 3301
AF526513.2 gg_id:57487 Ochrobactrum intermedium ADV14
EU352765.1 gg_id:265442 Ochrobactrum anthropi str. NK 2.T-3
AB120120.1 gg_id:94870 Ochrobactrum anthropi
AB091758.1 gg_id:59527 Ochrobactrum tritici AS1
AM490617.1 gg_id:247109 Ochrobactrum anthropi str. DSM 7216
FJ984528.1 gg_id:451696 Ochrobactrum haemophilum str. NBSL23
AF229848.1 gg_id:31117 Ochrobactrum sp. str. PR17
AF229879.1 gg_id:24208 Ochrobactrum sp. str. 4FB13
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DQ112028.1 gg_id:130527 Ochrobactrum anthropi str. T1
AM084018.1 gg_id:140347 Ochrobactrum sp. str. R-25055
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EU370421.1 gg_id:271876 Ochrobactrum sp. str. 45C2
EU352762.1 gg_id:268033 Ochrobactrum tritici str. NK 2.X-2
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EF028152.1 gg_id:179539 Ochrobactrum sp. str. xll-3
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GQ451252.1 gg_id:534015 Fecal Yunnan snub-nosed monkey feces clone J187
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FJ950551.1 gg_id:415870 Pseudochrobactrum saccharolyticum str. c299
FJ493040.1 gg_id:589752 Pseudochrobactrum asaccharolyticum str. 2G-2
AM263420.1 gg_id:161116 Pseudochrobactrum kiredjianae str. CCUG 49584
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GQ451230.1 gg_id:564278 Fecal Yunnan snub-nosed monkey feces clone J145
FJ950554.1 gg_id:407459 Pseudochrobactrum asaccharolyticum str. c72
FJ950543.1 gg_id:417632 Ochrobactrum grignonense str. c15

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AF417546.1	68929	1109.9	2066.9	8011.1	1666.4	6754.1	6270.7
GQ848213.1	586303	2420.5	2480.9	2861.2	4574.6	10097.3	6098.8
AY904786.1	111454	5660.9	6118.8	8891.5	5898.6	17904.9	15188.1
AM990460.1	277676	6442.4	8997.1	6084.8	4304.3	15682.8	9601.6
L37584.1	5189	1319.4	2392.7	5418.6	1454.4	7875.3	3848.0
X13695.1	5204	8685.5	9317.3	7805.1	6202.4	16560.7	11765.2
EU165529.1	255878	846.7	1559.8	5045.9	1984.0	4243.9	5423.7
U70978.1	5195	1024.0	2220.3	1108.0	1306.1	11426.0	4792.7
AF526513.2	57487	896.9	1952.6	1220.7	1171.0	9928.7	4390.8
EU352765.1	265442	1318.6	2481.9	2204.3	1815.8	10573.3	4539.9
AB120120.1	94870	1766.4	3000.5	2769.8	1931.0	13350.0	7640.8
AB091758.1	59527	7359.6	9745.7	3293.5	5839.4	15273.4	11940.2
AM490617.1	247109	2844.6	3500.9	4670.6	2243.0	6744.2	3844.1
FJ984528.1	451696	6875.8	6082.4	1413.2	1666.0	7442.6	3470.5
AF229848.1	31117	10062.1	9236.6	6023.6	7849.5	12911.3	11230.8
AF229879.1	24208	4928.0	5332.4	5293.8	3432.9	6668.3	5995.2
FJ859687.2	536560	1324.9	2585.9	3241.3	1177.0	3622.5	4114.2
DQ112028.1	130527	1515.7	1916.6	2864.6	1448.2	3795.0	6394.5
AM084018.1	140347	9517.5	10995.0	7134.6	5261.5	13790.5	11265.3
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DQ295875.1	142896	6146.6	8501.8	4956.9	2976.3	8658.8	9531.4
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EF028152.1	179539	4814.8	6210.5	3922.3	1129.2	10007.5	5503.7
EU399793.1	272191	6848.5	7984.8	7350.2	6225.8	10714.9	10593.2
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GQ451252.1	534015	1518.6	2659.3	2848.3	814.1	7251.4	4986.0
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AM263420.1	161116	3815.3	5367.1	6456.3	2880.1	12318.1	8641.7
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FJ950554.1	407459	814.9	2056.7	3404.7	1459.8	6942.9	5463.1
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DQ365923.2 gg_id:155200 Ochrobactrum pseudintermedium str. ADV43
AY914071.1 gg_id:113751 Ochrobactrum sp. R-3
AB369864.1 gg_id:253214 Pseudochrobactrum glaciale str. KMM 3858 (= Pi 26)
AM114407.1 gg_id:151281 Ochrobactrum anthropi str. CCUG 34735
FJ887929.1 gg_id:551972 Ochrobactrum intermedium str. AR9
AF526514.2 gg_id:62908 Ochrobactrum intermedium ADV21
EU352758.1 gg_id:271007 Ochrobactrum intermedium str. NK 2.HA-1
GQ280047.1 gg_id:591634 Ochrobactrum intermedium str. BJ-37
AF526515.2 gg_id:62909 Ochrobactrum intermedium ADV24
AF515675.1 gg_id:77381 Ochrobactrum sp. YYS-2002
AJ519939.1 gg_id:76582 Ochrobactrum gallinifaecis str. Iso 196
AM041247.1 gg_id:133461 Ochrobactrum aqua-oryzae str. MTCC 4195
FJ202509.1 gg_id:345537 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k
DQ446093.2 gg_id:172411 Surface Mucopolysaccharide Layer and Band Microbial Mat Black Band-Diseased Sid
GU118085.1 gg_id:560738 Threatened Corals Provide Microbial Habitats clone Apal_L09
FJ202721.1 gg_id:319280 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k
GU118071.1 gg_id:567305 Threatened Corals Provide Microbial Habitats clone Apal_M03
D25314.1 gg_id:4687 Blastochloris viridis str. ATCC19567
AM502287.1 gg_id:261580 Blastochloris gulmargensis str. JA248
AF084509.1 gg_id:200193 Blastochloris viridis str. B9
AJ401203.1 gg_id:78031 Blastochloris sp. AT2101
AY117148.1 gg_id:63558 Blastochloris sulfoviridis str. OK3G7
AJ012089.1 gg_id:4711 Blastochloris sulfoviridis str. ToP1
AJ548824.1 gg_id:82396 Candidatus Devosia euplotis str. CAMP4.4
EU589260.1 gg_id:260684 China Ningxia rice paddy field soil clone 1_C6
EF433460.1 gg_id:212196 Devosia sp. str. IPL15
EU812979.1 gg_id:311842 Microbial structure thermophilic reactors biogas reactor fed corn silage clone TUM-M
EF540476.1 gg_id:224522 Devosia sp. 6_4V
FJ807418.1 gg_id:550842 Presence and iron oxidizing landfill leachate impacted groundwater surface water int
EU362140.1 gg_id:355188 and Mesquite Flats Site Death Valley dune sand clone 11
DQ125710.1 gg_id:130155 uranium contaminated soil clone AKAU3805
EF612399.1 gg_id:255206 historic semiarid lead-zinc mine tailings site soil clone OS-C20
GQ396877.1 gg_id:573755 Functional unvegetated perhumid recently-deglaciated soils do not correlate shifts s
AY512822.1 gg_id:105993 Devosia riboflavina
DQ279337.1 gg_id:144518 Dynamic during maturation Tuber magnatum Pico ascoma Xanthomonas clone TM1
EF067859.1 gg_id:174315 Devosia terrae str. DCY11
FN421512.1 gg_id:573013 proteogenomics physiology phyllosphere Arabidopsis thaliana clone 12_F07
EU289427.1 gg_id:245814 metagenomic approach biosynthesis ansamycin endophytes or symbionts enriched s
GQ472390.1 gg_id:544772 Microbial Dongping Lake lake sediment clone 4D3-5
FM253613.1 gg_id:333986 Rock gold mine unusually microbial biofilm clone F07-1

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AY914071.1	113751	2082.0	3038.9	7666.9	3334.7	13519.1	6767.3
AB369864.1	253214	1850.3	4206.0	7810.5	2380.8	10173.3	9629.5
AM114407.1	151281	2419.3	4247.6	3705.0	3100.0	17251.2	8155.8
FJ887929.1	551972	1017.7	2169.9	1154.8	1261.0	10901.3	4606.4
AF526514.2	62908	1594.1	2806.2	2156.2	1798.9	12766.3	6911.0
EU352758.1	271007	7802.6	10110.7	8306.1	6379.7	16686.1	12307.8
GQ280047.1	591634	472.7	1109.6	1782.6	555.6	3720.3	4016.2
AF526515.2	62909	1047.0	2247.0	1451.5	1323.4	11181.0	4562.9
AF515675.1	77381	941.9	2081.6	1212.9	1249.7	11629.0	5091.6
AJ519939.1	76582	586.6	1835.1	3231.9	1147.4	6577.1	5096.6
AM041247.1	133461	1838.8	3103.3	6443.2	3072.2	4943.2	6222.0
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D25314.1	4687	1488.0	3331.3	3701.3	682.1	3080.9	2760.0
AM502287.1	261580	2564.6	4865.8	4191.0	2768.9	9743.0	7331.1
AF084509.1	200193	2215.1	4069.8	7489.7	3253.3	7990.5	9848.9
AJ401203.1	78031	714.5	1704.0	3336.9	398.4	1708.4	1321.7
AY117148.1	63558	414.9	1259.6	3257.0	178.6	1838.0	855.1
AJ012089.1	4711	2550.2	3465.1	5239.5	3930.5	10909.1	5805.0
AJ548824.1	82396	9194.3	8660.0	5070.2	7036.4	10021.4	9332.3
EU589260.1	260684	2902.7	3789.8	4441.0	2228.5	6276.4	4536.0
EF433460.1	212196	1927.5	3069.9	3270.9	1414.2	5617.5	6576.0
EU812979.1	311842	2877.1	3687.2	6251.2	2456.2	4792.3	5825.2
EF540476.1	224522	3501.3	5166.7	6943.6	3560.8	11076.1	9780.1
FJ807418.1	550842	4398.4	4439.9	6447.5	6104.2	8226.5	8577.2
EU362140.1	355188	4299.8	8220.2	6070.6	3677.6	8333.1	9274.5
DQ125710.1	130155	88.8	166.5	358.2	124.2	412.2	1694.7
EF612399.1	255206	6777.3	6900.7	6811.8	6852.6	12601.2	12081.8
GQ396877.1	573755	3018.6	4194.1	12741.0	5509.2	14645.2	17558.7
AY512822.1	105993	11106.2	13002.0	7370.0	9169.2	14122.5	13293.5
DQ279337.1	144518	2295.8	3228.0	3140.0	1787.1	3402.7	4403.5
EF067859.1	174315	835.7	936.9	2115.1	938.3	5456.9	3388.0
FN421512.1	573013	6551.2	7682.2	8667.8	9026.1	13652.5	11027.6
EU289427.1	245814	3600.6	3532.3	2198.1	3671.6	6071.1	4645.5
GQ472390.1	544772	218.9	689.0	3184.6	332.0	585.6	2602.5
FM253613.1	333986	3317.3	5774.6	3838.8	2399.9	5712.8	5672.5

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EF018449.1 gg_id:215447 aspen rhizosphere clone Amb_16S_1074
GQ263214.1 gg_id:581749 Structure Simulated Level Waste Site simulated level waste site clone F3_19X
EU709017.1 gg_id:301593 Devosia sp. str. B2
FJ560749.1 gg_id:550691 Prosthecomicrobium mishustinii str. 17
EF540486.1 gg_id:227483 Devosia sp. c4M
AM293857.1 gg_id:237298 Devosia subaequoris str. HST3-14
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CU927436.1 gg_id:573246 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
FM872901.1 gg_id:365288 occupant source house floor dust clone FB04D08
EF575560.1 gg_id:232353 Devosia sp. str. BD-c194
AY921786.1 gg_id:114008 farm soil clone AKYG1666
EU344945.1 gg_id:273185 Hepialus gonggaensis guts equalized library larval gut clone Hg5-35
GQ264021.1 gg_id:540672 Structure Simulated Level Waste Site simulated level waste site clone WC3_112
AJ318163.1 gg_id:25284 Waste-gas biofilter clone BIri24
AY695724.1 gg_id:107598 USA: New Mexico Carlsbad Lechuguilla Cave Rainbow Room clone RR3A4
GQ263858.1 gg_id:565555 Structure Simulated Level Waste Site simulated level waste site clone WC2_101
EU937979.1 gg_id:332501 Biogeochemistry Iron Oxidation Circumneutral Freshwater Habitat riparian iron oxidi
CU918672.1 gg_id:552248 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
GQ396880.1 gg_id:560208 Functional unvegetated perhumid recently-deglaciated soils do not correlate shifts s
DQ814270.1 gg_id:163314 zebrafish digestive tract clone aab66c07
EU133360.1 gg_id:257399 tallgrass prarie soil clone FFCH11455
DQ248307.1 gg_id:142990 carbon tetrachloride contaminated soil clone TF11
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FM877980.1 gg_id:553425 Microbial iron redox cycling circumneutral-pH groundwater seep Hyphomicrobium c
Y14307.1 gg_id:4627 Hyphomicrobium methylovorum str. DSM 5458
AB016812.1 gg_id:4626 Hyphomicrobium methylovorum str. MBIC3196
AF235089.1 gg_id:29178 Hyphomicrobium sulfonivorans str. S1; ATCC BAA-113; DSM 13863
FJ536921.1 gg_id:594171 Linking performance microbiology biofilters treating dimethyl sulphide presence and
Y14305.1 gg_id:4632 Hyphomicrobium zavarzinii str. ZV-622
AB252934.1 gg_id:167855 Identification Shibayama lagoon Ishikawa Japan iron-oxidation biofilm clone 225
EF019299.1 gg_id:210886 aspen rhizosphere clone Elev_16S_489
AF198623.1 gg_id:47454 Hyphomicrobium chloromethanicum str. CM2
AF234719.1 gg_id:52859 sludge clone A27b
AY328655.1 gg_id:88846 drinking water system simulator clone DSSF33
Y14302.1 gg_id:4636 Hyphomicrobium vulgare str. IFAM MC-750 ATCC 27500
DQ814327.1 gg_id:172883 zebrafish digestive tract clone aab67a09

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GQ006663.1	502999	9995.5	9751.4	6508.0	9577.7	12102.1	10849.0
FN594684.1	559356	2634.5	4695.1	5050.1	2614.8	2886.6	3794.7
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GQ263214.1	581749	260.1	664.1	3415.1	857.9	3565.0	8456.8
EU709017.1	301593	708.4	1302.0	1798.2	1779.6	2413.9	4748.2
FJ560749.1	550691	1554.5	3682.6	2039.3	735.4	880.1	3603.4
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AM293857.1	237298	1359.0	2151.1	3799.4	1315.2	2050.9	6157.0
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EF540440.1	224543	173.8	485.1	1061.4	213.2	828.2	1063.4
CU927436.1	573246	539.2	1060.3	2518.0	499.0	999.1	1216.8
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AY921786.1	114008	3927.7	4924.7	8278.4	4678.6	8074.5	9987.9
EU344945.1	273185	2822.3	3964.6	3413.2	4765.2	1865.7	5109.6
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GQ263858.1	565555	7813.9	9769.3	7270.4	7342.2	13179.1	13975.7
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DQ248307.1	142990	9018.3	7750.2	5460.0	3211.2	5054.0	5951.2
GQ093782.1	453654	893.2	1955.9	2336.8	1104.3	1676.2	3589.9
Y14309.1	4622	205.6	534.5	442.4	251.0	979.5	2944.3
FM877980.1	553425	5211.4	6131.9	2435.9	7158.3	10752.0	9493.7
Y14307.1	4627	2994.8	3189.3	4219.5	3541.2	3734.8	4066.7
AB016812.1	4626	34.2	92.0	208.8	98.9	210.3	909.6
AF235089.1	29178	1019.8	2123.6	2770.7	430.8	1618.6	3490.2
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AY957933.1 gg_id:115024 drinking water biofilm clone B3NR69D18
Y14303.1 gg_id:4630 Hyphomicrobium hollandicum str. IFAM KB-677
Y14304.1 gg_id:4635 Hyphomicrobium aestuarii str. DSM 1564
CU918149.1 gg_id:539592 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
AY328697.1 gg_id:88935 drinking water system simulator clone DSSF75
AY328659.1 gg_id:89720 drinking water system simulator clone DSSF37
AF097815.2 gg_id:4640 activated sludge clone 49520
AF279787.1 gg_id:26693 Hyphomicrobium sp. str. PMC
AY328635.1 gg_id:89164 drinking water system simulator clone DSSF12
AY328650.1 gg_id:90267 drinking water system simulator clone DSSF27
GQ500789.1 gg_id:573659 Surveys Biofilms and Sediments Mammoth Cave Karst Aquifers Bio-Sep beads conta
X53182.1 gg_id:34344 Hyphomicrobium vulgare str. MC-750
GQ263780.1 gg_id:558638 Structure Simulated Level Waste Site simulated level waste site clone WC1_b17
CU918043.1 gg_id:568017 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
AF097824.2 gg_id:4624 activated sludge clone 4953
DQ814766.1 gg_id:172128 zebrafish digestive tract clone aab53a04
CU920885.1 gg_id:547603 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
GQ264377.1 gg_id:513073 Structure Simulated Level Waste Site simulated level waste site clone WW2_57
AY328683.1 gg_id:88276 drinking water system simulator clone DSSF61
DQ815221.1 gg_id:168134 zebrafish digestive tract clone aab51g05
FM253620.1 gg_id:324555 Rock gold mine unusually microbial biofilm clone G04-1
Y14308.1 gg_id:4619 Hyphomicrobium denitrificans str. DSM 1869
GQ500820.1 gg_id:591347 Surveys Biofilms and Sediments Mammoth Cave Karst Aquifers Bio-Sep beads conta
FJ152725.1 gg_id:336999 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX5A_
GQ281066.1 gg_id:586097 Hyphomicrobium facile str. NBCS23
GQ500792.1 gg_id:579761 Surveys Biofilms and Sediments Mammoth Cave Karst Aquifers Bio-Sep beads conta
EF019856.1 gg_id:207848 aspen rhizosphere clone Elev_16S_1214
FJ439830.1 gg_id:550289 Investigation estrogen-degrading bioreactors membrane bioreactor biofilm clone M2
AY328674.1 gg_id:90421 drinking water system simulator clone DSSF52
EF125445.1 gg_id:198749 mangrove soil clone MSB-2E9
DQ814141.1 gg_id:172266 zebrafish digestive tract clone aab60d07
GU269548.1 gg_id:579387 Pedomicrobium ferrugineum str. ATCC 33119
GQ339120.1 gg_id:529888 Comprehensive Investigation on Iron Cycling Freshwater Seep ing Microscopy Cultiv
GQ264219.1 gg_id:585537 Structure Simulated Level Waste Site simulated level waste site clone WW1_b13
FJ478816.1 gg_id:573426 species richness estimates obtained nearly and simulated pyrosequencing-generated
FJ479530.1 gg_id:554597 species richness estimates obtained nearly and simulated pyrosequencing-generated
AY921654.1 gg_id:113465 farm soil clone AKYG1791
FJ478521.1 gg_id:556996 species richness estimates obtained nearly and simulated pyrosequencing-generated
GU269549.1 gg_id:571598 Pedomicrobium manganicum str. ATCC 33121
EF019229.1 gg_id:207866 aspen rhizosphere clone Elev_16S_398
EU644219.1 gg_id:285061 and Samoylov Island Lena active layer -centred polygon near surface horizon; Rim_T

AY957933.1	115024	96.6	355.5	728.9	165.2	829.5	605.1
Y14303.1	4630	614.1	1628.1	2339.7	553.5	2464.3	2744.5
Y14304.1	4635	865.9	1458.9	3050.5	1095.0	3079.6	2315.7
CU918149.1	539592	5814.1	7126.6	4067.8	4158.0	6028.2	7802.3
AY328697.1	88935	1167.3	3025.4	5777.5	4155.5	10812.4	13974.7
AY328659.1	89720	17566.3	17713.8	8364.3	14334.7	20080.7	17017.4
AF097815.2	4640	3250.7	1830.1	3923.7	5199.2	10999.9	6382.2
AF279787.1	26693	2864.4	3733.9	4580.0	2332.8	4171.1	7354.3
AY328635.1	89164	12806.4	12597.0	4116.8	8835.1	14052.4	12262.5
AY328650.1	90267	8260.0	6811.9	5901.9	8458.0	9203.4	9623.2
GQ500789.1	573659	4213.9	3595.6	6071.8	2896.2	6212.4	8777.8
X53182.1	34344	1989.7	2871.8	1832.7	1222.0	6568.5	4142.1
GQ263780.1	558638	8011.2	7546.5	6249.6	6631.0	9750.8	10131.1
CU918043.1	568017	2464.8	2122.3	2894.4	1529.4	3626.0	3531.3
AF097824.2	4624	555.6	1058.7	1559.7	626.8	1219.5	1654.9
DQ814766.1	172128	4446.3	4752.9	4880.6	3782.1	3505.3	5945.3
CU920885.1	547603	2297.0	2901.7	3522.3	2956.0	4789.9	4684.6
GQ264377.1	513073	2097.9	3591.2	6111.8	4130.5	10057.3	10601.8
AY328683.1	88276	3407.8	3781.4	4479.8	3602.3	6397.2	6644.6
DQ815221.1	168134	1667.2	2269.7	2478.3	3848.7	4791.3	6369.1
FM253620.1	324555	612.0	1551.8	1999.5	262.2	1595.5	2167.7
Y14308.1	4619	137.6	326.4	653.7	192.2	635.2	2147.2
GQ500820.1	591347	2600.2	4939.6	5789.0	2964.1	4148.5	3627.2
FJ152725.1	336999	3654.0	4647.5	4759.4	3912.2	8879.0	8764.4
GQ281066.1	586097	58.4	150.8	1027.2	144.9	379.9	894.3
GQ500792.1	579761	6941.0	9693.4	10210.4	6075.5	14891.9	13896.2
EF019856.1	207848	697.3	1436.8	1306.5	1363.7	2422.1	4483.7
FJ439830.1	550289	2999.9	3706.2	5798.7	2108.2	4525.6	4734.7
AY328674.1	90421	5154.4	5231.6	4696.1	5726.4	8669.6	9938.7
EF125445.1	198749	3873.1	4069.8	5254.6	3867.3	5450.0	7581.3
DQ814141.1	172266	1451.8	2601.0	3377.1	1376.9	3388.4	5017.2
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GQ339120.1	529888	1896.7	1673.9	3876.1	2444.0	7018.9	8327.3
GQ264219.1	585537	4651.1	6147.3	2471.9	4693.6	7287.8	6463.6
FJ478816.1	573426	4084.1	3482.1	6412.9	6313.4	5901.9	7639.7
FJ479530.1	554597	2574.9	4385.8	6845.0	4421.1	6454.0	8809.3
AY921654.1	113465	178.5	527.4	1000.6	233.5	1805.3	2794.2
FJ478521.1	556996	6512.0	8281.9	8534.8	4499.3	13136.7	10542.7
GU269549.1	571598	4997.9	5077.1	5005.7	3822.8	5133.1	6852.1
EF019229.1	207866	749.8	1195.1	2172.7	1040.0	3909.0	4613.4
EU644219.1	285061	2349.4	3011.3	4149.1	1928.1	5527.8	7311.5

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g__Pedomicrobium
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EU335234.1 gg_id:240757 Changes microbial metabolic and along hydrogeochemically variable profile unsatura
EF153296.1 gg_id:187340 Rhodomicrobium sp. str. ShRmc01
EF650482.1 gg_id:238973 Rhodocista sp. str. GP-7
D25313.1 gg_id:4680 Rhodoplanes roseus str. 941
AM712913.1 gg_id:247905 Rhodoplanes piscinae str. JA266
EF019983.1 gg_id:212484 aspen rhizosphere clone Elev_16S_1370
EU133616.1 gg_id:254348 tallgrass prarie soil clone FFCH2026
EU335329.1 gg_id:245987 Changes microbial metabolic and along hydrogeochemically variable profile unsatura
AY921820.1 gg_id:113474 farm soil clone AKYG712
AY922092.1 gg_id:114396 farm soil clone AKYH1064
EF018397.1 gg_id:208293 aspen rhizosphere clone Amb_16S_1010
GQ263521.1 gg_id:534454 Structure Simulated Level Waste Site simulated level waste site clone FW2_47B
EU335450.1 gg_id:235975 Changes microbial metabolic and along hydrogeochemically variable profile unsatura
EF020096.1 gg_id:210974 aspen rhizosphere clone Elev_16S_1506
GQ500727.1 gg_id:576799 Surveys Biofilms and Sediments Mammoth Cave Karst Aquifers Charon's Cascade sa
AY622245.1 gg_id:107444 subsurface soil clone B-L17
FJ479010.1 gg_id:561693 species richness estimates obtained nearly and simulated pyrosequencing-generated
FJ625323.1 gg_id:570840 Influence lead contamination on boreal pine forest soil clone HF_M_20
EF019513.1 gg_id:207374 aspen rhizosphere clone Elev_16S_1015
EF032737.1 gg_id:179877 cyanobacterial mat in lava cave clone HAVOmat148
EF018835.1 gg_id:215423 aspen rhizosphere clone Amb_16S_1316
AY234497.1 gg_id:111439 soil isolate Ellin5080
EU937846.1 gg_id:315986 Biogeochemistry Iron Oxidation Circumneutral Freshwater Habitat riparian iron oxidi
AY921720.1 gg_id:113725 farm soil clone AKYH1040
FJ807419.1 gg_id:570413 Presence and iron oxidizing landfill leachate impacted groundwater surface water int
EF020128.1 gg_id:215872 aspen rhizosphere clone Elev_16S_1545
DQ537531.1 gg_id:163571 manganese oxidation soil clone JH-GY22
FJ152854.1 gg_id:316335 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX5A_
DQ984560.1 gg_id:237595 Mt. Nan-Jen soil clone IFD_31
AY326602.1 gg_id:136172 Amazon soil clone 711-1
AJ581617.1 gg_id:93792 soil near uranium mill tailings clone KCM-C-24
FJ479160.1 gg_id:551343 species richness estimates obtained nearly and simulated pyrosequencing-generated
FJ479575.1 gg_id:585582 species richness estimates obtained nearly and simulated pyrosequencing-generated
AB286367.1 gg_id:204919 Reducing production and domination comamonadaceae reducing oxygen supply was
EF018437.1 gg_id:212776 aspen rhizosphere clone Amb_16S_1057
AY395414.1 gg_id:105676 pasture soil clone EB1095
EF019188.1 gg_id:208963 aspen rhizosphere clone Amb_16S_1857
DQ451455.1 gg_id:156816 forest soil clone FAC16
EU133294.1 gg_id:251152 tallgrass prarie soil clone FFCH12843
AY913382.1 gg_id:113588 forest soil clone DUNssu176 (-7A) (OTU#160)
AY963313.1 gg_id:151184 structures and correlated ecological factors soils two evergreen broad-leaved forests

EU335234.1	240757	4596.4	5993.4	8122.2	5652.0	10353.5	10727.4
EF153296.1	187340	6910.0	8772.3	5563.4	2376.3	7412.5	6194.7
EF650482.1	238973	14054.9	14504.0	8492.9	10408.7	18282.4	15043.6
D25313.1	4680	3543.2	5087.8	6261.9	4556.4	13381.6	12690.2
AM712913.1	247905	601.2	1203.6	3525.3	1292.0	5904.1	7040.7
EF019983.1	212484	1027.8	1994.3	2869.0	684.4	4194.3	5418.4
EU133616.1	254348	1072.9	1918.8	3942.9	990.5	5983.9	3394.0
EU335329.1	245987	18048.0	16723.3	11459.9	12971.1	19624.5	14676.8
AY921820.1	113474	2036.2	3125.5	1950.4	1154.4	4636.1	3048.5
AY922092.1	114396	3204.4	4682.7	4659.9	2145.1	7980.6	7527.9
EF018397.1	208293	2808.0	5964.3	12797.4	4256.2	17359.5	16339.7
GQ263521.1	534454	1950.3	3157.4	7031.6	2909.4	10512.4	11612.2
EU335450.1	235975	10789.5	9563.0	5253.2	8914.9	14236.6	11034.8
EF020096.1	210974	832.0	1258.9	5150.3	1198.3	1065.4	2834.1
GQ500727.1	576799	5413.4	2999.9	6898.4	7120.6	6222.0	7276.5
AY622245.1	107444	3293.0	5347.7	5518.3	3092.4	7044.2	7655.8
FJ479010.1	561693	801.1	1308.4	3653.9	1255.6	1465.1	2883.5
FJ625323.1	570840	515.9	1365.6	3428.1	1736.6	5330.9	7038.1
EF019513.1	207374	7853.8	7246.6	15215.9	7648.4	9328.5	10901.2
EF032737.1	179877	113.4	188.7	649.2	159.8	351.8	687.0
EF018835.1	215423	400.2	574.5	3845.0	1029.0	3986.0	6988.2
AY234497.1	111439	3773.9	5883.2	6026.4	4318.2	7323.8	8809.8
EU937846.1	315986	1393.1	2539.8	5787.4	2672.0	9032.2	9793.1
AY921720.1	113725	1937.5	2718.6	5077.0	1721.4	4602.4	3887.6
FJ807419.1	570413	2523.8	3788.4	5295.0	3818.4	9883.3	6449.4
EF020128.1	215872	56.9	96.2	287.8	91.3	77.5	91.5
DQ537531.1	163571	1989.5	3678.6	4227.4	1425.5	3104.4	6266.7
FJ152854.1	316335	620.6	1290.6	2779.6	1002.2	3794.6	4395.0
DQ984560.1	237595	558.9	1082.2	5019.6	1092.9	400.5	962.8
AY326602.1	136172	3806.3	5373.9	6312.0	3519.5	4091.2	6403.7
AJ581617.1	93792	370.4	846.8	294.9	278.6	1250.6	2612.3
FJ479160.1	551343	4923.3	4775.7	2902.7	5637.7	14285.0	8057.6
FJ479575.1	585582	7884.5	9113.2	9273.6	7937.6	12089.2	12131.8
AB286367.1	204919	207.0	469.7	742.8	618.0	1397.2	3677.5
EF018437.1	212776	3767.6	5206.5	2658.1	2617.9	7246.6	5478.7
AY395414.1	105676	750.8	1633.7	5051.9	3089.1	10600.3	13604.1
EF019188.1	208963	133.1	181.7	1216.3	296.3	568.3	1167.6
DQ451455.1	156816	188.1	307.3	1455.4	218.2	889.0	468.3
EU133294.1	251152	3525.5	5173.8	4852.8	2924.6	7276.5	9255.0
AY913382.1	113588	9750.8	8919.7	11190.3	10315.7	24333.1	23411.3
AY963313.1	151184	2464.4	3917.3	6427.4	2645.8	9953.4	8856.8

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GQ262926.1 gg_id:566311 Structure Simulated Level Waste Site simulated level waste site clone F1_73X
DQ837247.1 gg_id:244310 Archaeal and pristine National Park Spain Donana coastal aquifer clone 49S1_2B_37
FJ478974.1 gg_id:584077 species richness estimates obtained nearly and simulated pyrosequencing-generated
EF540400.1 gg_id:217826 oil-shale semi-coke solid waste clone 4_24MK
AY724055.2 gg_id:111888 soil clone DUNssu006
AB121773.1 gg_id:98457 Bradyrhizobium sp. str. Shinshu-th2
AY921846.1 gg_id:114139 farm soil clone AKYG1898
GQ397068.1 gg_id:575164 Functional unvegetated perhumid recently-deglaciated soils do not correlate shifts s
EU335327.1 gg_id:250714 Changes microbial metabolic and along hydrogeochemically variable profile unsatura
AJ810382.1 gg_id:159481 Rhizobiales genosp. AB CsBT10/2
EU429497.1 gg_id:544454 producing pigmented colonies aerosol and soil remote glaciated areas (Antarctica Al
EF516064.1 gg_id:218539 grassland soil clone FCPS586
GU444101.1 gg_id:515709 Effects amendments on fertility and microbial structure cucumber Cucumis sativus L
GQ402598.1 gg_id:566207 Accessing microbial biodiversity and metabolic potential tropical -based approach p
EF018075.1 gg_id:211128 aspen rhizosphere clone Amb_16S_400
DQ404666.1 gg_id:152904 contaminated sediment clone 654997
EU644207.1 gg_id:282627 and Samoylov Island Lena active layer -centred polygon near surface horizon; Rim_T
GQ264285.1 gg_id:555816 Structure Simulated Level Waste Site simulated level waste site clone WW2_06
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DQ125920.1 gg_id:136171 uranium contaminated soil clone AKAU4191
EU669630.1 gg_id:314708 soil clone S22-33
EF020062.1 gg_id:213736 aspen rhizosphere clone Elev_16S_1469
AY426439.1 gg_id:101471 full-scale anaerobic UASB bioreactor treating paper mill wastewater clone B14
EF018152.1 gg_id:216748 aspen rhizosphere clone Amb_16S_487
CU918797.1 gg_id:534993 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
EU133549.1 gg_id:253944 tallgrass prarie soil clone FFCH2918
AB240329.1 gg_id:144888 microbial structure Phragmites rhizosphere biofilm reed bed reactor laboratory clon
GQ264159.1 gg_id:584598 Structure Simulated Level Waste Site simulated level waste site clone WW1_a15
GQ263836.1 gg_id:592746 Structure Simulated Level Waste Site simulated level waste site clone WC1_b83
EU289423.1 gg_id:256335 metagenomic approach biosynthesis ansamycin endophytes or symbionts enriched s
GQ500841.1 gg_id:546305 Surveys Biofilms and Sediments Mammoth Cave Karst Aquifers Bio-Sep beads conta
EF019976.1 gg_id:206188 aspen rhizosphere clone Elev_16S_1362
EU335194.1 gg_id:256477 Changes microbial metabolic and along hydrogeochemically variable profile saturate
GQ093920.1 gg_id:452881 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
EU289515.1 gg_id:256361 metagenomic approach biosynthesis ansamycin endophytes or symbionts enriched s
EF520408.1 gg_id:228499 structure lakes: what controls ? acid-impacted lake clone ADK-BTh02-5
AY921875.1 gg_id:112834 farm soil clone AKYH1162
EU133623.1 gg_id:254308 tallgrass prarie soil clone FFCH929
EU881166.1 gg_id:317632 Karst region primary forest soil clone KPF200711-134
DQ125603.1 gg_id:136238 uranium contaminated soil clone AKAU3608
DQ269121.1 gg_id:191415 marine macro-alga surface clone DPC255

GQ262926.1	566311	1072.9	1672.0	6770.1	2389.6	7451.1	8697.5
DQ837247.1	244310	4948.5	4685.7	9349.9	4380.4	16066.3	15739.3
FJ478974.1	584077	895.7	1449.0	2404.0	1327.3	3997.7	5323.2
EF540400.1	217826	8168.1	7112.1	7910.2	8761.5	8508.7	7919.2
AY724055.2	111888	7127.1	7215.3	4099.0	7748.6	12926.1	11794.8
AB121773.1	98457	2078.8	2860.3	2709.2	2448.6	7382.6	12630.8
AY921846.1	114139	694.4	1214.5	979.1	532.4	1170.4	793.5
GQ397068.1	575164	812.9	1236.4	4724.9	1477.1	7367.1	6674.0
EU335327.1	250714	10613.2	11186.3	11945.2	10847.2	20326.2	13528.8
AJ810382.1	159481	7022.4	8084.5	6398.2	6121.9	12622.7	8294.3
EU429497.1	544454	5991.1	7348.1	9416.2	8157.0	7513.2	7180.9
EF516064.1	218539	70.0	431.6	83.9	116.0	72.3	42.5
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GQ402598.1	566207	2604.9	3178.2	1574.7	1394.2	3065.4	3730.0
EF018075.1	211128	3912.5	5565.7	6165.5	4761.6	11829.0	8692.5
DQ404666.1	152904	913.1	1445.0	6400.5	1488.8	7959.0	4804.7
EU644207.1	282627	307.1	1074.9	1515.6	344.2	3611.9	3045.1
GQ264285.1	555816	754.3	1765.9	6656.4	1389.6	4602.1	5137.9
EF019849.1	205156	807.3	1296.4	4705.4	1078.2	3816.0	6168.2
DQ125920.1	136171	1814.2	1857.3	5497.6	2948.2	9949.3	13632.4
EU669630.1	314708	1568.4	1792.7	4769.1	1932.7	6769.1	6771.0
EF020062.1	213736	139.2	819.9	433.2	426.7	167.1	385.8
AY426439.1	101471	1670.6	3220.9	4369.0	1143.5	4093.0	4136.7
EF018152.1	216748	3158.4	3963.6	3425.5	3124.5	9661.7	8615.3
CU918797.1	534993	1106.6	1969.5	2182.2	1195.4	6210.7	2673.8
EU133549.1	253944	2185.1	1719.4	3975.0	3428.5	2108.7	1888.5
AB240329.1	144888	139.8	301.8	2489.4	262.0	358.4	1230.2
GQ264159.1	584598	5260.9	7076.6	10039.0	6238.9	12734.1	15026.7
GQ263836.1	592746	1133.9	1686.1	4325.3	902.5	3617.0	4997.5
EU289423.1	256335	4561.2	5748.0	5854.7	7021.2	10325.4	12362.8
GQ500841.1	546305	67.3	114.3	2174.8	226.2	364.6	915.8
EF019976.1	206188	71.7	70.9	2198.1	129.2	146.4	72.0
EU335194.1	256477	648.7	1423.0	2209.9	706.5	2826.4	3489.8
GQ093920.1	452881	2630.5	3944.9	7183.3	3532.4	13553.4	13695.0
EU289515.1	256361	676.6	1461.0	2484.9	1078.6	4706.2	6884.8
EF520408.1	228499	2926.1	4363.5	7278.5	6212.7	9367.9	12108.5
AY921875.1	112834	827.2	1676.6	3141.3	1017.8	3585.8	5814.7
EU133623.1	254308	6260.3	6238.6	7974.2	7077.9	17765.5	19296.2
EU881166.1	317632	2564.6	3500.2	5553.8	4026.7	7881.5	6430.2
DQ125603.1	136238	233.0	705.9	2700.0	728.8	3172.5	2964.6
DQ269121.1	191415	2095.0	3030.2	3851.3	1724.4	4242.7	4263.6

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EU703268.1 gg_id:547851 taxon richness -altitude lakes eastern tin plateau predominance Bacteroidetes and S
AB240517.1 gg_id:141913 microbial structure rhizosphere biofilm Sapporo root-base (80 160 mm) Phragmites S
EF520393.1 gg_id:233793 structure lakes: what controls ? acid-impacted lake clone ADK-BTh02-93
AY934488.1 gg_id:138039 Hyphomicrobium sp. str. WG6
GQ397055.1 gg_id:583185 Functional unvegetated perhumid recently-deglaciated soils do not correlate shifts s
AM934937.1 gg_id:572993 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
EU491418.1 gg_id:263450 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X4 clone
AM935138.1 gg_id:564931 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
GQ264131.1 gg_id:588269 Structure Simulated Level Waste Site simulated level waste site clone WC3_68
EU881135.1 gg_id:318155 Karst region primary forest soil clone KPF200711-156
DQ413077.1 gg_id:151855 Microbial -dependent and Approaches Anaerobic/Aerobic SBR Reactor EBPR sludge
EU491437.1 gg_id:274058 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X4 clone
GQ263776.1 gg_id:579939 Structure Simulated Level Waste Site simulated level waste site clone WC1_b11
AM889180.1 gg_id:579421 structure superficial sediments Bizerte (Tunisia) southern Mediterranean coastal an
EU491407.1 gg_id:260794 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X4 clone
Y14313.1 gg_id:4638 Filomicrobium fusiforme str. DSM 5304
FJ203575.1 gg_id:338671 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h
CU927236.1 gg_id:567895 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
DQ860029.1 gg_id:248682 anchovy intestinal microflora clone F1W
FM242368.1 gg_id:305774 sequences sediment clone 64 T9d+oil
GQ264526.1 gg_id:589466 Structure Simulated Level Waste Site simulated level waste site clone WW3_80
DQ125521.1 gg_id:136194 uranium contaminated soil clone AKAU3482
FM253663.1 gg_id:344787 Rock gold mine unusually microbial biofilm clone F01-2
EU488066.1 gg_id:552142 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and
EU491718.1 gg_id:262760 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39
GU362945.1 gg_id:572272 and archaeal biogeochemical cycling genes within Qiongdongnan basin Sea: pilot stu
EU491544.1 gg_id:260534 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR4C
CU926506.1 gg_id:549098 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
FM872754.1 gg_id:363198 occupant source house floor dust clone FB01E01
EU246798.1 gg_id:256471 polyphasic description Pocillopora meandrina Palmyra Atoll Calcinus obscurus abdon
AB453748.1 gg_id:550276 Sulfur-Oxidizing Deep-sea Sponges deep-sea Poecilosclerida sponge clone GM-BSS-B
AB487448.1 gg_id:574086 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNIR0
EF117253.1 gg_id:178313 Hyphomicrobium sp. str. SLG5B-19
FJ264674.1 gg_id:306677 Manganese and Iron Dependent Anaerobic Oxidation Methane methane seep sedime
AB099999.1 gg_id:150659 Microbial dead chimney structures systems Mid-Okinawa Trough and Indian Ocean F
EF018886.1 gg_id:205881 aspen rhizosphere clone Amb_16S_1374
EU753663.1 gg_id:353953 modern freshwater stromatolites Ruidera Pools Natural Park Spain dry stromatolite
EF540511.1 gg_id:226508 Devosia sp. 4_C16_46
AM162442.1 gg_id:156227 and situ identification acidic sphagnum peat bog clone B60
EU335176.1 gg_id:238442 Changes microbial metabolic and along hydrogeochemically variable profile saturate
EF644804.1 gg_id:303233 genes and citrate lyase deep-sea microbial MAR Logatchev hydrothermal vent syster

EU703268.1	547851	962.3	1563.4	2807.3	1697.9	3337.5	3296.6
AB240517.1	141913	4214.0	4413.3	4202.2	1048.6	2636.4	2150.5
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AY934488.1	138039	161.4	314.8	2550.7	536.2	1574.3	2623.8
GQ397055.1	583185	11464.8	13702.3	10855.9	9896.4	15260.7	17567.0
AM934937.1	572993	6709.4	7658.2	5107.1	6761.7	7599.9	9319.8
EU491418.1	263450	4681.9	4881.0	3655.8	4963.6	9912.5	8800.9
AM935138.1	564931	3246.2	4835.9	4259.5	2141.1	6488.3	7177.0
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EU881135.1	318155	1338.7	2001.8	4487.6	1771.8	10119.8	7420.3
DQ413077.1	151855	1928.0	3503.8	5473.2	1760.5	6123.7	4355.4
EU491437.1	274058	3972.3	6141.7	9742.5	6172.8	13246.6	11886.6
GQ263776.1	579939	170.1	387.9	2262.4	169.5	4891.1	1034.6
AM889180.1	579421	2876.7	4361.7	3324.5	2880.6	4782.4	5634.2
EU491407.1	260794	4729.8	4323.6	3890.2	4219.2	3648.3	4554.2
Y14313.1	4638	793.4	1845.3	2968.7	1019.3	2974.8	3601.8
FJ203575.1	338671	4394.8	7658.9	5932.0	4523.2	8167.8	9439.3
CU927236.1	567895	3595.5	4387.8	4796.3	1089.1	2715.4	2576.1
DQ860029.1	248682	715.2	626.1	1676.3	959.1	909.0	1871.1
FM242368.1	305774	674.0	1064.2	1366.5	784.5	1023.3	870.2
GQ264526.1	589466	1533.9	1719.7	5078.7	3407.4	9918.2	7221.2
DQ125521.1	136194	2451.3	3260.7	3091.9	3857.5	3220.1	4052.7
FM253663.1	344787	625.7	1087.5	1654.4	476.2	1134.6	2193.0
EU488066.1	552142	5940.3	8352.7	12887.6	7956.4	15018.0	14910.6
EU491718.1	262760	3076.6	4577.1	5792.8	5913.3	8152.4	7049.6
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AB487448.1	574086	5096.8	7502.3	4317.7	6050.4	11759.4	13268.0
EF117253.1	178313	2677.0	3805.8	7657.9	2637.1	8010.7	8905.0
FJ264674.1	306677	2679.7	3019.1	2405.5	672.2	2704.4	2726.1
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EF018886.1	205881	567.1	1438.1	4337.5	940.1	3120.5	2334.9
EU753663.1	353953	1970.0	2621.5	3665.5	2327.5	9568.0	7421.3
EF540511.1	226508	1696.7	2340.8	7847.1	2711.4	9519.7	8843.8
AM162442.1	156227	2242.9	3969.5	4492.9	1409.3	5597.3	6934.6
EU335176.1	238442	6646.4	8940.7	9805.0	6231.0	13116.6	13970.8
EF644804.1	303233	4391.0	6157.1	9122.4	4754.6	13027.8	14411.1

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EF020326.1 gg_id:203923 aspen rhizosphere clone Elev_16S_1905
FJ157965.1 gg_id:583678 Methylobacterium sp. str. 5a.1.5
AB220073.1 gg_id:131580 Methylobacterium sp. str. PB20
AJ635303.1 gg_id:106826 Methylobacterium aquaticum str. GR16
AB252205.1 gg_id:238917 Methylobacterium brachiatum str. Hojyo2
EF116592.1 gg_id:190418 Methylobacterium fujisawaense str. TNAU14
FJ382176.1 gg_id:574655 Potentially pathogenic and air stem cell transplant summer hospital shower water BM
GQ181028.1 gg_id:588577 Methylobacterium fujisawaense str. LNW7
EF015477.1 gg_id:189399 Methylobacterium fujisawaense str. MP1
EU379265.1 gg_id:266548 Methylobacterium hispanicum str. 2N-2A
EU867320.1 gg_id:581205 Methylobacterium hispanicum str. CCGE2229
EU379303.1 gg_id:259601 Methylobacterium hispanicum str. 6R-J-4b
AJ888240.1 gg_id:132019 Methylobacterium sp. str. AR25
AY169421.1 gg_id:81189 Methylobacterium fujisawaense
GQ113305.1 gg_id:404095 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor
FJ593719.1 gg_id:528281 midgut tropical caterpillars fed on diets egg clone 298EGG8
AB252202.1 gg_id:250748 Methylobacterium persicinum str. 002-165
AB252201.1 gg_id:237732 Methylobacterium komagatae str. 002-079
NZ_ABIP01000058.1 gg_id:251181 Methylobacterium nodulans str. ORS 2060
EF019402.1 gg_id:208196 aspen rhizosphere clone Elev_16S_637
AB024616.1 gg_id:4808 Methylobacterium sp. str. MBIC4305 MIF2
AY468364.1 gg_id:99777 Methylobacterium podarium str. FM3
ABFR01000001.1 gg_id:238083 Methylobacterium populi str. BJ001
NC_010725.1 gg_id:289369 Methylobacterium populi str. BJ001
GU294326.1 gg_id:574537 Methylobacterium radiotolerans str. 5310
AB175637.1 gg_id:152031 Methylobacterium organophilum str. DSM 760
GQ077459.1 gg_id:411824 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1209a(
EU730904.1 gg_id:305729 Methylobacterium fujisawaense str. 151
NC_010505.1 gg_id:264722 Methylobacterium radiotolerans str. JCM 2831
GQ281074.1 gg_id:545132 Methylobacterium radiotolerans str. NBCS05
AB175641.1 gg_id:154811 Methylobacterium radiotolerans str. IAM 12098
AB175646.1 gg_id:151826 Methylobacterium thiocyanatum str. DSM 11490
GQ281068.1 gg_id:543707 Methylobacterium extorquens str. NBCS12
D32230.1 gg_id:4776 Methylobacterium zatmanii str. JCM 2819
AB175647.1 gg_id:150755 Methylobacterium zatmanii str. DSM 5688
GU294335.1 gg_id:543270 Methylobacterium zatmanii str. 6012
EF682985.1 gg_id:242745 Eastern Mediterranean atmosphere clone F13_9A_FL
GQ084916.1 gg_id:374179 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw26
U58018.1 gg_id:4788 Methylobacterium thiocyanatum str. ALL/SCN-P
AY741725.1 gg_id:101778 Methylobacterium sp. str. SKJH-20
DQ507203.1 gg_id:159608 Methylobacterium sp. str. K611B

EF020326.1	203923	3301.5	4578.9	4236.7	2013.3	7198.4	4316.4
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AJ635303.1	106826	1872.5	3026.7	4603.0	2118.0	9175.0	4056.8
AB252205.1	238917	490.5	1355.4	1864.7	965.0	4763.0	821.3
EF116592.1	190418	6830.1	8343.9	6192.0	8351.5	13560.9	11221.4
FJ382176.1	574655	3915.6	5144.8	5716.9	4226.4	10336.4	8602.5
GQ181028.1	588577	566.1	867.0	1630.1	661.6	1847.0	2327.2
EF015477.1	189399	2532.1	3704.3	4893.1	2158.2	6550.5	6177.8
EU379265.1	266548	2961.6	2844.2	1619.9	2881.2	8369.1	3561.3
EU867320.1	581205	1279.1	1587.8	2607.6	1133.6	5693.4	2429.9
EU379303.1	259601	2147.1	2292.6	371.1	3472.8	5404.8	4570.1
AJ888240.1	132019	553.0	877.2	2088.5	426.1	3799.8	2214.4
AY169421.1	81189	5709.3	5318.2	13340.2	10338.4	12623.9	12888.3
GQ113305.1	404095	1359.3	2461.2	3482.8	2308.4	7204.6	5628.0
FJ593719.1	528281	880.7	1713.1	4661.0	2049.4	7153.6	6680.0
AB252202.1	250748	1518.7	2354.4	6136.5	3175.1	7497.0	7011.4
AB252201.1	237732	323.1	673.6	1962.9	390.4	2773.9	1335.4
NZ_ABIP01000058.1	251181	790.1	1023.1	892.7	978.4	2916.7	1877.8
EF019402.1	208196	126.0	338.7	786.4	251.0	1122.7	2097.6
AB024616.1	4808	167.5	333.6	422.6	277.3	442.2	732.8
AY468364.1	99777	4734.5	5006.1	5715.2	3415.6	10073.2	6203.9
ABFR01000001.1	238083	4915.2	5122.5	4916.1	3324.3	9044.7	6675.8
NC_010725.1	289369	5481.2	4325.1	4573.8	3101.4	5517.3	5401.3
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AB175637.1	152031	1147.3	2036.1	2926.4	1147.9	5328.5	2868.7
GQ077459.1	411824	602.4	970.0	2392.9	697.9	3917.5	1556.6
EU730904.1	305729	6786.9	8733.1	9903.0	6322.5	12898.8	11459.0
NC_010505.1	264722	538.1	1191.4	4103.8	834.4	1937.3	2038.0
GQ281074.1	545132	587.9	957.9	2177.7	727.8	3596.9	2073.4
AB175641.1	154811	779.4	1506.0	2070.9	760.2	5286.7	2307.9
AB175646.1	151826	787.4	1228.2	1909.8	632.3	3767.7	3303.1
GQ281068.1	543707	8792.1	7303.6	5598.5	6326.4	10985.0	8848.7
D32230.1	4776	1042.8	1772.8	3245.4	1660.8	8757.2	5104.7
AB175647.1	150755	1067.4	1875.7	3317.6	1699.1	8618.1	5549.2
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EF682985.1	242745	1190.1	1990.2	1880.0	3676.6	9568.3	5865.9
GQ084916.1	374179	2191.7	2710.1	4285.4	3658.3	7371.9	5811.3
U58018.1	4788	4267.1	4675.5	6832.5	5136.0	12357.5	9227.1
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DQ507203.1	159608	1057.5	2127.2	3236.3	1752.9	9172.9	6476.1

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

GQ004577.1	505086	3880.8	5896.5	6382.9	3678.7	11351.9	8590.5
EF116586.1	178333	3224.3	4963.5	1792.1	2129.2	8558.7	6948.3
AY436812.1	105470	12531.3	14439.9	12374.9	12788.3	19081.9	17747.0
AY616142.1	110238	1161.6	2060.1	2972.2	1230.8	6077.8	3757.7
EU528225.1	284643	1118.7	1299.0	1849.3	1875.5	2199.4	2320.1
AB220086.1	134057	750.9	1309.4	3724.0	632.6	9412.7	3375.7
AB175635.1	154997	1578.8	1415.1	1021.5	409.6	1622.3	1646.6
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AY838487.1	109372	145.5	266.4	672.4	232.0	2985.8	1952.8
EU379312.1	277255	1975.5	3077.8	3803.7	1954.2	5836.2	5941.1
M95654.1	4785	882.0	2440.4	2230.1	1536.9	3514.2	4131.0
EF015479.1	196467	1736.0	2064.5	3857.5	1120.1	7237.9	4303.0
DQ339624.1	146461	1976.1	2683.3	6640.9	1938.8	7054.8	6558.5
EF116591.1	177690	6023.0	7402.2	8629.0	6885.2	13356.0	10570.2
AM910532.1	268349	1271.1	2061.7	4386.8	1398.2	5954.1	5116.6
GQ008625.1	501040	582.9	1115.4	3292.7	508.8	6563.9	2451.7
NR_029082.1	584448	4541.4	6391.9	6226.2	3773.2	15295.5	7760.6
AF198624.1	52319	451.0	821.3	2163.7	1445.6	5656.0	5136.9
EF116585.1	191242	4897.1	7725.2	3922.9	5003.2	19311.9	12684.4
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EF015478.1	187464	3855.3	4238.8	6483.5	4623.9	12675.8	8393.8
AY366072.1	93863	7224.6	8587.4	10939.2	9058.4	18780.6	18457.6
AF267912.1	43152	4874.4	8047.0	5218.5	4537.8	13975.3	9909.1
EF116584.1	190499	3200.9	3908.3	2287.0	5199.6	10932.0	7903.5
EF116583.1	180676	3752.2	3222.5	5330.7	2237.9	6417.5	8758.9
FJ225120.1	332818	2939.2	3380.1	5207.3	4063.0	7737.4	6257.2
DQ223682.1	161482	797.5	1386.4	910.4	991.6	3628.3	2610.6
EF426729.1	204294	3800.7	4905.4	8272.4	4266.1	12681.5	6459.1
AB252208.1	253017	621.7	949.1	1934.4	728.7	3531.3	1307.9
AY365229.1	93518	1513.1	1690.2	995.0	2738.7	6158.5	5154.0
AB252209.1	246889	5841.7	4701.3	8314.9	5053.0	6913.4	5690.0
GQ002395.1	507267	907.9	1700.9	2976.6	1596.6	7986.2	7103.3
AB369041.1	555620	217.8	331.0	761.5	171.9	914.8	1153.1
EU250227.1	249628	584.0	880.4	2273.7	660.5	3568.7	1507.6
AB220102.1	138655	567.9	1142.8	3028.8	910.1	2890.4	3673.3
FJ192175.1	329760	10926.4	12449.6	9171.5	7529.7	13733.8	12957.6
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D32228.1	4786	790.6	1221.2	1980.5	620.1	2955.0	2528.9
AJ851087.1	112210	229.8	432.8	1301.7	244.4	2935.5	528.7
GQ059305.1	374704	3250.3	3060.9	1193.3	3546.0	7400.7	3178.9

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AY569289.1 gg_id:102246 pink microbial mat clone YJQ-13
DQ471331.1 gg_id:157883 Methylobacterium jeotgali str. S2R03-9
AF409010.1 gg_id:102764 Methylobacterium sp. str. Ellin168
Z23159.1 gg_id:4797 Methylobacterium sp. str. PC30.44 (pale pink colony type)
AB252204.1 gg_id:312016 Methylobacterium sp. Hojyo1
D32229.1 gg_id:4784 Methylobacterium rhodinum str. JCM 2811
DQ129299.1 gg_id:138274 microarray level air two cities Texas urban aerosol clone AKIW886
DQ532273.1 gg_id:164604 Geographical Variation Microbial Burden and Spacecraft Assembly Johnson Space Ce
FJ193768.1 gg_id:341095 Genetic inventory 'KSC-Astrotek' spacecraft assembly clean room during DAWN missi
EU289454.1 gg_id:256447 metagenomic approach biosynthesis ansamycin endophytes or symbionts enriched s
AF107461.1 gg_id:32547 Methylosinus pucelana str. MTS
AJ458508.1 gg_id:64197 Methylocystis parvus str. 57
AF150805.1 gg_id:4738 Methylocystis parvus
DQ852349.1 gg_id:176777 Methylocystis sp. str. m1511
AJ458510.1 gg_id:72367 Methylocystis sp. str. 50/54
AJ458467.1 gg_id:64230 Methylocystis sp. str. 495/4
FJ502233.3 gg_id:558957 Methylopila sp. str. JZL-4
DQ404188.1 gg_id:212879 Schlegelia plantiphila str. S1
AB007842.1 gg_id:58407 methylotroph str. Hohenstaufen
M95665.1 gg_id:4737 Methylosinus sporium
AJ458495.1 gg_id:111428 Methylosinus sporium str. KS16a
M95664.1 gg_id:4735 Methylosinus sp str. LAC
AJ458481.1 gg_id:64219 Methylosinus trichosporium str. 33/1
AF150804.1 gg_id:4739 Methylosinus trichosporium
L20845.1 gg_id:4736 methanotrophic str. IMV B-3060
AJ458483.1 gg_id:64217 Methylocystis sp. str. Pi5/4
AY921958.1 gg_id:113362 farm soil clone AKYG1554
AJ431385.2 gg_id:64234 Methylosinus trichosporium str. KS21
AY922142.1 gg_id:113005 farm soil clone AKYH643
EF515258.1 gg_id:224728 Electricigen Enrichment MFC upf microbial fuel cell anode clone 22a11
AY297803.1 gg_id:89669 waterlogged archaeological wood clone pACH83
EF515279.1 gg_id:220495 Electricigen Enrichment MFC upf microbial fuel cell anode clone 22c11
CU924338.1 gg_id:560880 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
AB127972.1 gg_id:101532 Kaistina koreensis str. Y9
GQ060654.1 gg_id:467965 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw03g03
GQ064493.1 gg_id:418162 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw7
AJ458504.1 gg_id:64202 Methylocystis sp. str. F10V2a
AB095950.1 gg_id:87497 Ancalomicrobium adetum
AJ458500.1 gg_id:64205 Methylocystis sp. str. 10
GQ055294.1 gg_id:371984 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1113d(
CU925731.1 gg_id:548842 Towards definition core microorganisms involved digestion mesophilic anaerobic dig

AY569289.1	102246	2733.5	4670.1	6417.7	3922.6	15400.1	12105.8
DQ471331.1	157883	190.8	344.4	2054.2	621.2	5612.2	4130.7
AF409010.1	102764	2367.0	4679.8	5229.1	1448.2	6934.2	10406.6
Z23159.1	4797	2337.2	3186.4	4219.0	2725.8	5014.8	7327.3
AB252204.1	312016	3510.8	4246.6	5476.3	3684.2	10570.6	7100.8
D32229.1	4784	3846.2	3759.3	4593.9	3773.7	12595.4	6048.0
DQ129299.1	138274	10517.9	11772.7	12095.3	7647.1	18316.2	11784.7
DQ532273.1	164604	30.5	35.7	46.9	70.2	118.0	189.7
FJ193768.1	341095	5954.2	6959.1	5895.4	3811.2	9252.9	9986.0
EU289454.1	256447	2991.0	3591.0	3648.4	1666.9	6129.6	3275.3
AF107461.1	32547	6270.8	9198.4	7189.3	6338.5	11326.5	10302.1
AJ458508.1	64197	2046.5	4319.3	5095.7	2536.1	7438.0	5824.8
AF150805.1	4738	4182.9	6219.9	5080.4	6214.0	6001.9	7177.8
DQ852349.1	176777	6737.9	5332.0	6055.3	7904.2	9417.8	7727.0
AJ458510.1	72367	1948.8	2540.6	3550.9	2990.5	3915.2	3538.3
AJ458467.1	64230	1071.8	2062.7	4061.5	747.9	1480.7	2351.8
FJ502233.3	558957	10089.2	8949.1	8394.9	7837.8	15827.1	13093.3
DQ404188.1	212879	87.2	358.3	111.3	398.9	4024.1	4278.6
AB007842.1	58407	10974.6	10532.8	8600.7	9802.4	13640.1	11248.6
M95665.1	4737	3063.8	2723.4	1107.4	1164.6	2106.4	2003.7
AJ458495.1	111428	2374.0	4978.5	8957.4	3710.2	10833.1	11558.6
M95664.1	4735	2272.4	2761.2	2173.6	1319.6	4558.7	3482.2
AJ458481.1	64219	1439.3	3178.8	5157.5	1720.9	6249.9	7354.5
AF150804.1	4739	954.1	2026.6	2549.9	1381.4	6284.9	7085.7
L20845.1	4736	201.2	519.1	231.5	126.0	112.2	94.0
AJ458483.1	64217	1038.7	2500.6	5264.8	1179.1	3204.7	4569.9
AY921958.1	113362	3790.6	4067.7	6087.6	2773.0	5931.8	5928.4
AJ431385.2	64234	1255.6	2332.7	5988.8	1381.8	7107.2	8763.3
AY922142.1	113005	2302.5	4571.4	7826.7	2847.6	11022.7	8809.9
EF515258.1	224728	3043.8	3426.2	6174.2	6645.8	8035.3	10877.5
AY297803.1	89669	4903.9	5617.9	6803.0	7689.6	7621.8	7359.0
EF515279.1	220495	6425.6	7552.8	4402.0	7944.1	7716.6	5738.7
CU924338.1	560880	3112.0	5650.0	6560.4	4890.3	6891.7	6977.3
AB127972.1	101532	1621.4	1880.5	3033.7	4762.2	4114.3	5594.7
GQ060654.1	467965	312.7	898.0	1515.8	380.3	1789.8	2499.2
GQ064493.1	418162	2110.0	3096.3	5272.7	3710.7	7555.2	8891.4
AJ458504.1	64202	328.0	1004.1	1300.2	263.8	506.4	622.0
AB095950.1	87497	4666.6	7176.6	9567.6	5084.1	12036.3	14259.3
AJ458500.1	64205	2394.1	4291.1	6628.7	2574.1	7702.2	5233.0
GQ055294.1	371984	1527.5	3324.2	8962.1	1883.2	6438.7	7904.3
CU925731.1	548842	2276.1	4779.0	4950.4	1994.5	9503.2	10634.1

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DQ202244.1 gg_id:140112 Enrichment s Type II Methane-Oxidizing Inhabiting Northern Peatlands peatland clo
GQ221762.1 gg_id:582735 Prosthecomicrobium hirschii str. 6
AM162434.1 gg_id:156044 and situ identification acidic sphagnum peat bog clone B112
AY138237.1 gg_id:107461 human stomach biopsy clone Sto3-1
AJ458473.1 gg_id:56422 Methylocystis echinoides str. IMET 10491
GQ402774.1 gg_id:537864 Accessing microbial biodiversity and metabolic potential tropical -based approach p
AM283543.1 gg_id:165785 Methylocystis heyerii str. H2
FJ478572.1 gg_id:541918 species richness estimates obtained nearly and simulated pyrosequencing-generated
EU979087.1 gg_id:304412 Effects intercropping Rhizobium inoculation on microbial biomass and rhizosphere b
GU208455.1 gg_id:591539 Study on Sediment Dongping Lake sediment clone Fr1-9
GQ500824.1 gg_id:540718 Surveys Biofilms and Sediments Mammoth Cave Karst Aquifers Bio-Sep beads conta
GQ500812.1 gg_id:556729 Surveys Biofilms and Sediments Mammoth Cave Karst Aquifers Bio-Sep beads conta
AM934956.1 gg_id:546522 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
FJ755762.1 gg_id:552837 vertical archaeal water and Lake Taihu sediment clone LT-SB-B39
CU923583.1 gg_id:566212 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
FJ542854.1 gg_id:530919 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone A
CU921271.1 gg_id:550854 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
CU926316.1 gg_id:532947 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
EF019602.1 gg_id:214638 aspen rhizosphere clone Elev_16S_1127
AY921960.1 gg_id:113860 farm soil clone AKYG1560
FM874050.1 gg_id:362109 occupant source house mattress dust clone MB05G07
EF032656.1 gg_id:182489 structure riverine biofilms river biofilm clone SepB-8
EU589298.1 gg_id:272318 China Ningxia rice paddy field soil clone 2_D3
GQ093788.1 gg_id:382544 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
EF590055.2 gg_id:230239 changes structure sediments Songhua River contaminated nitrobenzene -DGGE cloni
AF370880.1 gg_id:66822 Nordella oligomobilis str. N21
DQ984605.1 gg_id:236172 LY oil-contaminated soil clone LYC075
AJ582085.1 gg_id:102514 Ahrensia sp. DFL-33
AJ582087.1 gg_id:95153 Ahrensia sp. DFL-44
AJ582086.1 gg_id:94505 Ahrensia sp. DFL-42
AJ582084.1 gg_id:95110 Ahrensia sp. DFL-13
L20802.1 gg_id:5138 Aminobacter ciceronei str. ER2
DQ196478.1 gg_id:139758 Aminobacter sp. str. MI-p2a
GQ254285.1 gg_id:544184 Aquamicrobium sp. str. H15
FJ167676.1 gg_id:307902 Chelatovorus multitrophus str. LPM-6
EF457242.1 gg_id:237931 Chelatovorus oligotrophus str. LPM4
GU111569.1 gg_id:537767 Nitratireductor sp. str. SL014B-25A2
EF157205.1 gg_id:249985 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon
EU564843.1 gg_id:267825 Nitratireductor sp. str. CC-MHSW-5
EU281628.1 gg_id:243131 Bacillus sp. B2(2007b) str. B2
EU024398.2 gg_id:238204 Isolation cyclohexylalkyltetralin degradation sediments marine sediment clone WBI3

DQ202244.1	140112	609.0	1644.0	2064.9	555.1	991.5	1248.9
GQ221762.1	582735	816.5	1839.6	2101.9	1325.1	6587.1	7278.2
AM162434.1	156044	4817.9	5643.9	6642.9	4433.3	6708.5	8207.0
AY138237.1	107461	1209.6	1967.7	2495.9	1402.6	8610.1	9360.0
AJ458473.1	56422	955.6	2507.1	2505.2	851.2	1424.0	2176.8
GQ402774.1	537864	945.9	1667.7	2339.5	1420.7	3137.8	4025.2
AM283543.1	165785	2094.6	4738.9	7911.4	2654.2	8063.1	8729.4
FJ478572.1	541918	1142.4	844.3	1198.0	1600.9	5281.5	3224.9
EU979087.1	304412	619.2	1548.9	1140.3	1702.4	7120.6	5367.2
GU208455.1	591539	2302.8	4575.3	7819.0	2798.1	5847.4	8003.5
GQ500824.1	540718	5149.2	6309.4	5318.8	4583.2	6737.3	9064.6
GQ500812.1	556729	2914.0	4536.3	6252.9	3962.6	9390.4	10591.7
AM934956.1	546522	423.1	759.9	5328.4	623.5	1282.8	2439.2
FJ755762.1	552837	12100.4	14587.9	5160.8	5293.0	7721.2	6742.6
CU923583.1	566212	7038.0	9868.7	6150.6	5623.3	9618.1	7059.1
FJ542854.1	530919	6046.6	7747.3	10433.7	6201.9	15228.1	16087.5
CU921271.1	550854	2796.3	4587.7	3250.2	2474.5	3662.0	5604.7
CU926316.1	532947	12670.6	16911.0	11554.6	7330.7	16502.8	13795.4
EF019602.1	214638	133.9	85.9	113.7	69.1	116.3	156.4
AY921960.1	113860	11449.3	15812.2	7359.4	6310.9	7366.1	8404.2
FM874050.1	362109	2352.6	5737.6	2835.9	1053.5	2742.9	3817.2
EF032656.1	182489	369.0	1038.2	1797.6	799.4	1627.8	2276.1
EU589298.1	272318	1366.8	3236.8	1000.6	650.9	2345.9	1699.5
GQ093788.1	382544	2770.3	4625.1	4532.4	1406.4	9760.2	7317.7
EF590055.2	230239	6310.2	10001.2	5176.9	3558.1	8695.1	9126.4
AF370880.1	66822	28.2	81.6	95.4	79.6	125.5	542.3
DQ984605.1	236172	5007.7	6162.5	4531.0	2408.0	6550.8	7236.9
AJ582085.1	102514	2711.3	4132.0	5280.3	2243.5	10088.0	5354.5
AJ582087.1	95153	1005.7	1681.6	1170.2	356.4	1180.2	2132.9
AJ582086.1	94505	1370.6	2118.0	2410.0	591.8	3088.3	3665.5
AJ582084.1	95110	1867.7	2450.4	1689.9	568.4	2258.6	3298.6
L20802.1	5138	2452.4	3714.6	2839.2	2875.4	10228.6	6227.8
DQ196478.1	139758	495.0	706.3	2359.5	1811.6	4557.1	6026.9
GQ254285.1	544184	174.2	509.6	599.0	394.7	2077.0	2603.5
FJ167676.1	307902	6495.1	5824.0	5434.3	4915.5	8592.1	8830.2
EF457242.1	237931	6884.9	7433.1	4453.2	6040.9	11926.6	11335.1
GU111569.1	537767	362.9	446.5	790.6	254.2	1227.6	1522.5
EF157205.1	249985	1127.1	1285.4	3615.0	845.7	3513.6	3891.8
EU564843.1	267825	4061.8	5207.0	5219.4	6184.7	9717.2	7937.3
EU281628.1	243131	2749.8	3370.2	4022.1	1971.7	2280.2	1637.6
EU024398.2	238204	3331.5	2962.5	2444.1	3657.4	1813.7	1557.2

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o__Rhizobiales	f__Phyllobacteriaceae
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GU201842.1 gg_id:516545 Rhizobium leguminosarum str. Qtx-1
AJ487829.1 gg_id:66200 Mesorhizobium ciceri str. Rch9816
FM209490.1 gg_id:314928 Mesorhizobium ciceri str. TS56
U07934.1 gg_id:5127 Mesorhizobium ciceri str. UPM-Ca7
X67230.1 gg_id:5122 Mesorhizobium loti str. LMG 4284
EU256435.1 gg_id:251597 Mesorhizobium plurifarium str. CCBAU 85060
EF061111.1 gg_id:186691 Mesorhizobium huakuii str. CCBAU 25053
EF061107.1 gg_id:198842 Mesorhizobium amorphae str. CCBAU 45122
GU083820.1 gg_id:593690 Mesorhizobium amorphae str. DBT14
DQ310706.1 gg_id:186218 Mesorhizobium loti str. U261
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EF061106.1 gg_id:194940 Mesorhizobium amorphae str. CCBAU 45139
EU399717.1 gg_id:273591 Mesorhizobium huakuii str. CCBAU 03094
EU849580.1 gg_id:554748 Mesorhizobium sp. str. CCNWYC132
EU410952.1 gg_id:276865 Mesorhizobium temperatum str. CCNWSX0012-2
AY195843.1 gg_id:82201 Mesorhizobium mediterraneum str. PECA03
EU074171.1 gg_id:253654 Mesorhizobium mediterraneum str. CCBAU 01409
AF508208.1 gg_id:102422 Mesorhizobium temperadae str. CCBAU 11018; SDW 018
AY725261.1 gg_id:136815 decayed velvetleaf seed clone S1-4-CL6
FJ234902.1 gg_id:352327 Microbial structure mesophilic biogas mesophil anaerobic reactors fed corne silage cl
AF410897.1 gg_id:20161 Mesorhizobium sp. str. Lo7-12
FJ550306.1 gg_id:512978 Mesorhizobium tianshanense str. BIHB 4151
FJ025121.1 gg_id:324436 Mesorhizobium tianshanense str. SEMIA 3012
EU707156.1 gg_id:290008 Mesorhizobium tianshanense str. CCBAU 15528
Z94807.1 gg_id:5084 Mesorhizobium genosp. T str. BDV5908
DQ407284.1 gg_id:156049 Mesorhizobium tianshanense str. RCAN08
GQ500629.1 gg_id:558777 Mesorhizobium sp. str. S948
FJ544261.1 gg_id:580951 Mesorhizobium sp. str. CA17
DQ100068.1 gg_id:135924 Mesorhizobium plurifarium str. CCBAU 51276
AY922072.1 gg_id:113594 farm soil clone AKYG882
FJ025123.1 gg_id:306937 Mesorhizobium amorphae str. SEMIA 849
AF325770.1 gg_id:47902 Rhizobium sp. str. TM-5
AY688622.1 gg_id:136093 Mesorhizobium plurifarium str. Sp42
DQ859034.1 gg_id:204637 Mesorhizobium plurifarium str. ORS 3324
FJ550307.1 gg_id:548722 Mesorhizobium tianshanense str. BIHB 4154
D14514.1 gg_id:5142 Mesorhizobium loti str. ATCC33669
EU256441.1 gg_id:248289 Mesorhizobium loti str. CCBAU 85068
D14511.1 gg_id:5149 Rhizobium sp str. TAL 1148
GQ088394.1 gg_id:443339 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
AF508207.1 gg_id:102269 Mesorhizobium nortea str. CCBAU 11014; SDW 014

DQ311089.1	149931	1317.3	1740.1	1518.0	3115.6	4190.5	8748.9
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AJ487829.1	66200	2073.6	3008.1	2362.3	2339.6	6818.6	10360.3
FM209490.1	314928	684.5	1457.7	3152.5	1466.4	4374.5	5652.8
U07934.1	5127	1918.3	2989.8	2924.2	2350.2	6870.2	10763.8
X67230.1	5122	1014.4	1882.3	2212.0	1870.9	4299.6	9604.8
EU256435.1	251597	603.0	1415.7	3872.4	1454.0	7273.2	8175.3
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EF061107.1	198842	1405.4	2943.0	3109.1	1742.8	5614.7	7977.2
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EU849580.1	554748	581.2	1360.9	1469.0	503.7	1263.2	3150.7
EU410952.1	276865	1435.9	2526.6	3488.1	2095.0	4794.0	6221.7
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AF508208.1	102422	2636.4	3824.6	4946.7	3189.1	6248.5	7876.3
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FJ234902.1	352327	3197.6	4218.8	4687.0	2996.9	5311.4	5089.6
AF410897.1	20161	570.2	1429.3	1180.7	625.8	3180.2	4903.1
FJ550306.1	512978	3079.2	4671.0	2662.3	2260.3	3295.3	5234.3
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EU707156.1	290008	3082.8	4893.9	2726.6	3671.4	9758.7	10413.2
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D14514.1	5142	1748.6	3241.2	5521.6	3339.9	8906.8	11818.0
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D13431.1 gg_id:5091 Mesorhizobium huakuii str. IFO15243
U50166.1 gg_id:5085 Mesorhizobium loti str. ICMP3153 USDA 3455 261
CU919824.1 gg_id:566028 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
AB166876.1 gg_id:99830 Mesorhizobium sp. str. M01
AF041447.1 gg_id:5146 Mesorhizobium tianshanense str. -1BS; USDA 3592
AY195844.1 gg_id:81838 Mesorhizobium mediterraneum str. PECA20
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CU926186.1 gg_id:540566 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
FJ542962.1 gg_id:511099 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone B
AJ295079.1 gg_id:74017 Mesorhizobium plurifarium str. ORS1096 (LMG 15298)
EU874893.1 gg_id:308046 Mesorhizobium sp. W12
CU915140.1 gg_id:466324 and dynamics adapted microbiota during degradation Tunisian zarzatine enriched se
CU915133.1 gg_id:381876 and dynamics adapted microbiota during degradation Tunisian zarzatine enriched se
EU440986.1 gg_id:317496 Nitratireductor aquibiodomus str. PR57-9
EU874875.1 gg_id:344328 Mesorhizobium sp. W66
CU915137.1 gg_id:413807 and dynamics adapted microbiota during degradation Tunisian zarzatine enriched se
NR_025262.1 gg_id:570268 Nitratireductor aquibiodomus str. NL21; DSM 15645
CU915181.1 gg_id:401720 and dynamics adapted microbiota during degradation Tunisian zarzatine enriched se
AM498744.1 gg_id:254465 Nitratireductor kimnyeongense str. KY 101 = JBRI2113
CU915166.1 gg_id:423734 and dynamics adapted microbiota during degradation Tunisian zarzatine enriched se
CU915156.1 gg_id:377929 and dynamics adapted microbiota during degradation Tunisian zarzatine enriched se
CU915082.1 gg_id:409815 and dynamics adapted microbiota during degradation Tunisian zarzatine enriched se
EU143347.2 gg_id:253753 Nitratireductor sp. str. J3
DQ659453.1 gg_id:160997 Chelatobacter sp. Pht-3B
GU447302.1 gg_id:518497 Nitratireductor sp. str. C115
FJ182044.1 gg_id:313217 Parvibaculum sp. str. P31
DQ015855.1 gg_id:139871 Antarctic lake water clone WLB16-101
FJ536887.1 gg_id:563896 Linking performance microbiology biofilters treating dimethyl sulphide presence and
AB186821.1 gg_id:101714 polychlorinated dioxin dechlorinating microcosm clone TSAC02

GQ221766.1	575053	616.6	1187.8	3338.4	1770.0	10886.0	9008.8
D13431.1	5091	1586.4	3059.2	5309.5	1811.5	7503.0	9458.4
U50166.1	5085	2355.1	4007.8	1425.9	2356.4	5502.7	9191.0
CU919824.1	566028	888.0	2076.3	1578.1	1574.3	3526.2	7307.0
AB166876.1	99830	518.8	778.1	1019.9	847.2	1887.2	3426.5
AF041447.1	5146	2152.2	3658.0	4308.7	3339.0	7260.6	8614.9
AY195844.1	81838	1802.9	3053.4	4604.7	2396.6	5793.3	6698.4
AF325769.1	23504	1289.6	2222.4	1179.9	529.6	1659.0	3292.1
AY490116.1	109828	1837.0	3183.6	1346.7	2318.5	7313.7	9789.0
FJ544258.1	563420	158.8	518.6	475.0	424.7	1252.7	3363.2
EU410950.1	271237	1152.7	3037.1	1507.4	1568.8	7471.2	8551.4
EU867314.1	556935	2395.6	3243.8	4990.5	2047.5	7283.3	7304.6
EU074176.1	236357	1693.0	3026.8	2560.6	2251.5	7047.9	10189.6
AJ785293.1	159531	1712.5	3175.7	2213.1	2064.5	8157.4	11262.1
Z94819.1	5097	1561.6	3317.2	3356.0	1837.0	5702.2	6584.6
AY509218.1	99286	669.7	1336.8	932.9	749.1	2541.4	3549.3
EU256445.1	235712	607.3	1207.1	2931.8	1219.3	5170.4	5996.2
EU256442.1	252097	2040.6	3752.6	5490.9	4085.7	9963.6	11208.1
EU074175.1	240934	721.6	1494.4	3451.8	1336.7	5925.6	6118.5
CU926186.1	540566	175.4	659.1	1193.8	264.1	2197.3	2735.3
FJ542962.1	511099	8211.6	7186.2	4609.3	6869.2	10265.2	10614.1
AJ295079.1	74017	1304.0	2533.3	5770.1	2559.0	8038.4	12190.3
EU874893.1	308046	376.0	881.5	2233.0	821.5	2559.0	5381.6
CU915140.1	466324	3381.1	3447.9	2092.3	1495.0	3629.8	4829.6
CU915133.1	381876	2310.3	2644.8	2455.1	4293.0	6246.5	6546.3
EU440986.1	317496	941.3	1165.8	2268.6	1436.5	3204.0	5912.1
EU874875.1	344328	827.9	962.8	1397.8	511.0	1664.2	3631.1
CU915137.1	413807	12197.0	9131.1	12431.8	12928.6	14420.7	14043.7
NR_025262.1	570268	348.3	567.2	1502.4	1063.0	2898.4	6929.8
CU915181.1	401720	1182.1	2314.2	4218.2	3047.0	6100.7	8359.6
AM498744.1	254465	1662.3	2694.4	4542.8	1011.1	5051.0	3879.2
CU915166.1	423734	3373.8	4782.3	7662.8	4463.6	9068.8	11712.8
CU915156.1	377929	4258.2	4478.2	4451.7	2648.2	4913.2	7581.9
CU915082.1	409815	4068.9	4188.5	2960.5	1472.5	4708.8	7804.4
EU143347.2	253753	4704.5	6640.2	7773.0	7686.8	13517.7	11534.7
DQ659453.1	160997	5012.8	4551.5	5239.2	3745.8	9255.5	10096.0
GU447302.1	518497	1283.7	2074.0	3560.7	929.7	6123.6	6248.0
FJ182044.1	313217	2967.1	3239.5	3501.3	1898.5	10807.4	5622.2
DQ015855.1	139871	717.9	1048.4	871.8	291.7	512.4	563.5
FJ536887.1	563896	5321.1	7254.5	8840.9	4213.6	7848.6	5849.3
AB186821.1	101714	9192.9	12462.0	8938.4	6536.7	10193.1	12970.7

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FM242452.1 gg_id:311978 sequences sediment clone 9 T12d+oil
AY387398.1 gg_id:101358 Parvibaculum lavamentivorans str. DS-1; DSM13023; NCIMB13966
FN430653.1 gg_id:537152 Parvibaculum sp. str. MBNA2
FJ154092.1 gg_id:333292 Phyllobacterium ifriqiyense str. CCNWGS0184
EU169165.1 gg_id:236290 Phyllobacterium myrsinacearum str. B65
EU420076.1 gg_id:541971 Phyllobacterium myrsinacearum str. Sp-0
AY636000.1 gg_id:104486 Phyllobacterium callistus str. CSC19
DQ917820.1 gg_id:219107 Microbial profiles bleached and wild-type Muricea elongata Phyllobacterium clone B
FJ405362.1 gg_id:367932 Phyllobacterium myrsinacearum str. SPc
EU169173.1 gg_id:253647 Phyllobacterium myrsinacearum str. B18
AY785319.1 gg_id:144696 Phyllobacterium brassicacearum str. STM 196
AJ011330.1 gg_id:5118 Phyllobacterium myrsinacearum HM35
EU928863.1 gg_id:345333 Phyllobacterium sp. str. T1018
X98418.1 gg_id:5120 Nanobacterium sanguineum Seralab FBS batch 901045
AY785329.1 gg_id:142779 Phyllobacterium myrsinacearum str. STM 958
EF364390.1 gg_id:225459 Phyllobacterium sp. str. Hue-5
AY635999.1 gg_id:107799 Phyllobacterium callistus str. CSC32
AY512821.1 gg_id:105844 Phyllobacterium myrsinacearum
GU257961.1 gg_id:593356 Bartonella elizabethae str. HXG-C15
AY331575.1 gg_id:91742 Pseudaminobacter sp. str. mp-1
D32248.1 gg_id:5112 Thiobacillus sp. str. THI 051
FJ203076.1 gg_id:337809 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c
FJ203650.1 gg_id:356370 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h
GU118765.1 gg_id:542574 Threatened Corals Provide Microbial Habitats clone Mfra_M12
FJ203080.1 gg_id:338592 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c
FJ203059.1 gg_id:303869 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c
FJ203057.1 gg_id:350236 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c
DQ396147.1 gg_id:155758 deep-sea octacoral clone ctg_NISA060
AB099936.1 gg_id:79338 inactive deep-sea hydrothermal vent chimneys clone IheB2-3
EU491659.1 gg_id:270912 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39
AF358017.1 gg_id:26724 peat soil microcosm clone LO13.3
EU491413.1 gg_id:269457 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X4 clone
EF572341.1 gg_id:228614 Coco's Island site 23 marine clone S23_440
DQ351777.1 gg_id:147394 Microbial Adherent Sediment Particles Heavy Metal Contaminated North Sea Surfac
GQ250606.1 gg_id:545163 bulk sea water column Gulf Mexico clone GOM_WB10-41
EU246807.1 gg_id:248919 polyphasic description Pocillopora meandrina Palmyra Atoll Calcinus obscurus abdon
EU488046.1 gg_id:568753 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and
FJ478659.1 gg_id:548335 species richness estimates obtained nearly and simulated pyrosequencing-generated
FM253615.1 gg_id:337543 Rock gold mine unusually microbial biofilm clone F09-1
EU735674.1 gg_id:343405 archaeal structures oil contaminated and soils China pristine soil Jidong Oilfield clone
AY913401.1 gg_id:113418 forest soil clone DUNssu195 (-7A) (OTU#173)

FM242452.1	311978	67.1	98.2	242.0	84.1	114.9	89.2
AY387398.1	101358	3758.4	5644.7	13094.4	4079.5	11897.3	12714.5
FN430653.1	537152	2164.8	2747.7	2770.1	2792.8	6737.5	5285.9
FJ154092.1	333292	77.1	199.3	463.6	147.9	305.9	1217.5
EU169165.1	236290	1047.4	2468.1	2332.9	668.7	4686.8	2782.2
EU420076.1	541971	2197.8	4565.3	6691.8	3113.4	12654.3	9692.2
AY636000.1	104486	1381.2	3160.5	2291.1	1378.7	8795.2	6425.3
DQ917820.1	219107	2668.3	3176.7	1514.2	1927.7	3826.6	3901.2
FJ405362.1	367932	391.9	1361.7	249.3	291.5	4788.6	2311.1
EU169173.1	253647	1386.7	1393.3	1265.8	1002.3	2077.2	2626.3
AY785319.1	144696	488.6	994.5	2425.9	607.4	4111.2	3896.4
AJ011330.1	5118	1452.7	3020.3	3578.0	1641.0	6974.4	5350.7
EU928863.1	345333	2157.8	2098.0	3583.5	2337.9	4814.0	5945.3
X98418.1	5120	7042.7	6925.8	4172.2	8774.7	12200.8	11077.5
AY785329.1	142779	2303.3	4090.5	5753.1	2578.1	11175.4	9498.0
EF364390.1	225459	1814.9	3518.3	5250.1	2677.1	7966.6	8413.7
AY635999.1	107799	14454.6	14034.7	11224.3	10620.2	12871.5	14052.9
AY512821.1	105844	1355.2	1828.4	3738.2	2466.6	5992.0	6630.2
GU257961.1	593356	343.1	1215.9	592.3	209.2	2006.2	4203.7
AY331575.1	91742	679.0	1263.8	2211.4	411.4	4216.0	3840.9
D32248.1	5112	1013.9	2635.5	7386.5	3524.6	6960.9	7789.3
FJ203076.1	337809	2724.0	3027.8	4142.6	3765.4	7754.4	6162.2
FJ203650.1	356370	9015.6	8832.2	6307.3	8530.9	17146.4	11436.8
GU118765.1	542574	2654.8	3320.2	2733.8	4607.4	9078.1	6373.6
FJ203080.1	338592	9481.4	7953.2	4769.0	8829.5	13207.7	10671.0
FJ203059.1	303869	1065.0	1267.6	2896.9	1267.6	4277.8	5067.6
FJ203057.1	350236	2285.0	2572.2	3093.2	3462.3	6030.3	3355.0
DQ396147.1	155758	25.5	49.3	64.3	60.9	97.6	252.4
AB099936.1	79338	3589.1	4876.0	2922.2	4148.0	4285.6	2836.5
EU491659.1	270912	980.3	737.6	4989.0	3484.4	1279.2	1338.6
AF358017.1	26724	12740.0	13701.6	11404.7	11173.4	13143.8	11117.7
EU491413.1	269457	3585.3	4624.4	8434.7	4179.9	10198.6	8643.3
EF572341.1	228614	3070.0	5626.7	8710.2	9636.5	4550.7	10264.6
DQ351777.1	147394	1238.7	1528.9	4943.8	938.1	1561.6	2380.6
GQ250606.1	545163	303.4	464.8	1210.5	481.7	2729.8	1068.5
EU246807.1	248919	7154.5	5388.7	8928.1	7858.2	10546.6	8833.2
EU488046.1	568753	17669.3	20523.7	14020.3	13455.3	21327.4	17140.5
FJ478659.1	548335	5902.9	7295.2	7991.3	5708.4	14134.9	14716.2
FM253615.1	337543	9819.5	13960.3	5597.1	5307.9	13660.4	7430.8
EU735674.1	343405	1116.4	1106.5	1248.3	532.5	902.4	866.1
AY913401.1	113418	4380.8	4634.2	3644.6	2736.6	5554.1	5250.4

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AY923020.1 gg_id:114265 Sargasso Sea waters clone D92_92
AY922026.1 gg_id:112779 farm soil clone AKYG492
AY913262.1 gg_id:113787 forest soil clone DUNssu042 (-2A) (OTU#176)
GQ263181.1 gg_id:510769 Structure Simulated Level Waste Site simulated level waste site clone F3_139X
EU881134.1 gg_id:308120 Karst region primary forest soil clone KPF200711-010
EU236381.1 gg_id:288220 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg91H4
AY913338.1 gg_id:114183 forest soil clone DUNssu131 (+7A) (OTU#177)
EF019626.1 gg_id:215375 aspen rhizosphere clone Elev_16S_770
EU488067.1 gg_id:548592 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and
FJ152813.1 gg_id:308393 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX5A_
EU386115.1 gg_id:270010 Biogeographical and microbes sediments on subseafloor sediment South China Sea c
GQ262947.1 gg_id:549426 Structure Simulated Level Waste Site simulated level waste site clone F1_85X
AJ633940.1 gg_id:114727 host's accessory nidamental gland clone 52ANG2
EU386026.1 gg_id:272493 Biogeographical and microbes sediments on subseafloor sediment South China Sea c
AY913351.1 gg_id:112770 forest soil clone DUNssu144 (+7A) (OTU#173)
FJ479146.1 gg_id:588630 species richness estimates obtained nearly and simulated pyrosequencing-generated
EU491428.1 gg_id:260972 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X4 clone
DQ070827.1 gg_id:147965 Prokaryotic Structures Seafloor Basalts Varying Age East Pacific Rise and Ridge basal
GU369888.1 gg_id:529803 and mats vents Arc white filamentous microbial mat photic shal hydrothermal vent
AB491708.1 gg_id:559688 Microbial control lamina formation Crystal geyser central Utah travertine clone CG1(
DQ814512.1 gg_id:161858 zebrafish digestive tract clone aaa30b10
GQ262857.1 gg_id:567747 Structure Simulated Level Waste Site simulated level waste site clone F1_33X
EU491525.1 gg_id:271177 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR4C
AY162106.1 gg_id:150582 Cultivating Sargasso Sea clone GMD21A06
AY913263.1 gg_id:113892 forest soil clone DUNssu043 (-2A) (OTU#173)
GQ262821.1 gg_id:534554 Structure Simulated Level Waste Site simulated level waste site clone F1_12X
EU735621.1 gg_id:339556 archaeal structures and pristine soils China oil contaminated soil Jidong Oilfield clone
EU799979.1 gg_id:351580 It's all ranking aquatic Newport Harbour RI clone 1C227658
EU491596.1 gg_id:264919 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39
FJ745115.1 gg_id:575156 Transporter genes expressed coastal response dissolved organic carbon surface wate
EU385898.1 gg_id:259577 Stratified microbes sediments Core MD05-2902 subseafloor sediment South China S
EU181478.1 gg_id:245815 Prokaryotic enhanced organic matter remineralization continental margin marine se
AF406520.1 gg_id:106379 complex marine community d at depth 200 m North Aegean Sea (Station 3) clone AE
GQ262936.1 gg_id:575894 Structure Simulated Level Waste Site simulated level waste site clone F1_79X
AM936572.1 gg_id:547134 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
GU369924.1 gg_id:518338 and mats vents Arc white microbial film on pebble aphotic zone shal hydrothermal v
AM936135.1 gg_id:553156 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
AM712634.1 gg_id:257971 Anderseniella baltica str. BA141
GU220743.1 gg_id:571033 Microbial mineralization and involved microbial Basin field temperature hydrotherm
FJ152698.1 gg_id:346361 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX1A_
DQ334628.1 gg_id:176463 Impact metals on sediments heavy metal polluted marine sediment clone HB2-33-2

AY923020.1	114265	3280.3	3731.8	4071.6	3069.4	9704.5	5989.4
AY922026.1	112779	12.9	29.4	108.2	61.8	64.6	83.1
AY913262.1	113787	6857.2	8739.1	10272.5	5384.8	9546.9	10722.6
GQ263181.1	510769	6388.9	7184.8	6697.9	5556.6	11613.4	7182.6
EU881134.1	308120	324.2	792.7	2746.7	491.0	2743.9	5300.0
EU236381.1	288220	686.4	1593.9	1162.2	975.8	2082.4	3729.8
AY913338.1	114183	5871.1	7434.1	6612.1	5123.1	13869.6	10441.1
EF019626.1	215375	783.2	2096.1	2253.9	883.7	4795.9	4092.1
EU488067.1	548592	10362.4	10808.1	10984.9	10071.0	13782.0	13566.6
FJ152813.1	308393	1897.3	3945.2	5082.2	1295.6	2176.3	4303.1
EU386115.1	270010	1596.8	1953.8	1898.0	739.1	4377.7	5529.7
GQ262947.1	549426	4473.8	2819.0	6063.3	4476.1	5867.1	5752.8
AJ633940.1	114727	2112.3	3370.9	2954.6	734.7	4474.2	4987.1
EU386026.1	272493	946.0	2259.3	1514.3	448.1	2872.5	2853.7
AY913351.1	112770	6912.2	6856.1	4194.2	6583.0	8524.4	10731.8
FJ479146.1	588630	2012.7	3656.6	7634.9	2357.3	7046.3	9034.0
EU491428.1	260972	11999.4	12411.4	10064.9	14816.5	25829.2	16939.2
DQ070827.1	147965	83.9	176.5	98.3	247.5	177.1	83.6
GU369888.1	529803	9428.7	12563.9	12292.6	8019.3	14165.7	13215.9
AB491708.1	559688	825.6	2056.2	2942.9	908.3	2823.1	4149.5
DQ814512.1	161858	1508.5	2389.0	4325.6	1820.2	1847.1	3933.3
GQ262857.1	567747	1044.5	3067.9	3798.1	2414.3	4283.5	4505.6
EU491525.1	271177	5480.5	6558.4	4691.4	4919.2	9314.6	7902.8
AY162106.1	150582	1210.9	1735.9	1660.3	1060.4	2191.0	4112.3
AY913263.1	113892	6325.5	6539.1	5583.0	5025.2	10562.2	10901.1
GQ262821.1	534554	431.6	690.0	1627.4	598.9	1853.6	863.4
EU735621.1	339556	5876.0	5046.8	4183.2	5013.5	8150.3	11527.4
EU799979.1	351580	1832.2	2678.6	1241.2	1909.3	7885.8	4860.2
EU491596.1	264919	2668.2	3019.2	2779.2	2330.8	2986.2	4575.6
FJ745115.1	575156	7480.7	9713.3	6252.4	7673.7	11678.6	12235.9
EU385898.1	259577	3808.6	4542.5	7285.7	4743.7	8031.4	7551.1
EU181478.1	245815	877.7	1206.0	3223.5	1140.9	3335.2	3541.9
AF406520.1	106379	1097.4	2016.5	2695.3	1144.0	4632.5	3984.6
GQ262936.1	575894	8783.9	10388.7	6171.8	4789.0	17844.5	10752.2
AM936572.1	547134	1641.7	3468.3	6702.6	1918.3	5082.2	7489.7
GU369924.1	518338	7940.6	8080.8	5305.4	6701.6	12615.9	10155.7
AM936135.1	553156	7435.1	8831.5	13494.4	7002.8	14283.2	12628.4
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GU220743.1	571033	2245.5	3167.3	3375.3	2753.3	9424.6	9315.8
FJ152698.1	346361	2736.4	4466.3	3902.5	1789.4	5639.1	4327.8
DQ334628.1	176463	4669.4	4643.3	2287.8	3060.0	7430.8	5095.6

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EU236304.1 gg_id:289355 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg1a1A9
EF208711.1 gg_id:201560 Vertical and horizontal structure microbial sandy carbonate sediment clone Cl75cm.2
EU881167.1 gg_id:342537 Karst region primary forest soil clone KPF200711-032
GQ347790.1 gg_id:592876 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
AF382114.1 gg_id:79210 bacterioplankton clone ZA3318c
FJ203577.1 gg_id:322591 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h
GU118597.1 gg_id:581316 Threatened Corals Provide Microbial Habitats clone Mfav_F16
FJ152626.1 gg_id:304121 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX1A_
FJ024326.1 gg_id:358115 Prokaryotic and their role biogeochemical cycling marine basalts basalt Juan de Fuca l
DQ395471.1 gg_id:156247 deep-sea octacoral clone ctg_CGOAA69
FJ203565.1 gg_id:315490 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h
EU491292.1 gg_id:276298 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak
GQ848473.1 gg_id:538386 Microbial sediments vents along East Lau Spreading Centre deep sea hydrothermal
FJ152991.1 gg_id:340224 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX4CE
GQ009791.1 gg_id:499876 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw77
DQ104986.1 gg_id:137534 Mesorhizobium sp. str. JS 12
EU332813.1 gg_id:360547 FACS assist identification TFO present aerobic enhanced biological phosphorus remo
FJ167442.1 gg_id:342632 microbiology granular sludge under autotrophic mixotrophic and heterotrophic denit
AB374372.1 gg_id:259747 sequences Weissenstein (white rock) / few millimeters be surface rock called 'Weiss
FJ203570.1 gg_id:316649 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h
AB246806.1 gg_id:146335 Mesorhizobium sp. str. Q-2
DQ001642.1 gg_id:158376 Microbial seeps asphalt seep clone E101-27
EF471634.1 gg_id:269321 Fast Screening and Estuarine Operon Libraries whole surface water Chesapeake Bay
AF234721.1 gg_id:32754 sludge clone A7
AJ864462.1 gg_id:109471 Mesorhizobium thiogangeticum str. SJT
FJ674841.1 gg_id:529939 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface
CU922361.1 gg_id:547097 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
AY598817.1 gg_id:105079 Hoeflea marina str. LMG 128
NR_025411.1 gg_id:547162 Mesorhizobium chacoense str. PR5; DSM 17287
GU118307.1 gg_id:538811 Threatened Corals Provide Microbial Habitats clone Dstr_L15
GU118284.1 gg_id:589090 Threatened Corals Provide Microbial Habitats clone Dstr_M18
AF280865.1 gg_id:72907 bioreactor clone mle1-44
AB167198.1 gg_id:107911 Rhizobium sp. str. c19
AF150703.1 gg_id:24111 Elbe River snow isolate Iso26 Iso26_1389
FJ670878.1 gg_id:524118 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface
EF019808.1 gg_id:206948 aspen rhizosphere clone Elev_16S_999
FJ152680.1 gg_id:332848 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX1A_
FN436146.1 gg_id:554537 Molekularbiologische Charakterisierung der bakteriellen Populationsdynamik eines t
AY942778.1 gg_id:145164 but species richness marine sponge Cymbastela concentrica clone Cc173
AM934887.1 gg_id:573454 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
AY690674.1 gg_id:99235 Mesorhizobium sp. str. GC08

EU236304.1	289355	997.5	1548.4	3333.2	1307.4	5834.3	5278.3
EF208711.1	201560	8651.2	8429.6	5799.0	2797.7	4389.1	3469.2
EU881167.1	342537	4505.6	6016.1	8485.9	3622.2	8375.8	9097.8
GQ347790.1	592876	2446.4	3674.7	5446.3	6162.0	5510.4	6252.1
AF382114.1	79210	676.1	1038.3	1214.9	1149.9	1521.9	1982.4
FJ203577.1	322591	226.1	470.2	1043.1	449.0	2464.8	1849.4
GU118597.1	581316	567.7	972.9	1022.5	815.3	558.9	1257.9
FJ152626.1	304121	4873.9	5343.0	2794.7	6694.0	9456.7	7488.0
FJ024326.1	358115	1120.6	189.1	835.5	1669.8	1564.8	372.6
DQ395471.1	156247	935.3	1005.0	1549.7	1460.9	121.9	2060.6
FJ203565.1	315490	42.2	66.7	651.7	131.8	626.3	215.7
EU491292.1	276298	9763.5	10494.3	8588.2	10047.3	13710.3	11675.1
GQ848473.1	538386	4643.7	5256.1	3504.7	4627.8	6236.0	4754.9
FJ152991.1	340224	1452.7	1997.6	2579.0	1581.5	7802.8	6414.6
GQ009791.1	499876	612.8	1795.8	2403.0	1057.9	2886.1	4656.1
DQ104986.1	137534	1433.6	2851.3	3456.6	948.7	5353.7	4678.6
EU332813.1	360547	3148.3	1859.9	7835.6	4270.3	5405.9	9197.9
FJ167442.1	342632	711.6	1200.7	1697.8	758.6	5487.1	4139.5
AB374372.1	259747	2126.5	3391.6	4204.5	2171.8	6001.0	6678.6
FJ203570.1	316649	2228.9	4175.1	8360.3	3481.2	8938.1	9988.2
AB246806.1	146335	5147.8	4423.6	3271.3	3249.6	3615.2	3959.9
DQ001642.1	158376	808.5	1062.4	2295.8	1494.3	1602.0	1733.6
EF471634.1	269321	240.3	408.5	754.5	210.4	1397.7	1346.9
AF234721.1	32754	1106.8	1799.2	3803.5	1587.1	5299.8	5367.1
AJ864462.1	109471	315.9	617.0	1820.4	1048.8	6538.1	5697.3
FJ674841.1	529939	567.9	797.0	1540.2	1878.1	5551.7	4256.3
CU922361.1	547097	2589.8	5890.9	7098.0	3631.8	12241.7	12130.4
AY598817.1	105079	1692.6	2275.6	1491.1	722.6	2755.7	3368.5
NR_025411.1	547162	776.2	1932.4	3134.8	1652.5	6849.6	5894.0
GU118307.1	538811	410.8	1308.2	2192.6	1069.1	4040.8	6176.2
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AF280865.1	72907	4806.0	4661.8	4303.2	3508.8	11749.6	11438.8
AB167198.1	107911	1095.6	2348.5	3840.6	2133.0	3211.2	6570.4
AF150703.1	24111	638.3	2027.4	839.4	779.3	1667.9	1793.8
FJ670878.1	524118	2999.8	4959.7	8633.2	6102.4	17895.5	17246.6
EF019808.1	206948	3737.5	6145.7	4036.3	4638.7	8978.1	9260.9
FJ152680.1	332848	300.4	767.7	2001.2	1396.8	7184.5	10152.1
FN436146.1	554537	101.8	239.2	687.9	113.6	3324.0	1062.0
AY942778.1	145164	56.3	93.5	177.8	187.4	528.3	808.9
AM934887.1	573454	158.5	387.1	3348.8	356.0	2992.9	5093.4
AY690674.1	99235	838.0	1988.6	2046.5	451.7	2444.0	4737.8

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FJ671319.1 gg_id:524448 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
AY332151.1 gg_id:100524 Mesorhizobium sp. str. GWS-SE-H103
FJ671077.1 gg_id:519193 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
AB265157.1 gg_id:164464 Mesorhizobium sp. str. E11
AJ318199.1 gg_id:73511 Waste-gas biofilter clone BIwii1
FJ542875.1 gg_id:521776 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone A
FJ203541.1 gg_id:316301 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h
GQ263841.1 gg_id:548137 Structure Simulated Level Waste Site simulated level waste site clone WC1_b89
EU287328.1 gg_id:243907 Pacific arctic surface sediment clone S26-28
FJ671628.1 gg_id:529153 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
FJ675300.1 gg_id:527154 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
DQ860072.1 gg_id:170119 Symbiotic aerobic anoxygenic phototrophic colonial tunicate clone L9
AY307924.1 gg_id:90640 Aminobacter sp. str. COX
EU236387.1 gg_id:287433 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg92A11
EU223941.1 gg_id:246412 -RFLP microbes Qinghai-Tin rail soil clone 56
FJ671907.1 gg_id:514109 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
DQ814869.1 gg_id:162010 zebrafish digestive tract clone aab54f12
GU454867.1 gg_id:523337 Understanding short-chain fatty acids accumulation enhanced alkaline digestion: kir
DQ364238.2 gg_id:157010 Rhizobium sp. str. WH2K
FJ542989.1 gg_id:528720 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone B
Y15403.1 gg_id:5113 Aquamicrobium defluvii str. DSM 11603
DQ860063.1 gg_id:167582 Symbiotic aerobic anoxygenic phototrophic colonial tunicate clone C7
FJ674998.1 gg_id:518661 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
FJ907162.1 gg_id:552671 Aminobacter sp. str. Sokolova
FJ542969.1 gg_id:531912 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone B
AB257631.1 gg_id:267976 Microbial few millimeters be surface dolomite rock 'Val Piora' Alps 1965 meters abov
AY515416.1 gg_id:99884 bulk water German Wadden Sea May 1999 clone GWS-BW-H52M
AB257653.1 gg_id:273074 Microbial few millimeters be surface dolomite rock 'Val Piora' Alps 1965 meters abov
EU404018.1 gg_id:306709 Microbial septic tank effluent and soil biozone infiltrative surface clean water clone (
EU769196.1 gg_id:329286 velvetleaf seed clone S4-6-CL4
Z30542.1 gg_id:5416 Agrobacterium larrymoorei str. 3-10
D14503.1 gg_id:5409 Agrobacterium rubi str. IFO13261
X67228.1 gg_id:5430 Agrobacterium rubi str. LMG 156
D12787.1 gg_id:5414 Agrobacterium rubi str. IAM 13569
AJ389912.1 gg_id:33557 Agrobacterium vitis str. CFBP2736
DQ466575.1 gg_id:156733 Agrobacterium tumefaciens str. B8LH
FJ493020.1 gg_id:556421 Agrobacterium tumefaciens str. T0H5
EU295450.1 gg_id:241317 Agrobacterium sp. str. LKXJ-3
AB208737.1 gg_id:115126 Agrobacterium sp. AEOC022
DQ803328.1 gg_id:190446 human fecal clone RL311_aam24b01
EU652866.1 gg_id:280086 Agrobacterium sp. str. ZY068

FJ671319.1	524448	1053.9	1951.5	4421.0	810.5	3053.9	5788.7
AY332151.1	100524	5511.5	4571.4	5610.9	3396.2	8377.1	9032.0
FJ671077.1	519193	635.9	1490.4	2853.9	2289.0	4732.5	4179.9
AB265157.1	164464	62.2	125.2	465.5	186.0	668.5	2487.5
AJ318199.1	73511	200.8	332.6	1675.6	360.5	1606.3	917.4
FJ542875.1	521776	90.8	279.4	938.1	1115.9	5105.1	8280.7
FJ203541.1	316301	640.2	1257.9	477.9	234.5	501.4	911.6
GQ263841.1	548137	248.0	744.1	1163.1	474.9	1102.7	2203.4
EU287328.1	243907	1022.7	2303.0	1691.0	1167.9	4863.2	5451.2
FJ671628.1	529153	11264.0	13694.0	10022.1	8914.8	18482.3	16009.7
FJ675300.1	527154	6176.8	8673.9	5146.9	6563.4	9367.4	9008.8
DQ860072.1	170119	2531.3	3833.2	4523.0	3011.6	8009.0	7134.8
AY307924.1	90640	171.1	539.0	1937.5	925.8	3116.1	4913.1
EU236387.1	287433	87.2	181.8	44.0	61.2	71.2	48.6
EU223941.1	246412	7395.2	8346.8	7278.2	9682.5	15417.7	11920.4
FJ671907.1	514109	1284.0	2394.8	5097.4	3951.8	10435.4	9750.2
DQ814869.1	162010	259.8	601.4	1173.1	545.1	1478.7	4086.2
GU454867.1	523337	2272.7	4288.2	4425.9	2134.9	6509.3	9359.4
DQ364238.2	157010	2219.2	3344.9	3507.4	2588.6	2871.4	6216.8
FJ542989.1	528720	1443.8	2051.8	1467.4	1451.0	3234.9	4169.2
Y15403.1	5113	959.2	1862.2	3237.3	1100.2	3714.1	3684.3
DQ860063.1	167582	1116.1	2377.4	4011.8	2084.2	5311.3	4742.2
FJ674998.1	518661	2114.6	3740.7	6674.7	2762.2	8506.7	9090.7
FJ907162.1	552671	1051.3	2203.8	4195.5	970.6	3554.1	5372.7
FJ542969.1	531912	1843.4	3466.4	2138.2	1977.1	6086.1	7919.2
AB257631.1	267976	2181.3	3575.4	6648.6	3132.7	7077.5	8955.9
AY515416.1	99884	461.9	1087.3	3119.3	1063.7	4943.9	5302.6
AB257653.1	273074	1032.1	1208.7	2688.0	1161.0	1866.3	3190.5
EU404018.1	306709	3048.9	4505.3	5752.4	4669.9	15613.9	16468.0
EU769196.1	329286	4280.6	7207.4	7281.0	4928.7	15458.5	7786.0
Z30542.1	5416	2613.4	4475.0	6118.8	3786.6	8720.3	9762.7
D14503.1	5409	1478.1	1900.5	3742.8	2811.8	5745.8	5087.2
X67228.1	5430	4515.0	5460.2	6092.6	5397.5	6929.6	5565.1
D12787.1	5414	3293.9	3942.9	4574.3	3839.0	6211.3	4973.2
AJ389912.1	33557	1940.9	3358.4	4063.9	2518.8	9670.0	8232.1
DQ466575.1	156733	1538.7	2875.2	2131.3	787.4	1733.3	2628.8
FJ493020.1	556421	966.8	1603.0	3263.2	1201.9	2705.0	3053.5
EU295450.1	241317	5111.9	5143.5	6399.7	3434.2	7851.0	7110.8
AB208737.1	115126	404.5	1275.8	1496.1	364.5	4370.7	2505.5
DQ803328.1	190446	7079.9	8065.0	8313.5	7716.9	16936.7	19166.0
EU652866.1	280086	1026.2	1872.5	2423.0	1823.7	3732.3	4615.3

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EF152286.1 gg_id:179195 Rhizobium sp. str. sc-w
AY438103.1 gg_id:155955 Rhizobium sp. str. EGY
DQ119110.1 gg_id:134359 Zoogloea ramigera
GQ444136.1 gg_id:587424 Agrobacterium tumefaciens str. VKLR 01
EF377321.1 gg_id:214126 Agrobacterium sp. str. CCBAU 10749
AM157353.1 gg_id:142761 Agrobacterium tumefaciens
DQ278905.1 gg_id:143494 Agrobacterium sp. str. 24DA-1
EU022589.1 gg_id:330237 Agrobacterium tumefaciens str. KBA3RM1
EF025327.1 gg_id:184622 Agrobacterium tumefaciens str. SREPS2
DQ383276.2 gg_id:217367 Agrobacterium tumefaciens str. 7406
DQ288946.1 gg_id:144288 Agrobacterium tumefaciens TG32
GQ258493.1 gg_id:561134 Rhizobium galegae str. Ca2
GQ169812.1 gg_id:577612 Agrobacterium tumefaciens str. B986
EU295451.1 gg_id:242798 Agrobacterium sp. str. LKXJ-2
DQ648579.1 gg_id:161239 Rhizobium undicola str. Liujia-81
FN640463.1 gg_id:514145 Agrobacterium sp. str. ZX09
DQ009494.1 gg_id:127447 Agrobacterium tumefaciens str. CCBAU 81181
AB368996.1 gg_id:549668 and microbial oils produced Asia petroleum crude oil (Arabian Extra light) clone PT-A
AY353708.1 gg_id:92988 Azotobacter chroococcum str. DSM2286
EF620435.1 gg_id:241441 Agrobacterium tumefaciens str. ISSDS-381
EU256457.1 gg_id:254367 Agrobacterium tumefaciens str. CCBAU 85023
EF102818.1 gg_id:253586 Agrobacterium tumefaciens str. G-1-22
AY626383.1 gg_id:99992 Agrobacterium tumefaciens str. ICMP 369
AF422644.1 gg_id:26211 TCE-sediment clone d035
AJ295683.1 gg_id:26338 Agrobacterium tumefaciens str. IrT-JG-6
EU155875.1 gg_id:244531 Agrobacterium tumefaciens str. D6
X73041.1 gg_id:5266 Blastobacter aggregatus str. IFAM 1003
GQ267695.1 gg_id:562519 Agrobacterium tumefaciens str. CCNWSX539
FJ444745.1 gg_id:561714 Cotton Rhizosphere cotton rhizosphere clone 4y-57
AY576874.1 gg_id:101430 Agrobacterium tumefaciens str. BY6
AB535700.1 gg_id:545894 Agrobacterium tumefaciens str. Pl.2-1
EU834271.1 gg_id:315015 Agrobacterium tumefaciens str. DS54
AJ306769.1 gg_id:66930 DCP-dechlorinating consortium clone SHA-91
DQ860031.1 gg_id:250206 anchovy intestinal microflora clone F1Y
AY048887.1 gg_id:33043 rhizosphere clone Q3-24C12
AF239848.2 gg_id:47953 Bradyrhizobium japonicum str. PRY65
DQ288890.1 gg_id:144720 Ensifer adhaerens
EU373406.1 gg_id:261377 Agrobacterium tumefaciens str. TPR09
AY626382.1 gg_id:99841 Agrobacterium larrymoorei str. ICMP 15237
AY568505.2 gg_id:107283 Agrobacterium tumefaciens str. C-
AJ389905.1 gg_id:34745 Agrobacterium tumefaciens str. Mushin6

EF152286.1	179195	1493.6	2325.5	3771.8	1478.9	3636.6	3619.8
AY438103.1	155955	2107.8	3925.0	6751.9	4699.6	12239.2	7581.9
DQ119110.1	134359	50.3	112.7	147.1	95.0	245.7	353.4
GQ444136.1	587424	6202.7	6995.6	5863.9	7568.1	8589.5	10026.9
EF377321.1	214126	751.4	989.1	1516.3	792.4	3144.5	1834.3
AM157353.1	142761	189.1	601.4	216.3	329.7	1843.7	1436.6
DQ278905.1	143494	233.8	634.4	521.5	215.3	646.2	536.3
EU022589.1	330237	1580.4	2743.4	3145.8	1445.9	3861.1	4292.1
EF025327.1	184622	2341.2	3907.7	3940.6	2467.4	9912.6	9443.3
DQ383276.2	217367	1429.6	2455.1	2481.6	2115.4	4536.4	5774.6
DQ288946.1	144288	888.4	1765.3	1009.8	704.8	3420.3	1443.0
GQ258493.1	561134	2437.3	4630.4	5919.5	4856.9	10365.4	10682.5
GQ169812.1	577612	1678.2	2581.3	2992.7	2130.6	4140.5	5122.2
EU295451.1	242798	3202.6	4871.1	4184.9	1717.8	6880.7	5746.6
DQ648579.1	161239	2842.8	4843.2	5286.8	3356.7	10643.2	6503.4
FN640463.1	514145	2377.1	2255.2	3161.5	1561.0	4902.3	3877.9
DQ009494.1	127447	961.5	1702.6	3439.0	1765.1	4730.3	4021.3
AB368996.1	549668	5737.3	7004.3	6034.5	6625.7	13730.8	9214.3
AY353708.1	92988	4070.5	4829.1	5102.0	7167.7	10637.9	10072.9
EF620435.1	241441	1952.8	2775.6	2843.3	2778.2	4575.8	6026.0
EU256457.1	254367	1759.6	2133.5	3176.9	2426.9	5973.0	5106.9
EF102818.1	253586	1395.8	2667.8	4043.4	2428.0	5861.8	5091.7
AY626383.1	99992	998.7	1656.5	3664.7	2565.5	4823.7	4898.1
AF422644.1	26211	2532.2	3255.6	3654.6	4025.5	10888.7	8856.0
AJ295683.1	26338	299.3	784.2	1409.2	227.3	820.8	1482.7
EU155875.1	244531	1132.0	2015.2	3006.0	2214.4	4748.3	3010.3
X73041.1	5266	1866.7	3366.5	2793.0	2123.8	9309.0	6138.7
GQ267695.1	562519	1448.3	3226.5	5493.8	2912.0	5771.6	6064.7
FJ444745.1	561714	6126.4	6064.5	5402.8	6533.2	10367.6	10522.0
AY576874.1	101430	702.6	1090.2	2596.6	1507.3	3493.1	3134.5
AB535700.1	545894	414.4	818.5	1527.1	867.5	4074.8	1478.0
EU834271.1	315015	840.4	1500.3	2646.7	1345.0	7841.7	5550.9
AJ306769.1	66930	948.8	1725.0	2398.8	1056.2	5077.6	3803.7
DQ860031.1	250206	2098.8	3646.1	1739.4	1337.9	4598.0	3725.8
AY048887.1	33043	4670.1	4182.4	5288.4	3347.0	8759.6	7279.2
AF239848.2	47953	9326.3	11690.8	9827.8	10598.4	18122.5	14824.8
DQ288890.1	144720	1772.0	1898.7	3793.3	1872.2	5978.3	7540.2
EU373406.1	261377	11182.4	11620.6	8074.7	7882.5	14936.7	12434.0
AY626382.1	99841	937.4	1510.2	2489.9	817.8	6146.5	3148.2
AY568505.2	107283	504.9	1059.4	1450.1	842.9	2904.0	2297.9
AJ389905.1	34745	1350.9	2367.9	2769.8	2644.4	3296.6	4919.2

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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
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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

AF003374.1	5424	8041.2	9524.5	6794.1	9119.5	11941.4	12552.5
AB362777.1	244116	5480.9	6345.6	3485.7	4690.9	6025.6	5938.2
D13294.1	5417	783.0	1011.8	1524.1	1689.1	5011.3	2198.1
AY826796.1	111301	5801.2	7149.9	7416.6	5460.7	12065.4	9495.6
AB508898.1	587039	1557.8	2547.6	2938.9	1642.6	6624.8	6359.5
EU221403.1	255931	1540.1	2797.1	3598.4	2648.7	6987.6	5611.9
GU233958.1	584818	3231.4	5019.8	1859.2	5542.8	14650.1	11461.2
EU373439.1	269871	776.7	1374.1	1983.8	1473.2	4815.3	1760.4
AY682683.2	142056	668.1	1209.2	1460.6	984.4	3458.3	2301.6
DQ357728.1	580478	8045.2	7155.6	8561.6	8683.1	10840.8	12676.1
AY221180.1	79849	820.9	1577.1	2085.2	1239.4	4128.3	3219.5
EU618037.1	279343	168.1	555.2	581.6	340.4	2346.2	2687.3
FM209485.1	323633	958.1	2026.9	3545.4	1819.6	5136.6	3944.5
L22533.1	199880	9416.9	11015.4	10210.1	8248.5	15935.0	12899.4
AM181747.1	161523	3336.9	6216.2	6443.5	4423.9	12877.4	10057.0
AY034028.1	43724	4013.1	5004.8	7437.9	4704.3	12306.7	13461.6
X68390.2	5210	1844.9	3794.6	3116.7	1199.1	4908.6	7230.9
AJ295073.1	25282	1481.4	2994.1	1935.8	1225.6	6017.2	4852.8
AF250353.1	20311	2728.9	4020.7	6690.0	2854.9	8820.3	10072.9
AF250354.1	52806	3216.0	3744.0	7867.7	4521.3	11788.6	14376.4
FJ418688.1	366662	3772.1	4939.4	7783.2	3636.4	10619.3	9748.8
AF250377.1	39113	4104.7	6975.5	2978.7	2798.3	11465.9	9536.3
AF452129.1	69312	3103.5	2902.3	9366.3	3681.5	11205.7	12415.6
EU221356.1	249920	6053.7	4957.6	14191.8	4099.0	10574.8	12332.9
DQ786803.1	169278	2575.8	3791.1	6327.9	2801.9	9540.1	11599.0
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FJ418687.1	359351	3404.8	4672.0	6827.4	3307.2	10705.2	9521.7
EU301688.1	235385	12292.9	9899.0	6739.5	12132.3	14738.1	13556.0
AB433352.1	272085	2139.4	3609.1	7715.8	1674.2	7560.5	10235.3
AB433350.1	265416	2583.5	3750.7	6140.1	2820.1	9526.9	10996.7
EU930422.1	351757	2765.8	3805.5	6156.8	2945.1	10338.4	11748.9
FJ405371.1	360590	1353.4	1520.0	1964.3	1827.8	4063.0	5167.4
EF506205.1	225990	3356.5	3585.9	5378.1	2897.5	10521.5	11320.0
EU139306.1	235960	2882.5	4131.5	6274.5	1963.4	6691.6	9856.1
DQ786804.1	163644	3276.1	4008.3	6987.4	4536.7	14341.2	14847.0
DQ411930.1	193675	3404.7	5244.6	9925.8	3087.8	13600.5	15145.3
EU410949.1	262494	2711.2	3645.6	6437.8	2304.4	8424.0	9721.8
D12796.1	5260	2560.9	3718.2	6082.4	2775.9	9247.2	11397.1
D14516.1	5217	2928.2	3985.7	6988.6	3105.1	9161.2	11624.1
DQ859043.1	204451	10325.0	9929.2	9317.5	10238.0	15848.4	17665.9
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AM409365.1 gg_id:174460 Kaistia sp. str. B6-12
FJ542971.1 gg_id:527906 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone B
AM409364.1 gg_id:180502 Kaistia sp. str. B6-8
AY394871.1 gg_id:95247 Rhizobium sp. str. EPR 13
DQ768630.1 gg_id:238108 Martelella mediterranea MARC4N
EF207562.1 gg_id:215523 mangrove system sediment
EU258744.1 gg_id:235404 Mycoplana peli str. AN419
DQ419569.1 gg_id:153696 Rhizobium sp. str. -1
EU256384.1 gg_id:245182 Sinorhizobium borbori str. DN316-1
GU433460.1 gg_id:521715 Rhizobium multihospitium str. CCBAU 31043
AY221178.1 gg_id:80113 Rhizobium tropici EBRI 32
AY221176.1 gg_id:79981 Rhizobium etli EBRI 21
AY221177.1 gg_id:80442 Rhizobium etli EBRI 26
U89820.1 gg_id:5300 Rhizobium mongolense str. USDA 1877
AY117636.1 gg_id:63517 Rhizobium etli str. PRF164
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AF025853.1 gg_id:5454 Rhizobium galegae str. 59A2
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AY775170.1 gg_id:107864 Rhizobium sp. str. CCBAU 23084
EU256413.1 gg_id:248308 Rhizobium giardinii str. CCBAU 85014
FJ445210.1 gg_id:547364 Rhizobium sp. str. CCNWGS0271
EU399693.1 gg_id:271840 Rhizobium giardinii str. CCBAU 01209
U89826.1 gg_id:5357 Rhizobium leguminosarum bv. viciae str. USDA 2434 bv.
FJ025091.1 gg_id:331780 Rhizobium leguminosarum str. SEMIA 3025
U29386.1 gg_id:5334 Rhizobium leguminosarum bv. viciae str. USDA 2370; ATCC 10004; SEMIA 032
FJ025089.1 gg_id:352984 Rhizobium leguminosarum str. SEMIA 388
DQ406712.1 gg_id:154460 Rhizobium leguminosarum str. RP422
FJ449665.1 gg_id:551782 Rhizobium leguminosarum CCNWSX0855
AY491062.1 gg_id:112424 Rhizobium leguminosarum str. ICMP 14642
EF525223.1 gg_id:224132 Rhizobium leguminosarum str. PB166
FJ025094.1 gg_id:328736 Rhizobium leguminosarum str. SEMIA 2082
AY904729.1 gg_id:112447 Rhizobium leguminosarum str. SEMIA 222
DQ835293.2 gg_id:171581 Rhizobium leguminosarum bv. viciae str. CCBAU 03321
AY509900.1 gg_id:112446 Rhizobium leguminosarum str. ATCC 14480
U89831.1 gg_id:5335 Rhizobium leguminosarum bv. viciae str. USDA 2508
AY904742.1 gg_id:112445 Rhizobium leguminosarum str. SEMIA 3007
EU256416.1 gg_id:257453 Rhizobium leguminosarum str. CCBAU 85142
EU637927.1 gg_id:548867 Rhizobium leguminosarum bv. viciae str. XtP1
DQ989228.1 gg_id:186910 Rhizobium leguminosarum str. CCBAU 73374
EU256418.1 gg_id:251645 Rhizobium leguminosarum str. CCBAU 85010

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AY394871.1	95247	1666.6	1828.8	1863.6	779.6	5213.8	3052.1
DQ768630.1	238108	7461.6	9419.8	5249.0	6961.2	10336.4	11627.5
EF207562.1	215523	1194.6	2301.7	1503.6	1142.1	6188.6	4252.7
EU258744.1	235404	1204.7	2231.5	3048.4	1084.8	2350.8	3224.1
DQ419569.1	153696	2965.6	6163.3	6032.5	4268.8	8826.1	8353.8
EU256384.1	245182	2935.0	3861.0	5124.1	1911.5	5479.9	6708.0
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AY221178.1	80113	12631.6	14854.4	11014.7	10333.7	18186.4	16064.5
AY221176.1	79981	6013.9	6592.5	8419.7	8225.1	16227.4	8491.1
AY221177.1	80442	2022.0	3987.8	5900.7	3497.8	5052.0	5012.3
U89820.1	5300	2311.7	4514.0	7143.0	4563.8	8194.9	6915.2
AY117636.1	63517	5966.8	6156.1	4509.5	7643.1	10627.3	9476.0
AF511497.1	87964	809.7	1418.4	1710.6	1086.6	5051.4	3541.2
AF025853.1	5454	164.8	313.5	749.6	163.1	868.7	836.6
AY509213.1	107491	313.2	690.3	1215.4	479.0	2269.0	2594.2
DQ267108.1	143997	856.2	982.8	1893.4	2080.4	3931.3	6433.3
AY775170.1	107864	541.2	1336.1	1750.2	412.2	2514.1	2148.6
EU256413.1	248308	11024.2	11211.3	7331.8	7255.4	12428.2	12100.7
FJ445210.1	547364	1286.1	2463.3	2940.1	1417.8	3724.1	4874.2
EU399693.1	271840	1404.6	2237.2	3670.6	1785.0	4344.2	6041.5
U89826.1	5357	4024.8	6057.6	5357.2	4371.3	11397.4	9775.5
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U29386.1	5334	3266.9	4116.1	3521.1	2977.6	8804.0	10053.8
FJ025089.1	352984	2209.2	3322.9	5442.7	4444.5	11862.9	7649.3
DQ406712.1	154460	1211.1	1179.2	1300.8	899.9	1488.3	3141.2
FJ449665.1	551782	482.7	739.1	1145.9	276.1	1413.6	1067.5
AY491062.1	112424	930.3	1909.3	3673.4	2446.0	6795.9	4903.5
EF525223.1	224132	12460.2	11630.0	7898.4	11199.1	14970.1	15628.0
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AY509900.1	112446	1309.0	2193.9	3998.2	3538.5	7474.2	6732.9
U89831.1	5335	9002.8	8737.9	4863.7	8321.6	12310.0	11833.7
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EU637927.1	548867	1348.5	2302.2	2835.9	2853.6	6063.8	7001.3
DQ989228.1	186910	2974.6	2208.0	5156.3	3342.4	9018.2	3199.9
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DQ786802.1 gg_id:164124 Rhizobium leguminosarum str. DdE4
DQ993270.1 gg_id:184444 Rhizobium leguminosarum str. CCBAU 43201
U89830.1 gg_id:5361 Rhizobium leguminosarum bv. viciae str. USDA 2501 bv.
EF525221.1 gg_id:225304 Rhizobium leguminosarum str. PB164
EU074196.1 gg_id:248930 Rhizobium leguminosarum str. CCBAU 03285
EF364380.1 gg_id:224417 Rhizobium leguminosarum str. Mad-3
EU329018.1 gg_id:248964 Rhizobium leguminosarum str. CCNWXJ0104
U89824.1 gg_id:5355 Rhizobium leguminosarum bv. viciae str. USDA 2377
FJ025087.1 gg_id:355511 Rhizobium leguminosarum str. SEMIA 344
EF634452.1 gg_id:279482 Rhizobium leguminosarum str. PP6
DQ989227.1 gg_id:196413 Rhizobium leguminosarum str. CCBAU 81422
DQ993269.1 gg_id:186689 Rhizobium leguminosarum str. CCBAU 61381
EU170564.1 gg_id:248471 Rhizobium leguminosarum str. CCBAU 71205
GQ118966.1 gg_id:414744 Rhizobium leguminosarum bv. viciae str. BKBLV17
GU083840.1 gg_id:581334 Rhizobium indigoferae str. ZY7-2
EU256422.1 gg_id:252040 Rhizobium leguminosarum str. CCBAU 85022
EU410946.1 gg_id:261545 Rhizobium leguminosarum str. CCNWSX0011-1
EF525222.1 gg_id:219478 Rhizobium leguminosarum str. PB165
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NZ_ABRA01002618.1 gg_id:541025 Rhizobium etli str. 8C-3
DQ835291.2 gg_id:166841 Rhizobium leguminosarum bv. viciae str. CCBAU 01253
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DQ406707.1 gg_id:151503 Rhizobium leguminosarum str. RP399
EU730599.1 gg_id:292520 Rhizobium leguminosarum bv. viciae str. BIHB 1191
EF525228.1 gg_id:217795 Rhizobium leguminosarum str. PB171
U89827.1 gg_id:5358 Rhizobium leguminosarum bv. viciae str. USDA 2443 bv.
DQ993268.1 gg_id:178826 Rhizobium leguminosarum str. CCBAU 65102
AY946012.1 gg_id:114608 Rhizobium leguminosarum bv. phaseoli str. RRE6
EF525219.1 gg_id:218373 Rhizobium leguminosarum str. PB162
EF525231.1 gg_id:218153 Rhizobium leguminosarum str. PB180
EF525212.1 gg_id:226245 Rhizobium leguminosarum str. PB129
GQ246944.1 gg_id:564777 Rhizobium sp. str. PM25
EU748920.1 gg_id:303700 Rhizobium sp. str. ML96
AF417558.1 gg_id:49093 Rhizobium gallicum str. DASA12005
AF417557.1 gg_id:39270 Rhizobium gallicum str. DASA12020
AF239242.1 gg_id:41578 Rhizobium sp. YAS34
AF417559.1 gg_id:74262 Rhizobium gallicum str. DASA12010

AY904740.1	112421	7131.0	5232.7	5332.2	6132.7	11011.0	8936.0
DQ786802.1	164124	1274.1	2193.3	4275.4	3366.3	8181.9	6658.2
DQ993270.1	184444	392.8	793.9	958.3	323.5	1652.0	1348.2
U89830.1	5361	1625.4	2478.6	1895.6	1468.2	5344.7	1562.8
EF525221.1	225304	1232.6	2123.3	3376.7	2252.9	7404.5	3341.2
EU074196.1	248930	2157.7	2081.4	5029.9	2354.7	8032.5	3513.8
EF364380.1	224417	1352.2	2425.3	2102.6	1045.2	2492.1	3892.2
EU329018.1	248964	632.0	1134.5	1061.0	480.7	1224.5	1572.1
U89824.1	5355	6429.5	7747.7	7352.1	6294.9	13771.7	11415.7
FJ025087.1	355511	823.7	1219.1	2780.1	2074.0	6523.3	1875.0
EF634452.1	279482	2496.2	3429.1	5559.5	4497.5	12111.3	9477.7
DQ989227.1	196413	772.6	1715.2	1588.4	778.0	2569.2	1179.9
DQ993269.1	186689	1102.7	748.1	1548.6	573.2	1496.7	1068.3
EU170564.1	248471	1284.9	1640.4	2676.8	1269.8	3176.8	1661.1
GQ118966.1	414744	2582.3	3943.2	3885.8	3225.9	3902.1	3438.9
GU083840.1	581334	1815.9	1306.4	3703.7	2292.0	6313.5	1302.2
EU256422.1	252040	1839.1	3537.5	3419.7	2399.4	4730.6	5330.0
EU410946.1	261545	1175.3	808.3	1001.8	656.9	2074.7	768.3
EF525222.1	219478	1395.3	1987.3	1250.4	782.3	1892.2	2413.0
FM209478.1	322548	4889.7	5903.0	3620.4	3342.1	9456.1	3847.0
EF364382.1	221307	3356.9	5346.2	7763.2	4777.7	12777.6	8879.5
FJ787328.1	566975	7464.8	9048.5	5707.6	4980.8	11753.5	11110.6
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DQ835291.2	166841	3153.9	2382.2	5899.3	3576.9	8270.3	5354.1
EF525230.1	219443	2355.8	2359.1	1854.2	4078.6	9417.1	7707.6
U89829.1	5360	1905.8	2680.5	3566.0	2842.5	7528.9	5119.2
DQ406707.1	151503	3920.8	5808.3	6769.5	4541.9	11041.6	7909.7
EU730599.1	292520	1356.7	2316.7	4567.3	3526.1	7825.2	6653.2
EF525228.1	217795	4015.4	5426.0	6365.2	4378.4	12045.5	11201.3
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AY946012.1	114608	10272.6	7929.3	3848.2	14784.4	14921.6	17605.3
EF525219.1	218373	2921.2	4523.9	4844.6	4400.8	14559.7	11331.0
EF525231.1	218153	846.1	1507.3	1822.4	1015.9	3671.7	3652.8
EF525212.1	226245	1265.1	2121.5	3011.0	2342.4	7223.0	2918.4
GQ246944.1	564777	3328.3	2814.6	7053.1	4034.7	9560.7	7129.3
EU748920.1	303700	2055.6	3582.7	5125.2	1922.6	7605.8	7521.6
AF417558.1	49093	3623.6	4307.6	3276.3	5279.2	12802.6	10637.0
AF417557.1	39270	3561.2	6215.2	3015.9	3212.8	10846.6	7431.4
AF239242.1	41578	1120.2	2372.7	3027.5	1172.0	2998.6	5086.8
AF417559.1	74262	1965.8	3332.0	2267.9	1903.2	6522.2	3796.2

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AY509212.1 gg_id:107348 Rhizobium mongolense str. S110
AF417561.1 gg_id:45894 Rhizobium gallicum str. DASA12024
EU399924.1 gg_id:264788 Rhizobium tropici str. CAF333
DQ422964.1 gg_id:155498 Sinorhizobium sp. str. Lv6.1Se
AB487888.1 gg_id:554002 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSSUR0
EU420078.1 gg_id:563426 Agrobacterium rhizogenes str. Cy-0
AY509210.1 gg_id:107049 Rhizobium etli str. S1
GQ015299.1 gg_id:494367 Topographical and Temporal Human Skin Microbiome skin palm clone nbw766g05c1
GQ015367.1 gg_id:494299 Topographical and Temporal Human Skin Microbiome skin palm clone nbw767e11c1
EU399914.1 gg_id:275574 Rhizobium tropici str. CAF224
GU129569.1 gg_id:583148 Rhizobium giardinii str. Qtx-3
EU694389.1 gg_id:299472 Rhizobium huautlense str. MI-7
U89817.1 gg_id:5320 Rhizobium mongolense str. USDA 1844
D14515.1 gg_id:5330 Rhizobium sp str. OK-50
AJ810381.1 gg_id:159130 Rhizobium genosp. AK CsB1B3
GQ287633.1 gg_id:587508 Rhizobium tropici str. Sap110
EF540480.1 gg_id:219212 Rhizobium sp. 8_4V
EU399716.1 gg_id:268493 Rhizobium giardinii str. CCBAU 83011
EU881929.1 gg_id:346116 Rhizobium sp. str. DJA1
FJ025131.1 gg_id:334111 Rhizobium tropici str. SEMIA 4088
GQ397032.1 gg_id:574749 Functional unvegetated perhumid recently-deglaciated soils do not correlate shifts s
DQ815117.1 gg_id:166290 zebrafish digestive tract clone aab50c07
X67226.2 gg_id:5448 Rhizobium galegae str. LMG 6214
EU335452.1 gg_id:243842 Changes microbial metabolic and along hydrogeochemically variable profile unsatura
EU399916.1 gg_id:269266 Rhizobium tropici str. CAF226
FJ405384.1 gg_id:358164 Rhizobium tropici str. CAF446
U89832.1 gg_id:5277 Rhizobium tropici str. CIAT 899; USDA 9030
EF515979.1 gg_id:225133 grassland soil clone FCPU446
FJ821665.1 gg_id:562882 Rhizobium sp. str. M20
DQ406713.1 gg_id:154917 Rhizobium tropici str. RP261
FJ405376.1 gg_id:369125 Rhizobium tropici str. CAF344
EU074168.1 gg_id:255982 Rhizobium galegae str. CCBAU 01393
FJ405380.1 gg_id:370346 Rhizobium tropici str. CAF439
EU488741.1 gg_id:321329 Rhizobium tropici str. CFN 299
FJ671671.1 gg_id:530568 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
FJ528271.1 gg_id:573223 Rhizobium sp. str. Cs217
U71078.2 gg_id:5393 Rhizobium hainanense str. I66
AJ863373.1 gg_id:120422 poplar tree microcosm rhizosphere flooded clone 17RHF35
EU488743.1 gg_id:339515 Rhizobium tropici str. H12
EU399925.1 gg_id:273473 Rhizobium tropici str. CAF336

AM922177.1	235606	1198.6	2672.8	3384.5	903.6	5228.5	6851.0
AY509212.1	107348	4273.5	6500.2	2368.6	4016.2	13433.0	9296.0
AF417561.1	45894	8433.0	7298.5	9754.3	6956.8	10565.7	9808.1
EU399924.1	264788	1981.1	4153.5	4987.8	2398.0	8995.6	8697.1
DQ422964.1	155498	925.6	2010.6	7406.2	2117.1	9490.1	5540.9
AB487888.1	554002	1435.1	2457.4	2559.4	1192.5	6262.9	7289.5
EU420078.1	563426	782.9	1962.6	1473.5	1717.3	5033.1	5942.6
AY509210.1	107049	2225.8	2100.0	2604.8	1370.6	3498.9	2834.9
GQ015299.1	494367	708.8	1758.3	3816.0	1809.8	5315.9	6359.8
GQ015367.1	494299	467.2	1249.7	5655.8	820.1	4156.4	5228.6
EU399914.1	275574	7481.8	10850.9	4826.4	5828.4	10265.3	9388.3
GU129569.1	583148	994.6	559.0	514.2	314.1	3445.1	3517.0
EU694389.1	299472	2713.1	3089.6	4846.7	5891.1	5935.7	5891.8
U89817.1	5320	879.6	1518.3	2234.3	2632.7	5329.2	9334.3
D14515.1	5330	1509.1	3380.8	3948.8	904.6	5855.1	5283.8
AJ810381.1	159130	264.9	470.9	1320.3	376.1	1671.2	2077.2
GQ287633.1	587508	3813.7	6288.2	6685.2	4757.1	10729.2	9374.6
EF540480.1	219212	747.4	1490.7	728.9	325.3	1523.8	871.6
EU399716.1	268493	1274.2	2377.3	2582.2	952.1	5495.9	5694.8
EU881929.1	346116	867.0	1426.2	2229.0	1410.7	5167.1	8199.8
FJ025131.1	334111	3066.0	3198.7	6933.6	3648.6	9588.3	7733.1
GQ397032.1	574749	490.5	1077.4	1314.7	523.6	2944.4	1683.2
DQ815117.1	166290	1738.9	2740.3	3491.0	1282.5	4286.6	5142.5
X67226.2	5448	1327.8	1466.0	4326.4	2934.5	3427.8	8259.1
EU335452.1	243842	3563.6	4239.1	4631.2	1833.6	5282.2	3252.0
EU399916.1	269266	2240.9	3792.2	4486.4	2602.1	9090.4	8043.8
FJ405384.1	358164	3699.6	4663.4	5841.1	3082.0	9410.4	7972.8
U89832.1	5277	4514.8	6649.5	2190.2	1654.0	9060.3	6910.9
EF515979.1	225133	1857.4	2604.0	1250.7	1584.4	5722.2	2036.2
FJ821665.1	562882	1612.9	2316.0	2264.6	1805.0	4097.3	5369.3
DQ406713.1	154917	503.0	513.2	822.6	421.6	1199.9	2973.0
FJ405376.1	369125	2106.0	4062.1	5222.4	2387.5	8012.4	7991.8
EU074168.1	255982	73.2	134.3	254.5	112.9	502.3	519.0
FJ405380.1	370346	1739.1	4346.7	2480.5	1869.3	10658.8	6264.2
EU488741.1	321329	1765.4	3038.9	9501.3	4390.3	14634.9	12748.6
FJ671671.1	530568	2412.6	3195.1	2476.8	2791.8	7915.0	7379.5
FJ528271.1	573223	5672.4	8374.9	7285.5	5976.2	11747.4	11025.9
U71078.2	5393	2246.1	4018.2	5397.5	2357.0	7317.5	7515.2
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EU399925.1	273473	2109.5	4055.9	5101.8	2359.9	7677.9	7786.0

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FJ444645.1 gg_id:577522 Cotton Rhizosphere cotton rhizosphere clone 2h-14

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FJ527681.1	570278	1849.8	3235.1	5640.7	3202.2	9356.0	7033.7
EU256404.1	243982	1318.3	1672.5	2586.4	1706.3	3518.5	5144.8
AF417565.1	48790	3972.9	3559.3	7569.7	4605.2	10692.9	6430.5
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EF364372.1	225279	254.7	744.8	1538.4	327.5	3122.4	2629.6
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EU344941.1	262518	4079.4	3265.6	2557.3	3951.1	4603.6	5208.4
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FJ405378.1	369642	13258.5	16093.6	9903.0	10618.0	19321.7	15883.2
FJ154086.1	338916	4832.4	5477.5	4164.3	4474.8	8718.9	6622.0
DQ814224.1	162443	4062.5	4912.1	4601.7	3118.0	8183.8	9901.2
AF364068.1	77604	1260.1	2834.0	2661.0	1329.1	7006.7	4021.0
AY166841.1	76567	5732.8	4635.2	5630.7	4707.6	10781.2	10123.1
DQ337581.1	149175	1773.6	3350.1	1461.6	916.5	1150.5	837.8
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EU618036.1	278997	1588.9	2860.8	2618.3	2358.2	3646.2	5579.8
DQ337571.1	149885	1601.4	2316.4	1744.1	933.5	3646.6	3475.3
DQ814410.1	165081	1428.5	2721.0	5266.0	2444.1	8045.6	10725.2
AJ864848.1	131846	3343.3	3559.6	4887.1	6501.3	10559.0	12750.9
AY626396.1	105525	2319.3	3861.4	3922.7	2078.5	6311.3	7657.1
EU488749.1	336323	958.7	2301.8	1552.9	919.9	3133.8	4517.5
DQ532253.1	166577	1953.2	3826.0	3171.4	1026.9	2338.5	3108.8
FJ405385.1	366415	1770.7	3477.1	4617.4	2542.7	8436.0	7476.6
EU556969.3	271487	1336.7	3181.5	4129.1	2157.5	9241.7	8500.0
EF364377.1	223771	1159.6	2695.0	2857.7	944.3	4317.2	6032.1
GQ118964.1	443148	2901.2	6205.3	4593.8	3238.4	10232.6	8532.6
FJ675259.1	513708	2700.7	2852.1	2062.6	2311.0	3754.6	2668.4
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EU133607.1	240333	3805.5	3940.1	4734.8	4304.7	3406.6	6722.5
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EF100519.1 gg_id:243157 Rhizobium sp. str. STM 4023
EU344911.1 gg_id:267554 Hepialus gonggaensis guts equalized library larval gut clone Hg5-01
U86344.1 gg_id:5267 Rhizobium giardinii str. H152
AM697248.1 gg_id:221087 sequencing libraries indoor dust clone BF0001C089
Z94803.1 gg_id:5364 Rhizobium genosp. R str. BDV5365
GQ181047.1 gg_id:511579 Rhizobium lusitanum str. BLN7
EF157275.1 gg_id:243829 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon
AY034026.1 gg_id:31634 Rhizobium loessense str. CCBAU 7190B
AY117667.1 gg_id:63509 Rhizobium tropici str. PRF77
EU399920.1 gg_id:264590 Rhizobium tropici str. CAF279
CU927615.1 gg_id:567667 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
EU748922.1 gg_id:321970 Rhizobium sp. str. ML102
EU488756.1 gg_id:313755 Rhizobium tropici str. H52
FJ025129.1 gg_id:315875 Rhizobium sp. str. SEMIA 6411
AY064412.2 gg_id:76783 Rhizobium sp. str. DCP2
AB233492.1 gg_id:205713 Amorphomonas oryzae str. B26
EU867317.1 gg_id:586260 Rhizobium sp. str. CCGE2052
U29387.1 gg_id:5389 Rhizobium sp str. RCR 3618D; USDA 2947
EU256433.1 gg_id:255837 Rhizobium cellulosilyticus str. CCBAU 85045
DQ310471.1 gg_id:199327 Rhizobium sp. 28/2
DQ984537.1 gg_id:256496 FD oil-contaminated soil clone FD_52
AF417562.1 gg_id:24266 Rhizobium leguminosarum str. DASA23002
AF510386.1 gg_id:87585 Rhizobium sp. str. vgs-11
AB233494.1 gg_id:212299 Amorphomonas oryzae str. B47
AF417563.1 gg_id:47187 Rhizobium leguminosarum str. DASA23111
EU410948.1 gg_id:267876 Rhizobium giardinii str. CCNWGS0022
AY117623.1 gg_id:63522 Rhizobium tropici str. PRF34
FJ405382.1 gg_id:361567 Rhizobium tropici str. CAF443
Z79620.1 gg_id:5452 Rhizobium galegae str. NBIMTC 2246
AY904747.1 gg_id:111491 Agrobacterium rhizogenes str. SEMIA 6070
DQ303318.1 gg_id:150175 Dynamic during maturation Tuber magnatum Pico ascoma Rhizobium clone TM4_28
EU600086.1 gg_id:276672 Pueraria montana var. lobata
AM697022.1 gg_id:217449 sequencing libraries indoor dust clone BF0001B048
EF522124.1 gg_id:220384 Agrobacterium rhizogenes str. CU10
D11344.1 gg_id:5282 Rhizobium tropici str. IFO15247
GQ115602.1 gg_id:459244 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw688b1:
AF260298.2 gg_id:77278 Rhizobium tropici str. PRF35
FJ405375.1 gg_id:359783 Rhizobium tropici str. CAF341
EU488750.1 gg_id:322227 Rhizobium giardinii str. H152
AF510382.1 gg_id:87256 Rhizobium sp. str. Kusp-1
EU399714.1 gg_id:274169 Rhizobium tropici str. CCBAU 83795

EF100519.1	243157	373.5	1067.9	1929.3	353.3	1656.1	3119.2
EU344911.1	267554	3285.6	4130.3	4375.2	2699.7	7218.7	5112.4
U86344.1	5267	746.4	1629.3	2593.0	948.6	4304.3	5527.8
AM697248.1	221087	5626.4	9903.3	4235.6	6384.7	11493.3	8066.8
Z94803.1	5364	1462.7	2206.6	3037.3	1380.0	1974.4	2620.7
GQ181047.1	511579	2108.8	4041.4	5208.6	1882.3	7819.2	7422.2
EF157275.1	243829	8425.3	9341.0	8177.9	9172.2	13782.8	10717.1
AY034026.1	31634	2132.4	2519.7	1243.0	1721.9	3177.9	4926.7
AY117667.1	63509	1849.3	3547.4	4965.9	2515.1	8557.4	7251.5
EU399920.1	264590	2261.2	4237.8	5382.7	2540.4	8218.7	8394.2
CU927615.1	567667	644.5	2016.7	1624.4	639.2	8050.9	3799.3
EU748922.1	321970	231.6	640.5	315.0	268.2	1287.7	1512.1
EU488756.1	313755	1929.7	3610.5	4916.1	1877.3	7960.2	7888.1
FJ025129.1	315875	2482.4	2820.5	1865.4	1206.2	1516.3	890.2
AY064412.2	76783	2012.7	4410.2	6293.0	3099.3	8075.7	6661.6
AB233492.1	205713	1293.8	1564.9	6573.4	2213.0	8097.7	12916.6
EU867317.1	586260	135.6	370.6	1401.5	708.1	1026.9	581.1
U29387.1	5389	3002.7	4247.1	3680.9	1868.2	2973.5	1307.3
EU256433.1	255837	4155.3	4819.6	5525.5	3542.3	3940.1	5585.1
DQ310471.1	199327	1423.4	1453.7	737.4	221.7	672.2	839.0
DQ984537.1	256496	208.5	730.5	1221.4	331.9	4539.0	4115.4
AF417562.1	24266	6108.7	8227.9	7009.2	6746.2	13644.9	13134.1
AF510386.1	87585	67.8	257.9	266.6	154.3	1433.6	237.2
AB233494.1	212299	941.2	1277.7	2142.8	1370.0	5795.6	6074.7
AF417563.1	47187	4013.3	3605.4	6781.2	4713.3	10004.6	8245.8
EU410948.1	267876	512.2	672.0	1005.3	154.8	709.3	1930.7
AY117623.1	63522	2739.9	3287.3	6433.8	3278.0	10066.7	7174.9
FJ405382.1	361567	2582.4	5791.7	6791.6	2342.8	13282.2	7301.9
Z79620.1	5452	196.9	447.6	1191.1	222.0	782.7	994.9
AY904747.1	111491	10744.6	10237.6	10200.0	9585.7	14942.4	11985.2
DQ303318.1	150175	5986.9	6702.1	2195.7	5909.7	15642.3	11619.8
EU600086.1	276672	2982.6	5729.2	5778.5	2509.0	9749.0	8337.6
AM697022.1	217449	4936.1	4663.5	3375.5	4106.4	9972.7	7114.9
EF522124.1	220384	5108.5	4116.4	7229.3	4177.5	11756.5	8971.7
D11344.1	5282	2701.2	2866.5	6403.6	3855.3	10796.9	7622.8
GQ115602.1	459244	7873.0	9905.4	6646.8	5949.8	13761.7	11677.4
AF260298.2	77278	2962.9	5263.3	4299.4	4773.5	9920.1	10596.9
FJ405375.1	359783	1915.4	3626.6	4950.1	1861.1	7844.2	7784.8
EU488750.1	322227	1997.3	3312.8	5231.2	1884.5	10203.1	11032.7
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EU399714.1	274169	561.3	1356.4	1304.6	650.4	3734.1	2471.3

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EU584258.1 gg_id:352865 Rhizobium sp. str. ORS 3441
AY316683.1 gg_id:200464 Reichenowia parasiticae
EF173321.1 gg_id:192524 Sinorhizobium sp. MKI7
FJ517717.1 gg_id:560086 Disturbing epithelial homeostasis metazoan Hydra leads drastic changes microbiota e
EU399935.1 gg_id:260090 Rhizobium tropici str. CAF438
D12788.1 gg_id:5289 Agrobacterium rhizogenes str. IAM 13570
EU399919.1 gg_id:276979 Rhizopus oryzae str. CAF276
DQ304797.1 gg_id:154037 studies on and nifH Lasiurus sindicus Sewan grass Thar Desert India root clone C6
AB187585.1 gg_id:104322 Granulella daejeonensis str. Ch06
EU723213.1 gg_id:334997 Shinella sp. str. NP526a
FJ598327.1 gg_id:566021 Shinella sp. str. 2-9
EU346730.1 gg_id:267822 Shinella zoogloeoides str. BC026
AF502218.1 gg_id:55816 EBPR sludge lab scale clone HP1B02
GQ009804.1 gg_id:499861 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw77
DQ898296.1 gg_id:173668 Rhizobium sp. str. MTR-3A
EU104300.1 gg_id:345964 Evidence Comamonadaceae determinants settling performance activated sludge clo
AB285481.1 gg_id:232448 Sulfolanivorax yambarensis str. MS4
FJ154090.1 gg_id:351849 Shinella kummerowiae str. CCNWGS0228
EF437254.1 gg_id:249079 Rhizobium sp. str. RZ6
FN436071.1 gg_id:573545 Molekularbiologische Charakterisierung der bakteriellen Populationsdynamik eines t
FN555404.1 gg_id:511375 Sinorhizobium sp. I-Bh25-4
D14255.1 gg_id:5205 Zoogloea ramigera str. IAM12669
DQ984584.1 gg_id:256527 Mt. Nan-Jen litterfall clone IYF06
DQ096644.1 gg_id:132981 Rhizobium sp. PIP4 str. PIP4; JCM 12219
EU888002.1 gg_id:349041 Microbial structure hydrolytic stage two-stage anaerobic digestion grass silage leach
DQ814239.1 gg_id:162359 zebrafish digestive tract clone aab65g10
X74915.1 gg_id:5207 Shinella zoogloeoides str. ATCC 19623
AM181744.1 gg_id:160209 Sinorhizobium arboris str. LMG 14919
D14509.1 gg_id:5245 Sinorhizobium meliloti str. IAM12611
EU379945.1 gg_id:270061 Sinorhizobium meliloti str. CCBAU 83856
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AM946566.1 gg_id:325210 Ensifer maghrebium str. ORS 1410
EU625296.1 gg_id:278661 Sinorhizobium meliloti str. 27
FJ025127.1 gg_id:351945 Sinorhizobium meliloti str. SEMIA 6162
EU545511.1 gg_id:342747 Sinorhizobium meliloti

DQ993272.1	193836	7420.2	11632.7	6776.5	7836.3	15003.2	10784.5
EU584258.1	352865	1247.2	1981.7	1480.6	634.2	1781.2	2822.1
AY316683.1	200464	3631.0	5038.2	9624.2	4722.0	13027.6	12710.1
EF173321.1	192524	373.3	965.8	1972.4	2283.4	1852.1	1036.2
FJ517717.1	560086	2601.5	4079.5	5184.0	3814.6	7804.4	7163.5
EU399935.1	260090	2103.0	3832.4	5199.2	2433.6	8221.8	8098.6
D12788.1	5289	3651.2	4277.3	5425.4	3980.0	12332.6	7816.5
EU399919.1	276979	2726.1	4036.9	6241.6	3232.4	8818.0	9108.9
DQ304797.1	154037	4595.7	6618.3	7498.3	5023.3	9784.0	10774.9
AB187585.1	104322	2702.8	4420.1	5255.0	2924.7	7311.0	9032.5
EU723213.1	334997	1366.4	2513.1	2199.2	747.3	2908.9	4270.2
FJ598327.1	566021	66.1	216.4	538.3	198.0	2370.7	1308.8
EU346730.1	267822	766.5	1949.4	1699.2	452.5	1993.8	3398.5
AF502218.1	55816	6950.3	9401.2	10449.1	7583.9	12676.8	13562.8
GQ009804.1	499861	1164.0	1914.9	3728.5	2409.9	2472.6	5043.1
DQ898296.1	173668	701.8	1858.4	2752.8	984.3	3525.6	2521.4
EU104300.1	345964	418.2	992.0	1690.6	980.4	1582.9	3203.8
AB285481.1	232448	3579.6	5583.7	7391.5	4288.1	10794.0	11889.8
FJ154090.1	351849	6614.3	7944.6	10109.4	5129.4	11711.0	12504.6
EF437254.1	249079	90.9	267.1	485.3	85.0	963.3	1574.8
FN436071.1	573545	2157.4	2578.6	4075.7	1593.0	2505.3	5986.8
FN555404.1	511375	888.9	1536.6	3330.8	2982.8	3942.2	3868.5
D14255.1	5205	489.6	1122.9	1294.4	441.6	2569.6	3256.1
DQ984584.1	256527	1012.4	2440.0	2741.5	927.8	4587.4	3930.2
DQ096644.1	132981	2797.9	3540.7	3473.0	2417.9	5382.6	7175.7
EU888002.1	349041	1047.9	1811.8	1355.5	852.8	2893.9	2028.4
DQ814239.1	162359	2716.0	3130.7	4510.2	3520.0	9931.3	12894.7
X74915.1	5207	107.1	327.4	479.5	178.2	726.5	1645.8
AM181744.1	160209	1040.3	2135.4	5688.6	1343.2	6633.6	7592.2
D14509.1	5245	1007.0	1451.7	3497.0	1749.7	5377.8	6823.3
EU379945.1	270061	1547.8	2168.5	4718.6	1930.4	6686.6	7861.3
EF531326.1	278035	304.9	342.7	811.1	812.3	933.6	2036.8
GU433464.1	517976	1024.1	1552.5	3723.9	1759.4	5857.7	7304.1
EU256454.1	253057	1786.3	1911.0	3956.2	1626.1	6022.2	8801.0
EF634450.1	278262	1202.2	2027.8	4893.9	2348.3	6551.0	8437.9
DQ989230.1	176599	6685.5	6493.9	6497.2	7753.3	13126.4	12207.0
AY904726.1	111921	1316.6	2110.4	4528.0	2547.6	7235.3	8483.2
AM946566.1	325210	145.9	374.9	706.2	503.4	2916.2	2538.9
EU625296.1	278661	1647.1	2489.6	4954.9	1440.1	7441.3	7205.1
FJ025127.1	351945	1931.1	3400.2	5340.1	1084.5	4121.8	6363.1
EU545511.1	342747	6399.7	5537.7	4237.6	4890.0	11012.8	10315.7

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AB535696.1 gg_id:557105 Sinorhizobium medicae str. Cl.3-2
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AY904727.1 gg_id:111751 Sinorhizobium meliloti str. SEMIA 134
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EU488378.1 gg_id:565999 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and
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EU488131.1 gg_id:534712 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and
AB232339.2 gg_id:155467 Bartonella sp. str. TFC2
EU488467.1 gg_id:553301 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and
EF540509.1 gg_id:219954 Rhizobium sp. 4_C16_39
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EU488463.1 gg_id:571469 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and
EU488371.1 gg_id:534308 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and
EU817493.1 gg_id:326733 Rhizobium sp. str. XJ-L72
EF090606.1 gg_id:197918 Agrobacterium sp. str. Mei-QS6
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EU256452.1	244861	3609.3	4957.7	8948.8	4516.2	12945.5	12820.5
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AM946567.1	343932	309.1	546.7	1462.5	321.7	1577.6	1486.1
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AB535703.1	545858	2019.6	3050.2	7126.1	3819.6	10117.4	12510.8
AB015420.1	34931	667.9	1090.6	1418.4	1212.6	6264.5	8547.2
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FJ821001.1	512395	432.5	649.0	564.6	1315.7	3850.3	4940.0
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EF645800.1	240354	1413.3	2564.1	4437.0	1305.4	6583.1	5659.2
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AB017203.1	50238	133.8	356.8	951.8	240.5	1274.6	1292.7
EU488283.1	551681	10505.5	10706.6	7497.4	8684.1	15331.8	12484.9
FJ793198.1	564313	1483.3	3365.2	2893.9	745.0	4428.0	3990.9
CU920781.1	563220	521.1	1543.0	3832.6	655.9	3992.6	5814.0
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EU488378.1	565999	5487.2	4899.3	5114.9	5460.3	9198.3	8967.9
EU488368.1	542279	367.5	709.2	1557.3	375.2	3796.7	1623.0
EU488131.1	534712	1091.2	2042.7	2858.0	1554.6	5909.5	3972.7
AB232339.2	155467	1144.3	2544.4	5289.7	1582.6	4799.0	6120.2
EU488467.1	553301	7442.7	8469.1	5158.7	7958.8	15740.3	11631.6
EF540509.1	219954	1401.9	1019.2	1217.6	216.7	421.4	1239.3
EF516927.1	218154	1315.3	1803.2	2588.0	1280.5	4471.6	2657.3
EU488260.1	547565	5611.9	6550.1	4810.4	6248.4	16023.1	11988.5
AY133103.1	56163	5637.3	6917.4	7883.7	7700.4	13651.4	12368.1
EU488463.1	571469	7483.7	5832.7	4062.4	8498.6	11384.9	12177.5
EU488371.1	534308	12607.6	13557.2	8504.8	9233.0	15640.9	11606.8
EU817493.1	326733	636.4	1409.2	2175.8	1332.8	6391.5	3602.8
EF090606.1	197918	3984.0	5583.1	7090.3	3398.0	9563.3	7621.4
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o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified

g__Pannonibacter
g__Pannonibacter
g__Pseudovibrio
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g__Pseudovibrio
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g__Afifella
g__Afifella
g__Rhodobium
g__unclassified
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g__unclassified
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g__sfA

s__Pannonibacter phragmitetus	61633
s__unclassified	61718
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s__unclassified	62667
s__unclassified	62811
s__unclassified	62887
s__Afifella marina	60542
s__Afifella marina	60815
s__unclassified	60973
s__unclassified	61098
s__Rhodobium orientis	59356
s__unclassified	58949
s__unclassified	59203
s__unclassified	59237
s__unclassified	59407
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s__unclassified	58953
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s__unclassified	58979
s__unclassified	59026
s__unclassified	59035

EU841534.1 gg_id:340002 Pannonibacter phragmitetus str. 224
EF608175.3 gg_id:535229 Pannonibacter sp. str. HT23
AM990762.1 gg_id:279133 Pseudovibrio sp. MOLA 539
FJ169215.1 gg_id:342767 microbial and polyketide biosynthetic potential palmerolide-producing tunicate Synoi
FJ169195.1 gg_id:321382 microbial and polyketide biosynthetic potential palmerolide-producing tunicate Synoi
EU726271.1 gg_id:342195 Stappia sp. str. B106
EU581698.1 gg_id:275806 Rhodobacteraceae sp. MEBiC05064T marine sponge Geomun-Island South Korea
DQ985041.1 gg_id:193166 Halomonas sp. str. JL1044
EF101502.1 gg_id:194356 Stappia meyerae str. GA15
EU167953.1 gg_id:269625 Stappia sp. str. 16-23
AY162083.1 gg_id:135498 Cultivating Sargasso Sea clone GMD37F4
FJ202909.1 gg_id:325677 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k
AY628423.1 gg_id:99161 Stappia marina str. mano18
D85832.1 gg_id:111501 Roseibium denhamense str. OCh 254
AY588950.1 gg_id:122223 Pacific Ocean deep sea sediment clone DE6.8
EU168019.1 gg_id:269506 Stappia sp. str. 23-28
EU999013.1 gg_id:304551 Predominance Methanolobus and Methanoculleus spp. Archaeal Saline Gas Field Fo
DQ270709.1 gg_id:144694 Halomonas sp. B-3046
GU199002.1 gg_id:593115 Mycoplana sp. str. G110
GU322907.1 gg_id:524664 Labrenzia sp. str. YC6927
EF101504.1 gg_id:185052 Stappia conradae str. MIO
DQ660386.1 gg_id:161779 Pseudovibrio sp. str. SPO723
AJ889009.1 gg_id:139632 Stappia alba str. 5OM9
DQ416561.1 gg_id:151808 s1cb71
DQ985044.1 gg_id:196145 Rhodopseudomonas sp. str. JL1015
AM696707.1 gg_id:224191 Rhodobium marinum str. JA211
GU370102.1 gg_id:521541 Rhodopseudomonas sp. str. P530(9)
EU445271.1 gg_id:272585 Rhodobium pfennigii str. AR 2102
AM180706.1 gg_id:161325 Rhodobium gokurnum str. JA 173
DQ532207.1 gg_id:166078 Geographical Variation Microbial Burden and Spacecraft Assembly Johnson Space Ce
AB374392.1 gg_id:269733 sequences Weissenstein (white rock) / few millimeters be surface rock called 'Weiss
AB257630.1 gg_id:273081 Microbial few millimeters be surface dolomite rock 'Val Piora' Alps 1965 meters abo
EU133571.1 gg_id:245274 tallgrass prarie soil clone FFCH4802
FJ152795.1 gg_id:310212 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX5A_
DQ451507.1 gg_id:156833 forest soil clone FAC68
AY862042.1 gg_id:112593 Washburn Spring 1 community clone WB1B012
GQ093827.1 gg_id:452509 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
FJ152772.1 gg_id:315470 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX5A_
AF050531.1 gg_id:4714 contaminated aquifer clone WCHB1-55
GQ402732.1 gg_id:538998 Accessing microbial biodiversity and metabolic potential tropical -based approach p
EU104345.1 gg_id:338628 Evidence Comamonadaceae determinants settling performance activated sludge clo

EU841534.1	340002	5238.4	9315.6	8498.0	5129.6	19209.7	14474.8
EF608175.3	535229	1361.0	1172.4	3247.8	870.9	2002.3	2861.2
AM990762.1	279133	86.4	125.0	260.3	209.1	1042.3	312.0
FJ169215.1	342767	9729.9	12367.8	9894.3	9450.5	18362.0	15363.1
FJ169195.1	321382	6828.2	12119.5	8494.9	8448.4	13819.5	12089.2
EU726271.1	342195	2406.8	3349.6	6306.6	4811.4	9434.0	6914.5
EU581698.1	275806	430.3	858.7	2489.3	1415.0	2273.3	1582.7
DQ985041.1	193166	837.3	1426.0	3569.1	2350.9	3601.6	3997.4
EF101502.1	194356	5057.5	6050.2	13810.9	4496.2	7687.2	7671.4
EU167953.1	269625	3269.3	4493.4	5158.1	3333.8	8832.6	7197.8
AY162083.1	135498	420.3	755.1	1549.1	593.4	3063.6	2394.8
FJ202909.1	325677	394.4	502.7	38.0	129.2	96.0	87.2
AY628423.1	99161	463.6	856.4	802.3	1554.5	5758.3	2019.3
D85832.1	111501	1952.3	2381.2	2971.6	2967.4	7104.7	3732.2
AY588950.1	122223	173.3	236.1	613.6	491.2	702.8	937.3
EU168019.1	269506	2175.7	2259.9	1671.1	1890.7	3586.5	2039.5
EU999013.1	304551	1350.6	2295.5	4596.6	2835.2	4145.2	4399.8
DQ270709.1	144694	2680.9	2705.8	2622.1	3787.3	4599.1	4631.0
GU199002.1	593115	466.7	1218.4	743.7	1086.1	4806.0	1603.4
GU322907.1	524664	18177.2	14629.7	15970.9	13069.4	19785.8	15055.5
EF101504.1	185052	4259.6	4885.8	4521.7	3831.0	9450.5	7337.4
DQ660386.1	161779	1250.7	2770.2	2818.0	1516.7	4722.8	2945.1
AJ889009.1	139632	2029.8	1664.8	1793.7	1440.3	4854.6	1917.8
DQ416561.1	151808	4447.5	4352.2	2180.0	777.1	6860.5	2875.1
DQ985044.1	196145	2760.9	2587.4	1385.4	3167.4	4949.5	1133.6
AM696707.1	224191	776.2	1431.2	1220.5	1161.8	4032.4	2719.3
GU370102.1	521541	2056.6	2182.4	1965.2	1138.8	8236.8	3528.7
EU445271.1	272585	147.5	399.8	1144.1	463.4	2019.8	3869.5
AM180706.1	161325	1575.5	1474.0	3081.3	1410.4	8953.5	3052.3
DQ532207.1	166078	407.5	820.2	1367.7	328.9	4502.7	1957.7
AB374392.1	269733	5437.7	6659.4	11895.6	5171.0	15996.0	14348.5
AB257630.1	273081	3549.7	3533.2	5373.6	3421.0	5370.3	5137.3
EU133571.1	245274	3612.4	5124.9	5311.1	3234.7	11031.3	8358.3
FJ152795.1	310212	1013.5	2250.9	2651.1	2055.1	6198.6	3428.5
DQ451507.1	156833	9060.0	10127.0	5661.4	8028.6	10341.1	10462.1
AY862042.1	112593	6673.8	10317.1	10634.7	7305.8	15581.5	15425.1
GQ093827.1	452509	5011.3	6891.5	5148.3	3912.0	13244.7	11321.3
FJ152772.1	315470	2885.7	4250.9	4967.5	2028.3	5242.1	6311.4
AF050531.1	4714	4912.2	7280.8	11645.4	4331.5	8775.1	9992.8
GQ402732.1	538998	2935.3	5465.5	3344.1	2484.3	5250.8	4546.5
EU104345.1	338628	11353.1	12634.7	7732.6	9282.8	13722.6	14952.5

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EU887986.1 gg_id:304250 Microbial structure hydrolytic stage two-stage anaerobic digestion grass silage leach
AF200695.1 gg_id:51286 13C- extracted 13C-methanol exposed soil clone UP2 proteobacterium
EF516292.1 gg_id:222685 grassland soil clone FCPT613
EF465533.1 gg_id:225699 Pseudoxanthobacter soli str. CC-CC4
GQ263890.1 gg_id:510008 Structure Simulated Level Waste Site simulated level waste site clone WC2_141
EU881257.1 gg_id:332410 (long-term grazing and burned annual) Karst region serious disturbance field soil clor
DQ984620.1 gg_id:257087 YK oil-contaminated soil clone YK_31
GQ262949.1 gg_id:538739 Structure Simulated Level Waste Site simulated level waste site clone F1_86X
AJ229208.1 gg_id:25697 anoxic bulk soil flooded rice microcosm clone BSV56 clone
AM162440.1 gg_id:155413 and situ identification acidic sphagnum peat bog clone B83
U87772.1 gg_id:4760 Afipia genosp. 6 str. G8665
EF020321.1 gg_id:207430 aspen rhizosphere clone Elev_16S_1897
X97077.1 gg_id:4765 peat bog clone TM19
FJ380167.1 gg_id:360221 ornithogenic Ross Sea region Antarctica AB1 soil clone 13/1/8F
AF358012.1 gg_id:29077 peat soil microcosm clone LO13.2
DQ129631.1 gg_id:137916 microarray level air two cities Texas urban aerosol clone AKIW856
DQ823159.1 gg_id:162179 Techniques Microbial Studies Oregon Caves National Monument Quad 3 off trail clo
GQ350414.1 gg_id:586170 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
EF516212.1 gg_id:225488 grassland soil clone FCPP499
FJ152802.1 gg_id:308948 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX5A_
EU881153.1 gg_id:310925 Karst region primary forest soil clone KPF200711-196
GQ402664.1 gg_id:548721 Accessing microbial biodiversity and metabolic potential tropical -based approach p
AM936498.1 gg_id:559544 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
EF019286.1 gg_id:209662 aspen rhizosphere clone Elev_16S_473
GQ402711.1 gg_id:546022 Accessing microbial biodiversity and metabolic potential tropical -based approach p
DQ451452.1 gg_id:156829 forest soil clone FAC13
GQ097820.1 gg_id:417366 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw397h0
AM935446.1 gg_id:547229 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
FM253652.1 gg_id:332834 Rock gold mine unusually microbial biofilm clone D06-2
EU861875.1 gg_id:338761 effects chronic fertilization on alpine tundra microbial implications carbon and cyclin
CU925666.1 gg_id:553033 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
CU926879.1 gg_id:567435 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
DQ813987.1 gg_id:162431 zebrafish digestive tract clone aab58b10
AY913367.1 gg_id:137744 forest soil clone DUNssu160 (+7B) (OTU#170)
CU923391.1 gg_id:570766 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
GQ021391.1 gg_id:488276 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbu27
FJ658644.1 gg_id:555885 Metalworking Fluids and Aerosols Metallurgy Plant metalworking aerosol clone Sumn
NR_025428.1 gg_id:548469 Chelatococcus asaccharovorans str. TE2
GQ848214.1 gg_id:552413 and Archaeal Xiarinur Soda Lake Water-sediment Interface water-sediment interfac
FJ592562.1 gg_id:574090 Fumarole-supported islands biodiversity within hyperarid -elevation landscape on Pu
AY792286.1 gg_id:124699 Humic Lake clone CrystalBog021H4

EU887986.1	304250	5039.7	6405.9	4303.7	3588.6	7067.5	6516.2
AF200695.1	51286	574.3	1410.5	2394.6	1053.4	1971.9	3474.0
EF516292.1	222685	838.5	1800.6	2150.1	379.8	3808.7	2058.6
EF465533.1	225699	4604.8	7904.7	10676.5	4956.9	18158.6	15107.7
GQ263890.1	510008	1867.0	2281.0	7284.3	2576.5	2294.1	3901.4
EU881257.1	332410	2042.6	1854.0	5450.3	3337.2	7654.1	8445.3
DQ984620.1	257087	5551.8	7521.8	12078.1	6229.4	13581.3	12690.3
GQ262949.1	538739	4357.5	4029.1	5163.9	2303.2	7345.6	8190.2
AJ229208.1	25697	2043.0	4012.4	7684.8	3803.4	12330.0	12597.0
AM162440.1	155413	2821.7	5683.1	7970.4	3818.9	13303.8	10903.1
U87772.1	4760	224.0	485.6	424.0	272.5	1227.3	1540.7
EF020321.1	207430	3564.6	6083.6	6729.6	4391.2	10675.7	6885.9
X97077.1	4765	1611.9	2658.7	1932.1	1982.4	9455.0	6594.2
FJ380167.1	360221	2193.0	3766.1	4365.6	2434.6	10892.5	10095.5
AF358012.1	29077	6035.9	7059.0	4018.4	5436.3	11608.1	12004.9
DQ129631.1	137916	4058.2	4531.0	3910.8	4929.0	9416.8	5773.0
DQ823159.1	162179	3893.8	3571.6	7288.6	5584.7	6488.4	6107.4
GQ350414.1	586170	2981.4	4479.0	6323.0	3955.3	7236.0	7276.2
EF516212.1	225488	3643.4	5003.0	5417.0	3705.4	7543.3	7365.2
FJ152802.1	308948	8332.3	9374.7	14730.5	7172.0	14060.8	16503.8
EU881153.1	310925	1422.1	2776.3	4122.2	1073.8	2778.7	3082.4
GQ402664.1	548721	2474.7	4558.8	9417.3	3669.7	9513.6	11562.6
AM936498.1	559544	3551.5	5250.6	7492.6	6510.2	11445.9	9292.2
EF019286.1	209662	6797.7	5387.4	3987.3	2132.1	5850.0	3361.5
GQ402711.1	546022	3505.3	4970.4	6367.4	4106.3	7417.0	6605.8
DQ451452.1	156829	49.1	72.2	267.8	144.6	99.0	89.3
GQ097820.1	417366	3571.7	5897.9	10998.3	4229.3	13225.2	15928.1
AM935446.1	547229	8371.8	7622.7	8709.8	7080.0	9305.8	8141.1
FM253652.1	332834	3505.4	4192.7	2473.5	3999.2	6393.1	6287.4
EU861875.1	338761	2461.4	3493.2	3127.9	2558.2	5823.6	5545.5
CU925666.1	553033	3108.2	6975.8	4546.3	4806.1	9934.4	7576.2
CU926879.1	567435	4952.9	8278.5	14447.6	5032.6	16391.6	15491.6
DQ813987.1	162431	425.1	1110.2	907.0	481.0	1241.0	1531.2
AY913367.1	137744	11065.5	13290.8	5601.5	7560.9	12564.8	10348.4
CU923391.1	570766	1879.8	3063.3	5864.6	1766.9	8104.2	7203.1
GQ021391.1	488276	10430.1	9895.0	3224.4	6353.1	9285.6	10434.4
FJ658644.1	555885	655.0	1612.4	3789.8	1084.5	4864.6	4102.7
NR_025428.1	548469	1322.6	1435.0	1795.2	869.1	6357.6	4363.2
GQ848214.1	552413	2959.0	3902.8	3401.7	5030.0	4037.5	5937.1
FJ592562.1	574090	73.0	170.5	964.9	148.9	578.0	628.6
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FJ542954.1 gg_id:513048 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone B
FJ624896.1 gg_id:544990 Influence lead contamination on boreal pine forest soil clone HF_C_23
GQ065523.1 gg_id:452998 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw89d08
AY212626.1 gg_id:106732 water 20 m upstream manure clone 175up
FM253660.1 gg_id:338715 Rock gold mine unusually microbial biofilm clone E09-2
DQ660884.1 gg_id:254810 DongChuan copper pyrites PRC determined acid mine drainage (AMD) clone DCK-I-2
AY921699.1 gg_id:113477 farm soil clone AKYG1801
EU133586.1 gg_id:247599 tallgrass prarie soil clone FFCH5858
AB240233.1 gg_id:144675 microbial structure rhizosphere Phragmites bulk soil reed bed reactor laboratory clo
EU617827.1 gg_id:344447 Seasonal variation microbial Yel Sea sediment clone D13S-4
EF079080.1 gg_id:252325 seeps sulfur-rich neutral pH ecosystem ochre-colored flocculent iron seep ditch fresh
EU050753.1 gg_id:256661 libraries sediment Kings Bay Svalbard Arctic clone ss1_B_08_05
EF018669.1 gg_id:209579 aspen rhizosphere clone Amb_16S_956
FM253680.1 gg_id:310692 Rock gold mine unusually microbial biofilm clone H07-2
AY921829.1 gg_id:114266 farm soil clone AKYH1529
AM935046.1 gg_id:566962 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
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GQ008167.1 gg_id:501498 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
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GQ263279.1 gg_id:534132 Structure Simulated Level Waste Site simulated level waste site clone FW1_a25
DQ230971.1 gg_id:141437 subsurface water clone DR938CH110701SACH95
GQ263757.1 gg_id:584708 Structure Simulated Level Waste Site simulated level waste site clone WC1_a78
GQ263601.1 gg_id:589565 Structure Simulated Level Waste Site simulated level waste site clone FW3_155C
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FJ998414.1 gg_id:390344 Amorphus sp. str. YIM D10
FJ477551.1 gg_id:509105 gut symbionts are tightly linked herbivory ants whole extracted single ant clone 83f
FJ416098.1 gg_id:368583 sediments sediment station NEC5 Northern Bering Sea clone 061M64
FJ430076.1 gg_id:360023 Rhizobium sp. str. CCNWGS114
DQ454123.3 gg_id:229692 Rhizobium sp. str. J3-A127
EF580937.1 gg_id:277780 Survey Microbial Freshwater Calcareous Mats freshwater calcareous mat clone CM4
DQ113411.1 gg_id:143364 microflora ants genus Bartonella Tetraponera attenuata RT13 clone
GU118131.1 gg_id:535654 Threatened Corals Provide Microbial Habitats clone Apal_F11
FJ477662.1 gg_id:591010 gut symbionts are tightly linked herbivory ants whole extracted single ant clone UAB-
EU056822.1 gg_id:354679 Rhizobium oryzae str. Alt 501
DQ269119.1 gg_id:197574 marine macro-alga surface clone DPC247
GQ199732.1 gg_id:591717 Mycoplana sp. str. 210_30

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DQ129276.1	137669	2848.3	3714.2	4262.1	6884.8	6627.0	8969.5
FJ542954.1	513048	2272.4	3794.4	7570.8	2459.8	10932.5	9473.2
FJ624896.1	544990	1440.0	1981.6	962.6	1869.8	4469.4	3676.5
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AY212626.1	106732	1830.3	3380.7	6033.1	2123.3	8532.4	7592.4
FM253660.1	338715	5396.6	6913.8	10774.5	5818.4	13379.6	14230.9
DQ660884.1	254810	1911.2	2777.7	6080.8	2426.2	5734.9	5083.8
AY921699.1	113477	396.1	1228.3	2648.5	406.7	3068.8	3053.2
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AB240233.1	144675	2435.8	3143.2	5228.5	3018.8	8497.4	10640.1
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EF079080.1	252325	11691.7	13741.5	15453.5	9454.9	15906.6	15887.6
EU050753.1	256661	1910.6	2917.4	2178.9	1149.3	2762.0	3677.1
EF018669.1	209579	151.2	381.3	1222.0	117.9	167.6	231.1
FM253680.1	310692	2925.8	2487.1	2360.2	3918.0	5232.2	4111.4
AY921829.1	114266	416.3	730.9	685.3	513.8	1632.6	1585.3
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GQ263169.1	511500	7156.7	5643.8	7689.4	8582.9	10764.0	9267.1
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GQ263279.1	534132	3310.7	4366.9	9682.9	3948.4	14685.8	11108.9
DQ230971.1	141437	297.9	758.9	2124.3	876.0	8833.7	5924.2
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GQ263601.1	589565	5997.5	5466.4	6251.5	6504.2	12698.8	7745.6
DQ097300.1	161408	113.6	128.2	30.5	92.2	556.9	36.3
FJ998414.1	390344	572.7	1315.3	2865.9	1723.4	7731.2	2988.8
FJ477551.1	509105	2589.6	3084.5	2870.1	2440.7	6127.2	6848.0
FJ416098.1	368583	968.0	1752.3	1389.1	669.0	4258.3	3564.7
FJ430076.1	360023	1400.1	2083.1	4125.9	2502.6	3370.4	5702.8
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FJ477662.1	591010	4622.5	4083.6	5065.0	3654.5	9107.5	7415.2
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FJ202935.1 gg_id:348688 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k
FJ230932.1 gg_id:323791 under Level Antibiotic Selection Pressures river water clone F30
EU290679.1 gg_id:254474 microbial structure biogeochemical contrasting shelf sediments Namibian upwelling
EF125460.1 gg_id:176046 mangrove soil clone MSB-2G6
EU022307.1 gg_id:256730 Mycoplana dimorpha str. DSM 7138
AB476277.1 gg_id:567915 Compositional and functional transition epibiotic microbial hydrothermal vent galath
FJ203608.1 gg_id:318738 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h
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AM403234.1 gg_id:165611 Nitrate-reducing and Denitrifying Marine Aqua Biofilter marine aqua
AJ318143.1 gg_id:46411 Waste-gas biofilter clone BIhii25
GQ093939.1 gg_id:462605 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
GQ033083.1 gg_id:432897 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
EF363715.1 gg_id:215874 Rhizobium soli str. DS-42
GU118128.1 gg_id:548423 Threatened Corals Provide Microbial Habitats clone Apal_H04
GU118281.1 gg_id:563202 Threatened Corals Provide Microbial Habitats clone Dstr_J12
EU491593.1 gg_id:273684 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR4C
AF423220.1 gg_id:51992 soil clone 1315-2
FJ712592.1 gg_id:517638 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) K
AY642558.1 gg_id:155596 and carbonate precipitation giant microbialites ly alkaline Lake Van Turkey microbiali
GQ054602.1 gg_id:405655 Topographical and Temporal Human Skin Microbiome skin back clone nbw1092d01c
DQ917801.1 gg_id:217617 Microbial profiles bleached and wild-type Muricea elongata Mesorhizobium clone BI
AJ294417.1 gg_id:22665 Rhizobium sp. str. TCK
EU246825.1 gg_id:240545 polyphasic description Pocillopora meandrina Palmyra Atoll Calcinus obscurus abdon
EF532794.1 gg_id:221752 Mycoplana caeni str. K107
GU369925.1 gg_id:525633 and mats vents Arc white microbial film on pebble aphotic zone shal hydrothermal v
AM930452.1 gg_id:259822 involved Tripneustes gratilla (Echinoidea) cloning and FISH host body wall lesions cl
EF649779.1 gg_id:244917 Rhizobium sp. str. J3-AN59
DQ330994.1 gg_id:159335 Guerrero Negro hypersaline microbial mat clone 09D2Z18
CU920079.1 gg_id:535750 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
AM697186.1 gg_id:223514 sequencing libraries indoor dust clone BF0001C027
GQ093897.1 gg_id:466355 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
FJ425633.1 gg_id:365493 communnities healthy and diseased colonies Caribbean coral Montastrea faveolata cl
EU528264.1 gg_id:286797 Seasonal Dynamics Mudflat Mouth Major Kentucky Lake Reservoir Tributary sedime
GQ365715.1 gg_id:548464 Hoeflea sp. str. AY-2
DQ289935.1 gg_id:167459 Microbial Carbon and Nitrogen Cycling Sediments South Atlantic Bight Permeable Sh
FJ193930.1 gg_id:340714 Genetic inventory 'KSC-Astrotek' spacecraft assembly clean room during DAWN missi
FJ203409.1 gg_id:331011 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h
AF359524.1 gg_id:38898 Alexandrium lusitanicum NEPCC 253
U78037.1 gg_id:5136 Ophiactis balli symbiont
EU753666.1 gg_id:306406 modern freshwater stromatolites Ruidera Pools Natural Park Spain dry stromatolite

FJ516967.1	557392	5201.3	7901.4	7099.0	7061.0	11476.3	10844.0
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EU290679.1	254474	5743.1	6647.3	6146.0	6234.3	11098.3	8587.4
EF125460.1	176046	6339.3	7586.1	10587.2	5761.2	16610.0	8293.4
EU022307.1	256730	587.8	1243.9	2219.8	2345.6	5119.1	8712.7
AB476277.1	567915	975.7	1423.5	905.2	556.9	3647.6	3671.0
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GU118008.1	558255	2606.7	3021.9	4328.7	1391.9	7686.9	5090.0
AM403234.1	165611	42.0	90.2	41.8	55.7	176.4	287.0
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GU118128.1	548423	1119.3	1663.6	2408.1	665.5	3770.6	3885.1
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AF423220.1	51992	662.5	1571.2	1706.5	1344.5	3564.7	3100.7
FJ712592.1	517638	4097.6	5668.6	7604.9	4275.9	12954.2	11776.2
AY642558.1	155596	1073.2	1483.4	2645.2	497.0	2416.0	4002.3
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GQ365715.1	548464	2860.3	4404.1	9537.5	4627.0	7369.4	10547.9
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FJ203409.1	331011	822.8	1125.7	2133.7	635.3	6345.5	5589.1
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EU753666.1	306406	5730.1	6083.6	7066.0	6905.8	10942.6	11065.2

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

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DQ103632.1	150577	145.0	161.6	122.6	108.2	155.2	473.2
DQ103628.1	150589	979.2	1980.3	5404.4	1034.5	9537.5	8252.3
AF004845.1	4722	5888.5	5630.6	5905.5	5593.3	13646.5	9369.4
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AY904784.1	111946	2471.0	4508.8	3914.5	2693.8	9556.6	8041.9
EU876663.1	317195	118.6	227.9	1435.4	317.2	2821.5	4752.9
AB236172.1	148902	679.7	956.8	1677.9	712.8	2659.7	3025.2
FJ707292.1	572030	290.3	677.8	1698.5	448.6	1898.6	1036.0
AB236169.1	147634	4139.9	7040.0	4897.4	3488.9	10023.4	7782.0
FJ478661.1	543156	245.6	541.9	2317.4	618.2	2093.1	1402.6
EF019390.1	209096	276.2	698.0	1978.0	220.6	1025.5	1363.7
AJ535707.1	105233	358.9	832.3	2168.4	1065.8	3132.6	4857.6
EF516667.1	218772	926.9	2182.1	1902.7	1284.8	3208.8	2415.2
AB236170.1	149143	2022.8	3596.5	6175.2	2950.6	10863.0	12154.4
EF516470.1	224138	118.8	203.2	1138.8	219.8	193.1	1051.2
AB271044.1	166471	1538.0	1716.3	3112.7	787.3	2260.5	3028.8
DQ986319.1	174214	176.6	422.6	1027.9	275.7	1106.6	469.4
GQ046109.1	464010	10204.7	10721.2	10437.9	8626.6	11346.2	12421.7
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X99469.1	4700	682.2	1839.5	1091.8	497.4	1743.0	516.5
EF540453.1	221589	3769.2	4749.9	10003.2	4730.0	9209.4	8824.9
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EU289458.1	239819	1477.7	2305.5	4951.8	2133.0	1894.8	3207.4
AJ306541.1	68682	3951.8	4895.5	7640.3	3884.2	9646.7	9697.0
DQ533878.1	231483	3306.5	5192.1	4039.5	2118.5	9207.7	6236.8
X94201.1	4654	764.1	1729.9	2110.2	466.1	1165.3	1433.4
X94202.1	4673	1686.5	4129.3	3672.4	1603.5	3918.9	4969.8
AF399969.1	62751	3487.7	3969.4	3131.4	3953.3	6069.2	4827.0
AJ421782.1	43442	1939.6	2094.7	3734.2	3739.0	12032.9	3618.1
FM202386.1	570096	636.9	1464.6	2922.6	2272.3	3843.4	2376.8
AJ227814.1	5865	2239.3	1735.6	2994.0	2475.0	2900.2	3723.8
CP000158.1	162510	280.7	500.7	579.1	317.2	1595.6	901.5
AF082795.1	5870	5913.1	7812.9	5881.4	6593.0	13203.8	9120.5
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DQ396058.1 gg_id:151886 deep-sea octacoral clone ctg_NISA280
DQ160243.2 gg_id:139361 Hyphomonas taiwanensis str. HYP1
NR_024938.1 gg_id:572877 Hyphomonas johnsonii str. MHS-2; ATCC 43964
AF082797.1 gg_id:5859 Hyphomonas oceanitis str. SCH-89
AJ007807.1 gg_id:5841 Maricaulis maris str. ACM 5106 (T)
EU528177.1 gg_id:286163 Seasonal Dynamics Mudflat Mouth Major Kentucky Lake Reservoir Tributary sedime
AJ301667.1 gg_id:26948 Maricaulis virginensis str. VC 5
DQ768642.1 gg_id:245137 Maricaulis virginensis MARC4M
FJ797347.1 gg_id:567500 Arenicola marina bioturbated mesocosm marine sediment clone 20
AY162105.1 gg_id:135262 Cultivating Sargasso Sea clone GMD21C01
NR_025323.1 gg_id:545614 Maricaulis parjimensis str. MCS 25; DSM 16078
AJ309862.1 gg_id:40525 Oceanicaulis alexandrii str. C116-18
DQ644012.1 gg_id:236476 Production cyanobacterial toxin Microcystin disease corals black band diseased (BBI
AY701470.1 gg_id:108547 dinoflagellate symbiont clone GCDE08_V
AJ227811.1 gg_id:5847 Caulobacter sp. str. MCS33
GQ441337.1 gg_id:593605 and dynamic mat present vs. active nitrogen-fixing microorganisms marine microbia
FJ152756.1 gg_id:347767 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX5A_
DQ395426.1 gg_id:154213 deep-sea octacoral clone ctg_CGOAB48
FJ203305.1 gg_id:307703 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c
AB286621.1 gg_id:209532 Reducing production and domination comamonadaceae reducing oxygen supply was
AF359547.1 gg_id:18991 Scrippsiella trochoidea NEPCC 15
AY942774.1 gg_id:148699 but species richness marine sponge Cymbastela concentrica clone Cc118
FJ497641.1 gg_id:542217 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun
EU881181.1 gg_id:303607 Karst region natural restoration land soil clone KNR200711-027
AF234756.1 gg_id:18609 sludge clone S36
GU118388.1 gg_id:538371 Threatened Corals Provide Microbial Habitats clone Gven_P10
EU196330.1 gg_id:244514 Investigation heterotrophic and autotrophic microbial perennial springs cold saline (
EU245307.1 gg_id:241958 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-H5-G02
DQ376579.1 gg_id:150962 Microbial ecology removing phosphate wastewater EBPR process aerobic sequencin
AB294313.1 gg_id:205348 Microbial structure deep coal seem groundwater stream clone SWB02
AY654758.1 gg_id:105062 Oculina mucus isolate 111
AM990862.1 gg_id:278552 Caulobacter sp. MOLA 88
FM242321.1 gg_id:337659 sequences sediment clone 83 T9d-oil
AJ578477.1 gg_id:102289 Woodsholea maritima str. CM251
AB286463.1 gg_id:208631 Reducing production and domination comamonadaceae reducing oxygen supply was
EF495229.1 gg_id:222908 Croceitomaculum antarcticum str. IMCC3195
AJ617875.1 gg_id:110283 oxic-anoxic interphase flooded paddy soil clone D14429
FM242450.1 gg_id:332051 sequences sediment clone 21 T12d+oil
EU665092.1 gg_id:571737 Soil are Changed Agricultural Practices agricultural soil clone Plot22-2G04
GQ500759.1 gg_id:590926 Surveys Biofilms and Sediments Mammoth Cave Karst Aquifers Bio-Sep beads conta
FJ826144.1 gg_id:514038 Succession during spring Sea filtered surface sea water decay period after diatom blo

DQ396058.1	151886	2827.4	3058.3	3359.9	2339.9	8212.6	5574.8
DQ160243.2	139361	1818.7	3232.3	3533.6	2618.7	8003.9	4640.8
NR_024938.1	572877	3397.2	2964.7	3835.1	4171.3	2578.0	3202.4
AF082797.1	5859	637.6	713.7	1071.2	388.8	2012.5	1607.9
AJ007807.1	5841	9757.7	11632.6	6976.7	10327.4	14251.9	11874.7
EU528177.1	286163	5677.1	7150.0	5393.1	7822.7	12324.7	10327.7
AJ301667.1	26948	4971.7	6418.4	4330.8	5061.9	7913.2	6010.3
DQ768642.1	245137	11209.6	12964.0	8736.0	11296.5	17251.9	12431.4
FJ797347.1	567500	4490.0	6739.9	7967.1	4870.8	9813.2	11723.5
AY162105.1	135262	2960.0	4688.2	8026.4	3208.2	10588.2	6628.5
NR_025323.1	545614	1105.9	3093.0	2095.4	1483.5	5429.3	2957.8
AJ309862.1	40525	2572.9	3221.4	3660.7	5475.5	7484.0	5106.4
DQ644012.1	236476	4188.0	5287.0	4897.1	5720.5	10966.7	7998.6
AY701470.1	108547	6691.4	7622.5	7725.2	6372.8	12880.1	10181.6
AJ227811.1	5847	434.1	1217.4	1922.7	714.9	2048.5	3533.1
GQ441337.1	593605	7184.2	5793.3	6255.4	5837.6	11394.3	8487.5
FJ152756.1	347767	3995.7	6264.6	8206.1	4057.0	12294.1	9917.4
DQ395426.1	154213	96.0	61.5	82.0	493.3	147.3	72.4
FJ203305.1	307703	6846.3	6221.7	4016.4	8552.6	14941.5	12513.9
AB286621.1	209532	438.8	765.5	658.8	164.8	226.5	373.7
AF359547.1	18991	1377.6	1823.1	1553.6	568.4	5223.8	2695.7
AY942774.1	148699	321.0	500.3	2050.0	350.9	2547.7	1512.8
FJ497641.1	542217	6659.1	11122.0	11448.6	7860.2	17735.6	14017.1
EU881181.1	303607	322.0	781.3	3162.6	2166.0	3972.7	3982.5
AF234756.1	18609	2633.0	3505.6	4684.5	2078.8	5960.4	5585.3
GU118388.1	538371	3834.7	4253.1	2477.1	2925.7	6942.6	5744.5
EU196330.1	244514	690.7	846.4	1822.2	955.3	7204.2	6213.6
EU245307.1	241958	3373.6	4835.0	1527.0	4500.1	8784.5	3818.1
DQ376579.1	150962	1479.2	2235.0	938.2	1182.4	7027.8	5786.0
AB294313.1	205348	1200.6	1747.1	2396.0	983.9	6495.4	2950.2
AY654758.1	105062	773.3	1513.0	856.8	671.1	2151.2	2837.2
AM990862.1	278552	2550.0	2013.4	2421.4	1659.2	8382.5	2137.5
FM242321.1	337659	632.9	1444.2	2076.1	1488.9	7575.7	4353.0
AJ578477.1	102289	2238.2	1536.9	3222.0	4030.0	3305.9	2960.9
AB286463.1	208631	62.9	525.7	776.3	70.3	58.2	34.7
EF495229.1	222908	119.5	191.7	60.2	217.5	80.8	37.6
AJ617875.1	110283	134.8	540.2	1590.0	125.8	449.1	1330.8
FM242450.1	332051	500.9	969.7	1568.7	523.0	6531.8	2960.3
EU665092.1	571737	647.5	1904.3	1225.3	469.3	2064.0	2814.1
GQ500759.1	590926	1652.0	2706.8	5955.9	2993.4	7815.6	8346.3
FJ826144.1	514038	488.0	1007.0	1236.9	640.4	1753.0	3674.8

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AY921760.1 gg_id:112748 farm soil clone AKYH1490
FJ516864.1 gg_id:565583 semiarid 'Tablas de Daimiel National Park' wetland (Central Spain) unravelled lower s
GU444088.1 gg_id:530619 Effects amendments on fertility and microbial structure cucumber Cucumis sativus L
EU491552.1 gg_id:263491 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR4C
EU236280.1 gg_id:296183 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg5aCo7
EU236341.1 gg_id:298881 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg5a2G5
EU104323.1 gg_id:309713 Evidence Comamonadaceae determinants settling performance activated sludge clo
GQ441341.1 gg_id:581650 and dynamic mat present vs. active nitrogen-fixing microorganisms marine microbia
NR_026060.1 gg_id:570345 Amaricoccus tamworthensis str. Ben103; ACM 5097
U88042.1 gg_id:5811 Amaricoccus macauensis str. Ben104
DQ130031.1 gg_id:151324 microbial biota normal forearm human skin clone GL97
NR_029203.1 gg_id:580499 Amaricoccus veronensis str. Ben102; ACM 5098
FJ152897.1 gg_id:336456 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX4CE
DQ346506.1 gg_id:154801 during composting libraries compost clone 2B22
FJ152955.1 gg_id:323451 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX4CE
EF489005.1 gg_id:245310 Antarctobacter sp. str. TG22
EU053204.1 gg_id:246019 Catellibacterium terrae str. QMT-4
NC_009952.1 gg_id:250733 Dinoroseobacter shibae str. DFL 12
FJ202183.1 gg_id:343990 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k
DQ289933.1 gg_id:167723 Microbial Carbon and Nitrogen Cycling Sediments South Atlantic Bight Permeable Sh
AF452106.1 gg_id:62868 Rhodobacter massiliensis str. Framboise
DQ342310.1 gg_id:205946 Haematobacter massiliensis str. H2443
AJ534225.1 gg_id:75300 Jannaschia helgolandensis HEL-43
AM990650.1 gg_id:278279 culturable oligotrophic ocean (South Pacific Gyre) sea water
AJ748747.1 gg_id:110922 Jannaschia rubra str. 4SM3
AY906862.1 gg_id:112620 Jannaschia sp. str. CL-SP26
EF202612.1 gg_id:200932 Jannaschia donghaensis str. DSW-17
DQ643999.1 gg_id:159971 Jannaschia pohangensis
EU034641.1 gg_id:253055 Ketogulonicigenium vulgare str. VC-2-2
DQ915605.1 gg_id:320216 Ketogulonicigenium robustum str. NRRL B-12627
AF136849.1 gg_id:135903 Ketogulonicigenium vulgare str. DSM 4025
AY005463.1 gg_id:45273 Leisingera methylohalidivorans str. MB2
AJ582229.1 gg_id:93357 Loktanella salsilacus str. LMG 22002
DQ533555.1 gg_id:163668 Loktanella tamlensis str. SSW-27
FJ172067.1 gg_id:327793 Microbial athalassohaline Tirez lagoon (Spain) water clone MJZ2
AJ582227.1 gg_id:94079 Loktanella vestfoldensis str. LMG 22006
AY576770.1 gg_id:138842 Ruegeria sp. str. 3X/A02/236
AF173971.1 gg_id:73505 Roseobacter sp. str. KT1117
FJ172062.1 gg_id:354977 Microbial athalassohaline Tirez lagoon (Spain) water clone MJW2
EF659438.1 gg_id:246665 within Poole Harbour seawater clone PH-F10
AM691092.1 gg_id:220404 Rhodobacteraceae clone EG3

AY921760.1	112748	6035.3	7668.4	5725.6	5516.3	8823.9	8198.2
FJ516864.1	565583	2379.8	4801.0	6231.0	2645.8	8810.9	4550.7
GU444088.1	530619	4644.8	6191.5	6468.2	5798.1	5166.7	5760.7
EU491552.1	263491	693.4	1792.5	1139.0	615.0	4089.8	2606.8
EU236280.1	296183	651.9	1125.6	3198.4	2902.1	2238.6	2153.8
EU236341.1	298881	1270.0	2415.9	4177.3	3224.0	6103.2	3295.3
EU104323.1	309713	2021.6	3057.9	3876.3	3419.1	3420.5	3564.0
GQ441341.1	581650	5016.7	8374.4	9853.8	7392.6	9953.7	13366.1
NR_026060.1	570345	849.8	1433.4	1914.2	1597.7	4364.3	3095.7
U88042.1	5811	11699.8	15004.2	12134.8	12893.1	21326.3	17626.9
DQ130031.1	151324	48.5	94.6	210.1	101.6	328.5	162.6
NR_029203.1	580499	1576.9	2171.7	3469.4	3510.0	3399.5	3650.9
FJ152897.1	336456	1809.3	2243.7	4399.1	4402.2	4724.5	6706.7
DQ346506.1	154801	8181.9	10625.7	11328.2	10394.7	20040.6	12084.3
FJ152955.1	323451	12987.6	13648.6	9648.6	11722.2	18018.4	16655.5
EF489005.1	245310	2442.3	1333.4	3069.7	2551.9	3093.7	2556.5
EU053204.1	246019	295.9	778.9	787.2	1292.1	2387.3	3044.9
NC_009952.1	250733	532.4	875.4	545.0	981.1	1066.2	1213.1
FJ202183.1	343990	29.3	44.4	373.5	67.5	331.2	137.9
DQ289933.1	167723	3006.7	4090.7	6109.1	3439.9	6721.0	7849.7
AF452106.1	62868	5422.1	6063.5	4117.4	8266.0	7545.3	8147.7
DQ342310.1	205946	1318.8	2000.0	3350.9	2508.8	1407.2	4209.2
AJ534225.1	75300	2881.1	3400.9	2335.1	3220.0	6960.5	4424.7
AM990650.1	278279	384.2	403.1	626.0	265.3	1398.4	1589.4
AJ748747.1	110922	1750.4	2322.2	2017.1	2939.0	3728.6	3803.1
AY906862.1	112620	883.0	1002.9	1069.7	1377.1	4014.7	3101.8
EF202612.1	200932	993.5	1511.5	1321.1	2621.6	3049.1	2937.0
DQ643999.1	159971	456.9	526.6	411.3	226.4	1705.8	604.3
EU034641.1	253055	1339.0	2044.3	2758.8	2281.2	3728.4	7471.0
DQ915605.1	320216	3310.6	5122.6	1690.1	2576.1	4199.5	5230.7
AF136849.1	135903	476.3	698.9	737.5	1145.4	1508.1	3693.6
AY005463.1	45273	5405.3	5087.1	5676.8	3908.8	5197.1	6741.5
AJ582229.1	93357	419.7	1081.2	1827.9	827.2	707.4	1586.1
DQ533555.1	163668	321.1	695.0	1134.2	371.3	2098.9	2461.5
FJ172067.1	327793	1877.0	2599.3	2702.5	2876.2	4539.7	4464.6
AJ582227.1	94079	1952.3	2131.3	1170.0	2364.9	2434.3	2264.9
AY576770.1	138842	1354.0	1495.4	2165.3	1211.9	2608.9	3288.6
AF173971.1	73505	245.0	716.6	1421.6	622.8	1553.6	2215.0
FJ172062.1	354977	161.8	195.7	157.8	522.3	137.1	147.2
EF659438.1	246665	4606.3	4297.8	3516.4	6099.5	9009.0	10129.9
AM691092.1	220404	657.8	1218.4	2666.6	1660.2	4698.1	4927.1

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AJ505786.1 gg_id:61254 coastal sediment clone
FJ152873.1 gg_id:328838 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX4CI
FJ716887.1 gg_id:510302 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United Kingc
DQ397336.1 gg_id:153999 Thalassobius sp. str. UST050418-052
GU061095.1 gg_id:592005 Evaluation culturing methods cultivate previously Yel Sea intertidal beach clone TFS-
DQ344498.1 gg_id:145649 Loktanella koreensis str. GA2-M3
AY167339.1 gg_id:81378 Roseobacter sp. str. ARK9990
FJ203462.1 gg_id:307704 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h
AJ505788.2 gg_id:61250 coastal sediment clone
FJ889546.1 gg_id:563888 Phaeobacter sp. str. ZS356
AY654808.1 gg_id:103608 Oculina mucus isolate 78
AY654838.1 gg_id:100870 Oculina mucus isolate 40
AF170751.1 gg_id:5658 Roseobacter sp. str. QSSC9-8
DQ514326.1 gg_id:161345 Maribius bermudensis str. B5-6
AY162102.1 gg_id:135261 Cultivating Sargasso Sea clone GMD21D01
X78313.1 gg_id:5670 Ruegeria algicola str. ATCC 51441ML4
AB491842.1 gg_id:557828 affiliation (Litopenaeus vannamei) Banyuwangi East Java microbial flocs floating brac
AJ633967.1 gg_id:114827 host's accessory nidamental gland clone T65ANG1
FJ716854.1 gg_id:541703 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United Kingc
AJ295988.1 gg_id:26995 Ruegeria aff. gelatinovorans str. ch611
EU592330.1 gg_id:539299 Seasonal changes Salton Sea hypersaline water clone SSW55N
AY258078.1 gg_id:135688 Ruegeria sp. str. DG882
AY344411.1 gg_id:91079 Lake Kauhako surface clone K2-S-32
GU324080.1 gg_id:556772 Marivita sp. str. CB 1101
AY600300.1 gg_id:103542 Loktanella hongkongensis str. UST950701-009P
FN431787.1 gg_id:544367 Loktanella hongkongensis str. AMV3 AMV18
AM983542.1 gg_id:537512 Loktanella pyoseonensis str. JJM85
EU143345.1 gg_id:252067 Loktanella sp. str. J20
AM944522.1 gg_id:268667 Nautella italica str. R-28753
FJ202078.1 gg_id:310849 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k
FJ202115.1 gg_id:343849 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k
EU592375.1 gg_id:583983 Seasonal changes Salton Sea hypersaline water clone SSW89Au
EF092158.1 gg_id:267120 Persistent Axinella corrugata Roseobacter clone AC2_A2
DQ675021.1 gg_id:162482 Pseudoruegeria aquimaris str. SW-255
DQ917854.1 gg_id:219732 Microbial profiles bleached and wild-type Muricea elongata clone BME80
FJ202604.1 gg_id:318096 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k
FJ202395.1 gg_id:319436 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k
DQ915613.1 gg_id:346324 Nereida ignava str. CECT5292
DQ915614.1 gg_id:327289 Oceanibulbus indolifex str. DSM14862
NR_027563.1 gg_id:544041 Oceanibulbus indolifex HEL-45 str. Hel-45; DSM 14862
EU694388.1 gg_id:293008 Oceanibulbus indolifex str. D15

AJ505786.1	61254	378.5	530.5	1923.9	3553.1	77.3	1421.4
FJ152873.1	328838	8764.0	7826.9	4936.3	6671.0	9898.9	9882.5
FJ716887.1	510302	1622.6	1627.7	3426.1	3253.1	2763.4	3785.5
DQ397336.1	153999	126.5	146.0	263.3	152.0	256.5	243.2
GU061095.1	592005	264.2	720.7	2602.6	1698.5	983.8	1128.6
DQ344498.1	145649	741.9	1523.9	3393.0	2580.7	3163.6	3972.9
AY167339.1	81378	1003.2	2043.8	1955.1	2753.4	4200.6	3481.5
FJ203462.1	307704	1210.8	1471.5	2324.3	2704.7	6069.2	4828.6
AJ505788.2	61250	22.3	19.8	26.6	42.3	60.1	23.5
FJ889546.1	563888	174.3	310.9	1602.7	271.3	493.8	911.2
AY654808.1	103608	2391.3	3084.4	6004.1	2910.6	7771.8	8381.2
AY654838.1	100870	354.3	418.5	588.4	344.0	851.9	441.5
AF170751.1	5658	34.9	68.0	32.0	63.1	62.9	45.1
DQ514326.1	161345	4028.8	5495.4	4939.9	4546.2	11796.4	7771.6
AY162102.1	135261	736.8	904.2	918.1	692.4	819.1	1880.2
X78313.1	5670	733.3	2140.0	3209.3	1923.8	2850.5	3377.0
AB491842.1	557828	361.5	1466.0	1811.1	256.3	1687.0	2959.3
AJ633967.1	114827	61.5	370.1	967.6	241.1	446.8	514.1
FJ716854.1	541703	947.4	1942.8	2160.0	1330.3	5050.8	4132.6
AJ295988.1	26995	3761.2	4538.4	5350.0	3289.0	7746.6	5397.7
EU592330.1	539299	754.4	1327.0	3537.3	799.8	2052.9	2130.4
AY258078.1	135688	263.8	643.8	1924.2	424.5	1142.8	2332.0
AY344411.1	91079	924.6	1383.1	3766.6	1841.4	1662.1	3041.6
GU324080.1	556772	8560.7	5772.8	9042.1	9315.2	9390.6	9157.9
AY600300.1	103542	198.9	604.1	899.4	560.5	300.5	413.2
FN431787.1	544367	31.4	110.6	197.0	107.9	148.2	468.7
AM983542.1	537512	2083.4	2053.8	1080.4	2621.3	4485.3	4030.3
EU143345.1	252067	1090.7	1073.5	1152.4	2111.5	3308.6	2816.3
AM944522.1	268667	444.0	791.7	5394.6	2395.6	1327.1	3542.3
FJ202078.1	310849	1513.9	1593.0	3161.1	1164.8	2607.5	2253.7
FJ202115.1	343849	521.3	842.9	1960.1	826.0	2182.9	1406.0
EU592375.1	583983	126.8	98.9	178.8	154.5	159.5	149.4
EF092158.1	267120	66.6	189.9	128.8	305.0	360.1	715.8
DQ675021.1	162482	98.6	248.3	1293.8	497.4	366.4	979.3
DQ917854.1	219732	1310.2	1448.4	5686.9	3618.0	2302.0	4264.7
FJ202604.1	318096	3157.0	2671.7	2519.4	1787.9	2912.5	3029.2
FJ202395.1	319436	269.8	308.8	182.8	173.9	1345.1	704.3
DQ915613.1	346324	24.7	33.5	32.6	45.6	71.0	28.7
DQ915614.1	327289	1776.7	2958.7	2445.1	3656.2	5812.7	4732.6
NR_027563.1	544041	1715.6	2026.0	2364.5	2970.8	4356.1	3775.8
EU694388.1	293008	1398.9	1760.2	2020.4	2619.5	3742.4	3305.2

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DQ915616.1 gg_id:305517 Oceanicola granulosus str. KCTC12143
GQ250665.1 gg_id:544324 bulk sea water column Gulf Mexico clone GOM_WB10-7
AB166982.1 gg_id:101280 Roseobacter sp. str. NT N37
FJ230846.1 gg_id:341497 marine str. SD7
FJ196062.1 gg_id:310847 Octadecabacter sp. str. ZS6-9
AB180384.1 gg_id:109216 Octadecabacter sp. str. No. 49
AF030437.1 gg_id:5737 Methylarcula terricola str. h37; VKM B-2160
AF030436.1 gg_id:5762 Methylarcula terricola str. h1; VKM B-2159
DQ402044.1 gg_id:150822 Paracoccus alcaliphilus str. mku-E2
DQ469585.1 gg_id:158059 Paracoccus alcaliphilus str. Sty2-VH
D32240.1 gg_id:5761 Paracoccus aminovorans str. JCM 7685
GQ497295.1 gg_id:552938 Paracoccus sp. str. KSL5401-001
GU201846.1 gg_id:518236 Paracoccus aminophilus str. Zw-11
AY312056.1 gg_id:88947 Paracoccus sp. Ol18
AF376134.1 gg_id:24018 Paracoccus sp. str. T231
FM207553.1 gg_id:348847 Paracoccus denitrificans E4
FJ381982.1 gg_id:582190 Potentially pathogenic and air stem cell transplant winter hospital shower water BMT
EF070124.1 gg_id:190880 Paracoccus sp. TRP
DQ539490.1 gg_id:169913 Paracoccus sp. SBRD2
DQ270723.1 gg_id:142241 Pseudomonas sp. B-1015
AF139992.1 gg_id:5771 Paracoccus marcusii str. ML-003
AJ582185.1 gg_id:93958 soil near uranium mill tailings clone Gitt-GS-149
AY014175.1 gg_id:47316 Paracoccus solventivorans str. ATCC 700252
FJ950555.1 gg_id:410450 Paracoccus versutus str. c75
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DQ512861.1 gg_id:159464 Paracoccus sp. str. LW36
AY004210.1 gg_id:28386 Paracoccus versutus str. kps
EU434456.1 gg_id:276317 Paracoccus versutus str. a234
FM872636.1 gg_id:369875 occupant source house floor dust clone FA04D10
AY014179.1 gg_id:46743 Paracoccus yeei str. G3060
GU108563.1 gg_id:545865 active chemolithoautotrophic prokaryotes sulfidic zone Black pelagic redoxcline dete
FJ713782.2 gg_id:571011 Paracoccus sp. str. DEH99
AB275604.1 gg_id:212709 Paracoccus kamogawaensis str. YSFL3
AJ864466.1 gg_id:109475 Paracoccus pantotrophus str. JT001
GQ250442.1 gg_id:577514 Paracoccus sp. str. MJ17
AB025189.1 gg_id:5770 Paracoccus sp. str. MBIC4018 HI7
DQ923133.1 gg_id:180344 Paracoccus halotolerans str. YIM 90738
D32238.1 gg_id:5766 Paracoccus alcaliphilus str. JCM 7364
DQ108402.1 gg_id:137632 Paracoccus sp. Tibet-S9a3
FJ842690.1 gg_id:576262 Paracoccus sp. str. NII-0918

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GQ250665.1	544324	284.8	562.2	1636.4	575.3	1614.4	1517.4
AB166982.1	101280	116.1	307.6	645.2	197.1	601.2	901.3
FJ230846.1	341497	90.2	178.2	205.2	349.7	403.5	302.9
FJ196062.1	310847	1683.5	2603.2	4694.2	2734.4	7753.9	6770.7
AB180384.1	109216	663.2	1057.8	2278.3	815.5	2476.4	2385.2
AF030437.1	5737	166.2	204.7	213.4	541.1	129.3	403.9
AF030436.1	5762	42.0	52.6	52.5	122.7	79.5	45.2
DQ402044.1	150822	81.9	218.1	328.4	244.3	308.7	401.4
DQ469585.1	158059	7659.9	9135.0	7056.1	7082.8	9998.1	9121.1
D32240.1	5761	1077.8	2035.0	4660.2	2684.2	1569.9	4451.5
GQ497295.1	552938	888.9	1306.1	4340.9	2913.0	184.1	4956.1
GU201846.1	518236	453.0	1108.5	1922.2	1280.7	488.5	3476.7
AY312056.1	88947	297.8	888.3	2164.0	1981.0	314.6	951.2
AF376134.1	24018	3335.4	4104.4	4144.0	6013.5	8507.6	7340.5
FM207553.1	348847	802.1	1853.0	5765.2	2928.7	424.9	5377.8
FJ381982.1	582190	1063.9	2265.3	4627.3	2944.9	137.9	2173.8
EF070124.1	190880	941.4	1803.9	2721.2	1144.9	4410.1	4112.5
DQ539490.1	169913	6021.2	7428.8	6036.3	8685.3	14875.5	11836.6
DQ270723.1	142241	2398.4	3277.0	5731.0	3697.2	6566.0	8470.0
AF139992.1	5771	4887.7	4663.1	3960.3	5718.9	10095.9	8377.9
AJ582185.1	93958	7997.5	9398.6	7285.5	5277.0	11935.0	12798.3
AY014175.1	47316	6302.8	5580.0	5916.4	6036.8	7209.3	7911.9
FJ950555.1	410450	8753.7	9200.5	8151.2	6798.2	11154.9	8303.5
EU434343.1	275527	8438.2	7014.5	7452.2	10664.0	11514.0	10188.7
DQ512861.1	159464	218.8	431.2	1705.2	985.8	993.9	810.8
AY004210.1	28386	360.9	755.6	2252.5	583.3	3368.7	1515.1
EU434456.1	276317	647.9	1293.9	2832.6	2181.4	2572.1	1342.6
FM872636.1	369875	1041.2	2526.9	3379.0	947.0	3679.9	5362.1
AY014179.1	46743	808.0	1788.7	1604.6	583.6	2724.6	1664.2
GU108563.1	545865	2042.2	3650.4	7732.0	3680.7	8834.2	8125.3
FJ713782.2	571011	1126.9	1590.8	1299.2	2681.4	2651.8	4010.9
AB275604.1	212709	957.9	1442.3	2315.0	539.7	4274.5	2264.2
AJ864466.1	109475	795.3	1535.8	3002.8	1515.4	1882.4	2646.6
GQ250442.1	577514	2197.8	2992.5	2595.3	4000.7	4015.8	6337.4
AB025189.1	5770	312.2	740.6	1226.4	517.1	370.7	444.9
DQ923133.1	180344	855.7	1638.7	2371.0	441.9	2452.9	1743.0
D32238.1	5766	2973.4	4515.9	5594.4	4171.3	10800.8	9295.1
DQ108402.1	137632	763.7	1096.1	1835.7	1007.4	1130.9	2546.1
FJ842690.1	576262	385.1	1075.4	1631.6	647.9	1811.0	3287.6

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AY626831.1 gg_id:103986 Paracoccus sp. str. QD5-2-1
AM697590.1 gg_id:225243 sequencing libraries indoor dust clone BF0002D101
DQ423482.1 gg_id:155546 Paracoccus sp. str. HN-182
EU196530.1 gg_id:241681 Paracoccus sp. Ol18
FJ670987.1 gg_id:527854 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
FJ675504.1 gg_id:532336 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
AM231051.1 gg_id:159385 Paracoccus sp. str. R-24342
AJ864463.1 gg_id:109472 Paracoccus thiocyanatus str. SST
FJ675534.1 gg_id:519944 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
AY573045.1 gg_id:106521 Paracoccus sp. str. ARCTIC-P17
AJ534231.1 gg_id:202277 Methylarcula sp. HEL-8
AB255110.1 gg_id:172587 corroded concrete clone SC-148
FM874023.1 gg_id:370368 occupant source house mattress dust clone MB05C10
DQ116009.1 gg_id:130794 bovine teat canal clone D-64
DQ337586.1 gg_id:150080 Paracoccus sp. BBTR62
FJ774966.1 gg_id:559136 Symbionts Brown Planthopper (Homoptera: Delphacidae) symbiont Nilaparvata luger
EU368762.1 gg_id:267622 Paracoccus sp. str. B61 Ydz-zz
DQ129626.1 gg_id:138528 microarray level air two cities Texas urban aerosol clone AKIW1050
GQ129980.1 gg_id:370584 Genetic inventory 'JPL-SAF' during MSL mission spacecraft assembly clean room floc
DQ532252.1 gg_id:165945 Geographical Variation Microbial Burden and Spacecraft Assembly Johnson Space Ce
D32239.1 gg_id:5758 Paracoccus aminophilus str. JCM 7686
AB264130.1 gg_id:165184 Paracoccus sp. str. TDMA-10
GQ260189.1 gg_id:588165 Paracoccus sp. str. 22-5
D32241.1 gg_id:5779 Paracoccus kocurii str. JCM 7684
AM900779.1 gg_id:235419 Paracoccus sp. PA216
AY167832.1 gg_id:77519 Paracoccus sp. str. SAFR-029
AB264129.1 gg_id:164471 Paracoccus sp. str. TDMA-8
AM990798.1 gg_id:279292 Paracoccus sp. MOLA 22
EF157164.1 gg_id:237879 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon
FJ267566.1 gg_id:323776 Paracoccus sp. str. II_Gauze_W_10_18
FJ658279.1 gg_id:570280 Metalworking Fluids and Aerosols Metallurgy Plant metalworking aerosol clone Winte
AB098589.1 gg_id:78216 Paracoccus sp. str. TUT1021
AB185957.1 gg_id:265461 Paracoccus marinus str. KKL-A5
DQ856507.1 gg_id:243813 intestinal microflora Chinese mitten crab (Eriocheir sinensis) clone C1I
GQ452286.1 gg_id:582083 Paracoccus sp. str. MU2A-22
AJ580352.1 gg_id:107767 Paracoccus sp. BOG6
AB012914.1 gg_id:5765 Paracoccus sp. str. MBIC3345 Y4
AM084041.1 gg_id:139889 Paracoccus sp. str. R-24616
AB024613.1 gg_id:5740 Paracoccus sp. str. MBIC1145
FJ210812.1 gg_id:323743 Paracoccus sp. str. QDHT-17

EU341164.1	238449	2506.0	4577.1	2261.3	3330.2	7460.7	8084.6
AY626831.1	103986	644.6	1801.7	1856.8	2713.5	2310.1	3660.4
AM697590.1	225243	3008.4	2720.0	2699.6	2694.0	5279.3	5438.6
DQ423482.1	155546	165.3	311.1	838.8	350.6	610.3	297.6
EU196530.1	241681	2197.3	3462.4	4707.9	3206.4	8761.7	5749.0
FJ670987.1	527854	5802.3	8479.6	8951.2	5520.9	10437.7	8931.9
FJ675504.1	532336	577.2	1658.4	3614.6	2676.4	2721.3	5261.5
AM231051.1	159385	139.0	550.1	549.2	819.4	119.4	504.3
AJ864463.1	109472	3262.9	2929.0	4108.3	4081.5	4706.1	5304.3
FJ675534.1	519944	397.8	1219.3	486.0	606.0	2616.6	2263.4
AY573045.1	106521	5789.7	5102.8	5925.0	5954.5	6294.3	9178.3
AJ534231.1	202277	2219.4	3986.5	4115.5	2073.6	6374.3	4142.2
AB255110.1	172587	6459.7	8920.1	4524.3	5428.0	12385.7	7949.4
FM874023.1	370368	2374.8	4280.6	4813.2	3462.6	3633.4	4543.9
DQ116009.1	130794	635.6	1429.3	1802.9	1294.0	3996.6	5585.7
DQ337586.1	150080	1699.6	2612.4	1614.6	1356.7	2397.9	2274.9
FJ774966.1	559136	6688.2	6419.0	5600.0	4836.1	10447.7	8853.4
EU368762.1	267622	203.7	342.8	737.2	265.7	241.8	640.3
DQ129626.1	138528	3021.6	2825.1	2769.1	2058.7	2707.2	3480.3
GQ129980.1	370584	411.6	1410.6	1258.6	1271.3	2462.5	1543.4
DQ532252.1	165945	2478.8	3126.0	3902.7	2073.7	7487.4	6696.4
D32239.1	5758	833.1	1600.3	2519.9	1555.6	5148.4	5799.3
AB264130.1	165184	2303.3	2939.4	3457.2	3010.2	5149.9	4943.1
GQ260189.1	588165	1312.2	2217.0	4673.4	2135.4	5039.7	4657.3
D32241.1	5779	6903.6	9357.5	13245.1	11096.6	13603.3	13981.0
AM900779.1	235419	340.7	433.4	1854.5	1183.9	1031.3	1611.1
AY167832.1	77519	2752.4	4290.2	5347.2	3849.7	6720.4	6830.7
AB264129.1	164471	861.4	2820.0	1386.9	1442.9	671.5	1432.1
AM990798.1	279292	712.6	1508.7	2867.7	1622.5	4263.5	3867.7
EF157164.1	237879	663.4	1043.5	2562.1	1733.0	2045.8	1688.3
FJ267566.1	323776	320.6	816.5	1299.5	595.2	1736.7	2426.6
FJ658279.1	570280	1294.9	1887.4	3744.5	1376.0	3475.5	4225.5
AB098589.1	78216	830.1	1341.0	2815.7	875.5	2660.7	5320.0
AB185957.1	265461	302.7	990.2	3608.7	732.7	1356.8	2966.4
DQ856507.1	243813	490.7	1021.6	1572.2	832.8	2329.8	2556.1
GQ452286.1	582083	1722.2	3102.4	3792.8	1137.9	4760.9	6976.4
AJ580352.1	107767	823.2	1736.3	4001.0	2933.1	461.5	2720.0
AB012914.1	5765	616.5	609.7	1419.2	1388.6	2248.7	848.0
AM084041.1	139889	525.6	960.8	2201.2	524.3	3270.0	3547.2
AB024613.1	5740	419.4	1164.4	1554.1	902.1	419.3	724.4
FJ210812.1	323743	385.6	699.7	1173.2	554.3	1633.6	1814.4

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AF365991.1 gg_id:111393 marine str. BB2AT3
AJ867253.1 gg_id:111057 Roseobacter gallaeciensis X6
DQ514304.1 gg_id:161029 Roseobacter sp. str. BSs20188
AJ633943.1 gg_id:114641 host's accessory nidamental gland clone 53ANG1
DQ915619.1 gg_id:311058 Phaeobacter gallaeciensis str. NBRC16654
GQ250607.1 gg_id:588747 bulk sea water column Gulf Mexico clone GOM_WB10-40
FJ014973.1 gg_id:304780 Phaeobacter sp. str. M3-1.1
Y13244.1 gg_id:5654 Roseobacter gallaeciensis str. BS107T
FJ014985.1 gg_id:334868 Phaeobacter sp. str. M8-3.2
AY771774.1 gg_id:141703 Arctic Roseobacter gallaeciensis clone SE84
FJ232439.1 gg_id:364995 Phaeobacter sp. str. NH44C
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DQ906715.1 gg_id:163091 and marine microorganisms Antarctic sea water 20 m clone AntCL1C10
FJ202414.1 gg_id:334773 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k
AM884343.1 gg_id:275025 Ruegeria sp. str. SCS1
GQ348550.1 gg_id:533795 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
FJ203339.1 gg_id:314415 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c
FJ202225.1 gg_id:350338 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k
FJ716879.1 gg_id:554782 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United Kingc
FJ203234.1 gg_id:305694 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c
DQ811850.1 gg_id:172275 mangrove soil clone MSB-3ax5
EU799430.1 gg_id:308804 It's all ranking aquatic Newport Harbour RI clone 1C227029
FJ203312.1 gg_id:327709 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c
FJ664800.1 gg_id:554245 Quantitative dynamics cells plankton-fed microbial fuel cell clone plankton_D11
EU642854.1 gg_id:279275 Pseudoruegeria sp. JC2496 str. JC2496; IMSNU 14150
EU246829.1 gg_id:248590 polyphasic description Pocillopora meandrina Palmyra Atoll Calcinus obscurus abdon
AF384204.1 gg_id:23935 Rhodobaca bogoriensis str. CL1
EF554833.1 gg_id:224271 Rhodobaca barguzinensis str. VKM B-2406
AF513929.1 gg_id:62508 Rhodobacter group clone LA1-B42N
AJ605746.2 gg_id:148330 Rhodobacter sp. str. EL-50
AF454295.1 gg_id:63841 hypersaline Mono Lake clone ML812M-6
AJ132383.1 gg_id:73883 Natronohydrobacter thiooxidans str. AHO 1 sediments ly alkaline soda lakes
DQ659236.1 gg_id:170558 Roseinatronobacter monicus str. Ros35
AB369166.1 gg_id:243619 Microbiological Assessment Circulation Mud Fluids During First Operation Drilling De
DQ432310.1 gg_id:156883 prokaryotic alkaline hypersaline lakes Wadi Natrun Egypt Lake Hamra sediment clon
AF454292.1 gg_id:63844 hypersaline Mono Lake clone ML602M-13
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DQ432393.1 gg_id:156929 prokaryotic alkaline hypersaline lakes Wadi Natrun Egypt Lake Hamra water clone W

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DQ178660.1	138722	1860.5	2960.6	3021.1	2635.7	8697.5	6034.9
AY177712.2	83687	1449.6	834.9	1313.3	938.7	2026.9	2416.1
AF365991.1	111393	131.0	515.1	923.7	570.9	611.5	1093.0
AJ867253.1	111057	135.9	515.3	1002.9	539.1	609.2	1090.6
DQ514304.1	161029	6756.4	7623.2	5838.4	7319.8	11585.5	8007.0
AJ633943.1	114641	301.6	366.6	1085.2	385.7	980.2	2389.8
DQ915619.1	311058	366.2	872.5	6487.8	2219.6	336.5	3370.7
GQ250607.1	588747	64.2	67.6	283.8	102.7	125.2	138.1
FJ014973.1	304780	2799.6	3889.9	4344.1	5902.4	6549.6	8047.0
Y13244.1	5654	10026.7	9035.1	4929.5	9024.9	13848.3	12544.2
FJ014985.1	334868	56.0	388.9	1275.5	273.6	360.5	570.5
AY771774.1	141703	904.4	1448.2	3921.0	1527.2	1264.8	1878.0
FJ232439.1	364995	4651.7	4057.4	7361.8	4102.0	6880.4	6791.1
DQ660384.1	172912	88.0	248.9	962.3	358.4	342.7	767.4
DQ906715.1	163091	4562.6	6244.4	6104.0	6515.3	8993.0	9603.9
FJ202414.1	334773	198.6	418.0	357.1	375.3	293.1	642.8
AM884343.1	275025	2073.7	4015.6	3195.0	2988.8	7779.4	8096.2
GQ348550.1	533795	2038.7	2604.4	3496.8	2484.8	5044.3	4536.3
FJ203339.1	314415	3821.7	4644.7	3924.2	7162.3	8401.0	6483.9
FJ202225.1	350338	5716.2	6354.9	3456.6	5948.0	7317.5	7135.0
FJ716879.1	554782	1243.2	1527.3	1713.8	1989.6	3228.1	3729.0
FJ203234.1	305694	688.3	1520.6	1973.7	1733.0	1088.6	4334.1
DQ811850.1	172275	213.8	507.7	288.1	721.6	266.2	1625.8
EU799430.1	308804	2178.6	3078.0	3188.0	3852.7	3901.2	4586.6
FJ203312.1	327709	503.2	693.3	582.9	903.7	522.9	718.8
FJ664800.1	554245	57.4	153.8	236.3	232.5	228.1	225.3
EU642854.1	279275	210.3	489.6	2036.2	723.3	936.5	874.8
EU246829.1	248590	2093.6	1809.5	3975.4	3981.2	4057.4	5377.4
AF384204.1	23935	1191.0	2051.7	2388.0	3857.6	2350.9	5035.1
EF554833.1	224271	464.2	783.6	2132.5	1727.4	1942.6	4098.6
AF513929.1	62508	598.8	1454.7	1182.1	1831.2	766.4	1512.8
AJ605746.2	148330	3951.7	4415.1	6477.3	7446.1	7855.4	8711.7
AF454295.1	63841	15480.3	14159.0	12551.1	15390.8	18646.4	16387.6
AJ132383.1	73883	315.9	803.8	510.5	544.7	881.4	717.0
DQ659236.1	170558	1573.6	2761.8	1408.1	1844.7	1866.0	1692.8
AB369166.1	243619	526.8	1228.9	2310.3	2895.5	1794.6	3019.4
DQ432310.1	156883	414.8	997.2	1415.7	649.7	1342.9	2431.6
AF454292.1	63844	7355.8	8722.4	5851.1	9321.6	7768.5	9229.7
DQ432219.1	156640	1404.0	3474.2	8387.0	4786.0	7288.3	10025.4
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s__unclassified	62869
s__Rhodobacter azotoformans	62610
s__Rhodobacter capsulatus	61571
s__Rhodobacter sphaeroides	61632
s__Rhodobacter sphaeroides	62803
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s__unclassified	62787
s__unclassified	62813
s__unclassified	62906
s__unclassified	62923
s__Rhodovulum marinum	62152
s__Rhodovulum sulfidophilum	61671
s__Rhodovulum sulfidophilum	62073
s__Rhodovulum sulfidophilum	62211
s__Rhodovulum sulfidophilum	62324

DQ659237.1 gg_id:173742 Roseinatronobacter monicus str. Ros10
FJ153015.1 gg_id:332691 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX4CI
CP000663.1 gg_id:219103 Rhodobacter sphaeroides str. ATCC 17025
D16427.1 gg_id:5815 Rhodobacter capsulatus str. C5
GU370088.1 gg_id:514578 Rhodobacter sphaeroides str. P230(6)
GU370084.1 gg_id:532163 Rhodobacter sphaeroides str. P230(1)
GU455302.1 gg_id:522935 Understanding short-chain fatty acids accumulation enhanced alkaline digestion: kir
AF280854.1 gg_id:49391 bioreactor clone mle1-20
GU086365.1 gg_id:560393 Pseudorhodobacter sp. str. HDW-19
FN428770.1 gg_id:543416 Looking India metagenomic approach Mahananda river water clone MRM1024
EU703461.1 gg_id:377032 lakes on Eastern Tin Plateau freshwater lake altitude 4279 masl clone XZZLH1
AB355088.1 gg_id:240664 Monitoring and archaeal two heavy polluted areas lake Egypt based on sediment Ma
AY212706.1 gg_id:102583 water 10 m downstream manure clone 257ds10
EU580696.1 gg_id:268039 Rhodobacter sp. str. NP25b
GQ500826.1 gg_id:587231 Surveys Biofilms and Sediments Mammoth Cave Karst Aquifers Bio-Sep beads conta
DQ815272.1 gg_id:169528 zebrafish digestive tract clone aab52e09
EU104326.1 gg_id:321409 Evidence Comamonadaceae determinants settling performance activated sludge clo
GU257946.1 gg_id:566382 Rhodobacter changlensis str. HXG-D9
DQ342322.1 gg_id:214765 Rhodobacter blasticus str. ATCC 33485; KC2138
AB077986.1 gg_id:67721 Rhodobacter gluconicum
DQ676414.1 gg_id:225039 Archaeal and plankton freshwater pond suboxic freshwater-pond sediment clone M
AM690348.2 gg_id:225526 Rhodobacter katedanii str. JA234
EU652478.1 gg_id:277835 Catellibacterium sp. str. JPB-2.07
GU454898.1 gg_id:520640 Understanding short-chain fatty acids accumulation enhanced alkaline digestion: kir
EF192900.1 gg_id:201726 sediments temperate artificial lake Rapel reservoir sediment clone Rap2_6C
AF234745.1 gg_id:35565 sludge clone A26
FJ382199.1 gg_id:512277 Potentially pathogenic and air stem cell transplant summer hospital shower water BM
AF035433.1 gg_id:5793 Rhodobacter apigmentum
EU464681.1 gg_id:301082 Hartmann's mountain zebra feces clone AFZEB_aaj69a12
AY957924.1 gg_id:114895 drinking water biofilm clone B3NR69D9
DQ337005.1 gg_id:147896 subsurface water clone EV818CFSSAHH73
EU979475.1 gg_id:307279 Rhodobacter sp. str. CR07-8
AB122032.1 gg_id:98295 Rhodobacter sp. str. Jip03
D16429.1 gg_id:5800 Rhodobacter blasticus str. ATCC33485
AF368183.1 gg_id:58379 non-EBPR sludge clone SBRT155
FJ196030.1 gg_id:333434 Rhodobacter sp. str. ZS3-33
AM696303.1 gg_id:217363 Rhodovulum marinum str. JA219
D16420.1 gg_id:5840 Rhodovulum sp str. MB260
U55277.1 gg_id:5835 Rhodovulum sulfidophilum str. W-1S=FERM P-15320
GU370080.1 gg_id:519755 Rhodovulum sulfidophilum str. P210(4)
EU770422.1 gg_id:306266 Rhodovulum sulfidophilum str. sy59

DQ659237.1	173742	858.9	1312.5	2367.8	1755.9	1040.6	3393.6
FJ153015.1	332691	764.8	1247.0	1123.1	888.6	1921.3	2358.8
CP000663.1	219103	1278.3	2669.1	5194.6	3700.7	2174.9	5345.3
D16427.1	5815	529.4	1022.6	1057.6	1421.9	230.5	1148.0
GU370088.1	514578	3285.4	4169.3	6885.0	5261.8	5457.4	8084.0
GU370084.1	532163	327.0	949.4	1273.7	380.3	657.3	1828.2
GU455302.1	522935	6254.0	9104.6	8220.9	6759.3	7665.5	12263.6
AF280854.1	49391	2302.4	3409.9	3050.4	4249.6	9142.2	7957.6
GU086365.1	560393	3456.7	4635.3	7172.3	8041.9	8868.1	8701.0
FN428770.1	543416	1165.2	2253.7	3492.2	1316.4	848.3	5007.1
EU703461.1	377032	817.5	2245.8	1848.3	3854.7	251.3	2293.1
AB355088.1	240664	1680.4	3380.4	3868.1	3219.5	10276.5	10488.9
AY212706.1	102583	3984.1	6952.2	4432.3	5342.9	6827.3	11584.1
EU580696.1	268039	1115.1	2729.2	2516.3	1784.1	1798.3	5793.1
GQ500826.1	587231	3699.0	5469.5	2116.7	2433.0	5596.8	7095.0
DQ815272.1	169528	961.4	2020.9	4249.3	3206.5	558.6	3940.1
EU104326.1	321409	1504.5	3370.2	5343.2	4310.6	1876.8	6906.2
GU257946.1	566382	405.8	1253.3	1329.2	808.7	1441.2	3989.2
DQ342322.1	214765	1713.4	4417.2	4505.0	3832.9	1745.6	6533.4
AB077986.1	67721	2232.2	2939.5	5826.3	5464.1	2264.1	5266.9
DQ676414.1	225039	619.5	2509.2	2565.9	1572.5	4125.5	3996.4
AM690348.2	225526	1401.0	3024.4	5074.1	5216.8	4441.5	7265.4
EU652478.1	277835	298.6	1388.1	2129.2	985.6	582.6	3042.5
GU454898.1	520640	2052.1	3619.6	9267.7	6151.8	846.8	4843.8
EF192900.1	201726	2052.3	4386.6	5874.2	4697.4	3450.8	6394.4
AF234745.1	35565	881.4	2413.9	3968.3	2208.7	1237.0	6014.1
FJ382199.1	512277	2586.2	5421.7	5199.3	4029.5	4724.1	8077.9
AF035433.1	5793	8760.0	11303.2	8538.6	11926.4	13676.3	11557.3
EU464681.1	301082	1970.6	2018.3	2008.8	2125.7	270.2	3150.0
AY957924.1	114895	1777.3	3156.4	7864.2	5767.3	1322.7	6367.6
DQ337005.1	147896	507.3	1614.0	1394.5	1664.8	380.3	4209.6
EU979475.1	307279	4882.2	7253.0	5670.1	6820.7	12488.5	9328.5
AB122032.1	98295	1282.7	3293.0	3944.6	2702.2	879.9	3518.4
D16429.1	5800	9761.9	10067.2	10050.5	10311.5	11570.3	10462.2
AF368183.1	58379	576.7	1665.4	544.0	402.3	903.5	2822.9
FJ196030.1	333434	4177.1	4438.0	5755.8	5979.0	4590.5	7421.8
AM696303.1	217363	1396.5	1937.2	1651.8	2232.2	6352.3	8120.5
D16420.1	5840	4137.5	3434.5	5691.2	4282.5	6598.8	5448.0
U55277.1	5835	8606.0	6939.0	5948.6	6504.2	7482.2	7437.5
GU370080.1	519755	1126.8	1947.5	3938.0	3587.2	1695.2	4739.0
EU770422.1	306266	1216.0	1522.4	976.5	2221.9	2185.2	2462.6

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AM180479.1 gg_id:163018 Rhodovulum sp. C2B-PN-R4
AM696304.1 gg_id:220300 Rhodovulum marinum str. JA242
AM748927.1 gg_id:256512 Rhodovulum kholense str. JA297
AM921780.1 gg_id:291146 Rhodovulum puniceilacus str. JA322
NR_025222.1 gg_id:555568 Albidovulum inexpectatum str. FRR-10
AB079635.2 gg_id:62339 Rhodovulum strictum str. JCM 9221
NR_025608.1 gg_id:568416 Roseisalinus antarcticus str. EL-88; DSM 11466
FJ593905.2 gg_id:592117 Roseivivax sp. str. sw-2
FJ897782.1 gg_id:543161 Roseivivax sp. str. BH87090
AB166989.1 gg_id:102398 Roseivivax sp. str. NT N51
GQ243710.1 gg_id:578525 consortia immobilizing nitrifying bioreactors designed penaeid and non-penaeid larv
EF512126.1 gg_id:220146 Roseobacter denitrificans str. CSQ-3
NC_008209.1 gg_id:163757 Roseobacter denitrificans str. OCh 114
GQ249575.1 gg_id:513025 Microbial anaerobic sediments Bay Cadiz (Spain) marine sediment: 12-14 cm layer cl
AY654757.1 gg_id:104921 Oculina mucus isolate 112
AY177714.1 gg_id:83398 Rhodobacteraceae T11
DQ446103.2 gg_id:164817 Surface Mucopolysaccharide Layer and Band Microbial Mat Black Band-Diseased Sid
AJ844283.1 gg_id:160252 Rubellimicrobium thermophilum str. E-R2A-8a
FM874293.1 gg_id:360432 occupant source house mattress dust clone MC04B03
EU338486.1 gg_id:242423 Pararubellimicrobium aerilata str. 5715S-9
EF547368.1 gg_id:218626 Rubellimicrobium sp. str. MSL 20
DQ532142.1 gg_id:167156 Geographical Variation Microbial Burden and Spacecraft Assembly Jet Propulsion Lal
DQ532274.1 gg_id:172438 Geographical Variation Microbial Burden and Spacecraft Assembly Johnson Space Ce
EF682991.1 gg_id:243852 Eastern Mediterranean atmosphere clone F13_3E_FL
AJ968649.1 gg_id:144280 Ruegeria atlantica str. N5III
DQ915630.1 gg_id:330249 Silicibacter lacuscaerulensis str. DSM11314
DQ915631.1 gg_id:306399 Silicibacter pomeroyi str. DSM15171
EF092256.1 gg_id:264007 Persistent Axinella corrugata Roseobacter clone MAx29_D12
AM709700.1 gg_id:254802 symbiotic Ruegeria strains cuttlefish Sepia officinalis egg yolk clone B4SOVto5
AM709703.1 gg_id:254660 symbiotic Ruegeria strains cuttlefish Sepia officinalis shell sacs clone 2SOSC91
AM930441.1 gg_id:268418 involved Tripneustes gratilla (Echinoidea) cloning and FISH host body wall lesions clc
GU118794.1 gg_id:533437 Threatened Corals Provide Microbial Habitats clone Mfra_N19
FJ203171.1 gg_id:354074 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c
GU118756.1 gg_id:593469 Threatened Corals Provide Microbial Habitats clone Mfra_C19
FJ203011.1 gg_id:350278 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c
AM709701.1 gg_id:248371 symbiotic Ruegeria strains cuttlefish Sepia officinalis embryo clone B4SOEmb23
FJ403069.1 gg_id:357398 Disease- changes healthy and diseased colonies Caribbean coral Montastrea faveolat
AJ633996.1 gg_id:114809 host's egg clone IEGG2
DQ357745.1 gg_id:149148 Marine Hatchery: Balance Between Pathogenic and Potentially Probiotic Strains mo
FJ716889.1 gg_id:549008 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United Kingc
EF629830.1 gg_id:274739 Changes marine Mycale laxissima on transfer aqua sponge tissue

AM180479.1	163018	83.3	283.1	528.3	696.1	277.6	1703.1
AM696304.1	220300	555.6	814.1	1214.7	579.0	1231.1	2038.3
AM748927.1	256512	2392.9	3198.5	2915.3	5147.3	9276.9	10016.6
AM921780.1	291146	2746.4	3678.1	6389.3	3382.5	7146.5	10217.1
NR_025222.1	555568	455.0	1356.2	5296.9	917.7	3736.5	5666.1
AB079635.2	62339	535.3	1337.5	1093.0	1727.8	3459.1	4307.3
NR_025608.1	568416	2625.6	2404.8	2594.9	1846.7	2459.8	1697.1
FJ593905.2	592117	5600.9	6790.6	8410.2	7399.0	15225.6	11856.3
FJ897782.1	543161	1544.7	3017.0	5760.1	2107.1	6794.5	10366.5
AB166989.1	102398	1928.5	3246.1	3850.4	2937.6	6066.6	6130.2
GQ243710.1	578525	1866.2	3516.9	7707.9	2089.3	10380.8	11109.1
EF512126.1	220146	606.2	529.1	617.9	656.9	928.8	1329.7
NC_008209.1	163757	1039.7	1871.1	2557.0	1611.4	2254.4	2486.4
GQ249575.1	513025	542.4	675.6	1814.5	982.8	2030.9	1500.0
AY654757.1	104921	8128.1	10204.0	9474.2	9234.0	10534.2	12509.6
AY177714.1	83398	98.3	189.2	350.4	249.6	725.1	245.2
DQ446103.2	164817	174.7	272.9	619.2	668.2	410.8	200.7
AJ844283.1	160252	83.2	162.3	505.1	149.1	117.8	83.3
FM874293.1	360432	641.6	1444.4	1497.5	1767.1	1003.1	2324.4
EU338486.1	242423	4333.2	6618.8	5725.0	5129.4	11403.9	9747.2
EF547368.1	218626	4795.5	6553.2	7759.1	6063.4	12408.2	11654.4
DQ532142.1	167156	4401.0	4808.5	5359.7	6352.3	9556.1	10755.4
DQ532274.1	172438	6484.2	7591.9	6406.2	6218.8	15526.7	12472.5
EF682991.1	243852	8867.3	7803.8	3751.5	8835.3	14549.7	10699.0
AJ968649.1	144280	1007.6	1390.4	2609.9	2992.9	845.4	2092.7
DQ915630.1	330249	682.9	1417.7	1888.8	887.3	796.6	1863.6
DQ915631.1	306399	147.8	433.5	433.0	215.8	119.6	996.4
EF092256.1	264007	265.7	757.6	770.3	155.8	2762.7	368.3
AM709700.1	254802	237.8	603.6	1293.6	1202.0	591.4	1236.7
AM709703.1	254660	372.3	811.3	2332.3	2341.2	580.8	1630.3
AM930441.1	268418	308.5	979.5	1410.5	1615.2	3383.2	1836.5
GU118794.1	533437	1112.7	2073.3	3144.6	1804.1	3723.6	5273.3
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AM709701.1	248371	376.2	816.7	2194.8	2347.0	592.3	1476.6
FJ403069.1	357398	11786.7	11439.2	11087.9	8143.2	13590.3	12337.6
AJ633996.1	114809	1379.9	2073.2	3124.9	1699.8	2828.7	3390.9
DQ357745.1	149148	130.3	230.2	1418.6	575.9	1076.1	921.6
FJ716889.1	549008	10491.5	10983.3	14263.5	9061.9	13623.1	11235.8
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D88526.1 gg_id:5714 Ruegeria atlantica str. IAM14463
FJ403081.1 gg_id:369403 Disease- changes healthy and diseased colonies Caribbean coral Montastrea faveolat
EU195952.1 gg_id:251321 Roseobacter sp. str. P123
DQ917807.1 gg_id:220204 Microbial profiles bleached and wild-type Muricea elongata Oleiphilus clone BME10
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DQ917855.1 gg_id:223353 Microbial profiles bleached and wild-type Muricea elongata Ruegeria clone ME108
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EU907925.1 gg_id:328931 Ruegeria sp. str. SKUK MB1010
U58356.1 gg_id:5685 Sagittula stellata
AJ557871.1 gg_id:84036 Arctic deep sea Isolation common chemoorganotrophic oxygen-respiring polar current
FJ425632.1 gg_id:362713 communnities healthy and diseased colonies Caribbean coral Montastrea faveolata S
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AJ534237.1 gg_id:75228 Sulfitobacter sp. LM-16
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AY771778.1 gg_id:144788 Arctic Sulfitobacter brevis clone SE96
EU919845.1 gg_id:315930 Kongsfjorden western Spitsbergen Svalbard ocean water clone s81
GU061088.1 gg_id:593911 Evaluation culturing methods cultivate previously Yel Sea intertidal beach clone TFS-

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EU195952.1	251321	107.6	241.2	231.5	139.6	192.2	186.5
DQ917807.1	220204	3261.7	3961.4	5342.1	4630.8	9443.5	8319.2
FJ203260.1	346584	4080.5	7086.1	6856.4	4620.6	4347.6	8526.1
AM709702.1	256402	2062.3	2932.5	3245.7	2601.1	4046.1	4049.0
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GQ391987.1	522785	1614.1	2061.0	5638.4	3266.7	3721.8	3309.5
FJ203147.1	315763	150.5	195.5	504.0	276.8	313.5	1147.6
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DQ915638.1 gg_id:316408 Thalassobacter stenotrophicus str. CECT5294
AB121783.1 gg_id:104544 Jannaschia cystaugens str. CFPB-A5
AJ631302.1 gg_id:109582 Thalassobacter stenotrophicus str. CECT 5294 = 5SM22
DQ915639.1 gg_id:315323 Thalassobius gelatinovorus str. NBRC15761
AJ878874.1 gg_id:142415 Thalassobius mediterraneus str. CECT 5383 = XSM19
FJ202550.1 gg_id:341164 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k
AJ968650.1 gg_id:143564 Roseovarius pelophilus str. G5II
AF114484.2 gg_id:5704 CVSP isolate str. CV919-312
EU236364.1 gg_id:297563 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg91D8
FJ203176.1 gg_id:337783 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c
FJ203129.1 gg_id:341596 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c
DQ376573.1 gg_id:152175 Microbial ecology removing phosphate wastewater EBPR process aerobic sequencin
EF540436.1 gg_id:220130 oil-shale semi-coke solid waste clone PK_V
DQ640665.1 gg_id:233567 full-scale EBPR sludge clone Skagenf58
EU979473.1 gg_id:344892 Rhodobacter sp. str. CR07-5
AM403212.1 gg_id:163121 Nitrate-reducing and Denitrifying Marine Aqua Biofilter marine aqua
EF205262.1 gg_id:188150 Paracoccus sp. 'CJSPY1 (P-I)' str. CJSPY1 (P-I)
FJ872532.2 gg_id:593437 Rhodobacter sp. str. ZH15
AY656719.1 gg_id:99632 Thioclava pacifica str. TL2
AM745438.1 gg_id:243786 Rhodobacter maris str. JA276
AY914074.1 gg_id:114095 Rhodobacter sp. R-8
GQ355283.1 gg_id:593578 Thioclava sp. str. GT-5
FJ542826.1 gg_id:530503 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone A
AY172658.1 gg_id:77954 Rhodobacter sp. str. B-7005
AM408117.1 gg_id:186127 Rhodobacter vinaykumarii str. JA123
EF061947.1 gg_id:193660 Xiamen China mangrove sediment clone XME33
EU491911.1 gg_id:264288 Abundance and microbial life ocean crust deep seawater East Pacific Rise clone EPR4
FJ202842.1 gg_id:306401 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k
FJ497541.1 gg_id:586757 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun
GU220746.1 gg_id:591725 Microbial mineralization and involved microbial Basin field temperature hydrotherm
EU287008.1 gg_id:239638 Pacific arctic surface sediment clone B78-44
FJ905620.1 gg_id:568278 s Tonga-Kermadec iron oxide chimney-like structure on Volcano 19 Tonga Arc clone V
AF468367.2 gg_id:80906 Arctic sea ice ARK10115
EF573178.1 gg_id:231130 Coco's Island site 23 marine clone S23_1277
FJ905703.1 gg_id:552641 s Tonga-Kermadec iron oxide sediments Volcano 1 Tonga Arc clone V1F23b

DQ097527.1	132683	283.3	321.6	623.3	185.6	455.2	406.7
AJ534236.1	76438	2902.2	3096.3	3756.2	4191.4	5248.1	5731.7
DQ659417.1	166927	128.8	202.7	1249.2	173.2	1012.4	966.2
GU061005.1	572128	121.2	189.5	179.5	117.1	160.1	275.1
AY690671.1	107730	224.5	336.0	1410.8	224.0	1007.9	1092.6
AB121782.1	104397	6660.2	6938.6	4652.7	6331.4	14586.3	10044.9
DQ915638.1	316408	2639.7	3203.7	2409.8	3408.7	5625.8	4478.3
AB121783.1	104544	1004.6	1267.1	801.5	1947.6	3594.8	2358.6
AJ631302.1	109582	5830.5	6949.8	4245.1	6838.4	14479.1	10359.6
DQ915639.1	315323	111.8	216.4	1419.9	131.2	352.2	229.1
AJ878874.1	142415	2133.3	1150.8	1611.8	1202.2	2077.0	1791.0
FJ202550.1	341164	11557.1	8350.5	10535.9	6621.5	10038.7	7923.9
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AF114484.2	5704	2648.3	2330.7	1463.2	1766.8	3176.2	2381.8
EU236364.1	297563	724.1	1109.1	1878.9	1027.3	1267.2	1842.3
FJ203176.1	337783	28.2	107.6	264.7	46.7	55.1	154.4
FJ203129.1	341596	580.7	521.3	1400.2	488.0	2867.9	2205.5
DQ376573.1	152175	1898.7	4094.7	2030.6	3940.3	10174.1	9431.4
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DQ640665.1	233567	1800.0	3072.0	2785.5	3347.6	5044.6	7041.3
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AM403212.1	163121	858.3	2051.1	2129.7	2962.1	4457.9	5912.2
EF205262.1	188150	468.7	1320.4	4208.7	3092.1	600.3	3121.8
FJ872532.2	593437	473.8	839.4	2076.6	1757.3	1298.5	4986.0
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GQ355283.1	593578	325.7	577.0	1674.9	1138.0	2969.0	1439.4
FJ542826.1	530503	657.0	1743.7	1468.5	657.5	3554.5	5824.7
AY172658.1	77954	8033.0	8338.4	7633.6	6353.2	7056.2	8729.6
AM408117.1	186127	1539.4	3206.2	7667.4	3566.2	8910.1	18138.8
EF061947.1	193660	1597.4	3053.5	2522.6	3134.6	4721.8	4089.7
EU491911.1	264288	3538.1	4572.8	4578.3	3835.2	7557.3	5905.7
FJ202842.1	306401	4234.6	3674.6	3839.7	6270.5	6700.8	7546.9
FJ497541.1	586757	5047.1	5528.2	4145.7	3797.7	5403.7	5508.1
GU220746.1	591725	2365.6	1713.5	4273.0	7492.0	2106.8	4091.0
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AF468367.2	80906	351.1	413.2	514.6	480.7	739.2	1973.3
EF573178.1	231130	1000.4	3391.8	3835.4	4527.2	5611.5	10203.9
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AB476208.1 gg_id:541086 Compositional and functional transition epibiotic microbial hydrothermal vent galath
DQ270648.1 gg_id:141449 hydrothermal carbonate chimney clone LC1133B-90
FJ497658.1 gg_id:584890 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun
AB476190.1 gg_id:558885 Compositional and functional transition epibiotic microbial hydrothermal vent galath
FJ497592.1 gg_id:556056 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun
AY922245.1 gg_id:113571 whalefall clone 131839
FJ712530.1 gg_id:528280 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) K
FJ997596.1 gg_id:417573 Jannaschia sp. str. KYW137
GU061174.1 gg_id:542278 Evaluation culturing methods cultivate previously Yel Sea intertidal beach surface se
EU652595.1 gg_id:278420 Seasonal variation microbial Yel Sea sediment clone D8S-60
EU919756.1 gg_id:336543 Kongsfjorden western Spitsbergen Svalbard ocean water clone b9
FJ497563.1 gg_id:586645 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun
AM997674.1 gg_id:545505 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A
GU061093.1 gg_id:584111 Evaluation culturing methods cultivate previously Yel Sea intertidal beach clone TFS-
AY794100.1 gg_id:109050 soil clone F2C01
GU119343.1 gg_id:536065 Threatened Corals Provide Microbial Habitats reef water clone Reef_C17
FJ202553.1 gg_id:341986 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k
DQ103611.1 gg_id:135996 hypersaline endoevaporitic microbial mat clone E6bF01
AM745160.1 gg_id:296724 Impact oil er hydrocarbons on microbial and activity Gulf Mexico cold seep marine s
EU143368.1 gg_id:258074 Thalassobius sp. str. J86
AY573044.1 gg_id:106356 Roseobacter sp. str. ARCTIC-P4
AF468276.1 gg_id:80486 Arctic pack ice; northern Fram Strait; 80 31.1 N; 01 deg 59.7 min E clone ARKIA-77
AB355073.1 gg_id:242934 Monitoring and archaeal two heavy polluted areas lake Egypt based on sediment Ma
DQ167248.1 gg_id:138930 Pseudoroseobacter euryhalinus str. KOPRI 13595
FJ196006.1 gg_id:351622 Rhodobacter sp. str. ZS2-28
GQ349620.1 gg_id:539973 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
FJ203199.1 gg_id:342707 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c
DQ395756.1 gg_id:154523 deep-sea octacoral clone ctg_CGOF276
FJ153021.1 gg_id:308558 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX4CE
FJ230833.2 gg_id:310112 Citricella sp. ADB str. AD8
FJ152760.1 gg_id:316923 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX5A_
FJ516861.1 gg_id:562114 semiarid 'Tablas de Daimiel National Park' wetland (Central Spain) unravelled lower s
AJ534233.1 gg_id:75623 Staleya sp. LM-7
AJ534210.1 gg_id:76632 Sulfitobacter sp. DFL-10
AF473921.1 gg_id:41652 template extracted Diploria strigosa with BBD clone 128-27L proteobacterium
AF254109.1 gg_id:55371 hydrothermal vent strain str. TB66
AY862771.2 gg_id:160768 prokaryotic genetic Salar de Atacama Northern Chile athalassohaline lake water clon
AJ534232.1 gg_id:75166 Staleya sp. LM-4
EU156067.1 gg_id:257910 Jannaschia seohaensis str. SMK-146
FJ623372.1 gg_id:591092 Efficient polyhydroxyalkanoates production waste-activated submitted process seque
EU564842.1 gg_id:264951 Rhodovulum sp. str. CC-MHSW-4

AB476208.1	541086	694.7	1084.9	2140.7	3109.1	1051.5	3436.3
DQ270648.1	141449	2156.1	3453.2	6803.9	4377.0	2807.0	4453.6
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AB476190.1	558885	5459.3	7928.1	6790.6	4881.1	7944.0	8240.8
FJ497592.1	556056	2386.9	3780.1	2433.0	2442.2	6654.3	4265.3
AY922245.1	113571	2021.5	2584.6	3974.4	2878.2	3312.3	3337.9
FJ712530.1	528280	3977.0	3218.3	3377.7	3822.0	2530.3	3958.3
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GU061174.1	542278	1877.0	2309.3	2405.7	2970.8	3796.2	4085.0
EU652595.1	278420	1143.1	1364.5	1286.2	332.7	1234.9	1805.7
EU919756.1	336543	124.0	234.9	288.9	361.8	323.0	484.9
FJ497563.1	586645	5032.4	4314.7	3358.8	4358.2	4503.2	8809.3
AM997674.1	545505	16149.8	16999.3	11819.5	13780.4	20933.6	18452.8
GU061093.1	584111	196.4	540.9	780.5	423.7	428.0	259.7
AY794100.1	109050	685.9	889.8	1176.6	507.2	1874.2	1174.8
GU119343.1	536065	8874.6	8156.8	6154.5	6664.7	8578.2	8332.7
FJ202553.1	341986	507.4	1042.0	781.9	818.0	4429.1	1648.0
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AM745160.1	296724	539.6	1498.1	1456.8	1285.9	3550.5	3683.9
EU143368.1	258074	1392.4	2071.3	1625.7	1833.9	3610.1	2025.1
AY573044.1	106356	278.8	759.3	421.7	451.3	1545.7	1960.9
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AB355073.1	242934	186.8	294.7	546.3	1056.6	245.9	685.8
DQ167248.1	138930	924.8	2610.8	5414.8	3369.6	2615.3	4369.4
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GQ349620.1	539973	1500.4	3097.3	5239.5	3997.1	4105.6	3924.7
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DQ395756.1	154523	3356.2	3143.6	3952.6	8021.4	5707.6	7606.0
FJ153021.1	308558	8287.2	11367.4	15023.2	10786.3	13724.8	14441.9
FJ230833.2	310112	3556.8	3944.4	2503.0	2639.6	6498.2	4818.3
FJ152760.1	316923	703.2	1854.6	1756.8	2361.7	1798.9	3520.3
FJ516861.1	562114	1906.3	3287.4	3623.4	2888.2	4605.1	5352.7
AJ534233.1	75623	3395.9	3835.3	3200.7	3428.5	5545.8	1842.4
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EU564842.1	264951	1742.0	2710.9	2658.6	2635.4	1697.2	2414.5

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DQ001322.1 gg_id:115461 Pseudorhodobacter incheonensis str. KOPRI 13537
AM911350.1 gg_id:359759 Phenotype-specific (Scleractinia) their implications coral's nutrition health and cold-
DQ395796.1 gg_id:153730 deep-sea octacoral clone ctg_CGOF245
FJ152917.1 gg_id:310932 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX4CI
FJ203141.1 gg_id:347865 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c
FM242431.1 gg_id:346708 sequences sediment clone 17 T12d-oil
AF353234.1 gg_id:45295 marine clone Arctic96A-8
FJ889529.1 gg_id:560186 Sulfitobacter sp. str. KS8-4
FJ202949.1 gg_id:340342 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k
GU061063.1 gg_id:543382 Evaluation culturing methods cultivate previously Yel Sea intertidal beach clone TFS-
FM958454.1 gg_id:535414 situ detection (Hippocampus guttulatus) intestinal content and mucus farmed seahc
DQ915635.1 gg_id:308648 Sulfitobacter dubius str. LMG20555
DQ915629.1 gg_id:305904 Salipiger mucosus str. LMG22090
EU491858.1 gg_id:272287 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39
FJ202508.1 gg_id:341377 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k
AJ002565.1 gg_id:5632 Marine (isolate SRF3) clone
FJ202423.1 gg_id:345716 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k
DQ103627.1 gg_id:135997 hypersaline endoevaporitic microbial mat clone E4aC05
AJ002563.1 gg_id:25112 Marine (isolate SRF1) clone
AF365993.1 gg_id:29620 marine str. BBAT2
AF098494.1 gg_id:5645 Sulfitobacter sp. str. GAI-109
EF202614.1 gg_id:202204 Sulfitobacter donghicola str. DSW-25
EU573104.1 gg_id:277995 and Dependent Microbial Oil Reservoir North Sea Ekofisk oil field Norwegian sector c
AY654818.1 gg_id:99671 Oculina mucus isolate 80
FJ202330.1 gg_id:348420 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k
AB266065.2 gg_id:170549 Citreicella sp. str. 2-2A
GU061006.1 gg_id:564192 Evaluation culturing methods cultivate previously Yel Sea intertidal beach clone SF7!
AF513400.1 gg_id:69921 Rhodobacter sp. str. 1-5
FJ203661.1 gg_id:307998 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h
EU544713.1 gg_id:277244 free-living particle- aggregate- archaeal and Laptev Sea 0.22-1.0 um size fraction (fre
AY162098.1 gg_id:135249 Cultivating Sargasso Sea clone GMD21H11
DQ517132.1 gg_id:159870 Cultivation-intensive study ephemeral hypereutrophic aquatic microbial Mojave Des
EU236329.1 gg_id:301814 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg5a1F11
AY007684.1 gg_id:41631 marine isolate JP88.1
DQ856513.1 gg_id:245016 intestinal microflora Chinese mitten crab (Eriocheir sinensis) clone C1T
AY770942.1 gg_id:108310 water injection well Dagang oilfield clone W2
AY922214.1 gg_id:112728 whalefall clone 131693
AF468376.1 gg_id:79810 Arctic sea ice ARK10233
GU061139.1 gg_id:584007 Evaluation culturing methods cultivate previously Yel Sea intertidal beach clone SF33
AB491855.1 gg_id:562026 affiliation (Litopenaeus vannamei) Banyuwangi East Java microbial flocs floating brac
GU118249.1 gg_id:592387 Threatened Corals Provide Microbial Habitats clone Dstr_B07

DQ001322.1	115461	2094.7	2342.5	1518.6	2598.4	3935.9	4524.8
AM911350.1	359759	201.8	495.5	2174.5	1037.3	649.1	916.3
DQ395796.1	153730	586.0	1912.9	2577.3	1863.2	3389.0	2379.3
FJ152917.1	310932	909.4	1416.3	2710.8	729.8	2048.2	3019.6
FJ203141.1	347865	182.0	393.3	1683.3	1035.6	206.8	1249.4
FM242431.1	346708	246.0	633.7	390.3	197.2	447.9	197.1
AF353234.1	45295	1367.1	2229.2	1759.6	1595.5	2592.2	2768.1
FJ889529.1	560186	776.8	707.8	561.8	974.3	2331.7	2354.8
FJ202949.1	340342	1773.0	3035.8	2389.2	3668.7	6701.5	6211.4
GU061063.1	543382	1407.3	4684.3	1125.2	1828.0	2698.1	3958.4
FM958454.1	535414	432.5	656.2	302.7	418.8	751.0	281.9
DQ915635.1	308648	515.6	1134.8	2926.9	1374.0	3183.1	2986.6
DQ915629.1	305904	401.6	1038.5	2245.1	2132.5	116.5	524.5
EU491858.1	272287	4553.3	4868.5	4228.3	4388.7	6248.1	7344.8
FJ202508.1	341377	2954.1	3756.5	3104.6	5550.7	3856.2	6500.5
AJ002565.1	5632	815.5	2084.1	1809.3	1404.2	2504.6	6324.2
FJ202423.1	345716	2558.5	4859.0	1959.1	2326.9	6829.8	4825.3
DQ103627.1	135997	263.2	1021.9	817.2	1207.9	760.1	1077.8
AJ002563.1	25112	17.1	46.1	50.0	159.6	53.8	61.0
AF365993.1	29620	198.6	425.2	734.2	198.4	194.1	304.7
AF098494.1	5645	449.7	942.6	886.7	846.7	1251.9	1308.6
EF202614.1	202204	544.9	543.6	529.3	837.8	1231.6	1436.1
EU573104.1	277995	58.2	96.0	243.8	224.6	427.9	245.9
AY654818.1	99671	29.9	126.6	53.8	66.6	324.0	294.3
FJ202330.1	348420	1154.6	2534.1	1716.0	2240.3	1393.0	1873.1
AB266065.2	170549	1206.0	1657.3	1420.5	2464.4	2105.4	2494.1
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AF513400.1	69921	145.0	491.6	706.9	277.7	425.4	1141.6
FJ203661.1	307998	2620.4	3353.6	2480.3	2604.4	4902.6	4339.7
EU544713.1	277244	1466.4	1551.4	5882.6	1442.0	4390.8	4427.7
AY162098.1	135249	1473.0	1311.1	1975.8	1680.1	5326.9	4375.0
DQ517132.1	159870	1815.4	3051.0	8456.2	5375.5	4455.5	9828.8
EU236329.1	301814	569.5	843.7	1950.3	1277.6	2318.3	1260.0
AY007684.1	41631	370.3	425.2	1619.0	1113.4	98.3	1200.9
DQ856513.1	245016	3783.5	4280.6	6480.9	6626.4	2931.0	5265.8
AY770942.1	108310	1431.6	2265.4	4965.4	6824.9	603.1	4528.0
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GQ232737.2 gg_id:548120 Phaeobacter sp. str. G4
FJ973591.1 gg_id:451932 Periodic sulfide irruptions impact microbial structure and hypersaline lake water colu
DQ103619.1 gg_id:133336 hypersaline endoevaporitic microbial mat clone E6aG08
AAYC01000011.1 gg_id:215094 Roseobacter sp. str. SK209-2-6
FJ202158.1 gg_id:306945 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k
DQ395522.1 gg_id:152925 deep-sea octacoral clone ctg_CGOCA28
DQ015795.1 gg_id:140619 Antarctic lake water clone ELB16-005
AB114421.1 gg_id:104479 Roseovarius sp. str. S6V
AY682197.1 gg_id:103418 Sulfitobacter sp. str. KMM 3457
EF646118.1 gg_id:240900 Potential interactions particle- anammox and archaeal partners namibian Namibian u
DQ856529.1 gg_id:245982 intestinal microflora Chinese mitten crab (Eriocheir sinensis) clone C2J
EF123343.1 gg_id:249977 Microbial disease microbial mats on Siderastrea siderea three regions wider Caribbea
AJ968647.1 gg_id:144272 Roseobacter sp. str. N05I
AY701455.1 gg_id:108540 dinoflagellate symbiont clone GCHU11_G
GU061043.1 gg_id:568665 Evaluation culturing methods cultivate previously Yel Sea intertidal beach clone Mix-
FJ516790.1 gg_id:575915 semiarid 'Tablas de Daimiel National Park' wetland (Central Spain) unravelled biofilm
AY697879.1 gg_id:100581 Antarctica clone F2C25
AF235129.1 gg_id:39391 North Sea clone KTc0993
EU464692.1 gg_id:296206 Hartmann's mountain zebra feces clone AFZEB_aaj69c08
EF659442.1 gg_id:247277 within Poole Harbour seawater clone PH-A6
AM930445.1 gg_id:268773 involved Tripneustes gratilla (Echinoidea) cloning and FISH host body wall lesions cl
AF507828.1 gg_id:62731 Mono Lake at depth 35 m station 6 July 2000 clone ML635J-2 proteobacterium
AM697339.1 gg_id:220866 sequencing libraries indoor dust clone BF0002C036
FJ437982.1 gg_id:542595 Benthic okenone production Fayetteville New York Green Lake surface sediments 16.
AJ633963.1 gg_id:114571 host's accessory nidamental gland clone T63ANG236
AJ534243.1 gg_id:76030 Sulfitobacter sp. PIC-76
DQ915443.3 gg_id:168588 Maritimibacter alkaliphilus str. HTCC2654
AY862758.2 gg_id:161659 prokaryotic genetic Salar de Atacama Northern Chile athalassohaline lake water clon
CU467448.1 gg_id:313991 Prokaryotic Tunisian saltern Saltern solar multipond clone
GU117994.1 gg_id:591140 Threatened Corals Provide Microbial Habitats clone Acer_I13
FJ403075.1 gg_id:356799 Disease- changes healthy and diseased colonies Caribbean coral Montastrea faveolat
FJ202782.1 gg_id:315498 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k
FJ716900.1 gg_id:575317 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United King
FJ202529.1 gg_id:318405 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k
FJ202470.1 gg_id:321216 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k
FJ222605.1 gg_id:350516 Albidovulum sp. str. S1K1
GQ433928.1 gg_id:560840 Subseafloor ocean crust microbial observatories: (F-through Osmo Colonization Syst
GU118103.1 gg_id:532669 Threatened Corals Provide Microbial Habitats clone Apal_O05
EF123406.1 gg_id:251365 Microbial disease microbial mats on Siderastrea siderea three regions wider Caribbea
Y15011.1 gg_id:5826 Rhodovulum iodosum str. N1

FJ801189.1	571663	1840.1	3454.4	6260.0	7454.8	4723.3	7889.3
GQ232737.2	548120	37.4	69.1	243.2	61.5	75.2	148.8
FJ973591.1	451932	3142.5	4082.4	4868.9	5728.9	3842.1	3977.4
DQ103619.1	133336	529.0	1006.7	981.2	793.5	658.8	2393.9
AAYC01000011.1	215094	327.7	389.6	1056.1	409.4	407.1	422.2
FJ202158.1	306945	2412.2	1038.6	2096.1	2597.0	2086.4	1515.7
DQ395522.1	152925	867.7	1431.3	4460.6	2177.3	3229.9	5671.2
DQ015795.1	140619	448.9	595.2	1708.3	1306.3	1346.2	2008.6
AB114421.1	104479	4788.2	7089.8	11800.1	9620.3	10676.4	11771.8
AY682197.1	103418	997.7	1628.9	3494.6	2355.7	3583.8	3779.4
EF646118.1	240900	3270.6	3229.7	6506.1	3053.0	9412.1	6707.1
DQ856529.1	245982	7796.3	9039.6	10155.1	11448.1	14675.3	12317.8
EF123343.1	249977	2810.5	2055.0	5516.6	5751.2	2956.9	3688.3
AJ968647.1	144272	411.7	1334.1	1847.5	1091.7	1814.5	2312.5
AY701455.1	108540	5162.2	7165.5	7322.5	6190.3	8330.8	8010.9
GU061043.1	568665	664.3	908.8	1386.6	1112.2	1450.7	1292.9
FJ516790.1	575915	2359.3	4303.6	4106.7	3941.4	8678.5	7323.6
AY697879.1	100581	75.1	186.2	546.4	177.3	194.6	341.2
AF235129.1	39391	4695.7	6223.3	5079.8	3327.8	12583.5	7703.7
EU464692.1	296206	106.5	235.0	157.7	251.1	148.7	746.9
EF659442.1	247277	8446.3	8074.7	8763.1	9599.8	11469.7	8681.0
AM930445.1	268773	10000.2	10891.2	8504.9	6299.9	9742.8	8162.5
AF507828.1	62731	1927.8	2239.0	2272.7	1407.2	2664.2	2614.4
AM697339.1	220866	1457.1	3378.4	5441.6	2562.3	3402.9	7863.5
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DQ915443.3	168588	188.6	248.2	696.0	117.9	1077.3	455.0
AY862758.2	161659	62.6	104.7	146.5	144.7	381.0	1450.6
CU467448.1	313991	962.3	1695.1	2249.4	2384.1	4605.2	2945.5
GU117994.1	591140	303.9	483.4	746.7	837.1	1265.5	3305.9
FJ403075.1	356799	10580.4	11008.3	7848.7	7482.9	10298.8	8952.1
FJ202782.1	315498	10801.0	10444.6	5704.0	10664.0	11064.5	9626.1
FJ716900.1	575317	2868.9	3816.3	3613.9	5005.7	8207.8	6729.2
FJ202529.1	318405	299.1	222.8	74.1	167.4	868.1	477.8
FJ202470.1	321216	9383.5	9034.5	8845.8	10009.0	13355.4	11161.0
FJ222605.1	350516	6955.4	8415.1	10426.5	6697.8	16829.8	13846.0
GQ433928.1	560840	21398.5	18934.8	15748.8	16817.2	22987.0	18668.8
GU118103.1	532669	1581.8	2905.4	5505.2	2237.9	5662.9	4925.8
EF123406.1	251365	1331.2	1500.8	4240.7	2424.9	2568.6	4696.3
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EU491925.1 gg_id:268669 Abundance and microbial life ocean crust deep seawater East Pacific Rise clone EPR4
GU061120.1 gg_id:532672 Evaluation culturing methods cultivate previously Yel Sea intertidal beach clone YAF-
AJ294354.1 gg_id:46595 Roseobacter isolate 667-4 clone
EU246237.1 gg_id:257864 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-P5-F08
DQ234221.2 gg_id:142932 determined library mangrove clone DS139
EU236288.1 gg_id:297968 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone HgCo15
EF648144.1 gg_id:239526 dynamics during produced water treatment aerobic activated sludge clone XJ91
DQ372842.1 gg_id:153431 Pirellula and OM43 are among dominant lineages identified Oregon coast diatom bl
EU799185.1 gg_id:320827 It's all ranking aquatic Newport Harbour RI clone 1C226756
GU061099.1 gg_id:584882 Evaluation culturing methods cultivate previously Yel Sea intertidal beach clone TFS-
GU118238.1 gg_id:538100 Threatened Corals Provide Microbial Habitats clone Dstr_A04
DQ860070.1 gg_id:165645 Symbiotic aerobic anoxygenic phototrophic colonial tunicate clone L16
DQ659411.1 gg_id:168003 Roseobacter sp. str. B11
FJ516820.1 gg_id:548219 semiarid 'Tablas de Daimiel National Park' wetland (Central Spain) unravelled biofilm
FJ203293.1 gg_id:333321 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c
DQ856523.1 gg_id:257325 intestinal microflora Chinese mitten crab (Eriocheir sinensis) clone C2L
EF646123.1 gg_id:251424 Potential interactions particle- anammox and archaeal partners namibian Namibian u
EU573108.1 gg_id:279211 and Dependent Microbial Oil Reservoir North Sea Ekofisk oil field Norwegian sector c
FJ203568.1 gg_id:352275 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h
AY926462.1 gg_id:113266 Roseobacterium hispanicus str. B-33
FJ202177.1 gg_id:355194 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k
FJ976449.2 gg_id:548736 Shimia sp. str. SW-6
AB476254.1 gg_id:564346 Compositional and functional transition epibiotic microbial hydrothermal vent galath
DQ811851.1 gg_id:165140 mangrove soil clone MSB-3B6
EU336981.1 gg_id:240704 Saemankumia lutimaris str. SMK-117
EF632664.1 gg_id:245725 Unique microbial contrasting aquatic altitude Andean Altiplano (northern Chile) sedir
AY845238.1 gg_id:110731 sponge clone 310P14
DQ009316.1 gg_id:123474 bacterioplankton clone SPOTSAPR01_5m244
EU195951.1 gg_id:257413 Roseobacter sp. str. P81
FJ497575.1 gg_id:590937 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun
FJ203659.1 gg_id:336186 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h
AY794174.1 gg_id:109121 soil clone F3C91
FJ973603.1 gg_id:397618 Periodic sulfide irruptions impact microbial structure and hypersaline lake water colu
NR_026472.1 gg_id:567431 Sulfitobacter mediterraneus str. CH-B427; DSM 12244
GU118899.1 gg_id:553131 Threatened Corals Provide Microbial Habitats clone Past_G06
DQ357735.1 gg_id:145906 Marine Hatchery: Balance Between Pathogenic and Potentially Probiotic Strains sea
FM180527.1 gg_id:323927 Roseovarius aestuarii str. B13
EU799662.1 gg_id:310648 It's all ranking aquatic Newport Harbour RI clone 1C227285
FJ716861.1 gg_id:542437 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United King
AM990873.1 gg_id:278099 Structure and functions coastal NW Mediterranean ecosystem sea water
GQ359327.1 gg_id:556328 Oceanicola sp. str. YCWB25

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EU246237.1	257864	501.9	1084.4	1231.6	1135.2	4985.4	6746.7
DQ234221.2	142932	208.7	305.4	491.2	353.4	187.0	306.8
EU236288.1	297968	1589.9	2818.9	1742.2	3047.3	4010.9	6233.8
EF648144.1	239526	3738.3	5089.6	7025.1	4609.0	8876.5	8425.8
DQ372842.1	153431	2989.9	3943.4	2418.5	3587.1	6726.3	4140.7
EU799185.1	320827	109.8	196.6	436.7	133.6	351.0	634.9
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GU118238.1	538100	2440.5	3056.4	2281.4	2884.8	5208.1	5516.5
DQ860070.1	165645	1974.8	3018.7	2643.9	3556.6	7687.4	6302.9
DQ659411.1	168003	639.0	1174.0	368.4	1160.6	654.0	765.4
FJ516820.1	548219	1738.0	2344.8	1339.8	4086.8	5159.0	5429.6
FJ203293.1	333321	7525.8	9087.3	4581.0	5782.5	13011.8	8863.6
DQ856523.1	257325	2848.7	3505.5	2560.6	4349.9	5153.5	4993.3
EF646123.1	251424	95.8	100.0	86.5	345.0	75.1	151.3
EU573108.1	279211	172.5	240.9	238.3	325.9	542.9	480.9
FJ203568.1	352275	185.2	292.3	187.8	288.8	58.7	296.3
AY926462.1	113266	2001.1	2629.9	2659.6	3943.5	3178.2	2888.4
FJ202177.1	355194	344.3	934.5	1066.6	1426.9	2730.6	849.0
FJ976449.2	548736	3630.3	2828.0	5721.5	2587.2	4736.7	4414.1
AB476254.1	564346	82.3	115.9	581.8	133.4	280.8	304.8
DQ811851.1	165140	4020.6	6249.4	5730.8	5374.3	6569.3	8735.4
EU336981.1	240704	295.9	841.1	1277.0	370.6	769.2	1006.3
EF632664.1	245725	2421.6	3447.9	2374.5	3826.4	4064.4	4685.1
AY845238.1	110731	1037.3	1981.6	4244.0	2665.9	4365.5	6290.8
DQ009316.1	123474	105.3	305.1	231.5	99.0	1446.6	605.7
EU195951.1	257413	212.5	562.5	1142.4	341.0	886.4	1367.8
FJ497575.1	590937	779.9	1967.6	2106.2	1510.4	1044.6	2504.2
FJ203659.1	336186	961.3	1564.8	1583.2	1590.3	2900.0	2297.1
AY794174.1	109121	229.1	335.9	442.5	250.0	1240.2	1558.7
FJ973603.1	397618	1730.1	3146.9	2688.1	2493.7	11144.9	12258.5
NR_026472.1	567431	2736.8	3084.9	3842.6	3450.1	5314.5	4625.7
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FM180527.1	323927	3651.5	4169.8	6984.7	3934.2	6755.1	6628.9
EU799662.1	310648	567.6	1364.9	1254.5	2476.8	2895.5	6435.6
FJ716861.1	542437	512.6	950.2	2166.6	638.2	3349.4	2623.4
AM990873.1	278099	1712.1	1513.5	1275.9	1546.9	2570.0	2884.8
GQ359327.1	556328	1691.6	2563.3	3752.6	3363.5	2965.5	4896.5

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X78312.1 gg_id:5644 Roseobacter litoralis str. ATCC 49566
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DQ925858.1 gg_id:165917 and marine microorganisms Antarctic sea water clone ANT40B10
FJ516768.1 gg_id:545124 semiarid 'Tablas de Daimiel National Park' wetland (Central Spain) unravelled biofilm
AY258088.1 gg_id:135761 Roseobacter sp. str. DG942
AY845236.1 gg_id:111182 sponge clone 33P7
AY936186.1 gg_id:113980 Rhodobacteraceae clone F2C02
DQ432370.1 gg_id:156995 prokaryotic alkaline hypersaline lakes Wadi Natrun Egypt Lake Hamra water clone W
FJ203264.1 gg_id:306783 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c
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EF648060.1 gg_id:251297 dynamics during produced water treatment aerobic activated sludge clone HB53
AM930444.1 gg_id:272692 involved Tripneustes gratilla (Echinoidea) cloning and FISH host body wall lesions clc
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FJ826135.1 gg_id:534609 Succession during spring Sea filtered surface sea water decay period after diatom blo
FJ202682.1 gg_id:306222 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k
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EF016462.1 gg_id:182573 Near real-time autonomous detection marine on coastal mooring Monterey Bay Calif
EU592337.1 gg_id:535793 Seasonal changes Salton Sea hypersaline water clone SSW5Ap
EU016198.1 gg_id:252028 Antarcticicola litoralis str. IMCC3295
DQ917848.1 gg_id:221374 Microbial profiles bleached and wild-type Muricea elongata Roseobacter clone BME
FJ403109.1 gg_id:359190 Disease- changes healthy and diseased colonies Caribbean coral Montastrea faveolat
AY349460.1 gg_id:91740 Roseobacter sp. WHOI JT-08
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EF549587.1 gg_id:240979 Pseudoruegeria indica str. P73
FJ716847.1 gg_id:554517 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United Kingc
EF471665.1 gg_id:276906 Fast Screening and Estuarine Operon Libraries whole surface water Chesapeake Bay
EU073791.1 gg_id:252125 Microbial subsurface beds and methanogenic enrichment s coal clone SH2B-1C
DQ280370.1 gg_id:141539 Paracoccus sp. str. DS2
EU488233.1 gg_id:556227 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and
DQ146982.1 gg_id:150257 Vibrio sp. str. V261
AY162112.1 gg_id:135282 Cultivating Sargasso Sea clone GMD13C04
GU061952.1 gg_id:577629 and function microbial mesoscale eddy perturbations South China Sea clone S-DCM-
AF473932.1 gg_id:50418 template extracted Diploria strigosa with BBD clone 128-47L proteobacterium
AY167262.1 gg_id:81992 Roseobacter sp. str. ANT9276a
FJ203083.1 gg_id:323475 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c
DQ395613.1 gg_id:152062 deep-sea octacoral clone ctg_CGOF244
AY690720.1 gg_id:106101 Pseudomonas sp. str. MK12

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AY845236.1	111182	1124.4	2572.4	1724.3	2248.8	5822.3	3025.4
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EU246273.1	257210	621.2	1267.2	2155.6	932.6	7376.9	7820.5
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EF016462.1	182573	9850.3	11520.6	9231.0	9637.8	10162.7	12565.1
EU592337.1	535793	2870.5	2379.7	2444.7	3164.9	4005.7	2874.8
EU016198.1	252028	3397.5	4878.8	5460.2	4512.9	10503.7	7348.8
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EU073791.1	252125	1642.1	3030.6	5602.9	4770.1	1597.2	4831.3
DQ280370.1	141539	352.0	584.2	1871.3	1469.6	2426.6	1211.0
EU488233.1	556227	1059.5	1947.7	2562.5	2397.3	1684.5	2320.0
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AF253467.1 gg_id:21303 Key aromatic-ring-cleaving enzyme protocatechuate 34-dioxygenase ecologically impc
FJ716902.1 gg_id:567191 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United Kingc
EF186075.1 gg_id:194746 Rhodobacter sp. str. DQ12-45T
AM691099.1 gg_id:221022 Rhodobacteraceae clone EG11
FJ973583.1 gg_id:427025 Periodic sulfide irruptions impact microbial structure and hypersaline lake water colu
AB294959.1 gg_id:222231 -dependent & analyses hydrothermal system off Taketomi Island Japan microbial ma
FJ203203.1 gg_id:348315 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c
FJ623308.1 gg_id:583673 Efficient polyhydroxyalkanoates production waste-activated submitted process seque
GQ451279.1 gg_id:548853 Fecal Yunnan snub-nosed monkey feces clone J274
DQ269086.1 gg_id:189161 marine macro-alga surface clone DPC189
EU431217.1 gg_id:264215 Roseovarius halotolerans str. HJ50
FJ155038.1 gg_id:305323 seasonal fluctuation coastal Bohai Bay sequencing and RFLP soil clone CC
EU287064.1 gg_id:240530 Pacific arctic surface sediment clone B78-100
GU118141.1 gg_id:576886 Threatened Corals Provide Microbial Habitats clone Apal_B15
DQ103616.1 gg_id:131552 hypersaline endoevaporitic microbial mat clone E4aB11
EF205473.1 gg_id:210036 among geographically regions central Tibet geothermal spring mat clone YCB80
DQ535898.1 gg_id:159839 Thalassobius aestuarii str. TF-212
FJ403106.1 gg_id:362198 Disease- changes healthy and diseased colonies Caribbean coral Montastrea faveolat
AM930417.1 gg_id:275915 involved Tripneustes gratilla (Echinoidea) cloning and FISH host body wall lesions clc
EF659446.1 gg_id:240011 within Poole Harbour seawater clone PH-B1
FJ516806.1 gg_id:513963 semiarid 'Tablas de Daimiel National Park' wetland (Central Spain) unravelled biofilm
FJ203288.1 gg_id:322400 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c
GU369891.1 gg_id:515404 and mats vents Arc white filamentous microbial mat photic shal hydrothermal vent
AM696698.1 gg_id:217239 Rhodovulum adriaticum str. JA245
FJ202541.1 gg_id:311333 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k
AM888193.1 gg_id:237685 Rhodobacter sp. str. THWCSN29
EF092221.1 gg_id:262333 Persistent Axinella corrugata Roseobacter clone B255_A1h
AB473971.1 gg_id:568966 sequences microorganisms Alvaneu Bad sulfur containing freshwater spring clone AS
GQ441231.1 gg_id:577508 and dynamic mat present vs. active nitrogen-fixing microorganisms marine microbia
DQ521519.1 gg_id:184737 Antarctic lake ice cover clone ANTLV2_E06
DQ432231.1 gg_id:156862 prokaryotic alkaline hypersaline lakes Wadi Natrun Egypt Lake UmRisha sediment cl
AY214344.1 gg_id:82177 Rhodovulum sp. A_wp02224
EU342372.1 gg_id:261363 Thalassobacter sp. str. GA2-M15
DQ836762.1 gg_id:169231 attached biomass denitrifying bioreactor clone DB-89
EU978825.1 gg_id:591654 and metabolic potential metagenome glacier ice clone glb337c
FJ425647.1 gg_id:364960 communnities healthy and diseased colonies Caribbean coral Montastrea faveolata R
FJ592545.1 gg_id:549666 Fumarole-supported islands biodiversity within hyperarid -elevation landscape on Pu
DQ811852.1 gg_id:163280 mangrove soil clone MSB-3E12
FJ202586.1 gg_id:310049 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k
FJ943236.1 gg_id:546187 Ponticoccus sp. IMCC5002 str. IMCC 5002
AM990868.1 gg_id:279616 Structure and functions coastal NW Mediterranean ecosystem sea water

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AB294959.1	222231	236.6	417.3	551.4	814.7	273.7	1123.0
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EF205473.1	210036	177.0	380.5	698.8	360.6	1171.3	758.7
DQ535898.1	159839	5264.6	3197.7	4280.5	2910.3	6754.5	5711.5
FJ403106.1	362198	214.1	275.2	673.1	313.2	334.9	266.1
AM930417.1	275915	293.2	507.1	469.2	1379.7	157.9	169.8
EF659446.1	240011	6236.8	7044.6	3671.7	7462.6	10803.4	9454.1
FJ516806.1	513963	5242.4	6790.2	7325.8	9546.7	11306.1	10555.7
FJ203288.1	322400	34.5	160.1	396.4	182.9	973.6	332.4
GU369891.1	515404	3629.3	1964.6	8167.4	1012.6	3067.5	2188.3
AM696698.1	217239	267.7	533.2	883.1	481.1	1519.8	2194.6
FJ202541.1	311333	1161.0	5190.9	6515.9	3977.9	10533.5	8287.2
AM888193.1	237685	1180.2	1979.3	1792.4	3185.7	3008.3	2626.6
EF092221.1	262333	131.5	509.3	907.8	722.9	1209.5	1249.6
AB473971.1	568966	5918.9	7297.7	6658.4	7584.6	12396.3	13288.7
GQ441231.1	577508	5710.7	8214.9	6024.8	7782.1	12920.3	12386.1
DQ521519.1	184737	3141.7	3988.2	5214.6	4245.6	6648.4	9938.3
DQ432231.1	156862	650.2	1968.2	1506.7	1761.9	1597.9	4639.9
AY214344.1	82177	1044.7	1434.8	2806.6	567.7	4692.1	5138.2
EU342372.1	261363	712.8	1262.8	1063.0	1681.1	2356.1	2046.6
DQ836762.1	169231	522.1	761.5	300.3	784.2	2462.8	1599.4
EU978825.1	591654	1771.7	3169.5	5204.0	5045.2	7931.8	5897.8
FJ425647.1	364960	979.0	1365.2	2321.3	679.3	1721.6	1911.2
FJ592545.1	549666	4028.9	7206.7	7083.5	6367.9	8994.9	8816.8
DQ811852.1	163280	1192.5	2011.6	2679.8	1191.1	2219.8	2432.4
FJ202586.1	310049	3450.1	3592.2	2453.4	5268.8	5537.3	7278.7
FJ943236.1	546187	534.4	2026.7	2608.0	572.6	2900.6	6457.3
AM990868.1	279616	60.9	433.2	606.0	766.0	3442.6	2032.1

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EU581832.1 gg_id:546740 Oceanicola sp. str. JLT1210
AF445668.1 gg_id:21491 travertine hot spring clone SM1C11
DQ836751.1 gg_id:170685 attached biomass denitrifying bioreactor clone DB-9
DQ223020.1 gg_id:140881 Roseobacter sp. str. UAzPsK-5
DQ153145.1 gg_id:139458 Structure Biofilms on Artificial Surfaces and Free-living Estuarine Seawater surface b
FJ516819.1 gg_id:559891 semiarid 'Tablas de Daimiel National Park' wetland (Central Spain) unravelled biofilm
GU118190.1 gg_id:537679 Threatened Corals Provide Microbial Habitats clone Dstr_M20
DQ071102.1 gg_id:135986 marine surface water clone SJC1.11
FJ210801.1 gg_id:354233 Roseobacter sp. str. QDHT-05
AM945586.1 gg_id:263307 Sulfitobacter sp. MOLA:356
AB491831.1 gg_id:572325 affiliation (Litopenaeus vannamei) Banyuwangi East Java microbial flocs floating brac
AY563033.1 gg_id:100625 Rhodobacter litoralis str. Mano9
AB100002.1 gg_id:79260 inactive deep-sea hydrothermal vent chimneys clone IndB2-5
EU799262.1 gg_id:318713 It's all ranking aquatic Newport Harbour RI clone 1C226841
AY162081.1 gg_id:135247 Cultivating Sargasso Sea clone GMD37D2
DQ860059.1 gg_id:165826 Symbiotic aerobic anoxygenic phototrophic colonial tunicate clone C3
EU246226.1 gg_id:253444 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-P5-E03
EF123390.1 gg_id:247890 Microbial disease microbial mats on Siderastrea siderea three regions wider Caribbea
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DQ015815.1 gg_id:140242 Antarctic lake water clone ELB16-059
AJ440751.1 gg_id:66953 Gram-negative MM 1
EU907924.1 gg_id:335974 Roseobacter sp. str. SKUK MB1009
DQ070788.1 gg_id:146111 Prokaryotic Structures Seafloor Basalts Varying Age and Juan de Fuca Ridge deep sea
AF468352.1 gg_id:80289 Arctic sea ice ARK10013
FJ542926.1 gg_id:515949 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone B
EF123341.1 gg_id:239882 Microbial disease microbial mats on Siderastrea siderea three regions wider Caribbea
GQ500845.1 gg_id:533002 Surveys Biofilms and Sediments Mammoth Cave Karst Aquifers Bio-Sep beads conta
EU143346.1 gg_id:240707 Loktanella sp. str. J57
DQ446109.2 gg_id:173763 Surface Mucopolysaccharide Layer and Band Microbial Mat Black Band-Diseased Sid
GU362938.1 gg_id:548305 and archaeal biogeochemical cycling genes within Qiongdongnan basin Sea: pilot stu
FJ403096.1 gg_id:365829 Disease- changes healthy and diseased colonies Caribbean coral Montastrea faveolat
FJ825922.1 gg_id:569378 Succession during spring Sea filtered surface sea water period diatom bloom Yel Sea;
FJ516795.1 gg_id:545503 semiarid 'Tablas de Daimiel National Park' wetland (Central Spain) unravelled biofilm
FJ203262.1 gg_id:333817 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c
AY922228.1 gg_id:113238 whalefall clone 131735
FJ152875.1 gg_id:307203 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX4CE
GQ349657.1 gg_id:580330 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
AF473915.1 gg_id:46143 template extracted Diploria strigosa with BBD clone 128-19L proteobacterium
EU246804.1 gg_id:251325 polyphasic description Pocillopora meandrina Palmyra Atoll Calcinus obscurus abdon
GU061266.1 gg_id:548114 Evaluation culturing methods cultivate previously Yel Sea intertidal beach seawater

EU287297.1	255176	1696.4	2247.4	1306.1	2981.4	3251.0	2708.9
EU581832.1	546740	412.1	570.1	1133.1	612.8	2143.3	1494.6
AF445668.1	21491	276.3	678.7	282.5	595.4	583.4	315.1
DQ836751.1	170685	1462.8	2163.5	2120.5	2268.1	4072.1	4788.1
DQ223020.1	140881	374.1	1017.9	3285.3	1100.2	1138.6	1331.6
DQ153145.1	139458	3941.4	5317.4	5288.3	4010.4	11426.7	10293.9
FJ516819.1	559891	7304.6	7437.8	9276.0	8120.5	10016.6	11940.3
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DQ071102.1	135986	6099.1	9351.5	9571.0	5621.8	11966.6	9479.9
FJ210801.1	354233	206.9	273.0	1375.6	363.0	5064.8	497.2
AM945586.1	263307	33.4	35.4	42.5	51.8	69.8	41.1
AB491831.1	572325	966.9	1631.1	2293.9	1419.0	2194.6	5061.9
AY563033.1	100625	1139.6	2154.1	6279.9	6674.8	5349.9	5350.7
AB100002.1	79260	2158.1	3194.7	1768.6	2549.6	3993.0	3321.2
EU799262.1	318713	1492.5	2954.2	3864.0	3936.6	3846.0	5645.8
AY162081.1	135247	1208.6	1597.5	1364.9	1460.1	1846.6	1603.3
DQ860059.1	165826	5790.6	4928.1	7163.3	7134.4	9587.8	7593.6
EU246226.1	253444	356.1	666.5	2178.4	476.8	1171.7	2897.1
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AM779569.1	254618	385.8	501.6	1547.5	530.9	876.0	508.5
DQ015815.1	140242	809.4	1126.5	1895.9	1602.2	2945.7	6041.4
AJ440751.1	66953	3636.6	3967.8	3711.4	6536.1	8483.9	7476.8
EU907924.1	335974	63.9	221.8	195.4	146.1	164.5	188.0
DQ070788.1	146111	2198.1	4017.8	2008.4	2837.3	6506.2	8722.6
AF468352.1	80289	798.4	1218.7	1416.4	1211.2	2915.8	1890.2
FJ542926.1	515949	1070.7	1390.1	1851.1	1537.5	1974.5	1657.8
EF123341.1	239882	12843.7	6413.6	11691.1	11585.4	13525.9	11010.5
GQ500845.1	533002	2069.5	3012.9	4458.4	2309.6	6226.6	7354.7
EU143346.1	240707	366.5	724.3	1840.1	677.1	721.3	1428.3
DQ446109.2	173763	204.8	247.4	573.0	239.9	1033.9	724.4
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FJ403096.1	365829	5868.9	5980.1	6989.1	8491.7	9056.9	9792.4
FJ825922.1	569378	4840.9	3570.1	4184.0	6438.1	709.8	2462.7
FJ516795.1	545503	4992.2	7400.7	7481.6	6633.6	11042.7	13713.1
FJ203262.1	333817	1076.0	1997.4	2441.7	2560.9	6967.2	3627.6
AY922228.1	113238	1180.7	1878.1	1248.8	1419.5	3373.0	2374.6
FJ152875.1	307203	2511.1	1756.3	3285.4	2898.4	1973.0	2825.8
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AF473915.1	46143	3706.2	2758.1	3474.1	2575.9	6440.0	5102.7
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AF007256.2 gg_id:5663 coastal seawater isolate clone
FJ203181.1 gg_id:331968 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c
FJ716898.1 gg_id:511895 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United Kingc
DQ103625.1 gg_id:133177 hypersaline endoevaporitic microbial mat clone E2aE09
EU907918.1 gg_id:345550 Roseobacter sp. str. SKUK MB1003
FJ999598.1 gg_id:435644 sponge Haliclona simulans South China Sea clone B24
FM872825.1 gg_id:365967 occupant source house floor dust clone FB03D09
FJ664812.1 gg_id:548236 Quantitative dynamics cells plankton-fed microbial fuel cell clone plankton_H05
EU592363.1 gg_id:569744 Seasonal changes Salton Sea hypersaline water clone SSW81Au
DQ416564.1 gg_id:155908 s1cb87
GU117983.1 gg_id:555923 Threatened Corals Provide Microbial Habitats clone Acer_G14
FJ716866.1 gg_id:513386 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United Kingc
DQ191822.1 gg_id:140189 Microbial and geochemical heterogeneity 3 km deep South Africa fractured metaba:
EU050746.1 gg_id:245675 libraries sediment Kings Bay Svalbard Arctic clone ss1_B_02_95
EU799752.1 gg_id:341789 It's all ranking aquatic Newport Harbour RI clone 1C227397
GU117926.1 gg_id:569576 Threatened Corals Provide Microbial Habitats clone Acer_B13
FJ664788.1 gg_id:567643 Quantitative dynamics cells plankton-fed microbial fuel cell clone plankton_A05
EU624444.1 gg_id:286855 Ruegeria atlantica str. SS-05
FJ543062.1 gg_id:516831 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone B
EF632666.1 gg_id:255072 Unique microbial contrasting aquatic altitude Andean Altiplano (northern Chile) sedir
DQ153140.1 gg_id:138819 Structure Biofilms on Artificial Surfaces and Free-living Estuarine Seawater surface b
GU118199.1 gg_id:559757 Threatened Corals Provide Microbial Habitats clone Dstr_E23
DQ421597.2 gg_id:210820 Salt Marsh Prokaryotes salt marsh clone SIMO-4232
FJ202464.1 gg_id:323413 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k
FJ202775.1 gg_id:343203 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k
AB355069.1 gg_id:257450 Monitoring and archaeal two heavy polluted areas lake Egypt based on sediment Ma
EU835420.1 gg_id:349125 structure and quorum sensing reverse osmosis RO membrane biofilm clone 1B15
DQ421651.2 gg_id:211048 Salt Marsh Prokaryotes salt marsh clone SIMO-4286
DQ659415.1 gg_id:166922 Roseobacter sp. str. COL2P
AY167261.1 gg_id:81559 Roseobacter sp. str. ANT9274
EU196325.1 gg_id:243714 Roseobacter sp. NP30
EF123331.1 gg_id:239119 Microbial disease microbial mats on Siderastrea siderea three regions wider Caribbea
FJ230841.1 gg_id:304753 Phaeobacter sp. str. G8
DQ856532.1 gg_id:244293 intestinal microflora Chinese mitten crab (Eriocheir sinensis) clone C2N
EU835468.1 gg_id:317397 structure and quorum sensing reverse osmosis RO membrane biofilm clone 3M06
DQ234217.2 gg_id:141577 determined library mangrove clone DS134
DQ412059.1 gg_id:154395 Roseobacter sp. str. LOB-8
DQ667965.1 gg_id:170315 Orientalimare eburneum str. SW-277
EF207559.1 gg_id:215772 mangrove system sediment
EF471656.1 gg_id:270937 Fast Screening and Estuarine Operon Libraries whole surface water Chesapeake Bay
FJ203039.1 gg_id:307415 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c

AF007256.2	5663	232.3	751.1	2736.6	695.2	742.7	1579.7
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FJ999598.1	435644	3013.3	2526.5	4569.5	3194.4	8820.3	5334.3
FM872825.1	365967	4875.5	7325.7	11104.6	8528.3	12306.2	13998.7
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DQ667965.1	170315	379.8	809.2	915.8	712.8	888.1	1823.3
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EU685337.1 gg_id:294040 Rhodobacter sp. str. CC-SAL-30
DQ412074.1 gg_id:155494 Sulfitobacter sp. str. SPB-4
AY654837.1 gg_id:100715 Oculina mucus isolate 39
Y11551.1 gg_id:5675 Roseovarius tolerans str. Ekho Lake-172
AF076898.1 gg_id:5650 d isolate western Sargasso Sea clone D
AY967725.1 gg_id:115231 Sulfitobacter sp. IS1
EU287912.1 gg_id:244920 Rhodovulum thermophilus str. CC-MHSW-1
AF359530.1 gg_id:35622 Alexandrium tamarense NEPCC 407
DQ103624.1 gg_id:132289 hypersaline endoevaporitic microbial mat clone E4bD01
AY771769.1 gg_id:142124 Arctic Marinosulfonomonas methylotropha clone SE69
AY639888.1 gg_id:99168 Citricella thiooxidans str. CHLG 16
FM242220.1 gg_id:327863 sequences sediment clone 119 T0h-oil
EU700143.1 gg_id:296248 Study on Shantou Bay Marine Sediments Microorganisms sediment clone STU1
AF502214.1 gg_id:59351 EBPR sludge lab scale clone HP1A30
AJ633964.1 gg_id:114588 host's accessory nidamental gland clone T63ANG237
AF170736.1 gg_id:5781 Rhodobacter sp. str. QSSC1-20
AY344379.1 gg_id:92016 Lake Kauhako surface clone K2-S-3
DQ659414.1 gg_id:167392 Roseobacter sp. str. BS90
GQ396945.1 gg_id:593441 Functional unvegetated perhumid recently-deglaciated soils do not correlate shifts s
EU236337.1 gg_id:295747 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg5a2D1
AF076897.1 gg_id:5649 d isolate western Sargasso Sea clone C
FJ202870.1 gg_id:332743 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k
AY922243.1 gg_id:113817 whalefall clone 131821
EU360293.1 gg_id:271908 Pyrene-Degrading Consortium Deep-Sea Sediment West Pacific and its Key Member
EU799036.1 gg_id:305874 It's all ranking aquatic Newport Harbour RI clone 1C226589
DQ153126.1 gg_id:138759 Structure Biofilms on Artificial Surfaces and Free-living Estuarine Seawater surface b
GU118282.1 gg_id:587759 Threatened Corals Provide Microbial Habitats clone Dstr_I12
EU799596.1 gg_id:350463 It's all ranking aquatic Newport Harbour RI clone 1C227214
DQ412069.1 gg_id:156195 Sulfitobacter sp. str. KBB-2
FJ202786.1 gg_id:352366 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k
EU564840.1 gg_id:259482 Pseudoruegeria sp. str. CC-GIMAT-2
EU592378.1 gg_id:590969 Seasonal changes Salton Sea hypersaline water clone SSW59Au
AY845243.1 gg_id:110751 sponge clone 34P35
EU799556.1 gg_id:355768 It's all ranking aquatic Newport Harbour RI clone 1C227168
FJ202880.1 gg_id:319087 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k
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FJ202552.1 gg_id:331090 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k
AY548765.1 gg_id:103722 Sulfitobacter sp. str. PM03
FJ872535.1 gg_id:567410 Ruegeria sp. str. ZH17

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DQ103612.1	133856	1153.6	2506.6	3462.3	2433.6	8779.6	10811.3
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DQ412074.1	155494	354.2	708.0	917.0	1319.6	1543.4	2142.9
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Y11551.1	5675	1280.4	2423.9	2528.4	2801.0	10315.4	7114.2
AF076898.1	5650	10400.8	10749.2	7983.9	10834.9	15859.4	13092.8
AY967725.1	115231	601.5	1054.6	6501.1	2439.2	976.2	1907.0
EU287912.1	244920	17.4	51.0	65.8	62.6	70.4	84.3
AF359530.1	35622	241.1	329.7	1603.2	192.6	1040.2	1276.7
DQ103624.1	132289	434.2	664.0	376.7	462.3	2098.5	2679.9
AY771769.1	142124	257.9	657.6	1415.2	542.5	561.4	567.8
AY639888.1	99168	317.5	585.8	1253.2	843.3	1300.2	1956.9
FM242220.1	327863	402.7	695.9	1415.2	787.8	2560.0	2099.7
EU700143.1	296248	4206.1	3370.2	4929.9	4824.8	7345.0	7679.6
AF502214.1	59351	5591.6	7367.6	8126.6	6635.2	16898.0	14403.5
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AF170736.1	5781	144.2	280.1	249.4	445.7	150.6	392.6
AY344379.1	92016	3747.4	6327.4	8255.3	4839.9	11520.2	13054.5
DQ659414.1	167392	156.2	235.0	1047.8	208.9	353.3	651.6
GQ396945.1	593441	7194.6	6273.3	7051.5	7008.1	7053.4	7086.8
EU236337.1	295747	94.6	280.6	2106.6	266.8	286.2	1157.2
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AY922243.1	113817	2023.4	2216.1	2397.1	2119.1	3774.1	3655.5
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EU799036.1	305874	289.3	767.7	1684.8	1726.8	969.5	1502.7
DQ153126.1	138759	3640.8	4323.4	1707.7	4250.8	7473.7	6023.7
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EU799596.1	350463	3521.4	4870.7	9190.0	6772.1	8050.3	10873.1
DQ412069.1	156195	2204.6	2906.0	4267.9	3405.8	6572.4	6113.2
FJ202786.1	352366	4148.7	6076.3	9664.6	6789.8	8698.3	10545.7
EU564840.1	259482	222.3	488.4	289.4	478.6	172.9	380.0
EU592378.1	590969	147.5	320.4	578.0	244.8	1489.5	1460.0
AY845243.1	110751	6646.0	7452.9	7676.3	6352.2	12690.3	10890.0
EU799556.1	355768	2259.9	5056.5	6445.1	4693.5	7278.6	9017.2
FJ202880.1	319087	154.5	258.4	75.1	141.3	191.3	443.1
EU652592.1	277670	3272.1	4699.7	4860.9	4856.8	7226.3	6337.5
FJ202552.1	331090	5565.3	7150.1	7134.1	6360.5	15604.0	10266.1
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AY794143.1 gg_id:109093 soil clone F2C77
FJ906694.2 gg_id:575135 Rhodobacter sp. str. JS-43
EU799442.1 gg_id:354617 It's all ranking aquatic Newport Harbour RI clone 1C227041
EF471465.1 gg_id:276208 Fast Screening and Estuarine Operon Libraries whole surface water Chesapeake Bay
FJ232451.1 gg_id:368703 Phaeobacter sp. str. NH52F
EF659432.1 gg_id:239375 within Poole Harbour seawater clone PH-B6
AY845237.1 gg_id:111058 sponge clone 310P5
GQ349664.1 gg_id:579002 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
DQ008594.1 gg_id:121132 Roseobacter sp. str. HYL-SA-18
EU419924.1 gg_id:273372 Roseobacter sp. str. RW37
GU396991.1 gg_id:516703 Haematobacter sp. str. BC14248
EF573183.1 gg_id:234741 Coco's Island site 23 marine clone S23_1282
EU771820.1 gg_id:337345 African elephant feces clone AFEL_aai29h10
GU369903.1 gg_id:528643 and mats vents Arc white filamentous microbial mat photic shal hydrothermal vent
DQ357748.1 gg_id:149884 Marine Hatchery: Balance Between Pathogenic and Potentially Probiotic Strains Fuc
AM176846.1 gg_id:160274 Recovery mangrove sediment clone SZB5
GU061078.1 gg_id:580648 Evaluation culturing methods cultivate previously Yel Sea intertidal beach clone TFS-
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AB052711.1 gg_id:41554 Acetobacter cibinongensis str. 1BM-18C
AB052710.1 gg_id:29322 Acetobacter cibinongensis str. 4H-1
AJ419838.1 gg_id:58373 Acetobacter estunensis str. LMG 1626
FJ157232.1 gg_id:318111 Acetobacter indonesiensis str. KS9
GQ131205.1 gg_id:457643 Lactobacillus plantarum str. IMAU70089; BM3151
FJ157228.1 gg_id:324416 Acetobacter lovaniensis str. KS1
AB052706.1 gg_id:25818 Acetobacter orientalis str. 21F-2
AB470917.3 gg_id:535203 Acetobacter orientalis KL13-3
AB117965.1 gg_id:92224 Acetobacter orientalis SF18-1
AJ419845.1 gg_id:58362 Acetobacter orleanensis str. LMG 1583
AB264094.1 gg_id:187581 Acetobacter syzygii str. SKU19
AB052713.1 gg_id:22265 Acetobacter syzygii str. 22F-1B
AB032354.1 gg_id:34202 Acetobacter tropicalis str. NRIC 0312 No.3
AB032355.1 gg_id:34622 Acetobacter tropicalis str. NRIC 0312 No.39
AJ419836.1 gg_id:58365 Acetobacter peroxydans str. LMG 1633
EU341169.1 gg_id:245064 Evaluation Rapid Technologies Estimate Microbial Burden and Commercial Airline Ca
AF127399.1 gg_id:4453 Acetobacter aceti SRI1321
NR_025512.1 gg_id:561758 Acetobacter cerevisiae str. LMG 1625
GQ240641.1 gg_id:551528 Acetobacter pasteurianus str. DSM 2324
EF528281.1 gg_id:224755 Acetobacter pasteurianus str. CICCHLJ Q61
EU131161.1 gg_id:241962 Acetobacter oeni str. B7
DQ168837.1 gg_id:138760 Fermentative biohydrogen production heated anaerobic sludge clone J20
EU126660.1 gg_id:240163 Acetobacter pasteurianus

AY794143.1	109093	25.7	36.8	92.2	66.2	87.7	71.5
FJ906694.2	575135	1764.3	1825.7	3046.5	3430.6	3671.0	6396.1
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EF471465.1	276208	45.9	109.8	143.6	106.9	182.3	146.6
FJ232451.1	368703	1548.8	2124.3	1661.6	1960.9	4990.8	2931.3
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AY845237.1	111058	4465.8	5508.6	6196.2	5611.8	13874.1	11654.0
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AB052711.1	41554	1972.4	2752.2	3180.1	1943.3	5140.0	5818.5
AB052710.1	29322	3863.5	6289.1	3951.4	3098.7	6762.8	7352.2
AJ419838.1	58373	1312.4	2116.6	1575.8	1701.7	1760.8	1570.4
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FJ157228.1	324416	763.8	1631.9	912.6	253.3	519.5	673.4
AB052706.1	25818	2951.1	4127.2	1921.8	1877.1	3367.9	3031.2
AB470917.3	535203	7039.0	7238.5	6220.1	6074.9	9312.6	8569.1
AB117965.1	92224	1408.3	1906.2	2034.1	1414.3	2545.2	3001.5
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AB052713.1	22265	178.1	418.7	887.6	529.0	303.8	564.4
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AB006711.1 gg_id:4493 Acidiphilium multivorum str. AIU 301
DQ906056.1 gg_id:227409 nickel resistance genes metagenome Tinto River rhizosphere clone ERF-1C1
AY495956.1 gg_id:101146 Acidiphilium sp. str. WJ52
D30775.1 gg_id:4477 Acidiphilium organovorum str. ATCC 43141
Y18446.1 gg_id:4503 Acidiphilium cryptum str. Kuesel IFV
D30776.1 gg_id:4484 Acidiphilium rubrum str. ATCC 35905
AY632901.1 gg_id:101742 Acidiphilium symbioticum str. KM2
FJ915152.1 gg_id:541391 Acidiphilium cryptum str. nju-AMD11
AM502929.1 gg_id:246693 Acidiphilium cryptum str. YT1
AF376026.2 gg_id:40217 Acidiphilium sp. str. NO-17
DQ659235.1 gg_id:220234 acid mine drainage clone DBS-Clone60
AM697382.1 gg_id:222512 sequencing libraries indoor dust clone BF0002C079
AM947652.1 gg_id:268023 Acidisoma tundrae str. WM1
GQ264418.1 gg_id:581747 Structure Simulated Level Waste Site simulated level waste site clone WW3_107
AM749786.1 gg_id:243689 Acidicaldus sp. T163
AM749741.1 gg_id:253578 Isolation ing candidate division soils New Zealand steam-affected geothermal soil cl
AY882839.2 gg_id:112235 hot spring clone SK290
DQ906080.1 gg_id:223846 nickel resistance genes metagenome Tinto River rhizosphere clone ERF-G1
AB362219.2 gg_id:240252 Acidocella aluminiidurans str. AL46
D30771.1 gg_id:4491 Acidocella aminolytica str. 101
EU360486.1 gg_id:271114 pilot biological ferrous iron oxidation mine water treatment plant clone W-Z-59
X77468.1 gg_id:4470 Acidomonas methanolica str. LMG 1668
AB056321.1 gg_id:67745 Kozakia baliensis str. Yo-3
AB025928.1 gg_id:52420 Asaia bogorensis str. 71
AB230993.2 gg_id:145122 Asaia bogorensis str. BCC 15703
AB292238.1 gg_id:247489 Asaia bogorensis AG60
EF635915.1 gg_id:255006 Asaia sp. str. Gb16
AB025930.1 gg_id:33826 Asaia bogorensis str. 87
AB292240.1 gg_id:246483 Asaia krungthepensis AE76
AB292241.1 gg_id:254045 Asaia krungthepensis AE68
AB292242.1 gg_id:235750 Asaia krungthepensis AE73
AB102955.1 gg_id:95258 Asaia krungthepensis str. AA06
AB292239.1 gg_id:239498 Asaia siamensis AE97
AB230990.2 gg_id:149795 Asaia siamensis str. BCC 15670
CP001189.1 gg_id:306076 Gluconacetobacter diazotrophicus 5 str. PAl 5; ATCC 49037
DQ387435.1 gg_id:220341 Gluconacetobacter diazotrophicus str. 4L
AF127392.1 gg_id:4462 Gluconacetobacter diazotrophicus SRI1990
AF127397.1 gg_id:4461 Gluconacetobacter diazotrophicus SRI1212
X75620.2 gg_id:4423 Gluconacetobacter hansenii str. NCIB8746 LMG1527
AB166736.1 gg_id:100534 Gluconacetobacter hansenii str. NBRC 14820

GQ267957.1	548999	262.9	649.2	479.6	556.3	1680.2	1469.1
AB006711.1	4493	1504.6	1350.0	440.9	371.4	1386.9	1200.9
DQ906056.1	227409	126.5	117.1	71.6	199.3	71.3	58.4
AY495956.1	101146	5293.6	5275.0	2684.2	3127.2	9115.5	6695.4
D30775.1	4477	1951.1	2059.8	935.5	1271.2	2385.8	2177.7
Y18446.1	4503	1127.8	775.1	1329.0	1183.4	2260.9	1563.5
D30776.1	4484	1877.1	2339.6	2736.1	1992.9	5956.1	4632.0
AY632901.1	101742	8221.6	7775.9	4330.0	8555.7	11596.8	10637.4
FJ915152.1	541391	626.4	743.1	315.7	543.2	1066.1	1001.8
AM502929.1	246693	2086.9	2680.0	1549.1	1627.7	3007.5	2227.3
AF376026.2	40217	5921.9	8353.6	4107.7	5765.9	5240.2	3770.3
DQ659235.1	220234	1442.9	1682.3	1439.2	1574.3	1025.1	1646.1
AM697382.1	222512	1871.7	1797.6	4146.2	2089.1	2439.0	2152.6
AM947652.1	268023	1088.2	1069.7	1880.8	436.1	1622.5	1454.0
GQ264418.1	581747	5042.3	5893.8	4070.8	4578.0	8142.1	6596.8
AM749786.1	243689	573.8	1090.5	1905.2	480.2	1516.1	1645.7
AM749741.1	253578	1049.4	2555.6	2575.1	658.3	4882.6	3628.0
AY882839.2	112235	125.0	243.6	1013.3	193.2	182.8	243.4
DQ906080.1	223846	751.5	1783.0	2847.0	1131.8	1077.3	1872.4
AB362219.2	240252	199.6	518.5	684.5	338.0	856.8	1306.4
D30771.1	4491	1497.8	3456.4	2950.8	2489.8	3091.4	4066.1
EU360486.1	271114	4472.9	4818.7	3389.1	5967.0	8495.5	5642.2
X77468.1	4470	1457.7	2344.1	3126.5	2482.2	3352.8	3046.2
AB056321.1	67745	308.7	727.2	875.8	1391.6	494.6	581.4
AB025928.1	52420	1398.1	2275.5	2597.6	1618.7	2920.9	1801.4
AB230993.2	145122	626.7	1225.9	1496.7	1002.5	1070.1	1458.3
AB292238.1	247489	2877.6	4379.6	4230.0	2704.8	4543.6	3562.7
EF635915.1	255006	4871.3	3595.6	4578.5	6440.6	13751.9	8845.9
AB025930.1	33826	1215.6	1829.7	2009.2	1161.0	1179.2	932.7
AB292240.1	246483	1440.7	2198.1	2491.5	1654.2	3113.2	1806.9
AB292241.1	254045	3342.9	4867.9	4305.7	2798.2	5336.6	2277.7
AB292242.1	235750	2875.4	4081.8	4032.0	2703.4	4539.2	3571.2
AB102955.1	95258	1663.5	2531.4	2638.8	1630.2	2744.3	2610.5
AB292239.1	239498	662.2	580.5	1117.8	580.7	1795.4	1444.5
AB230990.2	149795	283.2	596.3	824.0	744.7	220.2	423.6
CP001189.1	306076	294.9	459.5	1249.6	443.0	604.9	1275.5
DQ387435.1	220341	558.9	756.6	1372.1	793.9	942.8	1430.1
AF127392.1	4462	554.9	766.2	1380.8	783.9	936.7	1423.3
AF127397.1	4461	563.0	745.1	1183.4	773.0	925.3	1366.2
X75620.2	4423	5029.3	4698.9	3786.2	5022.6	7661.3	6848.8
AB166736.1	100534	1109.1	1942.7	2148.3	2303.1	1318.8	1840.6

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AJ001631.1 gg_id:4449 Gluconacetobacter oboediens str. LTH2460
EU096236.1 gg_id:277233 Gluconacetobacter intermedius str. EW-i
AF127395.1 gg_id:4441 Gluconacetobacter liquefaciens SRI1994
AF127413.1 gg_id:4430 Gluconacetobacter sacchari IF9645
AF127406.1 gg_id:4437 Gluconacetobacter sacchari SRI1216
AJ012698.1 gg_id:4467 Gluconacetobacter europaeus str. ZIM B028 V3
X75619.1 gg_id:70289 Gluconacetobacter xylinus str. NCIB11664 LMG1515
AF111841.1 gg_id:23292 Gluconacetobacter johannae str. CFN-Cf55
AF192761.1 gg_id:36976 Gluconacetobacter azotocaptans str. CFN-Ca54
AY958232.3 gg_id:124373 Gluconacetobacter azotocaptans DS1
AB016865.1 gg_id:4420 Acetobacter sp
AB095100.1 gg_id:71559 Gluconacetobacter persimmonensis str. KJ145
AF127401.1 gg_id:4460 Gluconacetobacter diazotrophicus SRI1206
AB166741.1 gg_id:104836 Gluconacetobacter saccharivorans str. LMG 1584
AB205220.1 gg_id:114307 Gluconacetobacter europaeus str. DSM 6160
EU000272.1 gg_id:250024 Gluconacetobacter xylinus
X80775.2 gg_id:4456 Gluconobacter cerinus str. ATCC 19441 IFO 3267 = LMG 1368
AB308276.1 gg_id:231954 Gluconobacter cerinus
DQ523496.1 gg_id:159924 Acetobacter syzygii str. A265
AB308275.1 gg_id:231476 Gluconobacter oxydans str. LD51-2
AB178430.1 gg_id:108207 Gluconobacter oxydans str. NBRC 12118
AB128051.1 gg_id:98968 Gluconobacter thailandicus str. F142-1
AB178392.1 gg_id:108166 Gluconobacter oxydans str. NBRC 3250
AB308278.1 gg_id:229359 Gluconobacter frateurii str. CR16-1
AB470921.2 gg_id:533805 Gluconobacter frateurii GB222-1
EU096234.1 gg_id:274069 Gluconobacter sp. str. EW707
AB470922.2 gg_id:533831 Gluconobacter japonicus GB132-1
X82290.1 gg_id:4464 Gluconobacter frateurii str. IFO 3264 LMG 1365
AB308277.1 gg_id:234315 Gluconobacter thailandicus str. ZN22-2
AF173825.1 gg_id:4404 Antarctic clone LB3-94
AY682679.1 gg_id:144291 Microbial biofilms corroding systems heating system clone 24
EU012448.1 gg_id:255991 Roseococcus suduntuyensis str. SHET
AY150047.1 gg_id:75850 Roseomonas cervicalis str. ATCC 49957
EU742165.1 gg_id:314674 Roseomonas cervicalis str. XTD510
GQ047159.1 gg_id:446551 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1009d
AF227831.1 gg_id:26143 str. 47076
GQ043367.1 gg_id:395886 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw96
GQ043897.1 gg_id:458437 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw97
GQ038481.1 gg_id:399250 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu4
GQ045958.1 gg_id:387425 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ041000.1 gg_id:378028 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv

AJ001631.1	4449	1639.2	2554.8	2360.2	3538.7	4873.5	7076.0
EU096236.1	277233	1029.6	1812.4	2011.3	2526.9	3453.1	4756.0
AF127395.1	4441	698.7	1002.6	1750.5	1145.3	1808.5	2227.4
AF127413.1	4430	107.1	141.1	346.5	210.0	156.1	231.6
AF127406.1	4437	2669.3	2381.5	1992.0	1765.1	3315.7	3036.2
AJ012698.1	4467	1246.8	2336.1	2881.6	2434.9	3306.0	4941.5
X75619.1	70289	11277.3	10685.5	6518.5	8063.1	10149.1	13745.5
AF111841.1	23292	4441.5	6084.4	8550.3	7275.4	10156.2	10311.2
AF192761.1	36976	1937.5	2631.2	3296.3	2411.4	4953.8	5016.0
AY958232.3	124373	2096.8	3922.5	1833.3	3417.9	3768.7	1764.4
AB016865.1	4420	2331.5	2295.0	1930.3	3314.4	3304.6	1917.6
AB095100.1	71559	2264.6	2331.7	3496.7	2791.0	1812.3	2549.8
AF127401.1	4460	7200.7	4560.7	8558.6	6089.1	4940.1	7668.3
AB166741.1	104836	1681.0	3106.8	1836.9	2024.0	3447.9	2681.9
AB205220.1	114307	2029.8	3214.4	3104.4	3439.4	6529.2	7896.4
EU000272.1	250024	1391.5	2401.3	2656.8	2531.0	4323.1	5420.2
X80775.2	4456	2978.3	2741.7	4649.0	3550.8	3279.0	3077.9
AB308276.1	231954	7274.1	7965.7	7094.2	8093.8	12543.3	11861.2
DQ523496.1	159924	24253.4	42548.9	24365.8	21504.2	30321.1	8024.3
AB308275.1	231476	445.3	881.8	900.8	530.0	355.5	306.5
AB178430.1	108207	2825.3	3291.0	3649.4	3562.3	2511.1	2820.7
AB128051.1	98968	1004.8	1237.9	1382.1	1483.8	971.9	1078.7
AB178392.1	108166	502.1	862.8	3061.2	218.4	1615.0	1341.8
AB308278.1	229359	14562.4	13472.2	14025.9	11787.1	17674.0	19480.4
AB470921.2	533805	2022.3	2613.0	3176.4	2765.0	2916.7	3436.9
EU096234.1	274069	317.3	820.3	1021.7	618.8	407.4	85.3
AB470922.2	533831	6640.2	6920.4	8124.4	5478.8	7625.8	6339.5
X82290.1	4464	8563.4	9512.0	12071.9	7297.8	10279.9	9670.5
AB308277.1	234315	8957.9	8217.5	13188.2	10861.6	10721.7	11344.6
AF173825.1	4404	212.1	549.1	1682.0	277.5	538.2	1563.2
AY682679.1	144291	5909.3	6493.9	6835.2	5831.3	8830.1	8149.9
EU012448.1	255991	1905.7	2696.6	5176.7	2758.8	3739.4	3732.2
AY150047.1	75850	898.1	1597.0	3184.9	1363.7	3969.1	4388.4
EU742165.1	314674	1276.1	1761.5	3168.2	2452.6	4962.0	6294.2
GQ047159.1	446551	2380.6	3604.6	1453.4	816.4	3121.9	2729.3
AF227831.1	26143	544.0	1306.9	462.2	240.6	277.9	480.1
GQ043367.1	395886	13644.1	15353.0	7530.1	11246.2	14067.4	14137.9
GQ043897.1	458437	783.9	1385.8	441.7	345.0	1679.0	844.8
GQ038481.1	399250	6238.8	6072.2	3195.8	7360.0	9896.0	9777.3
GQ045958.1	387425	1260.0	2219.5	2549.0	1224.4	2963.7	3618.8
GQ041000.1	378028	9766.7	10141.8	3853.1	7323.9	9089.6	10949.1

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k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
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k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria

o__Rhodospirillales	f__Acetobacteraceae
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GQ037397.1 gg_id:377987 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ045672.1 gg_id:385279 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
DQ532240.1 gg_id:163716 Geographical Variation Microbial Burden and Spacecraft Assembly Johnson Space C
GQ042983.1 gg_id:383540 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1011g
GQ045701.1 gg_id:371940 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ046235.1 gg_id:458923 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw
GQ043724.1 gg_id:434279 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw97
GQ039151.1 gg_id:441025 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbu41
AM231587.1 gg_id:152603 Roseomonas aquatica str. TR53
GQ097336.1 gg_id:424616 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw453g04
FJ542999.1 gg_id:517152 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone B
AJ315073.1 gg_id:42326 Spain:Carmona clone
GQ097313.1 gg_id:459459 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw453d1
DQ130024.1 gg_id:154116 microbial biota normal forearm human skin clone BL102
AY922054.1 gg_id:114073 farm soil clone AKYG679
EF019939.1 gg_id:214556 aspen rhizosphere clone Elev_16S_1314
GQ039238.1 gg_id:415678 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbu41
AF227855.2 gg_id:24986 str. 96446
EU104101.1 gg_id:309755 Evidence Comamonadaceae determinants settling performance activated sludge clo
EU182887.1 gg_id:236056 Roseomonas sp. str. MH59
EF019649.1 gg_id:204768 aspen rhizosphere clone Elev_16S_801
GQ097316.1 gg_id:454621 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw453e0
AF443585.1 gg_id:88754 semiarid soil clone C-F-13
DQ815048.1 gg_id:163698 zebrafish digestive tract clone aab49c08
DQ990962.2 gg_id:197174 Microbial Rock Varnish Yungay Atacama Desert Chile rock varnish clone AYRV2-159
DQ129635.1 gg_id:194558 microarray level air two cities Texas urban aerosol clone AKIW418
FJ479560.1 gg_id:573663 species richness estimates obtained nearly and simulated pyrosequencing-generated
FM874262.1 gg_id:358386 occupant source house mattress dust clone MC03F05
GQ097319.1 gg_id:444359 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw453e0
NR_028984.1 gg_id:587551 Roseomonas rosea str. 173-96; DSM 14916
AJ488504.1 gg_id:64742 Teichococcus ludipueritiae str. 170-96
EF682998.1 gg_id:246217 Eastern Mediterranean atmosphere clone F14_5H_FL
AB114611.1 gg_id:102348 rice plant clone ER-17
DQ129249.1 gg_id:151603 microarray level air two cities Texas urban aerosol clone AKIW963
AJ871428.1 gg_id:110099 Paracraurococcus ruber CP2C
AF513983.1 gg_id:64695 Leahibacter roseus str. LCR1
GQ097329.1 gg_id:458521 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw453f08
AB009013.1 gg_id:4416 Paracraurococcus ruber str. NS102
AY150045.1 gg_id:75313 Roseomonas gilardii str. ATCC 49956
EU540200.1 gg_id:280239 profile human microbiota antecubital fossa (inner elbow) skin clone nbt247a02
AF170742.1 gg_id:4413 Paracraurococcus sp. str. QSSC5-3

GQ037397.1	377987	1228.7	2265.2	1710.8	620.5	2203.3	2787.5
GQ045672.1	385279	5898.8	7607.6	5738.7	5317.3	13935.5	15624.2
DQ532240.1	163716	7094.0	7183.0	4356.6	4914.3	10031.9	8698.7
GQ042983.1	383540	2688.6	3073.1	3821.7	2604.1	4366.2	7168.0
GQ045701.1	371940	3892.5	4195.5	3810.3	3726.2	7087.4	7667.4
GQ046235.1	458923	10824.0	12003.1	6273.6	9409.1	14343.0	12524.3
GQ043724.1	434279	5140.8	4890.5	5607.4	4771.6	6269.7	7329.7
GQ039151.1	441025	6656.8	7932.6	3860.3	3331.7	5884.1	5990.7
AM231587.1	152603	143.5	264.6	274.1	145.7	209.4	306.6
GQ097336.1	424616	5711.0	7460.2	5436.0	5850.9	9022.5	7275.9
FJ542999.1	517152	1242.7	1987.5	2048.8	838.5	3316.4	3596.9
AJ315073.1	42326	491.1	1165.7	1786.3	501.7	1024.4	1109.8
GQ097313.1	459459	8914.1	10641.0	5270.1	8392.6	10539.3	9568.1
DQ130024.1	154116	581.1	1062.9	1418.4	422.0	649.6	952.8
AY922054.1	114073	1212.0	2300.3	2733.1	1168.5	3140.1	3338.1
EF019939.1	214556	5590.6	6178.5	8356.3	6096.6	10463.9	8329.9
GQ039238.1	415678	8939.1	9107.9	7389.6	7346.2	10940.3	8891.1
AF227855.2	24986	3096.2	3453.8	3315.8	2760.1	3521.3	3202.8
EU104101.1	309755	1438.6	2314.2	1352.8	1123.8	2668.4	1276.2
EU182887.1	236056	115.5	263.1	1265.3	513.8	564.3	727.5
EF019649.1	204768	7274.4	7906.0	6694.0	7026.3	10253.7	8834.0
GQ097316.1	454621	9381.4	9861.7	6100.1	9730.9	11312.4	9659.1
AF443585.1	88754	898.0	1421.0	1421.8	1178.5	1685.6	2159.7
DQ815048.1	163698	163.2	204.0	209.6	143.3	557.0	721.5
DQ990962.2	197174	171.4	259.2	346.0	297.1	357.3	326.5
DQ129635.1	194558	337.4	169.3	150.5	93.4	65.1	73.0
FJ479560.1	573663	533.5	960.7	2401.8	361.8	2170.9	498.4
FM874262.1	358386	5164.2	6001.7	5503.6	5020.9	9294.0	7085.1
GQ097319.1	444359	1219.2	2412.8	2705.5	567.1	8229.8	861.0
NR_028984.1	587551	80.9	188.3	109.1	128.3	145.9	105.6
AJ488504.1	64742	659.6	1558.6	1656.5	903.4	3006.4	2163.7
EF682998.1	246217	590.5	1193.9	3572.8	565.6	4775.5	2448.5
AB114611.1	102348	76.7	141.6	367.0	126.3	235.7	469.8
DQ129249.1	151603	1004.8	1613.7	1877.9	461.6	1710.0	2162.3
AJ871428.1	110099	83.3	127.3	214.1	106.0	118.7	103.1
AF513983.1	64695	18.9	22.6	34.2	58.5	59.6	16.7
GQ097329.1	458521	1847.2	2445.8	3154.2	2068.1	5895.8	3585.7
AB009013.1	4416	87.7	145.4	111.7	100.8	145.6	185.6
AY150045.1	75313	1695.3	1229.9	258.8	1810.9	149.6	61.4
EU540200.1	280239	470.4	614.7	1833.3	312.8	2006.8	621.2
AF170742.1	4413	8095.9	8874.8	3949.6	6215.5	10769.9	7063.2

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o__Rhodospirillales	f__Acetobacteraceae
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EF520429.1 gg_id:230389 structure lakes: what controls ? acid-impacted lake clone ADK-BTe02-70
DQ984625.1 gg_id:242669 YK oil-contaminated soil clone YK_59
AB363646.1 gg_id:574723 Swaminathania salitolerans str. SI15-2
AF459455.1 gg_id:43009 Swaminathania salitolerans str. PA 12
AB445099.1 gg_id:315688 Swaminathania salitolerans str. NBRC 104436
AB304087.1 gg_id:249455 Tanticharoenia sakaeratensis str. NBRC 103193
AB303367.1 gg_id:257476 Ameyamaea chiangmaiensis str. BCC 15745
EF519867.1 gg_id:267119 Ronia tepidophila str. TU-7
D45202.1 gg_id:4575 Oleomonas sagaranensis str. HD-1
EF446228.1 gg_id:213763 Prokaryotic and Ecology Floating Macroscopic Filaments Extreme Acidic River Rio Tint
EF446204.1 gg_id:208105 Prokaryotic and Ecology Floating Macroscopic Filaments Extreme Acidic River Rio Tint
EF516844.1 gg_id:220042 grassland soil clone FCPN646
L22481.1 gg_id:8030 Heliothis virescens testis endosymbiont
AF465832.1 gg_id:79493 Rubritepida flocculans
AY234551.1 gg_id:112277 soil isolate Ellin5134
GQ088427.1 gg_id:407742 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw3
GQ402627.1 gg_id:593096 Accessing microbial biodiversity and metabolic potential tropical -based approach pe
DQ906085.1 gg_id:222665 nickel resistance genes metagenome Tinto River rhizosphere clone ERF-H8
GU172195.1 gg_id:537239 Microbial Eucalyptus plantation soil clone DSM-R23
AJ633644.1 gg_id:103476 Rhodovarius lipocyclicus str. CCUG 44693
AY370188.1 gg_id:104162 ground up bee tissues clone pAJ205
DQ378212.1 gg_id:152090 oil-polluted soil clone F50_Pitesti
FM874498.1 gg_id:361359 occupant source house mattress dust clone MD04D08
AB240243.1 gg_id:144065 microbial structure rhizosphere Phragmites bulk soil reed bed reactor laboratory clon
FJ915153.1 gg_id:583138 Acidisphaera sp. str. nju-AMDS1
DQ129264.1 gg_id:138221 microarray level air two cities Texas urban aerosol clone AKIW397
EF409853.1 gg_id:207022 acid mine drainage clone SLS-49-06
EU861903.1 gg_id:306635 effects chronic fertilization on alpine tundra microbial implications carbon and cyclin
FJ595556.1 gg_id:532895 rock Black Canyon New Mexico: and Geochemistry rocks no varnish clone NV12_7c7
DQ378204.1 gg_id:151650 oil-polluted soil clone F42_Pitesti
AB110421.1 gg_id:91691 Saccharibacter floricola str. S-877
AY913353.1 gg_id:112752 forest soil clone DUNssu146 (+7A) (OTU#150)
EU409119.1 gg_id:263028 Impacted Mine Drainage Dabaoshan Mining Area mine drainage sediment clone DBS
AM162403.1 gg_id:154314 and situ identification acidic sphagnum peat bog
Y07647.2 gg_id:4411 Drentse grassland soil clone vii
EU409601.1 gg_id:276553 Gluconobacter sp. str. EW707
DQ906066.1 gg_id:223618 nickel resistance genes metagenome Tinto River rhizosphere clone ERF-C4
AM697086.1 gg_id:221365 sequencing libraries indoor dust clone BF0002B036
AY395443.1 gg_id:102882 pasture soil clone EB1124
EU360476.1 gg_id:259611 pilot biological ferrous iron oxidation mine water treatment plant clone FS-Z1-34
AJ292597.1 gg_id:53994 PCB-polluted soil clone WD238

EF520429.1	230389	176.6	335.2	395.4	180.2	1456.8	951.5
DQ984625.1	242669	3674.2	3716.6	2324.2	4636.2	8435.8	9906.0
AB363646.1	574723	202.8	862.8	1277.2	618.1	427.5	796.5
AF459455.1	43009	382.3	940.3	967.5	1050.0	504.2	644.2
AB445099.1	315688	745.5	1777.1	1305.8	1763.2	1425.8	1476.0
AB304087.1	249455	1256.9	1076.2	1249.8	1139.5	387.8	628.7
AB303367.1	257476	4438.2	6049.4	5771.0	5630.8	5944.3	5581.6
EF519867.1	267119	187.1	339.1	285.0	101.1	175.3	337.3
D45202.1	4575	60.5	108.1	279.3	214.7	952.4	245.3
EF446228.1	213763	502.9	583.8	1444.1	1349.9	369.0	629.0
EF446204.1	208105	301.1	793.6	669.0	267.0	666.3	827.6
EF516844.1	220042	204.1	294.5	916.6	220.6	1359.4	884.2
L22481.1	8030	3689.7	4831.3	2440.7	3538.1	598.0	4256.2
AF465832.1	79493	437.0	1468.8	1287.5	436.4	2046.1	1833.3
AY234551.1	112277	2300.3	2011.8	3035.0	3801.6	2134.0	2320.7
GQ088427.1	407742	2121.2	3301.4	3811.4	2577.9	8046.3	5600.9
GQ402627.1	593096	3803.4	4981.7	3925.9	4052.0	3884.7	3819.9
DQ906085.1	222665	1520.5	1598.0	1069.3	2217.7	3097.9	1914.2
GU172195.1	537239	676.8	1148.0	1450.8	717.2	5318.0	1443.6
AJ633644.1	103476	170.0	39.3	33.6	84.7	238.6	109.2
AY370188.1	104162	27.4	47.3	65.3	89.2	82.5	36.6
DQ378212.1	152090	454.3	1144.9	1553.6	1343.6	1304.4	1488.7
FM874498.1	361359	1424.9	1886.7	2198.0	1182.5	1724.1	2627.1
AB240243.1	144065	6459.1	6517.6	4471.7	7350.1	9791.6	9283.9
FJ915153.1	583138	90.9	100.0	602.4	98.6	54.4	80.4
DQ129264.1	138221	2072.8	2888.1	2213.8	1143.0	6433.6	2706.5
EF409853.1	207022	1740.2	2929.5	4206.4	1778.5	6032.2	2470.5
EU861903.1	306635	6501.2	10591.5	7904.1	6049.5	10863.5	10589.8
FJ595556.1	532895	2993.2	4622.4	3801.2	2302.8	4305.0	4834.8
DQ378204.1	151650	586.4	854.2	2918.2	458.4	2692.2	1007.2
AB110421.1	91691	35.2	53.0	79.1	69.5	63.8	46.4
AY913353.1	112752	1805.6	2758.1	5180.2	1312.0	3978.2	4092.2
EU409119.1	263028	2403.1	3503.3	2866.2	2099.0	3986.1	3262.9
AM162403.1	154314	34.5	54.8	63.8	66.6	75.5	82.3
Y07647.2	4411	4866.2	7206.0	7284.9	4709.2	12051.4	9845.3
EU409601.1	276553	2371.8	3308.9	3826.0	2733.1	6126.7	2372.8
DQ906066.1	223618	179.9	135.0	267.6	98.2	286.9	149.2
AM697086.1	221365	2435.8	4452.7	3043.0	2215.5	7146.5	4940.8
AY395443.1	102882	48.0	48.6	118.3	86.2	75.9	52.9
EU360476.1	259611	1360.0	1648.7	3445.9	1079.7	2209.8	3012.2
AJ292597.1	53994	1780.5	2087.2	2723.5	941.4	3945.4	4102.3

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AJ292602.1 gg_id:32348 PCB-polluted soil clone WD271
EF520426.1 gg_id:230396 structure lakes: what controls ? acid-impacted lake clone ADK-SGh02-10
FJ465991.1 gg_id:509891 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea
GQ059256.1 gg_id:458919 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
AJ292598.1 gg_id:43037 PCB-polluted soil clone WD248
AM162450.1 gg_id:151048 and situ identification acidic sphagnum peat bog clone B78
EU250247.1 gg_id:250255 acid mine drainage clone GXDC-33
AB381935.1 gg_id:263857 Rhodovastum atsumiense str. G2-11
GQ402643.1 gg_id:585535 Accessing microbial biodiversity and metabolic potential tropical -based approach pe
AM691109.1 gg_id:222002 Acetobacteraceae clone BF15
EU445203.1 gg_id:554674 Isolation Weight Forest Topsoil Metagenomic tropical forest topsoil clone R16
DQ378187.1 gg_id:152683 oil-polluted soil clone F23_Pitesti
DQ378196.1 gg_id:155293 oil-polluted soil clone F33_Pitesti
AM696849.1 gg_id:226512 sequencing libraries indoor dust clone BF0002A034
AJ867914.1 gg_id:141085 Fluctuations Significantly Influence Microbial Present Nival Lakes lake water clone C2
FJ466191.1 gg_id:572984 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea
EU861954.1 gg_id:319672 effects chronic fertilization on alpine tundra microbial implications carbon and cyclin
EU250257.1 gg_id:253895 acid mine drainage clone GXDC-43
FJ228277.1 gg_id:315855 sulfate-reducing enriched during bioremediation experiment sediments (Brandenbur
DQ532333.1 gg_id:171696 Geographical Variation Microbial Burden and Spacecraft Assembly Kennedy Space C
AF465654.1 gg_id:21795 geothermal soil clone YNPRH71B
GQ495410.1 gg_id:591379 terrestrial volcanic rocks Iceland Hnausahraun lava f clone Bas-7-52
GQ402607.1 gg_id:509496 Accessing microbial biodiversity and metabolic potential tropical -based approach pe
AJ292611.1 gg_id:44239 PCB-polluted soil clone WD2108
GQ054463.1 gg_id:451765 Topographical and Temporal Human Skin Microbiome skin back clone nbw1089b08c
EF516502.1 gg_id:223286 grassland soil clone FCPT506
FJ774959.1 gg_id:509511 Symbionts Brown Planthopper (Homoptera: Delphacidae) symbiont Nilaparvata luger
DQ659205.1 gg_id:220971 acid mine drainage clone DBS-Clone30
DQ833767.1 gg_id:172972 Geochemical Controls on Microbial Rainbow and Springs Yellowstone National Park
AY192273.1 gg_id:81029 Rocky Mountain alpine soil clone W2b-8C
FM874399.1 gg_id:364038 occupant source house mattress dust clone MD01H12
AB286050.1 gg_id:229374 Asaia lannaensis str. BCC 15733
AB297501.1 gg_id:250834 Roseomonas sp. str. K-20 (=JCM 14634)
GQ055435.1 gg_id:432032 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1115c0
AM934721.1 gg_id:545175 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
AY594267.2 gg_id:122816 Photorhabdus luminescens
AY741146.1 gg_id:163171 Azospirillum amazonense str. 21R
GU256437.1 gg_id:580136 Azospirillum amazonense str. DSM 2787
DQ288688.1 gg_id:151705 Azospirillum brasilense str. MTCC4037
GQ284588.2 gg_id:542408 Azospirillum sp. str. ptl3

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AJ292602.1	32348	98.8	126.6	756.7	128.3	124.0	76.9
EF520426.1	230396	87.9	196.3	364.7	128.8	183.5	80.4
FJ465991.1	509891	1916.8	2953.4	1878.4	1743.1	5177.2	3503.6
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AJ292598.1	43037	1733.0	1502.9	1700.2	656.6	1705.8	1987.5
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AB381935.1	263857	4748.1	4990.0	5541.1	2552.0	12077.9	8235.6
GQ402643.1	585535	21.7	33.9	28.9	65.5	60.6	31.5
AM691109.1	222002	209.3	322.9	246.2	99.1	104.8	85.8
EU445203.1	554674	158.2	179.0	989.2	225.7	713.2	1248.8
DQ378187.1	152683	1182.0	2119.5	1195.3	1852.1	5439.4	6028.8
DQ378196.1	155293	3727.1	3418.5	3414.7	6419.5	8356.6	7559.6
AM696849.1	226512	2719.5	3971.4	5543.4	2551.1	5896.2	7053.3
AJ867914.1	141085	83.6	467.8	1546.3	222.6	1402.4	2249.9
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DQ532333.1	171696	204.9	354.6	615.0	231.3	347.6	907.8
AF465654.1	21795	178.2	421.6	969.5	480.5	369.5	375.4
GQ495410.1	591379	1223.1	1285.3	1619.6	344.2	1031.1	854.8
GQ402607.1	509496	1058.8	1507.5	3717.1	1587.8	4603.7	3713.8
AJ292611.1	44239	1381.7	1621.3	2095.5	1008.4	2533.6	1023.7
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EF516502.1	223286	703.1	1444.5	2073.9	439.0	1972.4	1459.2
FJ774959.1	509511	1266.9	2344.0	4009.9	1837.6	5630.8	4182.7
DQ659205.1	220971	814.7	1121.9	1171.0	2469.2	3262.6	2559.4
DQ833767.1	172972	2150.8	5282.6	1907.5	2941.8	5122.5	5392.9
AY192273.1	81029	39.8	106.5	381.3	75.2	233.5	547.8
FM874399.1	364038	692.8	1382.5	1355.6	273.9	755.7	804.7
AB286050.1	229374	1355.3	3732.8	1676.1	2601.7	3412.0	3190.9
AB297501.1	250834	193.2	395.9	501.6	99.0	366.7	251.7
GQ055435.1	432032	4949.6	6287.7	5864.2	4646.4	11162.8	7922.2
AM934721.1	545175	2080.8	2432.1	2645.6	2261.2	4585.2	5616.3
AY594267.2	122816	1650.9	3280.1	4033.4	1384.9	6471.3	3506.8
AY741146.1	163171	25.9	47.8	72.7	151.5	490.2	66.4
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GQ284588.2	542408	365.7	713.4	3185.4	1043.2	1598.9	2404.9

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AY958234.2 gg_id:114930 Azospirillum brasilense N8
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AP010947.1 gg_id:514463 Azospirillum sp. str. B510
DQ304794.1 gg_id:151417 studies on and nifH Lasiurus sindicus Sewan grass Thar Desert India root clone C3
AY344369.2 gg_id:91010 Lake Kauhako 30 m clone K2-30-36
AB542395.1 gg_id:546390 Azospirillum sp. str. TSA36t
AY283791.1 gg_id:86765 Azospirillum sp. str. LOD4
AB508899.1 gg_id:568722 Azospirillum sp. str. TSH98
FJ871055.1 gg_id:565380 Azospirillum lipoferum str. ATCC 29707
DQ288690.1 gg_id:156178 Azospirillum brasilense str. MTCC4039
AY563022.1 gg_id:104372 Azospirillum sp. WAI-19
AM922283.1 gg_id:248382 Azospirillum picis str. IMMIB Tar-3
AF521650.1 gg_id:58733 Azospirillum sp. str. Arm2-2
DQ676344.1 gg_id:220178 Archaeal sediment and plankton freshwater pond suboxic freshwater-pond clone M
AB307662.1 gg_id:260920 clay wall used Japanese traditional buildings clone R63
AJ238567.1 gg_id:4572 Azospirillum doebereinerae str. 63f
DQ104848.1 gg_id:131955 Azospirillum brasilense str. A154
DQ787330.1 gg_id:171362 Azospirillum lipoferum str. B2
EU678791.1 gg_id:283785 Azospirillum sp. str. BV-s
AY265875.1 gg_id:105629 perchlorate-reducing ABL1
EU264075.1 gg_id:344876 Azospirillum sp. str. CA6
GU256443.1 gg_id:590104 Azospirillum oryzae str. JCM 21588
AB208736.1 gg_id:115023 AEOC021 clone
DQ682470.1 gg_id:163594 Azospirillum oryzae str. N7
AY692040.1 gg_id:107382 UASB reactor clone I43
AY660962.1 gg_id:101185 Azospirillum lipoferum str. CN1
AF170353.1 gg_id:4586 Azospirillum sp. str. TTI
AY118224.1 gg_id:63341 Azospirillum sp. str. DA2-3-1
DQ288686.1 gg_id:152173 Azospirillum brasilense str. MTCC4035
AB508878.1 gg_id:573964 Azospirillum sp. str. TSH5
AB487643.1 gg_id:594099 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNSR0
AB508897.1 gg_id:562150 Azospirillum sp. str. TSH96
FJ970032.1 gg_id:439656 Inquilinus sp. str. CCBAU 01442
AM162580.1 gg_id:153285 and role capsules Sepia officinalis host egg clone 3SOMBO87
GU118836.1 gg_id:572584 Threatened Corals Provide Microbial Habitats clone Mfra_A15
AJ244806.1 gg_id:25832 Sepia officinalis symbiont
AM162572.1 gg_id:150158 and role capsules Sepia officinalis cuttlefish egg capsule clone 3iSOMBO24
GU118235.1 gg_id:537977 Threatened Corals Provide Microbial Habitats clone Dstr_L14
GU118741.1 gg_id:555264 Threatened Corals Provide Microbial Habitats clone Mfra_E20
AJ244796.1 gg_id:34409 Sepia officinalis symbiont
GU118225.1 gg_id:587505 Threatened Corals Provide Microbial Habitats clone Dstr_G01

AY958234.2	114930	663.9	1040.4	3874.0	1955.8	3537.2	3447.2
DQ022956.1	138398	7053.1	6958.7	5422.1	5753.7	9844.6	9508.4
AP010947.1	514463	7323.6	7185.3	9681.1	7176.9	15556.0	14493.7
DQ304794.1	151417	10095.0	8567.8	8100.2	9558.3	14883.5	11835.6
AY344369.2	91010	131.2	347.0	589.3	281.3	337.1	751.9
AB542395.1	546390	5501.8	7156.8	5685.6	5580.2	12033.9	12052.0
AY283791.1	86765	1155.1	1116.5	2251.5	1147.4	5686.7	2611.2
AB508899.1	568722	3779.7	4455.2	6468.3	5891.4	6975.5	8205.4
FJ871055.1	565380	3338.2	3981.6	6591.8	4922.8	6377.8	6926.2
DQ288690.1	156178	1279.1	1777.1	4647.1	2637.9	5839.8	6130.6
AY563022.1	104372	9722.8	7937.6	9307.2	11341.7	12539.8	12302.5
AM922283.1	248382	3415.7	6462.9	6463.3	4497.9	6818.9	8037.5
AF521650.1	58733	5653.3	6521.4	9478.2	5162.0	12425.8	12361.2
DQ676344.1	220178	358.8	297.1	497.1	394.3	959.0	2154.7
AB307662.1	260920	6072.1	8518.4	8601.8	5722.7	11111.9	10307.1
AJ238567.1	4572	4122.2	2918.0	3615.7	2786.6	5501.6	3965.5
DQ104848.1	131955	6301.7	6481.0	7708.6	6824.5	9123.8	9235.7
DQ787330.1	171362	2798.5	2925.7	4086.5	4113.1	5500.7	6634.1
EU678791.1	283785	6437.7	7905.6	9686.6	8938.8	11625.6	13247.6
AY265875.1	105629	1796.8	2011.6	3523.8	2480.4	4095.7	4239.6
EU264075.1	344876	12802.0	13033.1	10937.5	11356.3	17967.5	18959.5
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DQ682470.1	163594	4764.1	5015.5	6669.6	5849.4	10207.0	9693.2
AY692040.1	107382	4760.5	6925.2	8768.7	4463.5	12846.7	11958.4
AY660962.1	101185	5908.7	7917.1	7378.4	6717.2	11218.1	9887.9
AF170353.1	4586	6251.0	7675.6	7779.8	7356.1	16196.8	13280.3
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DQ288686.1	152173	4251.7	4771.5	3978.7	6994.9	7299.9	7861.9
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AB487643.1	594099	4132.2	7260.5	7146.1	5405.5	11000.0	12307.5
AB508897.1	562150	1383.9	1455.9	4580.4	785.3	2778.8	2967.0
FJ970032.1	439656	1315.7	1745.3	1073.7	1997.3	1302.3	2135.4
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GU118836.1	572584	7459.0	9276.5	12526.5	5968.7	12109.1	12388.6
AJ244806.1	25832	453.2	777.6	1016.8	401.8	2440.0	3329.0
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GU118225.1	587505	3311.6	5221.6	1931.1	2028.3	2175.9	4074.5

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DQ889913.1 gg_id:200287 natural product producing octocoral Erythropodium caribaeorum clone EC75
GU118960.1 gg_id:582926 Threatened Corals Provide Microbial Habitats clone Past_N22
GU118209.1 gg_id:561066 Threatened Corals Provide Microbial Habitats clone Dstr_P09
FJ203583.1 gg_id:329326 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h
AM709743.1 gg_id:256953 symbiotic Ruegeria strains cuttlefish Sepia officinalis renal appendages clone B4SOA
EF612768.1 gg_id:242309 Aquaspirillum peregrinum subsp. integrum str. LMG 5407
AM901294.1 gg_id:328525 Phaeospirillum cystidoformans str. JA317
NR_027605.1 gg_id:543918 Magnetospirillum gryphiswaldense MSR-1 str. MSR-1; DSM 6361
AJ488096.1 gg_id:66169 chlorobenzene-degrading consortium clone IIIA-9
D14433.1 gg_id:4535 Phaeospirillum fulvum str. NCIMB11762
AY171615.1 gg_id:78316 Dechlorospirillum sp. str. SN1
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AB250624.1 gg_id:155751 Phaeospirillum sp. str. TUT3101
AB307663.1 gg_id:276270 clay wall used Japanese traditional buildings clone B21
Y17390.1 gg_id:4531 Magnetospirillum sp. str. MSM-4
AB378599.1 gg_id:259049 dominate denitrification nitrate- succinate-ammended stable istope probing 13C fra
FJ230905.1 gg_id:306797 under Level Antibiotic Selection Pressures river water clone F56
AB487549.1 gg_id:580150 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNSR0
AJ292593.1 gg_id:37406 PCB-polluted soil clone WD229
AB111108.1 gg_id:200462 Electrochemically assisted iron respiration grow previously iron-reducing clone LS-2
DQ659219.1 gg_id:217481 acid mine drainage clone DBS-Clone44
AM990911.1 gg_id:279352 Nisaea sp. MOLA 137
FJ202804.1 gg_id:310439 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k
DQ665839.1 gg_id:162790 Nisaea denitrificans str. DR41_18
AB074520.1 gg_id:66304 Aquaspirillum itersonii subsp. nipponicum str. IAM 14945 subsp.
DQ234645.1 gg_id:143736 subsurface water clone DR546BH1103001SAD24
EU835446.1 gg_id:313151 structure and quorum sensing reverse osmosis RO membrane biofilm clone 2B21
AF293000.1 gg_id:50973 ferromanganous micronodule clone MNG3
NR_028855.1 gg_id:574444 Rhodocista pekingensis str. 3-p; JCM 11669
FM177580.1 gg_id:313312 Rhodocista pekingensis str. JA405
AM072288.1 gg_id:138132 Rhodocista xerospirillum
NC_011420.2 gg_id:326714 Rhodospirillum centenum SW str. SW; ATCC 51521
CP000230.1 gg_id:143149 Rhodospirillum rubrum str. ATCC 11170
D30777.1 gg_id:4516 Rhodospirillum photometricum str. E-11
D14431.1 gg_id:6144 Rhodothalassium salexigens str. ATCC35888
AM296500.1 gg_id:180810 Rhodovibrio salinarum str. JA137
FJ152947.1 gg_id:356548 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX4CE
GU447293.1 gg_id:524419 Rhodovibrio salinarum str. LYG30
DQ432379.1 gg_id:156957 prokaryotic alkaline hypersaline lakes Wadi Natrun Egypt Lake Hamra water clone W
DQ103606.1 gg_id:136158 hypersaline endoevaporitic microbial mat clone E4aB02
DQ103605.1 gg_id:133137 hypersaline endoevaporitic microbial mat clone E4aF06

DQ889913.1	200287	6104.5	7654.2	8101.7	5287.1	11750.4	11752.2
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GU118209.1	561066	406.4	1439.0	906.5	333.9	1504.8	2473.2
FJ203583.1	329326	3260.7	2723.7	3326.3	1516.0	3728.8	3714.4
AM709743.1	256953	4099.4	7687.2	5670.6	4692.0	7365.3	7283.7
EF612768.1	242309	166.3	383.6	215.9	169.5	379.9	121.2
AM901294.1	328525	4708.4	4564.2	6304.3	7438.2	8330.5	7931.6
NR_027605.1	543918	3461.4	4875.8	7954.8	4103.7	8147.3	9114.0
AJ488096.1	66169	5360.8	8406.3	6150.3	10038.8	12366.6	10763.6
D14433.1	4535	4048.7	6251.3	9782.7	4221.2	12264.0	11213.3
AY171615.1	78316	1999.8	4082.9	6416.4	2642.0	5971.1	6937.3
AJ617837.1	110792	25.2	49.7	138.6	60.3	89.5	40.7
AB250624.1	155751	289.4	897.2	3282.5	934.7	3203.6	4273.1
AB307663.1	276270	2721.8	4480.7	5340.0	4208.5	11454.2	9470.0
Y17390.1	4531	5531.2	7789.0	20291.3	6962.9	14306.5	10009.3
AB378599.1	259049	7934.3	9952.3	11746.5	9641.7	13407.5	13529.5
FJ230905.1	306797	1093.4	572.3	4183.4	1722.6	2817.4	922.5
AB487549.1	580150	347.0	789.7	3595.2	335.7	1263.9	1106.0
AJ292593.1	37406	2949.3	3257.3	4687.7	4652.0	5314.4	4807.0
AB111108.1	200462	5579.9	6520.8	6710.9	5846.1	7867.5	8546.1
DQ659219.1	217481	4234.8	4720.8	3410.1	2242.9	3535.8	3142.7
AM990911.1	279352	1155.8	1235.8	2960.5	2224.9	2098.7	4432.4
FJ202804.1	310439	1032.9	2758.6	3250.4	850.4	4880.2	6715.8
DQ665839.1	162790	3975.6	7043.8	8598.6	4448.6	9853.7	11238.7
AB074520.1	66304	66.8	190.5	361.5	138.2	598.1	485.4
DQ234645.1	143736	914.1	1330.3	3901.3	1263.7	3854.0	4590.2
EU835446.1	313151	209.4	564.8	770.9	658.0	4108.0	1798.5
AF293000.1	50973	1492.0	1530.9	2269.7	1725.2	5636.4	4387.2
NR_028855.1	574444	1100.7	1925.5	2505.4	1821.7	5450.9	4303.8
FM177580.1	313312	7080.0	8712.7	11481.8	7289.5	13327.4	12176.6
AM072288.1	138132	6653.2	7778.3	9079.3	5311.9	10848.1	9094.3
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CP000230.1	143149	3253.8	2869.1	5385.0	3196.8	3457.3	2631.2
D30777.1	4516	4170.2	5550.8	9336.7	5054.0	13693.5	9975.8
D14431.1	6144	115.3	87.2	200.3	464.0	324.5	433.2
AM296500.1	180810	1433.7	3210.1	4255.8	4082.3	6658.6	9722.0
FJ152947.1	356548	1598.2	1997.9	4062.5	1395.6	538.7	2926.7
GU447293.1	524419	4428.7	3908.9	6281.7	4890.6	5131.0	5602.2
DQ432379.1	156957	6874.1	9503.3	9975.1	6741.1	12869.1	13118.1
DQ103606.1	136158	1969.9	2963.9	2655.9	2770.2	3235.9	3096.7
DQ103605.1	133137	1128.8	1365.8	1100.8	1365.7	911.5	1067.1

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DQ103604.1 gg_id:131371 hypersaline endoevaporitic microbial mat clone E4bC07
AJ318524.1 gg_id:62473 Rhodovibrio sodomensis str. SG3105
AY987846.1 gg_id:136616 Rhodovibrio sp. 2Mb1
AM284389.1 gg_id:181835 Roseospira goa str. JA133
DQ103603.1 gg_id:132484 hypersaline endoevaporitic microbial mat clone E6aD01
AM691104.1 gg_id:225998 Rhodobacteraceae clone EG16
DQ672568.1 gg_id:172363 Skermanella sp. str. 5416T-32
GU195651.1 gg_id:584833 Skermanella sp. str. Py-2-1
EU979029.1 gg_id:306356 Effects intercropping Rhizobium inoculation on microbial biomass and rhizosphere b
AB240277.1 gg_id:143931 microbial structure rhizosphere Phragmites bulk soil reed bed reactor laboratory clo
GU134927.1 gg_id:560804 Acid-tolerant microaerophilic oxdizing enhance Fe(III) accumulation Fe(II) oxidizing
GQ402757.1 gg_id:510201 Accessing microbial biodiversity and metabolic potential tropical -based approach p
FJ823892.1 gg_id:529891 Controlling accumulation fermentation inhibitors biorefinery recycle water microbial
FJ823930.1 gg_id:525260 Controlling accumulation fermentation inhibitors biorefinery recycle water microbial
AM162451.1 gg_id:156377 and situ identification acidic sphagnum peat bog clone B85
AB071665.1 gg_id:67722 Tistrella mobilis
FN556563.1 gg_id:514434 Tistrella sp. str. JW16.1a
AM259857.1 gg_id:212680 Spatial sponge- Mediterranean Tethya aurantium sponge cortex clone TAA-10-13
EF682992.1 gg_id:235586 Eastern Mediterranean atmosphere clone F14_1C_FL
AM743175.1 gg_id:252146 Azospirillum sp. str. AP-500
EF125412.1 gg_id:176117 soil naked tidal flat sediment near mangrove clone MSB-1F1
DQ167235.1 gg_id:138716 Brucella sp. str. HJ114
AJ966587.1 gg_id:138336 and screening metagenomic library 5274m depth Pacific nodule province deep sea se
FJ746303.1 gg_id:568242 Microbial oligotrophic marine sediments: South Pacific Gyre ocean sediment 5306 m
GQ350189.1 gg_id:545318 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
EU881096.1 gg_id:331647 Karst region primary forest soil clone KPF200711-101
EF032744.1 gg_id:198274 cyanobacterial mat in lava cave clone HAVOmat83
AY598790.1 gg_id:102860 Germany: Lake Staffelsee clone SS31
AF391979.1 gg_id:45882 thermal soil clone YNPFFP3
EF494345.1 gg_id:225101 Nunnock River granitic landscape clone NR.1.078
AM293856.1 gg_id:206331 Subaequorebacter tamlense str. HST3-12
GQ264472.1 gg_id:588466 Structure Simulated Level Waste Site simulated level waste site clone WW3_179
EU050764.1 gg_id:241084 libraries sediment Kings Bay Svalbard Arctic clone ss1_B_04_78
EF020098.1 gg_id:206127 aspen rhizosphere clone Elev_16S_1509
EF471705.1 gg_id:259136 Fast Screening and Estuarine Operon Libraries whole surface water Chesapeake Bay
EU919770.1 gg_id:341359 Kongsfjorden western Spitsbergen Svalbard ocean water clone b31
EU048669.1 gg_id:250376 and archaeal surface marine sediment Slope South China Sea clone MD2896-B9
EU236336.1 gg_id:292058 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg5a2C6
DQ001629.1 gg_id:157721 Microbial seeps asphalt seep clone E91-35
AB193945.1 gg_id:108907 deep-sea vent clone Sc-EB05
AM935074.1 gg_id:552526 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd

DQ103604.1	131371	6377.9	6614.8	4993.3	8037.9	8941.3	9323.5
AJ318524.1	62473	103.1	183.2	330.9	286.7	482.7	150.7
AY987846.1	136616	6155.4	6915.3	7165.2	9517.4	14643.5	10240.1
AM284389.1	181835	3637.2	4040.7	3128.3	2587.8	11986.4	4786.1
DQ103603.1	132484	1830.3	3781.4	2673.7	1770.6	5996.6	3611.0
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DQ672568.1	172363	138.6	189.8	122.9	211.4	224.9	901.8
GU195651.1	584833	2219.7	2402.0	2336.1	2296.6	2937.8	4109.5
EU979029.1	306356	1839.9	3508.3	5298.3	2151.9	4515.7	4981.4
AB240277.1	143931	3586.4	5156.7	5055.0	3618.3	6522.3	8407.2
GU134927.1	560804	2946.7	3072.8	2896.6	4116.3	4954.4	5259.6
GQ402757.1	510201	4761.2	6786.9	6095.8	6979.0	16476.8	12213.7
FJ823892.1	529891	1305.5	2375.6	2948.9	1062.2	3899.9	3471.5
FJ823930.1	525260	25.5	62.6	512.4	78.3	127.1	31.6
AM162451.1	156377	492.3	866.3	1941.1	1974.9	1441.5	1521.6
AB071665.1	67722	1197.3	2229.8	4682.5	1377.4	6781.4	6290.6
FN556563.1	514434	1587.7	1717.2	3141.8	1551.6	5047.2	1924.8
AM259857.1	212680	3891.7	3428.4	3151.4	1955.8	1771.6	1922.3
EF682992.1	235586	6588.6	6405.3	10496.5	6983.5	10939.9	11459.9
AM743175.1	252146	1820.4	3487.9	5342.1	2456.3	8722.9	5353.0
EF125412.1	176117	21.2	19.4	19.5	58.1	64.0	23.2
DQ167235.1	138716	960.2	1205.0	676.2	1578.8	4541.3	2911.6
AJ966587.1	138336	617.7	1053.0	1761.9	715.0	2830.8	4532.6
FJ746303.1	568242	12799.5	16705.6	18989.6	14514.3	23839.2	19394.0
GQ350189.1	545318	296.5	373.0	550.4	276.6	880.5	569.1
EU881096.1	331647	6043.0	6091.3	7965.6	4913.9	10221.3	13066.1
EF032744.1	198274	1740.8	3208.3	2266.4	515.5	3527.7	2868.7
AY598790.1	102860	3941.1	4816.3	4657.3	3253.5	6854.5	5919.6
AF391979.1	45882	191.0	180.6	618.6	954.0	2607.4	4624.1
EF494345.1	225101	2144.0	2562.8	4582.7	2325.8	3744.1	4430.2
AM293856.1	206331	277.4	378.0	333.3	249.0	143.5	125.8
GQ264472.1	588466	1311.0	3029.7	7397.5	4164.9	3698.0	7415.7
EU050764.1	241084	2687.4	3554.9	2847.5	2042.5	4699.5	3381.2
EF020098.1	206127	174.4	244.5	1799.8	453.0	1326.3	2755.2
EF471705.1	259136	1572.4	3188.0	7405.1	3175.3	6577.3	7841.8
EU919770.1	341359	2713.2	4475.6	5157.5	4031.2	7608.8	9722.3
EU048669.1	250376	3368.5	4177.5	8159.4	4149.1	10522.7	12109.8
EU236336.1	292058	2479.9	3552.4	6350.4	4588.0	9341.5	11041.6
DQ001629.1	157721	4640.6	6977.2	6931.7	3943.9	12583.6	8409.8
AB193945.1	108907	114.1	482.0	732.3	231.8	643.5	897.8
AM935074.1	552526	4928.2	4492.5	8607.4	4896.0	8075.3	5841.9

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FJ202806.1 gg_id:342034 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k
GQ350131.1 gg_id:594295 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
FJ535047.1 gg_id:568244 Enhancement protein conversion volatile fatty acids accumulation during addition: ef
EU491336.1 gg_id:261444 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak
GU118173.1 gg_id:561208 Threatened Corals Provide Microbial Habitats clone Dstr_L03
AM997392.1 gg_id:555289 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A
GU118261.1 gg_id:583811 Threatened Corals Provide Microbial Habitats clone Dstr_K01
FJ517060.1 gg_id:512990 semiarid 'Tablas de Daimiel National Park' wetland (Central Spain) unravelled water c
EU043719.1 gg_id:250043 fluences structure fosters richness subtropical Altamaha Ohopee River Valley inland
EF018877.1 gg_id:211913 aspen rhizosphere clone Amb_16S_1361
AY963356.1 gg_id:152533 structures and correlated ecological factors soils two evergreen broad-leaved forests
DQ378220.1 gg_id:154249 oil-polluted soil clone F58_Pitesti
DQ640710.1 gg_id:232270 full-scale EBPR sludge clone Skagen52
EF516955.1 gg_id:226012 grassland soil clone FCPN514
AY326611.1 gg_id:136208 Amazon soil clone 178-2
EF515225.1 gg_id:223603 Electricigen Enrichment MFC upf microbial fuel cell anode clone 21e11
EU133518.1 gg_id:236426 tallgrass prarie soil clone FFCH17724
GQ350707.1 gg_id:550871 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
FJ746316.1 gg_id:540101 Microbial oligotrophic marine sediments: South Pacific Gyre ocean sediment 5306 m
EF125410.1 gg_id:182626 soil naked tidal flat sediment near mangrove clone MSB-1E8
GQ264148.1 gg_id:552057 Structure Simulated Level Waste Site simulated level waste site clone WC3_89
AF104474.1 gg_id:5172 Olavius loisae endosymbiont 3
AY921823.1 gg_id:112944 farm soil clone AKYG694
AJ347025.1 gg_id:60184 sponge clone TK03
AB248648.1 gg_id:147088 mesophilic anaerobic butyrate-degrading reactor clone BHB19
EU223956.1 gg_id:250075 -RFLP microbes Qinghai-Tin rail soil clone 127
EU834785.1 gg_id:587763 Microbiology Aerobic Phosphorus Removal Process aerobic phosphorus-removing se
AM259856.1 gg_id:211365 Spatial sponge- Mediterranean Tethya aurantium sponge cortex clone TAA-10-03
EF157247.1 gg_id:243543 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon
AM997745.1 gg_id:555861 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A
EU133614.1 gg_id:253675 tallgrass prarie soil clone FFCH18567
GQ350360.1 gg_id:584854 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
AB369165.1 gg_id:241639 Microbiological Assessment Circulation Mud Fluids During First Operation Drilling De
AF406524.1 gg_id:60649 complex marine community d at depth 200 m North Aegean Sea (Station 3) clone AEG
EU834769.1 gg_id:545652 methods extraction nucleic acid activated lab scale EBPR-activated sludge clone L24
GU134929.1 gg_id:583250 Acid-tolerant microaerophilic oxdizing enhance Fe(III) accumulation Fe(II) oxidizing e
DQ015800.1 gg_id:139714 Antarctic lake water clone ELB16-121
DQ070828.1 gg_id:147136 Prokaryotic Structures Seafloor Basalts Varying Age East Pacific Rise and Ridge basal
GQ337284.1 gg_id:572538 Hydrography shapes biogeography deep Arctic Ocean water depth 996m clone NB0
AY913404.1 gg_id:114085 forest soil clone DUNssu198 (-7B) (OTU#132)
AJ519623.1 gg_id:75071 Uranium mill tailings soil sample clone Sh765B-TzT-31 proteobacterium

FJ202806.1	342034	2223.1	721.8	462.7	1036.4	479.3	304.7
GQ350131.1	594295	2461.1	2581.1	4778.3	2872.0	6430.1	4762.1
FJ535047.1	568244	7228.6	7138.1	15562.6	6023.6	10001.6	10225.7
EU491336.1	261444	3548.6	4203.4	6332.0	4016.5	8563.3	7861.9
GU118173.1	561208	3790.8	4019.1	5420.9	3909.6	8250.8	8880.2
AM997392.1	555289	2364.4	3748.0	3577.5	3169.7	4376.2	4385.2
GU118261.1	583811	2781.3	2906.9	1832.4	1283.0	4345.4	988.0
FJ517060.1	512990	5818.9	7611.2	11075.9	4691.3	11058.9	10326.1
EU043719.1	250043	9052.5	9774.2	7467.8	7447.4	13297.8	12088.5
EF018877.1	211913	129.1	333.0	144.2	128.0	134.5	152.6
AY963356.1	152533	534.1	1188.5	1744.7	376.9	592.7	374.4
DQ378220.1	154249	1279.6	1495.4	1099.5	1285.8	3296.1	2700.0
DQ640710.1	232270	6523.6	7251.4	6531.2	5265.1	10360.9	10418.9
EF516955.1	226012	1913.2	2943.0	5402.3	1105.2	4943.3	4447.8
AY326611.1	136208	650.6	547.1	464.0	793.5	126.3	415.4
EF515225.1	223603	49.6	101.8	280.7	169.4	97.1	250.4
EU133518.1	236426	1621.3	2101.0	5106.0	2137.1	1821.9	2950.0
GQ350707.1	550871	583.9	1285.3	3026.5	676.1	6541.3	6231.3
FJ746316.1	540101	7451.8	8242.6	14042.0	6877.8	10733.6	9952.9
EF125410.1	182626	194.8	250.7	228.5	222.3	716.9	778.7
GQ264148.1	552057	227.3	546.4	2024.0	377.5	2464.9	1269.9
AF104474.1	5172	1956.7	3582.8	2750.5	2035.8	6651.1	4332.7
AY921823.1	112944	3226.0	3827.1	5652.2	2373.2	6532.6	7061.8
AJ347025.1	60184	30.6	66.6	172.3	104.5	84.6	95.1
AB248648.1	147088	229.3	663.2	3193.2	833.8	1842.5	1759.0
EU223956.1	250075	1639.7	3409.1	6232.2	1359.0	5636.3	6376.4
EU834785.1	587763	205.8	552.5	1394.5	256.1	1163.8	3183.2
AM259856.1	211365	39.6	68.2	50.9	60.3	86.2	60.0
EF157247.1	243543	749.6	1839.4	3098.1	545.0	4689.4	4918.6
AM997745.1	555861	8344.3	7031.0	7629.3	7537.8	11843.7	9885.9
EU133614.1	253675	6825.3	7173.3	7767.7	4694.5	11001.0	9137.7
GQ350360.1	584854	1517.9	1357.4	2429.8	1947.2	1942.7	3277.5
AB369165.1	241639	1329.0	2372.8	3378.2	1366.0	6659.3	2226.8
AF406524.1	60649	7075.5	8431.5	7130.7	4656.0	11023.4	8056.4
EU834769.1	545652	1375.8	1702.9	2157.3	750.6	2394.7	1786.8
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DQ015800.1	139714	1955.6	3328.2	4809.0	3506.5	3969.5	3814.7
DQ070828.1	147136	3279.3	4849.6	8725.1	3758.0	12002.3	11082.4
GQ337284.1	572538	6461.8	7885.8	11641.0	7956.9	16301.5	14091.3
AY913404.1	114085	1633.0	2354.7	905.0	2979.2	8051.5	6974.7
AJ519623.1	75071	13530.3	12083.8	11548.9	9633.6	14749.1	14937.3

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AF293001.1 gg_id:26566 ferromanganous micronodule clone MNC12
FJ479421.1 gg_id:511480 species richness estimates obtained nearly and simulated pyrosequencing-generated
GQ500775.1 gg_id:552221 Surveys Biofilms and Sediments Mammoth Cave Karst Aquifers Bio-Sep beads conta
DQ917851.1 gg_id:218252 Microbial profiles bleached and wild-type Muricea elongata Ochrobactrum clone BM
EU617825.1 gg_id:343695 Seasonal variation microbial Yel Sea sediment clone C13S-26
EU491409.1 gg_id:268557 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X4 clone
FM877531.1 gg_id:368599 Microbial several mining wastes Bulgaria uranium mill tailings clone BuhD-22
EU491319.1 gg_id:260202 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak
EU202862.1 gg_id:317723 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo
GQ347126.1 gg_id:553069 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
EU236340.1 gg_id:294380 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg5a2F3
DQ015803.1 gg_id:140565 Antarctic lake water clone ELB16-042
EU373886.1 gg_id:270370 southern Cretan margin (eastern Mediterranean Sea) canyon and slope sediment cl
GU118149.1 gg_id:577466 Threatened Corals Provide Microbial Habitats clone Dstr_F11
AB445108.1 gg_id:536442 Candidatus Monilibacter spp. common bulking filaments are members III Defluviicoc
DQ917837.1 gg_id:226756 Microbial profiles bleached and wild-type Muricea elongata Rhodovibrio clone BME
DQ450764.1 gg_id:160882 Microbial Alpine Tundra Wet Meadow Soil: Chloroflexi Cold Water-Saturated satura
AJ567596.1 gg_id:88278 deep-sea sediment clone MBAE43
AJ536857.1 gg_id:78724 uranium mining waste pile soil sample clone JG30-KF-C3 proteobacterium
GU118759.1 gg_id:580439 Threatened Corals Provide Microbial Habitats clone Mfra_O22
DQ451512.1 gg_id:156709 forest soil clone FAC73
AY234650.1 gg_id:111452 soil isolate Ellin5299
AY913379.1 gg_id:114006 forest soil clone DUNssu172 (-7A) (OTU#131)
GQ339163.1 gg_id:523098 Comprehensive Investigation on Iron Cycling Freshwater Seep ing Microscopy Cultiv
EU236410.1 gg_id:289382 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg92E10
GQ350571.1 gg_id:550448 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
FJ675120.1 gg_id:515036 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface
EU048609.1 gg_id:240749 Microbial surface marine sediment Xisha Trough South China Sea clone MD2902-B2
DQ300606.1 gg_id:146291 microbial ocean's interior amplicon single fosmid library pool 130m depth HOT stati
FJ902587.1 gg_id:565674 phreatic limestone sinkholes northeastern Mexico biofilm 1m deep hydrothermal ver
AY428766.1 gg_id:103846 activated sludge
EF540431.1 gg_id:222179 oil-shale semi-coke solid waste clone MK41
EU133493.1 gg_id:254436 tallgrass prarie soil clone FFCH8309
AJ011919.1 gg_id:5104 Roseospirillum parvum str. 930I
EU617826.1 gg_id:319668 Seasonal variation microbial Yel Sea sediment clone D13S-112
DQ815232.1 gg_id:171372 zebrafish digestive tract clone aab51h10
EF600578.1 gg_id:292508 soil clone E5-40
EU617823.1 gg_id:303939 Seasonal variation microbial Yel Sea sediment clone D13S-34
GQ264051.1 gg_id:568681 Structure Simulated Level Waste Site simulated level waste site clone WC3_148
FJ478931.1 gg_id:554483 species richness estimates obtained nearly and simulated pyrosequencing-generated
EF125433.1 gg_id:190304 mangrove soil clone MSB-2D4

AF293001.1	26566	325.9	493.6	386.6	436.0	1005.3	1504.3
FJ479421.1	511480	11189.5	12030.2	8523.3	9692.0	13202.4	13449.4
GQ500775.1	552221	56.2	81.5	83.7	85.7	82.1	54.9
DQ917851.1	218252	989.2	2262.3	2113.7	3852.6	3420.4	3833.4
EU617825.1	343695	8537.3	7712.7	5101.2	9378.6	10900.8	10457.1
EU491409.1	268557	13064.1	11018.3	8930.8	10946.0	14627.8	13917.9
FM877531.1	368599	1764.3	3063.6	3898.8	3003.4	3422.9	3554.8
EU491319.1	260202	5249.3	6720.4	7092.5	4279.4	10625.8	7659.8
EU202862.1	317723	169.3	420.0	766.5	243.6	1231.0	1570.2
GQ347126.1	553069	11802.5	14299.8	13151.4	13044.1	19690.5	18244.2
EU236340.1	294380	3449.8	3100.8	6447.2	3602.4	9636.0	6555.6
DQ015803.1	140565	1368.9	2215.0	4490.5	2211.1	9622.6	10902.9
EU373886.1	270370	9135.4	10301.9	4579.8	9367.4	13259.4	12715.2
GU118149.1	577466	1918.5	2913.3	5159.3	2388.5	7906.7	9495.6
AB445108.1	536442	113.5	114.3	504.8	244.6	923.1	261.9
DQ917837.1	226756	199.7	234.8	258.8	218.8	1055.6	554.1
DQ450764.1	160882	196.4	212.0	477.1	405.9	690.9	169.1
AJ567596.1	88278	9097.1	9444.4	6257.3	7493.4	9981.4	4199.7
AJ536857.1	78724	127.4	271.0	667.1	169.9	392.3	509.6
GU118759.1	580439	58.7	238.7	369.0	146.1	98.5	418.6
DQ451512.1	156709	97.3	229.3	597.1	214.1	898.5	2639.4
AY234650.1	111452	407.3	1072.4	1040.5	437.9	1794.9	2058.3
AY913379.1	114006	1464.3	1999.3	5302.6	2144.3	4910.2	2452.0
GQ339163.1	523098	4340.9	6052.6	14436.4	5831.8	18855.7	12999.6
EU236410.1	289382	5615.7	4917.6	8954.6	5769.9	4508.9	5347.6
GQ350571.1	550448	2928.7	4119.0	11190.6	4246.2	7999.9	8991.1
FJ675120.1	515036	912.4	1749.9	1011.0	452.2	3712.6	2474.8
EU048609.1	240749	1973.5	3788.2	3599.2	1671.6	4773.6	5368.2
DQ300606.1	146291	7882.2	6130.3	6028.1	7432.5	17108.1	8566.6
FJ902587.1	565674	3001.8	5139.7	4812.1	1513.4	5811.6	4450.2
AY428766.1	103846	64.7	106.7	71.5	77.3	298.7	137.0
EF540431.1	222179	4096.5	4947.0	7930.5	4635.9	10270.3	9392.9
EU133493.1	254436	9113.2	11231.5	4952.2	7094.7	14274.0	10772.5
AJ011919.1	5104	171.3	380.1	150.3	191.4	878.6	331.2
EU617826.1	319668	1948.2	2808.2	4622.2	3857.4	3316.3	6470.9
DQ815232.1	171372	1112.2	2655.6	534.8	1270.8	289.8	435.6
EF600578.1	292508	81.4	152.9	84.1	106.9	189.9	401.1
EU617823.1	303939	3672.4	5093.6	10650.1	3615.0	11601.8	11573.9
GQ264051.1	568681	1078.5	1790.1	2538.4	1650.8	2385.0	4264.8
FJ478931.1	554483	5650.4	5428.5	2307.8	6778.9	8576.4	8388.0
EF125433.1	190304	72.3	63.8	31.8	89.3	115.6	122.7

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EU799327.1 gg_id:304619 It's all ranking aquatic Newport Harbour RI clone 1C226909
AY627380.1 gg_id:106889 marine clone AY627380
AY913376.1 gg_id:112806 forest soil clone DUNssu169 (-7A) (OTU#134)
AF104473.1 gg_id:4539 Olavius loisae endosymbiont 2
CU923620.1 gg_id:545476 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
EU386000.1 gg_id:275575 Biogeographical and microbes sediments on subseafloor sediment South China Sea c
EU652588.1 gg_id:278603 Seasonal variation microbial Yel Sea sediment clone D8S-126
EU800562.1 gg_id:307071 It's all ranking aquatic Delaware Bay NJ clone 2C228703
EU369121.1 gg_id:304307 libraries oyster shell clone MBIOS-05
AM935823.1 gg_id:552916 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
AY913278.1 gg_id:114037 forest soil clone DUNssu056 (-2C) (OTU#127)
EU245313.1 gg_id:244972 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-H5-H03
GQ346810.1 gg_id:585746 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
EU656113.1 gg_id:282361 Thalassobaculum sp. P24
AY654771.1 gg_id:105164 Oculina mucus isolate 38
AM997954.1 gg_id:574275 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A
FJ592569.1 gg_id:574659 Fumarole-supported islands biodiversity within hyperarid -elevation landscape on Pu
GQ060714.1 gg_id:419408 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw04e09
GQ263876.1 gg_id:538639 Structure Simulated Level Waste Site simulated level waste site clone WC2_121
EF516055.1 gg_id:225294 grassland soil clone FCPU555
DQ395408.1 gg_id:154449 deep-sea octacoral clone ctg_CGOAA92
EU589252.1 gg_id:262768 China Ningxia rice paddy field soil clone 1_A7
EU675666.1 gg_id:300711 Magnetospirillum sp. str. QH-2
GQ246307.1 gg_id:513629 Temporal and spatial China North Yel Sea sediments clone Sd1-26
EF632901.1 gg_id:244241 Unique microbial contrasting aquatic altitude Andean Altiplano (northern Chile) fresh
EF018460.1 gg_id:210561 aspen rhizosphere clone Amb_16S_1086
GQ337197.1 gg_id:581302 Hydrography shapes biogeography deep Arctic Ocean water depth 1000m clone CB
AF407727.1 gg_id:60574 Great Artesian Basin clone B79
Z29637.1 gg_id:4555 Azospirillum species
GQ346973.1 gg_id:580534 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
DQ984631.1 gg_id:253590 YK oil-contaminated soil clone YK_106
GQ348477.1 gg_id:583127 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
EU861390.1 gg_id:318694 marine magnetite-containing magnetic spirillum str. MMS-1
GQ349430.1 gg_id:542625 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
DQ906721.1 gg_id:171043 and marine microorganisms Antarctic sea water 20 m clone AntCL1D10
EU202861.1 gg_id:351776 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo
EF515275.1 gg_id:222372 Electricigen Enrichment MFC upf microbial fuel cell anode clone 22c07
AY660963.1 gg_id:101335 Azospirillum irakense str. Rsb1
EF018935.1 gg_id:211514 aspen rhizosphere clone Amb_16S_1444
DQ396323.1 gg_id:152292 deep-sea octacoral clone ctg_NISA029
EU449569.1 gg_id:561462 Soil are Changed Agricultural Practices agricultural soil clone Plot4-A11

EU799327.1	304619	3909.9	6576.7	9265.6	3472.2	7313.3	6735.9
AY627380.1	106889	84.4	148.4	161.5	94.3	178.7	118.4
AY913376.1	112806	61.6	78.5	162.0	70.1	172.0	163.5
AF104473.1	4539	309.0	465.0	1461.3	997.5	3836.9	5722.5
CU923620.1	545476	2445.9	3594.6	3082.9	2233.5	6542.8	7001.7
EU386000.1	275575	3914.9	4409.5	5482.1	4344.7	6890.7	5794.5
EU652588.1	278603	8092.0	9834.0	10440.3	7841.4	15663.1	13136.8
EU800562.1	307071	7638.1	9114.1	6165.7	6858.2	10049.7	8936.6
EU369121.1	304307	1618.1	3460.5	4137.7	2320.5	6741.0	5869.0
AM935823.1	552916	291.2	525.6	2421.9	603.7	3074.6	1612.6
AY913278.1	114037	247.8	508.7	792.4	448.4	817.3	1544.5
EU245313.1	244972	4543.5	6721.6	5061.1	4476.3	7666.8	7842.1
GQ346810.1	585746	2856.3	3634.3	2734.0	4131.4	4890.9	4777.4
EU656113.1	282361	4995.8	5298.4	6746.9	7053.0	7629.0	6814.0
AY654771.1	105164	388.1	218.1	312.8	302.6	143.7	212.9
AM997954.1	574275	4568.3	5001.5	6594.4	4600.2	6324.0	6190.8
FJ592569.1	574659	5240.4	6448.5	8039.8	5582.1	13196.6	9922.6
GQ060714.1	419408	3257.0	4160.1	4267.0	2299.9	7830.5	5120.7
GQ263876.1	538639	7341.5	8583.7	11089.1	7136.2	9303.8	9039.6
EF516055.1	225294	54.8	140.7	1089.5	125.1	113.7	175.8
DQ395408.1	154449	106.4	332.3	509.6	180.2	254.6	390.8
EU589252.1	262768	5187.9	4604.4	1555.3	3836.4	6419.9	5250.4
EU675666.1	300711	2577.0	3350.4	5773.1	1947.5	6982.4	7630.6
GQ246307.1	513629	11060.2	10933.2	7644.0	8692.0	10530.5	10732.5
EF632901.1	244241	1646.6	1400.4	3713.5	1704.9	4921.4	8635.4
EF018460.1	210561	5582.2	6488.5	9531.0	6512.4	11881.9	7444.8
GQ337197.1	581302	4387.0	7007.7	11937.4	4237.2	13587.1	12499.4
AF407727.1	60574	1366.8	1838.9	3623.6	1027.8	4185.5	4952.9
Z29637.1	4555	86.5	137.2	1233.6	271.8	669.4	2239.8
GQ346973.1	580534	6287.9	7622.8	8572.3	5715.9	11467.4	8737.9
DQ984631.1	253590	3803.4	3192.2	2053.4	2275.6	6464.0	3446.0
GQ348477.1	583127	1461.0	3184.1	4720.5	2138.3	11133.6	10411.1
EU861390.1	318694	8022.8	8025.2	9905.4	7465.9	11172.5	8757.6
GQ349430.1	542625	3802.4	5901.6	6871.5	3892.5	14644.4	10428.7
DQ906721.1	171043	92.2	156.1	482.0	119.9	415.4	244.4
EU202861.1	351776	5361.4	5147.0	1996.8	4872.8	7573.3	6939.7
EF515275.1	222372	3740.2	3808.2	4159.4	1575.9	3542.8	3116.0
AY660963.1	101335	7294.6	7161.7	4417.6	5445.3	10356.2	9739.3
EF018935.1	211514	170.5	154.4	664.7	271.9	330.0	700.9
DQ396323.1	152292	1828.2	3347.6	1502.3	794.5	1488.4	2385.3
EU449569.1	561462	8007.9	8854.3	13677.4	8463.3	12786.5	13590.5

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GQ340152.1 gg_id:586348 Prokaryotic Marathonas Reservoir Greece water column clone K07-02-BAC
AM936893.1 gg_id:534867 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
GQ214100.1 gg_id:566368 China loess clone P828
FM201297.1 gg_id:557664 'Candidatus Cryptoprodotis polytropus' Rickettsia-Like Ciliated Protist Pseudomicrot
GQ264291.1 gg_id:568633 Structure Simulated Level Waste Site simulated level waste site clone WW2_11
GU118948.1 gg_id:545008 Threatened Corals Provide Microbial Habitats clone Past_M16
AM997985.1 gg_id:563558 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A
EU373875.1 gg_id:272622 southern Cretan margin (eastern Mediterranean Sea) canyon and slope sediment clc
EU133314.1 gg_id:248945 tallgrass prarie soil clone FFCH1031
AM934985.1 gg_id:542300 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
EU008565.1 gg_id:236520 Nisaea salexigens str. CZ41_10a
EU133267.1 gg_id:252811 tallgrass prarie soil clone FFCH1925
EU133443.1 gg_id:244312 tallgrass prarie soil clone FFCH15235
EU287138.1 gg_id:249446 Pacific arctic surface sediment clone P13-45
GU117956.1 gg_id:542538 Threatened Corals Provide Microbial Habitats clone Acer_C02
EF516857.1 gg_id:220224 grassland soil clone FCPS408
EF516694.1 gg_id:218380 grassland soil clone FCPO401
FM872931.1 gg_id:367617 occupant source house floor dust clone FB04G07
GQ261313.1 gg_id:573535 Study on Sediment sediment Dongping Lake clone 1S3-20
EU652589.1 gg_id:279075 Seasonal variation microbial Yel Sea sediment clone B8S-114
EU586202.1 gg_id:271304 Skermanella sp. str. 10-1-101
AF179678.1 gg_id:32841 Defluvicoccus vanus str. pilsen; Ben114
EU805031.1 gg_id:326771 It's all ranking aquatic 250 miles Panama City clone 6C233013
AM936395.1 gg_id:537674 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
GU118735.1 gg_id:580777 Threatened Corals Provide Microbial Habitats clone Mfra_G10
EF157262.1 gg_id:241911 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon
EU665131.1 gg_id:537780 Soil are Changed Agricultural Practices agricultural soil clone Plot22-2D03
EU335156.1 gg_id:242184 Changes microbial metabolic and along hydrogeochemically variable profile saturate
FJ592573.1 gg_id:564942 Fumarole-supported islands biodiversity within hyperarid -elevation landscape on Pu
EU799064.1 gg_id:318113 It's all ranking aquatic Newport Harbour RI clone 1C226620
FJ674890.1 gg_id:516834 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
EU802123.1 gg_id:305536 It's all ranking aquatic Chesapeake Bay MD clone 3C003533
GQ015990.1 gg_id:493677 Topographical and Temporal Human Skin Microbiome skin back clone nbw819g09c1
FJ202874.1 gg_id:330657 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k
GQ402572.1 gg_id:564337 Accessing microbial biodiversity and metabolic potential tropical -based approach p
GQ406147.1 gg_id:550141 Benthic submerged sinkhole ecosystems sediment clone -45-1
AB447630.1 gg_id:583557 Microbial Structure and Dynamics Granules Expanded Granular Sludge Bed (EGSB) R
FJ666170.1 gg_id:568338 Unseen stowaways: tank commercial cargo ship Port Houston Texas ballast water clo
AM997864.1 gg_id:571601 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A
GU220729.1 gg_id:581688 Microbial mineralization and involved microbial Basin field temperature hydrotherm
EF516586.1 gg_id:220363 grassland soil clone FCPS581

GQ340152.1	586348	6306.9	6623.5	7962.2	8216.1	10175.7	8398.4
AM936893.1	534867	6740.4	7306.9	7358.7	4318.7	6589.5	7024.7
GQ214100.1	566368	1212.9	2700.6	3796.1	1852.5	9870.6	4283.6
FM201297.1	557664	1515.2	2965.9	3631.4	1319.0	2668.5	5513.6
GQ264291.1	568633	3602.7	3573.2	9027.1	3829.1	8452.5	9894.8
GU118948.1	545008	2935.7	2852.1	987.0	1609.2	2760.7	2995.4
AM997985.1	563558	772.0	2175.4	3623.2	1694.5	3446.8	3690.4
EU373875.1	272622	140.5	309.6	788.4	224.6	1374.5	374.4
EU133314.1	248945	95.4	176.4	274.8	144.7	994.5	506.9
AM934985.1	542300	1968.7	2586.8	3985.7	2503.5	3535.3	4151.7
EU008565.1	236520	571.1	358.5	263.4	750.6	434.9	374.3
EU133267.1	252811	4583.4	5079.2	4182.1	3356.2	6156.1	7507.6
EU133443.1	244312	2859.4	5511.7	4861.4	1362.8	6268.2	6148.6
EU287138.1	249446	6440.8	9032.0	6477.2	7832.1	9940.1	10321.5
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EF516694.1	218380	5435.1	7061.6	2437.7	9569.0	6375.6	5732.2
FM872931.1	367617	89.1	374.8	193.5	84.1	126.4	134.4
GQ261313.1	573535	4283.5	7667.8	8511.2	3093.0	9882.1	11497.5
EU652589.1	279075	146.4	304.3	1626.7	677.0	3970.1	3705.1
EU586202.1	271304	1003.4	1153.5	2686.7	676.7	1474.5	2078.6
AF179678.1	32841	181.1	447.9	731.6	154.6	677.6	415.8
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EU335156.1	242184	7730.8	7023.3	9422.3	9559.9	14921.5	13736.4
FJ592573.1	564942	14.3	28.6	226.1	42.9	56.2	35.3
EU799064.1	318113	4730.1	9473.5	7325.7	5224.4	8889.0	11260.8
FJ674890.1	516834	3117.1	4706.7	4359.3	3023.0	6149.7	5872.1
EU802123.1	305536	7990.8	11621.7	9849.6	7857.2	12137.0	13057.4
GQ015990.1	493677	4516.8	6431.4	6293.5	4247.3	11508.1	10423.2
FJ202874.1	330657	2544.0	2595.4	6451.9	5104.6	3792.6	4860.4
GQ402572.1	564337	1058.9	2862.9	5334.8	1179.9	2465.4	3528.3
GQ406147.1	550141	825.5	1188.0	5514.1	1823.7	1974.1	1375.0
AB447630.1	583557	2686.3	5259.3	3903.4	3039.7	3336.6	5057.2
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GU220729.1	581688	2205.5	4386.5	7607.5	2437.0	7750.8	9436.1
EF516586.1	220363	68.9	82.7	111.0	96.8	211.4	120.0

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FJ203466.1 gg_id:353797 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h
AY963489.1 gg_id:154486 structures and correlated ecological factors soils two evergreen broad-leaved forests
GU220737.1 gg_id:535156 Microbial mineralization and involved microbial Basin field temperature hydrotherm
EU802633.1 gg_id:310636 It's all ranking aquatic Northeast Colon Panama clone 4C229990
GQ348385.1 gg_id:545576 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
CU925661.1 gg_id:555845 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
AM997811.1 gg_id:565394 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A
EF600571.1 gg_id:302726 soil clone E5-25
EU156155.1 gg_id:256677 thermal spring microbial and functional genes Coffee Pots Hot Spring clone pCOF_65
EU276561.1 gg_id:363728 -DGGE and Approaches Analyze Effect Agricultural Practices on Soil agricultural soil c
EU735612.1 gg_id:328739 archaeal structures and pristine soils China oil contaminated soil Jidong Oilfield clone
EU799183.1 gg_id:313413 It's all ranking aquatic Newport Harbour RI clone 1C226754
AF355036.1 gg_id:40077 marine clone Arctic95B-2
GQ346952.1 gg_id:583540 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
EU881179.1 gg_id:309422 Karst region natural restoration land soil clone KNR200711-087
AY555804.1 gg_id:102414 Bor Khlueng hot spring clone PK324
EF589979.2 gg_id:228872 changes structure sediments Songhua River contaminated nitrobenzene -DGGE cloni
GQ349354.1 gg_id:577322 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
GU118617.1 gg_id:548705 Threatened Corals Provide Microbial Habitats clone Mfav_B20
EU491294.1 gg_id:275770 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak
AY395352.1 gg_id:101876 pasture soil clone EB1033
EU048618.1 gg_id:240989 Microbial surface marine sediment Xisha Trough South China Sea clone MD2902-B11
EU050763.1 gg_id:245677 libraries sediment Kings Bay Svalbard Arctic clone ss1_B_07_73
L06455.1 gg_id:4597 magnetite-containing magnetic vibrio str. MV1
EU491108.1 gg_id:266612 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak
EF157245.1 gg_id:251478 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon
DQ917850.1 gg_id:222549 Microbial profiles bleached and wild-type Muricea elongata Rhodospirillaceae clone
EU445208.1 gg_id:559267 Isolation Weight Forest Topsoil Metagenomic tropical forest topsoil clone R21
AJ581583.1 gg_id:93503 soil near uranium mill tailings clone KCM-B-24
GQ060531.1 gg_id:405595 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw02h11
AB289439.1 gg_id:249530 Iambacter cinctapus str. IAM 15419
GU118285.1 gg_id:546121 Threatened Corals Provide Microbial Habitats clone Dstr_H24
AM176885.1 gg_id:161167 Recovery mangrove sediment clone SZB60
DQ070832.1 gg_id:149655 Prokaryotic Structures Seafloor Basalts Varying Age East Pacific Rise and Ridge basal
FJ744861.1 gg_id:552179 Transporter genes expressed coastal response dissolved organic carbon surface wate
GQ246388.1 gg_id:583912 Temporal and spatial China North Yel Sea sediments clone Cm1-51
Y12596.1 gg_id:4588 Drentse grassland soil Netherlands clone DA111
GQ060463.1 gg_id:426164 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw01g03
DQ396275.1 gg_id:151653 deep-sea octacoral clone ctg_NISA128
FJ203534.1 gg_id:340730 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h
DQ450755.1 gg_id:161246 Microbial Alpine Tundra Wet Meadow Soil: Chloroflexi Cold Water-Saturated satura

FJ203466.1	353797	76.0	74.7	223.1	61.5	60.9	57.9
AY963489.1	154486	2172.8	2598.2	2838.9	2479.2	2752.6	5103.8
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EU802633.1	310636	304.6	564.3	225.8	684.5	1097.8	979.8
GQ348385.1	545576	29.9	76.3	156.8	89.1	174.9	388.1
CU925661.1	555845	4155.5	4803.5	6836.0	5490.3	5718.4	7534.8
AM997811.1	565394	9479.7	11480.2	11411.3	6821.1	13863.6	12230.4
EF600571.1	302726	11168.3	13133.9	12376.9	6898.1	16658.7	12449.8
EU156155.1	256677	11515.2	11714.0	8714.9	11481.7	15470.8	11741.9
EU276561.1	363728	10152.1	12004.4	11724.6	9095.3	14576.8	13951.7
EU735612.1	328739	4619.8	5460.3	8617.1	5188.0	10183.6	6711.0
EU799183.1	313413	8649.1	9053.4	8779.7	9218.9	12550.5	10363.9
AF355036.1	40077	1067.2	2390.7	7759.3	1439.3	5282.5	7495.2
GQ346952.1	583540	763.7	1374.8	3041.7	640.3	3489.4	2722.5
EU881179.1	309422	5744.8	6035.3	4351.2	3844.6	6104.4	8127.7
AY555804.1	102414	51.2	104.1	110.8	110.2	115.9	88.7
EF589979.2	228872	2391.5	3199.2	3286.4	3216.9	6276.2	6881.4
GQ349354.1	577322	2370.2	2966.4	4467.0	2243.2	6104.1	8135.1
GU118617.1	548705	925.1	1575.6	2239.6	1176.4	5379.7	4906.2
EU491294.1	275770	3565.8	3726.2	8236.9	3856.8	7790.5	8079.4
AY395352.1	101876	99.9	195.5	158.9	112.0	133.2	208.0
EU048618.1	240989	4229.5	5522.8	9279.5	4685.0	7234.3	7551.4
EU050763.1	245677	2175.4	3029.7	3865.8	3585.3	4641.3	4904.5
L06455.1	4597	80.3	184.5	598.2	109.6	276.1	465.2
EU491108.1	266612	6584.4	6413.4	9816.3	8943.3	13404.4	13546.0
EF157245.1	251478	2837.8	3891.1	6467.6	5010.5	13369.6	7435.5
DQ917850.1	222549	69.5	175.1	83.8	168.8	204.6	292.8
EU445208.1	559267	2975.8	3406.2	3204.3	1947.7	2965.1	3377.0
AJ581583.1	93503	8538.2	6816.4	4084.6	2860.7	2197.6	7328.0
GQ060531.1	405595	4636.8	5927.0	5041.3	3830.9	7944.6	6779.8
AB289439.1	249530	1554.4	2963.3	3241.6	2326.0	7872.5	4743.9
GU118285.1	546121	120.8	221.1	1325.0	375.1	1433.0	2255.5
AM176885.1	161167	11590.6	11424.4	18977.5	11577.2	17705.5	13935.7
DQ070832.1	149655	2644.8	3224.6	3898.5	2134.9	2867.1	4461.1
FJ744861.1	552179	3819.7	2520.6	2076.8	2204.7	7057.3	5383.0
GQ246388.1	583912	6137.1	5045.2	7276.4	3231.6	2569.0	4784.7
Y12596.1	4588	3225.7	3651.0	2953.9	2582.0	6526.1	6443.7
GQ060463.1	426164	4786.9	7446.6	4063.3	3969.9	13528.8	9431.3
DQ396275.1	151653	826.0	1471.8	755.8	287.2	1478.3	1626.3
FJ203534.1	340730	3344.0	4279.7	4401.6	2192.9	6464.2	3829.1
DQ450755.1	161246	8014.3	9303.3	8344.6	4525.1	14175.0	15716.6

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EU236327.1 gg_id:296133 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg5a1E3
GU302497.1 gg_id:567827 Spatial structure and activity sedimentary microbial underlying Beggiatoa spp. mat h
FM242447.1 gg_id:339472 sequences sediment clone 28 T12d+oil
AJ581348.1 gg_id:92371 Mediterranean sponge clone E01-9C-5
DQ499294.1 gg_id:159606 acidic cave snottite biofilm clone CV43
DQ811855.1 gg_id:165418 mangrove soil clone MSB-4H3
AF355035.1 gg_id:33175 marine clone Arctic96B-9a
AM936708.1 gg_id:539426 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
FJ746319.1 gg_id:561304 Microbial oligotrophic marine sediments: South Pacific Gyre ocean sediment 5306 m
AM420239.1 gg_id:242807 Noma subgingival plaque clone 603003(oral)
EU799498.1 gg_id:346828 It's all ranking aquatic Newport Harbour RI clone 1C227104
AJ567552.1 gg_id:88580 deep-sea sediment clone MBMPE38
GU118834.1 gg_id:578664 Threatened Corals Provide Microbial Habitats clone Mfra_G08
FJ197425.1 gg_id:341281 deep Pacific Ocean and Eastern Mediterranean Sea sediment clone ALVIN24a_3D_FL
EU048622.1 gg_id:242336 Microbial surface marine sediment Xisha Trough South China Sea clone MD2902-B16
GQ264138.1 gg_id:563019 Structure Simulated Level Waste Site simulated level waste site clone WC3_78
AY907759.1 gg_id:136640 identification picoplankton contrasting waters Arabian Sea water clone A314902
EU236317.1 gg_id:290364 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg1bD5
EF157232.1 gg_id:257142 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon
GQ350356.1 gg_id:589836 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
EF515995.1 gg_id:222088 grassland soil clone FCPU464
GQ348251.1 gg_id:594329 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
AM935509.1 gg_id:534332 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
FM253629.1 gg_id:336148 Rock gold mine unusually microbial biofilm clone H08-1
AJ633959.1 gg_id:114556 host's accessory nidamental gland clone 30ANG6
GQ354964.1 gg_id:560931 structure between two geochemically distinct springs Alum Rock Park spring clone 4
DQ451508.1 gg_id:156725 forest soil clone FAC69
EU491777.1 gg_id:266165 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39
EF018173.1 gg_id:205399 aspen rhizosphere clone Amb_16S_515
EU592393.1 gg_id:548310 Seasonal changes Salton Sea hypersaline water clone SSW14N
GU302465.1 gg_id:545368 Spatial structure and activity sedimentary microbial underlying Beggiatoa spp. mat h
EF597705.1 gg_id:239558 Metagenomics deep mediterranean warm bathypelagic habitat 3010m depth Ionian
EF516219.1 gg_id:217798 grassland soil clone FCPP413
FJ746286.1 gg_id:571876 Microbial oligotrophic marine sediments: South Pacific Gyre ocean sediment 5306 m
EU491571.1 gg_id:273715 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR4C
GQ350038.1 gg_id:551365 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
GQ264041.1 gg_id:541154 Structure Simulated Level Waste Site simulated level waste site clone WC3_135
EF572964.1 gg_id:231481 Coco's Island site 23 marine clone S23_1063
EU528234.1 gg_id:284226 Seasonal Dynamics Mudflat Mouth Major Kentucky Lake Reservoir Tributary sedime
DQ070813.1 gg_id:147895 Prokaryotic Structures Seafloor Basalts Varying Age and Juan de Fuca Ridge basalt gl
EU491885.1 gg_id:271221 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39

EU236327.1	296133	2184.0	1837.7	2158.8	991.9	1460.2	1022.5
GU302497.1	567827	737.6	2128.1	2649.9	686.5	2678.5	3353.3
FM242447.1	339472	7923.8	7492.5	5350.8	7349.3	10772.1	9953.4
AJ581348.1	92371	82.7	93.9	61.2	74.0	90.6	44.7
DQ499294.1	159606	3209.7	4701.6	6239.5	2137.4	5407.6	5304.1
DQ811855.1	165418	365.0	557.6	650.3	694.5	1518.8	3044.9
AF355035.1	33175	1213.0	1821.2	1994.3	572.4	2305.0	2230.6
AM936708.1	539426	2051.4	3098.6	3565.5	4699.4	3670.3	4810.3
FJ746319.1	561304	416.3	1634.8	1973.1	375.0	1032.2	789.7
AM420239.1	242807	102.2	337.6	168.7	154.0	334.3	247.8
EU799498.1	346828	61.5	141.2	892.0	209.8	241.9	779.2
AJ567552.1	88580	4803.9	5260.0	9259.7	4964.0	8855.2	11155.4
GU118834.1	578664	2334.4	2752.4	3528.4	3371.1	4933.5	2928.6
FJ197425.1	341281	4444.8	6388.3	5144.0	3066.6	6923.3	6183.9
EU048622.1	242336	4915.1	6522.2	8751.9	5977.7	6960.2	7069.4
GQ264138.1	563019	13949.1	14965.4	9240.3	16342.3	19300.3	17488.8
AY907759.1	136640	599.3	1348.9	331.8	868.6	3357.7	4103.5
EU236317.1	290364	1320.7	1458.4	2318.0	1151.3	3692.8	3578.1
EF157232.1	257142	1542.7	2548.3	6553.5	2851.5	6487.1	6864.0
GQ350356.1	589836	3479.4	3969.7	4747.5	5506.7	6864.7	9315.3
EF515995.1	222088	993.8	1188.7	4266.4	1091.2	2116.5	3208.7
GQ348251.1	594329	7247.2	5835.2	2508.7	8912.4	8122.2	7143.9
AM935509.1	534332	6774.8	6419.3	7541.0	3130.2	8204.4	11346.5
FM253629.1	336148	7446.7	8814.0	7838.4	7002.2	11068.9	10233.3
AJ633959.1	114556	2071.1	3343.1	3541.4	3053.7	5928.4	5890.3
GQ354964.1	560931	3152.7	3974.1	5818.6	4741.0	6457.7	5809.4
DQ451508.1	156725	3664.9	3570.3	4030.1	6557.5	7102.6	6760.5
EU491777.1	266165	2591.1	3857.4	4312.5	2199.9	9091.6	8682.9
EF018173.1	205399	1645.9	2835.1	1776.8	1926.1	3204.7	2690.8
EU592393.1	548310	3511.3	6374.3	7683.4	5945.9	11663.6	11883.4
GU302465.1	545368	576.0	1083.8	4093.7	1001.6	3359.9	3135.9
EF597705.1	239558	5203.2	10460.2	2847.5	3364.2	4579.7	4542.0
EF516219.1	217798	2113.1	2390.5	1569.3	1399.5	5322.5	2965.7
FJ746286.1	571876	9771.7	13241.8	13074.6	8422.5	9949.3	9086.0
EU491571.1	273715	3253.3	4179.0	5396.5	3375.8	4896.9	4696.8
GQ350038.1	551365	2409.6	3715.5	3848.4	1895.5	5576.5	3003.1
GQ264041.1	541154	2970.8	3824.0	6469.9	1871.1	7137.0	6248.4
EF572964.1	231481	486.4	881.1	389.4	890.2	482.6	290.7
EU528234.1	284226	417.1	822.9	1904.8	527.6	5239.8	2977.2
DQ070813.1	147895	60.6	71.8	57.3	137.6	432.1	83.9
EU491885.1	271221	1653.8	2084.8	931.8	1346.4	2740.8	1613.2

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AJ535710.1 gg_id:100274 Stella humosa str. DSM5900
GQ351141.1 gg_id:564010 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Eastern
FJ902662.1 gg_id:578073 phreatic limestone sinkholes northeastern Mexico biofilm 1m deep hydrothermal ver
EU799997.1 gg_id:334995 It's all ranking aquatic Newport Harbour RI clone 1C227677
FJ755769.1 gg_id:509529 vertical archaeal water and Lake Taihu sediment clone LT-SB-B68
DQ378260.1 gg_id:155886 oil-polluted soil clone M43_Pitesti
EU801583.1 gg_id:322226 It's all ranking aquatic Chesapeake Bay MD clone 3C002913
GQ347647.1 gg_id:577589 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
DQ906739.1 gg_id:172572 and marine microorganisms Antarctic sea water 20 m clone AntCL1H5
EU133575.1 gg_id:256291 tallgrass prarie soil clone FFCH4971
EU386027.1 gg_id:273866 Biogeographical and microbes sediments on subseafloor sediment South China Sea c
AF465655.1 gg_id:33613 geothermal soil clone YNPRH85B
EF018202.1 gg_id:210884 aspen rhizosphere clone Amb_16S_548
X99671.1 gg_id:4509 Rhodospira trueperi
EU050757.1 gg_id:247141 libraries sediment Kings Bay Svalbard Arctic clone ss1_B_03_94
FJ624900.1 gg_id:514040 Influence lead contamination on boreal pine forest soil clone HF_C_27
DQ129334.1 gg_id:138266 microarray level air two cities Texas urban aerosol clone AKIW400
AM936707.1 gg_id:544803 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
EU799402.1 gg_id:341487 It's all ranking aquatic Newport Harbour RI clone 1C226994
AB054178.1 gg_id:22043 marine sponge clone HOC44
FM242428.1 gg_id:309504 sequences sediment clone 38 T12d-oil
FJ826483.1 gg_id:557922 Succession during spring diatom bloom Sea filtered surface sea water contrasting nor
AM935865.1 gg_id:548884 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
EF573465.1 gg_id:229444 Coco's Island site 23 marine clone S23_1564
AF143822.1 gg_id:72005 hydrocarbon-degrading consortium clone 4-Org1-14
AM997828.1 gg_id:547681 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A
EU799295.1 gg_id:343368 It's all ranking aquatic Newport Harbour RI clone 1C226876
AJ581592.1 gg_id:94143 soil near uranium mill tailings clone KCM-B-56
EU800342.1 gg_id:351874 It's all ranking aquatic Delaware Bay NJ clone 2C228398
EU799038.1 gg_id:352113 It's all ranking aquatic Newport Harbour RI clone 1C226591
EU287307.1 gg_id:256038 Pacific arctic surface sediment clone S26-7
GQ350021.1 gg_id:545223 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
EU804599.1 gg_id:355413 It's all ranking aquatic 250 miles Panama City clone 6C232548
FM242426.1 gg_id:326326 sequences sediment clone 62 T12d-oil
GU119311.1 gg_id:560169 Threatened Corals Provide Microbial Habitats reef water clone Reef_B20
AM935243.1 gg_id:543551 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
GU118274.1 gg_id:583340 Threatened Corals Provide Microbial Habitats clone Dstr_J21
FJ203516.1 gg_id:319588 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h
EU925871.1 gg_id:314210 sediments sediment station DBS1 northern Bering Sea clone 074F57
EU799960.1 gg_id:342027 It's all ranking aquatic Newport Harbour RI clone 1C227638
FM242370.1 gg_id:336124 sequences sediment clone 37 T9d+oil

AJ535710.1	100274	591.9	937.2	1476.9	1108.9	1836.4	2258.1
GQ351141.1	564010	4755.3	6142.0	8530.0	2741.7	5286.4	6974.0
FJ902662.1	578073	666.1	933.1	1872.0	628.2	690.9	1459.6
EU799997.1	334995	349.8	1080.2	887.9	472.8	4134.2	2792.8
FJ755769.1	509529	2764.5	4819.1	8127.9	2071.1	7153.8	9024.4
DQ378260.1	155886	590.9	877.5	3206.1	1353.3	4670.4	3820.5
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GQ347647.1	577589	5102.4	8656.0	4075.8	4875.6	8811.0	8191.5
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AF465655.1	33613	1209.3	2021.7	1320.0	613.2	2616.1	2359.6
EF018202.1	210884	1844.6	2029.0	3165.1	3048.4	3983.0	6324.4
X99671.1	4509	2799.0	2654.7	5291.7	2435.4	8056.9	4739.2
EU050757.1	247141	14443.5	15509.3	12896.6	8823.0	17610.4	12173.3
FJ624900.1	514040	122.0	289.1	704.2	199.5	286.8	704.2
DQ129334.1	138266	24.0	58.9	67.7	74.0	89.7	47.5
AM936707.1	544803	1056.0	1732.3	2314.4	630.9	3162.1	1954.0
EU799402.1	341487	5600.1	3214.7	3110.2	3430.6	6055.1	3560.6
AB054178.1	22043	4043.5	4955.9	5083.5	5049.2	12296.0	8252.2
FM242428.1	309504	1316.0	2873.1	6706.1	905.2	7893.2	5988.5
FJ826483.1	557922	2285.1	2550.7	5055.5	4538.5	9181.8	10733.7
AM935865.1	548884	701.7	1320.4	746.7	1222.5	3556.0	5832.3
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AF143822.1	72005	45.8	94.8	172.9	63.3	123.2	90.6
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AJ581592.1	94143	9158.8	10680.1	11284.1	6174.1	12871.8	10379.5
EU800342.1	351874	8869.9	8822.2	6636.9	9400.5	8918.2	9637.2
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EU287307.1	256038	3356.9	4631.6	4038.1	4061.1	8429.3	10162.7
GQ350021.1	545223	6988.6	7551.5	9077.5	8148.1	11393.5	11244.6
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EU258753.1 gg_id:237362 summer sea Dalian and Liaodong determined bay clone D1850
FM242371.1 gg_id:354142 sequences sediment clone 56 T9d+oil
AY913254.1 gg_id:113643 forest soil clone DUNssu035 (+2C) (OTU#147)
EU804078.1 gg_id:344865 It's all ranking aquatic 250 miles Panama City clone 6C231969
FJ826334.1 gg_id:510049 Succession during spring diatom bloom Sea filtered surface sea water contrasting nor
AY033313.1 gg_id:68981 marine bacterioplankton clone MB12C06
EF471702.1 gg_id:265895 Fast Screening and Estuarine Operon Libraries whole surface water Chesapeake Bay
AM936369.1 gg_id:545287 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
DQ513034.1 gg_id:160542 Microbial life fluids ridge flank crustal fluid clone FS142-43B-02
EF575022.1 gg_id:234907 site S25 near Coco's Island marine clone S25_1366
DQ071034.1 gg_id:131466 marine surface water clone Chl1.16
EU799958.1 gg_id:320279 It's all ranking aquatic Newport Harbour RI clone 1C227636
EU802957.1 gg_id:349161 It's all ranking aquatic Northeast Colon Panama clone 4C230356
FM242449.1 gg_id:354033 sequences sediment clone 34 T12d+oil
FJ826476.1 gg_id:558348 Succession during spring diatom bloom Sea filtered surface sea water contrasting nor
AB054154.1 gg_id:36213 marine sponge clone HOC20
U70679.2 gg_id:4573 Cape Hatteras picoplankton clone OM38
FM242318.1 gg_id:307417 sequences sediment clone 51 T9d-oil
EU802384.1 gg_id:308776 It's all ranking aquatic Northeast Colon Panama clone 4C229705
GQ350321.1 gg_id:586003 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
EU803029.1 gg_id:303610 It's all ranking aquatic Northeast Colon Panama clone 4C230433
GQ347926.1 gg_id:577083 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
AY744399.1 gg_id:108446 EBAC2C11 complete clone EBAC2C11
EF573783.1 gg_id:233886 site S25 near Coco's Island marine clone S25_127
AJ240913.1 gg_id:72555 5' clone CHAB-III-8
EU010169.1 gg_id:252561 Biogeography Singapore seawaters seawater clone B50
FM242430.1 gg_id:330363 sequences sediment clone 64 T12d-oil
FM242317.1 gg_id:329580 sequences sediment clone 2 T9d-oil
EU800341.1 gg_id:336625 It's all ranking aquatic Delaware Bay NJ clone 2C228397
GU061713.1 gg_id:555701 and function microbial mesoscale eddy perturbations South China Sea clone CEP-5m
EF540391.1 gg_id:226996 oil-shale semi-coke solid waste clone MJK32_MK
EU799440.1 gg_id:311029 It's all ranking aquatic Newport Harbour RI clone 1C227039
EF100695.1 gg_id:175841 Caenimicrobium bisanense str. K93
AB110414.1 gg_id:87741 Blastochloris sulfoviridis str. RN1
FJ169957.1 gg_id:346128 Anaplasma bovis str. Zhongxian
FJ226454.1 gg_id:350108 Anaplasma marginale str. Ishigaki-2007
AF318945.1 gg_id:50430 Anaplasma ovis 1/11/2/480 sheep 3573/7
AJ633050.1 gg_id:99202 Anaplasma ovis Yuzhong
AJ633051.1 gg_id:99352 Anaplasma ovis Zhangjiachuan
AY530806.1 gg_id:100745 Anaplasma platys
AF287153.1 gg_id:18302 Anaplasma platys

EU258753.1	237362	5204.0	4775.9	6870.7	6698.3	18341.4	7893.8
FM242371.1	354142	6564.8	8477.1	10228.0	7360.1	16982.7	15518.4
AY913254.1	113643	2115.5	3027.6	6167.1	3675.0	5014.5	6736.7
EU804078.1	344865	1245.9	3403.5	3024.7	1308.6	4261.6	3998.6
FJ826334.1	510049	10327.1	11378.8	8477.1	8395.7	13325.7	12895.9
AY033313.1	68981	7268.4	9750.4	6832.4	6826.7	13463.2	12775.9
EF471702.1	265895	5354.8	5538.0	9502.9	5566.4	14123.8	12746.4
AM936369.1	545287	3029.8	4814.2	3221.2	4140.1	2630.3	4083.6
DQ513034.1	160542	3419.3	3374.3	6056.2	2928.3	2343.0	2326.5
EF575022.1	234907	2979.6	2869.7	1769.9	1478.2	2555.9	1270.5
DQ071034.1	131466	2190.5	2415.8	1687.4	2156.6	2041.9	1661.2
EU799958.1	320279	5553.3	6823.6	9089.5	7299.8	15991.1	16444.6
EU802957.1	349161	6023.7	8110.9	7544.2	7435.1	12902.1	12168.2
FM242449.1	354033	16063.3	16102.7	12762.7	15391.1	23595.8	19420.1
FJ826476.1	558348	2943.2	5562.9	5831.0	3431.5	7683.4	7469.5
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U70679.2	4573	2069.9	2778.0	2636.9	1520.9	3740.8	3905.0
FM242318.1	307417	5387.1	6737.3	8185.1	5476.3	13141.5	8425.3
EU802384.1	308776	529.4	753.5	858.3	325.5	781.7	1465.9
GQ350321.1	586003	74.5	603.3	894.3	141.7	1008.4	654.8
EU803029.1	303610	8565.7	12950.4	8503.8	6687.5	13808.9	13128.1
GQ347926.1	577083	9003.6	11157.9	7725.2	6940.9	11022.1	9787.8
AY744399.1	108446	8610.5	11639.5	8432.6	11138.8	11786.1	11221.0
EF573783.1	233886	10040.2	10608.9	9586.1	8207.2	14264.3	13281.8
AJ240913.1	72555	74.8	110.6	201.3	92.5	120.3	87.6
EU010169.1	252561	3763.1	4152.1	4363.4	4514.1	6341.0	5882.7
FM242430.1	330363	13802.6	14049.2	10649.5	13227.3	20745.1	16152.0
FM242317.1	329580	5914.6	7069.9	9964.5	6879.6	13948.3	13229.7
EU800341.1	336625	14265.9	17369.8	17876.1	11447.5	22416.3	16572.7
GU061713.1	555701	6475.8	14393.9	7932.9	8587.1	13645.7	9344.6
EF540391.1	226996	846.8	1267.1	4143.4	1099.2	14244.9	5327.8
EU799440.1	311029	76.5	79.2	352.6	223.7	207.2	430.3
EF100695.1	175841	87.3	145.2	267.5	173.3	1337.2	316.0
AB110414.1	87741	4378.1	4905.5	4477.7	4842.8	6355.0	6915.3
FJ169957.1	346128	3500.9	4627.3	3453.2	3580.0	6964.1	5729.5
FJ226454.1	350108	6614.1	6119.7	6721.0	4134.6	7810.2	5620.2
AF318945.1	50430	5085.5	4616.2	4531.6	2788.9	6030.5	4542.7
AJ633050.1	99202	6525.9	6001.8	5279.3	4346.8	8055.1	5600.9
AJ633051.1	99352	3145.5	2372.1	2973.8	1126.3	3026.5	2312.4
AY530806.1	100745	2157.3	2891.7	2053.4	2186.5	4699.3	3832.6
AF287153.1	18302	3324.3	4680.6	4059.7	3947.9	5610.3	4999.9

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M82801.1 gg_id:6041 "Ehrlichia platys"
AF286699.1 gg_id:42949 Anaplasma platys
AY942762.1 gg_id:150441 but species richness marine sponge Cymbastela concentrica clone Cc045
GU118640.1 gg_id:590270 Threatened Corals Provide Microbial Habitats clone Mfav_F04
AJ566640.2 gg_id:136326 Ixodes ricinus endosymbiont 1 (IricES1)
FJ389575.1 gg_id:365478 cloning and Anaplasma sp. goat Chongqing blood clone szg-2
AY969011.1 gg_id:141855 Anaplasma phagocytophilum J4
EU978823.1 gg_id:536819 and metabolic potential metagenome glacier ice clone glb335c
EU491849.1 gg_id:264506 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39
GU118498.1 gg_id:587318 Threatened Corals Provide Microbial Habitats clone Gven_P15
AF069962.1 gg_id:5951 Acanthamoeba endosymbiont clone UWC36
AF283007.1 gg_id:25427 Anaplasma centrale
EF667897.1 gg_id:256410 Long-term maintenance species-specific microbiota basal metazoan Hydra epitheliun
AY527214.1 gg_id:112067 Anaplasma phagocytophilum str. Strong
FJ981659.1 gg_id:563266 Flea Vectors Plague clone XC1
AY969014.1 gg_id:143969 Anaplasma phagocytophilum J4
FJ478621.1 gg_id:513411 species richness estimates obtained nearly and simulated pyrosequencing-generated
AF497583.1 gg_id:82176 detected Haemaphysalis wellingtoni removed chicken Thailand clone Hw124
AM997528.1 gg_id:562891 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A
EF667921.1 gg_id:236767 Long-term maintenance species-specific microbiota basal metazoan Hydra epitheliun
EU799164.1 gg_id:355833 It's all ranking aquatic Newport Harbour RI clone 1C226733
AB196721.1 gg_id:152987 Anaplasma phagocytophilum str. SS33P-L
AY969013.1 gg_id:143770 Anaplasma phagocytophilum J4
GU118630.1 gg_id:582550 Threatened Corals Provide Microbial Habitats clone Mfav_B15
GU118616.1 gg_id:569314 Threatened Corals Provide Microbial Habitats clone Mfav_P11
AF156784.1 gg_id:6042 Anaplasma platys str. Gzh981
AF493952.1 gg_id:66159 tick-borne pathogen order Rickettsiales East: evidence ticks humans identical 2 Homo
EF633744.1 gg_id:278455 Neoehrlichia lotori str. RAC413
AY135531.1 gg_id:59553 Candidatus Neoehrlichia mikurensis str. Rattus strain mikurensis
DQ915970.1 gg_id:172589 Ehrlichia canis
M73226.1 gg_id:6033 Ehrlichia canis str. Florida
NC_007354.1 gg_id:139026 Ehrlichia canis str. Jake
U86664.1 gg_id:6016 Ehrlichia chaffeensis Jax
AB013009.1 gg_id:6031 Ehrlichia muris str. NA1
AF318021.1 gg_id:16712 Ehrlichia ruminantium str. Porto Henrique
M73227.1 gg_id:6026 Ehrlichia ewingii
NC_007798.1 gg_id:153370 Neorickettsia sennetsu str. Miyayama
AF037210.1 gg_id:6005 Neorickettsia risticii str. SHSN-1
AF206298.1 gg_id:17901 Ehrlichia sp. 'trout isolate' trout
AF037211.1 gg_id:6006 Neorickettsia risticii str. SHSN-2

AF303467.1	24415	3762.8	5117.5	3994.8	4350.9	6175.4	5485.4
M82801.1	6041	5739.2	6423.9	4408.1	6102.7	10667.6	9587.1
AF286699.1	42949	2888.2	3638.8	2643.6	3116.4	3204.6	3376.5
AY942762.1	150441	2422.0	4850.0	3491.3	1861.9	5146.9	3887.4
GU118640.1	590270	15564.7	16655.4	11257.9	13171.8	13176.8	15737.6
AJ566640.2	136326	3348.2	4384.4	7186.6	3956.9	8702.8	6616.5
FJ389575.1	365478	3905.9	3000.0	3303.7	705.5	584.6	1070.3
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EU978823.1	536819	2461.2	3514.5	6691.5	4612.4	5439.1	4626.6
EU491849.1	264506	6041.1	7409.6	8161.7	6321.4	4415.4	4942.5
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AF069962.1	5951	42.4	82.1	312.1	77.0	213.8	164.4
AF283007.1	25427	3942.8	3409.0	5165.3	1351.0	5725.6	5914.3
EF667897.1	256410	9327.7	11424.6	9317.7	8538.9	11835.8	10528.0
AY527214.1	112067	3606.0	4196.0	4090.3	3115.8	7349.7	4694.5
FJ981659.1	563266	48.2	147.2	229.5	79.5	104.3	78.7
AY969014.1	143969	6456.9	6889.4	2138.2	4348.8	6248.6	5315.5
FJ478621.1	513411	13254.9	11396.8	11632.6	15123.3	10639.8	11313.6
AF497583.1	82176	8574.0	8411.7	8770.5	6710.8	11987.8	8410.2
AM997528.1	562891	5033.0	5064.7	8719.1	7751.4	3552.6	3908.2
EF667921.1	236767	5151.3	6110.8	7450.0	5516.7	6745.7	4654.3
EU799164.1	355833	5623.9	7999.6	12716.3	6467.0	18679.9	11760.0
AB196721.1	152987	2583.4	3191.6	3145.9	1627.9	4637.5	3449.2
AY969013.1	143770	9371.9	6509.0	4158.4	7726.9	7383.4	8313.4
GU118630.1	582550	1778.3	3276.4	5961.4	2479.1	6774.3	6462.2
GU118616.1	569314	4367.6	6441.1	6408.2	5223.7	5946.0	6401.7
AF156784.1	6042	18922.9	18814.8	11107.5	13399.4	21149.7	16162.4
AF493952.1	66159	593.9	880.4	2630.8	802.9	1675.7	916.0
EF633744.1	278455	7063.8	7685.8	9565.3	7491.4	7780.4	6081.5
AY135531.1	59553	563.9	847.1	1389.4	1401.8	3920.4	809.8
DQ915970.1	172589	8795.7	8658.0	5779.7	8225.0	7864.5	6572.2
M73226.1	6033	9630.1	11372.9	11888.3	9564.6	11308.3	8931.3
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U86664.1	6016	5855.4	9447.1	10028.7	6376.5	11360.6	8032.6
AB013009.1	6031	9161.8	13746.0	15679.3	7713.4	13692.2	9133.0
AF318021.1	16712	2588.7	7111.1	5354.8	3571.6	7341.6	6774.3
M73227.1	6026	6172.6	10166.7	9093.9	6892.9	10171.0	7972.4
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AF037210.1	6005	5529.3	4812.5	11069.2	8963.6	13179.6	12683.7
AF206298.1	17901	1525.7	2416.1	1736.0	887.4	3793.3	6494.2
AF037211.1	6006	3139.4	4014.2	4047.3	3281.9	5664.1	6882.0

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s__Candidatus Pelagibacter ubique	73159

X71837.1 gg_id:5918 Caedibacter caryophilus str. 221
AF132138.1 gg_id:39058 Acanthamoeba polyphaga HN-3 symbiont
DQ129376.1 gg_id:154693 microarray level air two cities Texas urban aerosol clone AKIW1012
DQ537528.1 gg_id:173557 manganese oxidation soil clone JH-WH29
EF575101.1 gg_id:233724 site S25 near Coco's Island marine clone S25_1445
AM997318.1 gg_id:562327 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A
CU926702.1 gg_id:564680 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
FJ529991.1 gg_id:544240 Initial ammonia- and nitrite-oxidizing compromises successful nitritation counter-diffu
EU735608.1 gg_id:305493 archaeal structures and pristine soils China oil contaminated soil Jidong Oilfield clone
DQ925896.1 gg_id:252167 Microbes and Thermal Gradients Temperature Hydrothermal Chimneys hydrotherm
AY174894.1 gg_id:110755 Sinorickettsia chlamys
AB299552.1 gg_id:254738 Motility Symbiont Termite Gut Flagellate Caduceia versatilis Member 'Synergistes' G
DQ337066.1 gg_id:146295 subsurface water clone EV818SWSAP21
AB185652.1 gg_id:106778 rumen clone F24-H08
AB192232.1 gg_id:141713 termite gut homogenate clone RsTu1-71
AB089088.1 gg_id:78348 termite gut homogenate clone Rs-D21 proteobacterium
AB192283.1 gg_id:144338 termite gut homogenate clone RPK-86
FJ202085.1 gg_id:352689 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k
AB192282.1 gg_id:142916 termite gut homogenate clone RPK-49
AJ867903.1 gg_id:143746 Fluctuations Significantly Influence Microbial Present Nival Lakes lake water clone A1
EF409837.1 gg_id:208265 acid mine drainage clone YTW-34-06
AY493937.1 gg_id:136282 Fingerprinting aggregates soil clone 15
GQ008144.1 gg_id:501518 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw:
GQ385282.1 gg_id:566774 Biofilm formation on new membranes initiated and dominated Spinghomonas spp r
AF132139.1 gg_id:40401 Acanthamoeba endosymbiont UWET39
AF069496.1 gg_id:4551 Candidatus Odyssella thessalonicensis str. L13
EU305601.1 gg_id:244100 Short-term effect organic matter on nitrite oxidation performance structure nitrite-o
DQ464145.1 gg_id:157472 acid mine drainage clone D3-44
DQ336985.1 gg_id:148878 subsurface water clone EV818CFSSAHH30
EU133464.1 gg_id:247958 tallgrass prarie soil clone FFCH1626
FJ437938.1 gg_id:550142 Benthic okenone production Fayetteville New York Green Lake surface sediments 16.
AB089089.1 gg_id:78233 termite gut homogenate clone Rs-D39 proteobacterium
EF140635.1 gg_id:180865 Acanthamoeba sp. KA/E9 symbiont
GQ500786.1 gg_id:579026 Surveys Biofilms and Sediments Mammoth Cave Karst Aquifers Bio-Sep beads conta
AJ318202.1 gg_id:45099 waste-gas biofilter clone BIxi22
AF132137.1 gg_id:24244 Acanthamoeba endosymbiont UWC9
AY135665.1 gg_id:106090 Southern Ocean clone ANT18/2_83
EU804706.1 gg_id:348480 It's all ranking aquatic 250 miles Panama City clone 6C232664
FJ155034.1 gg_id:341080 seasonal fluctuation coastal Bohai Bay sequencing and RFLP ocean water clone BJ
EF572082.1 gg_id:232332 Coco's Island site 23 marine clone S23_181
EF573154.1 gg_id:233774 Coco's Island site 23 marine clone S23_1253

X71837.1	5918	2223.5	405.8	2359.6	2239.7	216.7	664.3
AF132138.1	39058	38.7	107.8	134.2	99.3	234.7	101.4
DQ129376.1	154693	204.0	534.8	581.2	507.9	1016.4	1213.2
DQ537528.1	173557	2699.4	2325.9	7605.5	3150.5	6978.6	6827.0
EF575101.1	233724	10798.8	13208.7	6090.3	7782.5	13074.4	11530.6
AM997318.1	562327	5054.5	5481.0	9660.8	6058.5	11014.2	9300.0
CU926702.1	564680	4892.6	4617.0	6594.3	4429.7	5846.6	5871.7
FJ529991.1	544240	2987.5	3761.0	5661.8	3531.1	6744.7	5930.9
EU735608.1	305493	6449.3	5873.5	5060.7	5508.3	9345.2	8549.8
DQ925896.1	252167	2728.7	3423.1	5255.3	5079.8	5508.3	6596.7
AY174894.1	110755	7467.4	7540.9	4944.5	6765.2	9314.5	7942.9
AB299552.1	254738	1724.1	2307.8	4089.2	3119.4	3369.2	1976.9
DQ337066.1	146295	293.4	571.9	2049.6	357.4	333.2	785.2
AB185652.1	106778	478.8	391.6	607.1	503.7	450.8	145.9
AB192232.1	141713	21.3	48.5	22.6	52.6	45.5	16.8
AB089088.1	78348	15705.4	14048.3	13553.7	16279.3	12166.0	10751.3
AB192283.1	144338	1183.3	2427.2	2033.5	439.8	3130.4	2274.9
FJ202085.1	352689	1665.0	1967.0	3094.1	3000.3	5320.7	4681.7
AB192282.1	142916	5890.8	6623.6	4488.3	5396.2	4434.4	3629.9
AJ867903.1	143746	4840.9	5047.4	5070.3	6382.2	5475.4	5274.3
EF409837.1	208265	82.3	123.8	350.0	121.1	104.1	84.4
AY493937.1	136282	9348.7	9753.0	4866.9	8161.1	11922.2	11167.4
GQ008144.1	501518	1111.2	2861.8	2678.1	1615.7	5229.8	4319.9
GQ385282.1	566774	9848.4	11227.7	12204.3	10675.2	18279.9	13999.9
AF132139.1	40401	3864.7	4620.7	6407.4	6292.9	3995.8	6297.0
AF069496.1	4551	4697.2	5027.5	3526.8	4041.3	5583.1	8541.0
EU305601.1	244100	13740.8	6633.8	20246.2	14165.8	9362.7	9491.5
DQ464145.1	157472	98.9	246.2	639.1	188.4	156.9	178.2
DQ336985.1	148878	371.9	555.7	968.6	503.0	1410.0	1949.4
EU133464.1	247958	6463.7	6840.0	10139.8	7994.1	11987.8	8955.9
FJ437938.1	550142	10083.8	10595.5	11497.7	8515.7	10983.9	10101.3
AB089089.1	78233	2365.2	3070.4	2056.2	2036.2	2497.4	3454.8
EF140635.1	180865	1228.8	853.2	2848.0	1303.7	690.6	1445.2
GQ500786.1	579026	2383.3	3636.8	6703.8	2801.8	8123.1	7666.8
AJ318202.1	45099	3710.7	4591.7	4426.5	3504.4	6705.7	6014.5
AF132137.1	24244	4807.2	6892.4	9970.4	5713.2	10921.9	10401.8
AY135665.1	106090	5816.1	4896.6	3022.3	4695.6	5390.9	4882.0
EU804706.1	348480	830.7	664.1	847.6	433.7	1182.0	1338.5
FJ155034.1	341080	2360.9	1628.3	631.9	1700.4	2657.7	2411.7
EF572082.1	232332	5268.8	4063.5	4973.3	4493.7	6503.8	7648.5
EF573154.1	233774	356.0	580.6	1022.9	464.7	493.3	847.3

k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
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o__Rickettsiales	f__Pelagibacteraceae
o__Rickettsiales	f__Pelagibacteraceae
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g__Candidatus Pelagibacter
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s__Candidatus Pelagibacter ubique	73164
s__Candidatus Pelagibacter ubique	73177
s__Candidatus Pelagibacter ubique	73179
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s__Candidatus Pelagibacter ubique	73187
s__Candidatus Pelagibacter ubique	73188
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s__Candidatus Pelagibacter ubique	73356
s__Candidatus Pelagibacter ubique	73361
s__Candidatus Pelagibacter ubique	73367

EU010190.1 gg_id:247318 Biogeography Singapore seawaters seawater clone C4
EF572152.1 gg_id:230071 Coco's Island site 23 marine clone S23_251
EU237277.1 gg_id:251339 Genes transcripts Eastern and Western Equatorial North Atlantic Ocean microbial as:
EU394583.1 gg_id:352939 Coccolithophore bloom dynamics shape (NE-Atl) northern Bay Biscay pelagic particle
EF573604.1 gg_id:228750 Coco's Island site 23 marine clone S23_1703
EU804172.1 gg_id:347854 It's all ranking aquatic 250 miles Panama City clone 6C232068
GQ337086.1 gg_id:550700 Hydrography shapes biogeography deep Arctic Ocean water depth 1191m clone NB:
DQ071035.1 gg_id:130275 marine surface water clone Chl1.17
EU268097.1 gg_id:249237 summer Dalian and Liaodong bay determined sea water clone L4163
EU804840.1 gg_id:322061 It's all ranking aquatic 250 miles Panama City clone 6C232806
EU804308.1 gg_id:348507 It's all ranking aquatic 250 miles Panama City clone 6C232210
GU119425.1 gg_id:538759 Threatened Corals Provide Microbial Habitats reef water clone Reef_H23
EU804403.1 gg_id:312309 It's all ranking aquatic 250 miles Panama City clone 6C232318
EU804919.1 gg_id:322681 It's all ranking aquatic 250 miles Panama City clone 6C232895
FJ744775.1 gg_id:553689 Transporter genes expressed coastal response dissolved organic carbon surface wate
GU061340.1 gg_id:569849 and function microbial mesoscale eddy perturbations South China Sea clone CE1-5m
GQ348144.1 gg_id:586176 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
EU800313.1 gg_id:349820 It's all ranking aquatic Delaware Bay NJ clone 2C228362
FJ826485.1 gg_id:562447 Succession during spring diatom bloom Sea filtered surface sea water contrasting nor
EF572554.1 gg_id:229787 Coco's Island site 23 marine clone S23_653
EU804543.1 gg_id:345570 It's all ranking aquatic 250 miles Panama City clone 6C232490
AF382134.1 gg_id:79390 bacterioplankton clone ZA3320c
EU804583.1 gg_id:316863 It's all ranking aquatic 250 miles Panama City clone 6C232532
GU119354.1 gg_id:548940 Threatened Corals Provide Microbial Habitats reef water clone Reef_P04
EF572954.1 gg_id:234414 Coco's Island site 23 marine clone S23_1053
FJ744853.1 gg_id:532890 Transporter genes expressed coastal response dissolved organic carbon surface wate
EU799492.1 gg_id:352428 It's all ranking aquatic Newport Harbour RI clone 1C227098
EU237401.1 gg_id:245547 Genes transcripts Eastern and Western Equatorial North Atlantic Ocean microbial as:
EU799198.1 gg_id:338982 It's all ranking aquatic Newport Harbour RI clone 1C226770
EU805287.1 gg_id:303698 It's all ranking aquatic 250 miles Panama City clone 6C233287
GQ350090.1 gg_id:575288 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
EU804214.1 gg_id:344952 It's all ranking aquatic 250 miles Panama City clone 6C232114
GU061805.1 gg_id:581967 and function microbial mesoscale eddy perturbations South China Sea clone CEP-DC
FJ545626.1 gg_id:567003 Diveristy Seawater and Sediment Northern North Yel Sea seawater clone W2-50
GU061372.1 gg_id:553174 and function microbial mesoscale eddy perturbations South China Sea clone CE1-5m
EU804569.1 gg_id:338938 It's all ranking aquatic 250 miles Panama City clone 6C232517
EU805276.1 gg_id:318071 It's all ranking aquatic 250 miles Panama City clone 6C233276
FJ744769.1 gg_id:550347 Transporter genes expressed coastal response dissolved organic carbon surface wate
EU800579.1 gg_id:340109 It's all ranking aquatic Delaware Bay NJ clone 2C228725
EF572965.1 gg_id:230129 Coco's Island site 23 marine clone S23_1064
EU804139.1 gg_id:353394 It's all ranking aquatic 250 miles Panama City clone 6C232032

EU010190.1	247318	10845.3	8699.1	6282.7	10165.2	11763.9	10694.4
EF572152.1	230071	2065.6	1569.2	2016.6	1496.8	2879.5	3581.4
EU237277.1	251339	5776.2	6104.9	3917.4	5107.5	6299.7	7691.0
EU394583.1	352939	337.8	181.7	146.8	134.7	78.7	64.3
EF573604.1	228750	2493.2	1480.9	1134.6	2044.2	2896.6	2434.9
EU804172.1	347854	185.0	144.1	253.7	103.8	259.1	211.5
GQ337086.1	550700	243.1	139.9	82.3	74.0	58.7	48.1
DQ071035.1	130275	1592.9	1406.5	1146.8	1769.7	2808.0	2785.9
EU268097.1	249237	10215.4	13608.2	3408.9	5778.5	7973.4	6465.6
EU804840.1	322061	402.7	223.6	131.4	166.5	353.4	111.5
EU804308.1	348507	3043.3	1778.8	2789.7	1606.2	3263.4	3722.6
GU119425.1	538759	5236.2	7461.9	3725.3	5374.5	6086.7	4320.7
EU804403.1	312309	3395.2	3027.9	2789.7	3298.4	4566.7	4903.4
EU804919.1	322681	2395.9	1465.0	1042.3	1975.8	3146.3	2853.9
FJ744775.1	553689	3443.1	2342.6	3680.6	2618.0	4741.6	5333.9
GU061340.1	569849	144.2	125.0	122.2	76.8	191.9	176.2
GQ348144.1	586176	5463.5	3838.0	5174.7	4636.6	6133.0	7071.4
EU800313.1	349820	1733.4	1256.8	901.7	1711.3	2464.3	2097.1
FJ826485.1	562447	13519.0	18578.0	8449.3	12851.1	15390.3	14543.8
EF572554.1	229787	2807.6	1758.5	2108.6	1731.0	2712.5	3114.1
EU804543.1	345570	5147.9	2869.4	3533.8	3444.6	5040.1	4888.2
AF382134.1	79390	5204.6	3061.6	924.5	2725.9	9748.6	4757.0
EU804583.1	316863	1560.6	2493.9	2989.3	2085.8	5081.9	5058.9
GU119354.1	548940	4938.4	3804.2	3091.2	4204.7	5812.1	4735.5
EF572954.1	234414	1293.3	634.9	503.3	621.1	1682.1	1142.9
FJ744853.1	532890	2380.2	1198.9	493.4	927.6	1870.3	1045.5
EU799492.1	352428	2406.9	1613.9	1469.9	2158.5	3224.5	2923.1
EU237401.1	245547	3402.2	1689.3	1569.6	2363.6	2640.0	2441.2
EU799198.1	338982	581.3	742.7	1216.9	529.9	485.5	973.8
EU805287.1	303698	1842.6	3320.6	1334.5	2079.5	5740.1	7696.3
GQ350090.1	575288	2849.5	3498.0	2736.4	2103.5	3503.1	2274.7
EU804214.1	344952	3010.7	1809.8	2904.3	1696.0	2821.6	3461.8
GU061805.1	581967	10824.5	10422.6	7174.6	8526.1	11440.4	11107.5
FJ545626.1	567003	467.4	746.6	929.3	682.4	608.8	786.7
GU061372.1	553174	1818.9	1568.4	1746.2	1542.9	2814.0	3631.4
EU804569.1	338938	5004.7	2947.1	3379.4	3204.9	5109.4	5370.0
EU805276.1	318071	2132.2	1408.7	914.0	1828.2	3517.9	2976.7
FJ744769.1	550347	2457.9	1491.1	1191.2	1873.8	2317.2	2573.9
EU800579.1	340109	2046.7	1454.9	1244.7	1971.4	2868.3	2582.8
EF572965.1	230129	3455.0	2367.3	3670.6	2617.4	4744.4	5344.4
EU804139.1	353394	2237.0	1510.7	2562.5	1571.6	2749.0	3604.3

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EU802744.1 gg_id:315894 It's all ranking aquatic Northeast Colon Panama clone 4C230111
EF572652.1 gg_id:228725 Coco's Island site 23 marine clone S23_751
EU010214.1 gg_id:249320 Biogeography Singapore seawaters seawater clone C8
GU230220.1 gg_id:584057 Multilevel approach along Rio de la Plata-South Atlantic Ocean coastal water clone A
EU805083.1 gg_id:327126 It's all ranking aquatic 250 miles Panama City clone 6C233068
EU802898.1 gg_id:305898 It's all ranking aquatic Northeast Colon Panama clone 4C230290
EU410957.1 gg_id:258240 Description SAR11 containing lighting region variable replacement within genome Ca
EU804893.1 gg_id:318781 It's all ranking aquatic 250 miles Panama City clone 6C232865
EU804562.1 gg_id:340648 It's all ranking aquatic 250 miles Panama City clone 6C232509
EU802304.1 gg_id:307321 It's all ranking aquatic Northeast Colon Panama clone 4C229615
EU804721.1 gg_id:329320 It's all ranking aquatic 250 miles Panama City clone 6C232679
GU119190.1 gg_id:554445 Threatened Corals Provide Microbial Habitats reef water clone Reef_G03
EU800774.1 gg_id:341025 It's all ranking aquatic Delaware Bay NJ clone 2C228971
U75253.1 gg_id:5912 marine planktonic clone SAR407
EU804381.1 gg_id:355665 It's all ranking aquatic 250 miles Panama City clone 6C232293
EF572413.1 gg_id:233290 Coco's Island site 23 marine clone S23_512
EU804710.1 gg_id:317021 It's all ranking aquatic 250 miles Panama City clone 6C232668
EF572687.1 gg_id:229583 Coco's Island site 23 marine clone S23_786
EU804612.1 gg_id:350897 It's all ranking aquatic 250 miles Panama City clone 6C232561
GQ350315.1 gg_id:592999 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
EU802940.1 gg_id:355076 It's all ranking aquatic Northeast Colon Panama clone 4C230336
EF573232.1 gg_id:231199 Coco's Island site 23 marine clone S23_1331
EU804547.1 gg_id:326831 It's all ranking aquatic 250 miles Panama City clone 6C232494
FJ826220.1 gg_id:554175 Succession during spring diatom bloom Sea filtered surface sea water contrasting nor
GQ348078.1 gg_id:593145 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
EU800420.1 gg_id:339916 It's all ranking aquatic Delaware Bay NJ clone 2C228516
GQ346823.1 gg_id:587245 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
EU804281.1 gg_id:328071 It's all ranking aquatic 250 miles Panama City clone 6C232183
GQ347719.1 gg_id:576263 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
EF571967.1 gg_id:231214 Coco's Island site 23 marine clone S23_66
EU801166.1 gg_id:335800 It's all ranking aquatic Delaware Bay NJ clone 2C229523
EF573156.1 gg_id:230611 Coco's Island site 23 marine clone S23_1255
GQ350674.1 gg_id:536841 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
FJ826114.1 gg_id:565466 Succession during spring Sea filtered surface sea water decay period after diatom blo
GQ346738.1 gg_id:538218 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
EF573022.1 gg_id:232263 Coco's Island site 23 marine clone S23_1121
EF572419.1 gg_id:228811 Coco's Island site 23 marine clone S23_518
EF571934.1 gg_id:230704 Coco's Island site 23 marine clone S23_33
FJ744970.1 gg_id:536126 Transporter genes expressed coastal response dissolved organic carbon surface wate
EF572311.1 gg_id:230398 Coco's Island site 23 marine clone S23_410

EF572314.1	240960	3658.6	2519.5	3286.5	2711.2	5010.3	5335.2
EU802744.1	315894	4199.6	2740.6	3384.0	3275.8	4829.8	5165.1
EF572652.1	228725	3055.2	1495.7	1245.1	2326.4	2901.8	2470.8
EU010214.1	249320	3487.4	1794.5	1531.6	2612.6	2951.5	2837.7
GU230220.1	584057	1448.5	700.3	879.4	788.1	816.7	955.1
EU805083.1	327126	3956.8	2561.8	3150.1	2630.5	5068.7	5803.1
EU802898.1	305898	4482.3	3486.4	3137.0	3728.2	4882.3	4956.9
EU410957.1	258240	1510.4	1359.3	875.0	1709.5	2995.4	3017.3
EU804893.1	318781	173.8	315.1	283.7	247.0	242.0	96.4
EU804562.1	340648	3728.3	2544.6	3474.0	2717.9	4948.2	5205.4
EU802304.1	307321	10080.2	8094.4	6253.1	8400.5	10564.0	10327.4
EU804721.1	329320	1277.3	740.4	736.2	694.8	1823.4	1526.7
GU119190.1	554445	5735.2	2999.5	4242.6	3749.6	4880.6	5041.4
EU800774.1	341025	883.1	319.1	349.3	421.6	182.1	122.8
U75253.1	5912	713.1	746.8	475.2	1610.5	1423.7	1423.7
EU804381.1	355665	1189.1	485.2	545.8	668.6	713.5	739.5
EF572413.1	233290	3432.7	2902.0	2837.2	3196.0	4570.5	5302.0
EU804710.1	317021	5157.4	2860.7	3904.0	3413.2	4847.9	4842.9
EF572687.1	229583	6620.2	4216.3	5929.3	4857.2	5432.9	6339.0
EU804612.1	350897	4415.9	2516.6	3495.0	4162.8	4383.1	4368.2
GQ350315.1	592999	4663.0	3135.5	4263.0	3366.3	4846.7	5566.1
EU802940.1	355076	5620.8	4673.2	2823.6	5819.7	8861.1	8334.5
EF573232.1	231199	3772.1	1822.2	1790.6	2631.5	3018.9	2780.1
EU804547.1	326831	6747.1	4663.9	3658.8	5456.1	6287.2	6002.6
FJ826220.1	554175	2165.8	1606.1	1659.9	2214.0	2567.2	3040.4
GQ348078.1	593145	213.7	138.2	144.0	87.2	189.2	192.6
EU800420.1	339916	3704.5	2032.8	1739.2	2789.7	2944.2	2826.5
GQ346823.1	587245	3164.5	1915.0	1410.2	2324.0	3154.4	3105.3
EU804281.1	328071	5361.7	4770.2	4805.2	6389.9	9173.2	8042.4
GQ347719.1	576263	1713.8	1291.2	1073.7	1676.6	2804.4	3231.7
EF571967.1	231214	914.9	843.4	1159.1	890.7	619.2	1052.4
EU801166.1	335800	5976.0	4764.1	1951.1	6067.8	7331.5	6257.4
EF573156.1	230611	328.6	437.1	384.0	345.7	262.6	97.3
GQ350674.1	536841	3593.5	1764.5	1384.1	2491.4	3031.7	2233.7
FJ826114.1	565466	640.1	606.2	408.6	280.8	1206.0	636.6
GQ346738.1	538218	3213.7	1661.3	1776.5	2539.8	2881.3	2823.7
EF573022.1	232263	3291.2	1701.4	2230.0	1886.9	2726.6	3150.1
EF572419.1	228811	3550.6	2683.5	3659.1	2869.5	4898.5	5005.7
EF571934.1	230704	4843.9	2865.2	3668.1	3414.7	4850.4	5188.3
FJ744970.1	536126	2540.1	3144.0	1674.0	3133.5	5929.6	6222.5
EF572311.1	230398	9941.7	9720.2	7805.7	7298.3	10368.1	9898.1

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s__Candidatus Pelagibacter ubique	73582
s__Candidatus Pelagibacter ubique	73590
s__Candidatus Pelagibacter ubique	73597
s__Candidatus Pelagibacter ubique	73600
s__Candidatus Pelagibacter ubique	73605
s__Candidatus Pelagibacter ubique	73606
s__Candidatus Pelagibacter ubique	73612
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s__Candidatus Pelagibacter ubique	73639
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s__Candidatus Pelagibacter ubique	73647
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s__Candidatus Pelagibacter ubique	73657
s__Candidatus Pelagibacter ubique	73658
s__Candidatus Pelagibacter ubique	73665
s__Candidatus Pelagibacter ubique	73670
s__Candidatus Pelagibacter ubique	73675
s__Candidatus Pelagibacter ubique	73677
s__Candidatus Pelagibacter ubique	73679
s__Candidatus Pelagibacter ubique	73682
s__Candidatus Pelagibacter ubique	73687
s__Candidatus Pelagibacter ubique	73695
s__Candidatus Pelagibacter ubique	73699
s__Candidatus Pelagibacter ubique	73706
s__Candidatus Pelagibacter ubique	73707
s__Candidatus Pelagibacter ubique	73708
s__Candidatus Pelagibacter ubique	73711
s__Candidatus Pelagibacter ubique	73717
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s__Candidatus Pelagibacter ubique	73744
s__Candidatus Pelagibacter ubique	73745
s__Candidatus Pelagibacter ubique	73747
s__Candidatus Pelagibacter ubique	73751
s__Candidatus Pelagibacter ubique	73758
s__Candidatus Pelagibacter ubique	73784

FJ826203.1 gg_id:537705 Succession during spring Sea filtered surface sea water decay period after diatom blo
GQ351049.1 gg_id:579779 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
GQ348133.1 gg_id:563097 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
EU802469.1 gg_id:338687 It's all ranking aquatic Northeast Colon Panama clone 4C229801
GQ350531.1 gg_id:538597 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
DQ071141.1 gg_id:136072 marine surface water clone Surf1.16
EU800481.1 gg_id:326350 It's all ranking aquatic Delaware Bay NJ clone 2C228595
EU804453.1 gg_id:348575 It's all ranking aquatic 250 miles Panama City clone 6C232382
EU805349.1 gg_id:346932 It's all ranking aquatic 250 miles Panama City clone 6C233353
EU804887.1 gg_id:339824 It's all ranking aquatic 250 miles Panama City clone 6C232859
EU800477.1 gg_id:331844 It's all ranking aquatic Delaware Bay NJ clone 2C228590
GQ350584.1 gg_id:538959 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
EU802582.1 gg_id:316095 It's all ranking aquatic Northeast Colon Panama clone 4C229931
EU800272.1 gg_id:327151 It's all ranking aquatic Delaware Bay NJ clone 2C228312
GQ350462.1 gg_id:562464 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
DQ655710.1 gg_id:161812 ocean) brackish zone shal coastal lagoon (South Atlantic Ocean) clone 8
DQ071057.1 gg_id:136068 marine surface water clone Chl1.44
EF573476.1 gg_id:228126 Coco's Island site 23 marine clone S23_1575
EF572494.1 gg_id:232394 Coco's Island site 23 marine clone S23_593
EU805294.1 gg_id:309191 It's all ranking aquatic 250 miles Panama City clone 6C233294
EU801916.1 gg_id:339935 It's all ranking aquatic Chesapeake Bay MD clone 3C003295
EU805290.1 gg_id:336652 It's all ranking aquatic 250 miles Panama City clone 6C233290
EU592342.1 gg_id:563209 Seasonal changes Salton Sea hypersaline water clone SSW26Ap
EF574158.1 gg_id:231586 site S25 near Coco's Island marine clone S25_502
EF572576.1 gg_id:234584 Coco's Island site 23 marine clone S23_675
GQ348209.1 gg_id:568564 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
EU804711.1 gg_id:311847 It's all ranking aquatic 250 miles Panama City clone 6C232669
EU805387.1 gg_id:316104 It's all ranking aquatic 250 miles Panama City clone 6C233396
EU805281.1 gg_id:329803 It's all ranking aquatic 250 miles Panama City clone 6C233281
GU061691.1 gg_id:586444 and function microbial mesoscale eddy perturbations South China Sea clone CEP-5m
GU061692.1 gg_id:591579 and function microbial mesoscale eddy perturbations South China Sea clone CEP-5m
EU005773.1 gg_id:276591 Major activity inside and outside natural iron-fertilized phytoplankton bloom 3 micro
EU800693.1 gg_id:345826 It's all ranking aquatic Delaware Bay NJ clone 2C228861
DQ071050.1 gg_id:132375 marine surface water clone Chl1.38
EU801209.1 gg_id:353280 It's all ranking aquatic Chesapeake Bay MD clone 3C002456
EU268085.1 gg_id:240606 summer Dalian and Liaodong bay determined sea water clone L2104
EF573262.1 gg_id:231495 Coco's Island site 23 marine clone S23_1361
EU805181.1 gg_id:334084 It's all ranking aquatic 250 miles Panama City clone 6C233174
GU230228.1 gg_id:535781 Multilevel approach along Rio de la Plata-South Atlantic Ocean coastal water clone A
EF572832.1 gg_id:229346 Coco's Island site 23 marine clone S23_931
EF573364.1 gg_id:232550 Coco's Island site 23 marine clone S23_1463

FJ826203.1	537705	240.2	331.6	325.8	257.8	245.2	87.9
GQ351049.1	579779	3601.5	1883.5	1441.3	2523.1	3193.2	2312.7
GQ348133.1	563097	1264.3	1012.3	767.2	1345.2	2268.1	2331.7
EU802469.1	338687	2238.5	969.8	1742.7	1787.1	1519.0	2377.7
GQ350531.1	538597	237.8	173.9	144.5	123.8	155.7	77.2
DQ071141.1	136072	1145.0	1036.6	839.0	1480.6	1533.2	1805.4
EU800481.1	326350	1544.8	1159.2	991.5	1583.4	2804.7	2777.3
EU804453.1	348575	3393.7	1571.0	1378.2	2324.3	2407.1	2215.4
EU805349.1	346932	3030.7	2316.6	1833.8	3320.1	4498.2	3556.0
EU804887.1	339824	5948.5	5459.0	4305.4	3946.3	7293.0	6005.3
EU800477.1	331844	3506.1	2704.5	3685.1	2805.2	4794.8	5339.5
GQ350584.1	538959	3291.0	1781.4	1546.5	2702.7	2331.1	2207.2
EU802582.1	316095	4071.6	3342.7	2854.8	4442.3	5357.7	4897.8
EU800272.1	327151	2615.1	1383.7	1378.6	2116.1	2829.7	2283.6
GQ350462.1	562464	4962.3	1446.1	1122.7	3392.2	1011.3	1361.6
DQ655710.1	161812	4673.9	3426.2	3019.8	3827.0	5315.2	4542.2
DQ071057.1	136068	3424.2	3527.7	2432.6	3372.6	5885.8	5082.0
EF573476.1	228126	1328.5	1064.2	738.6	1343.5	2268.9	2327.6
EF572494.1	232394	4453.2	2758.4	3464.9	4343.1	4381.8	4104.2
EU805294.1	309191	1227.4	1010.6	666.1	1321.9	2313.3	2167.5
EU801916.1	339935	1600.0	1659.4	974.2	1928.0	4411.1	4019.3
EU805290.1	336652	5661.5	2988.3	3953.9	3719.1	4877.5	5027.9
EU592342.1	563209	2260.6	1740.6	3273.2	1481.1	3379.4	4646.9
EF574158.1	231586	2808.2	1757.3	2257.7	1731.8	2716.5	2921.0
EF572576.1	234584	6466.8	3345.3	4405.1	4028.0	5708.1	4967.9
GQ348209.1	568564	8889.3	10232.9	7195.5	8183.7	10958.3	8978.6
EU804711.1	311847	1498.4	1259.7	1093.0	1611.1	3038.1	3003.9
EU805387.1	316104	6928.3	5267.4	5394.0	5444.3	8151.3	8667.4
EU805281.1	329803	2044.0	1401.4	1277.1	1944.2	3168.3	2797.5
GU061691.1	586444	3512.3	2370.0	3425.5	2631.0	4744.1	5746.5
GU061692.1	591579	2747.2	1735.5	2258.5	1722.8	2715.6	3112.0
EU005773.1	276591	3262.7	1908.7	1966.8	2533.1	2868.0	3060.4
EU800693.1	345826	4662.3	3130.9	4257.9	3358.4	4793.6	5989.0
DQ071050.1	132375	2065.4	1568.1	1874.6	1496.7	2876.8	3581.2
EU801209.1	353280	1151.8	506.6	134.1	372.3	394.4	236.8
EU268085.1	240606	654.9	295.1	39.6	200.4	56.3	14.2
EF573262.1	231495	4655.7	2922.1	3552.6	3283.2	5023.1	4549.3
EU805181.1	334084	5870.4	3147.4	3682.3	3678.9	4950.2	4887.6
GU230228.1	535781	2131.7	969.8	221.5	643.5	1322.3	377.7
EF572832.1	229346	7712.4	6039.9	4577.1	5056.7	5982.3	6363.5
EF573364.1	232550	1040.4	649.1	689.7	550.1	1241.0	1516.1

k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
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k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria

o__Rickettsiales	f__Pelagibacteraceae
o__Rickettsiales	f__Pelagibacteraceae
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o__Rickettsiales	f__Pelagibacteraceae

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s__Candidatus Pelagibacter ubique	73787
s__Candidatus Pelagibacter ubique	73788
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s__Candidatus Pelagibacter ubique	73954
s__Candidatus Pelagibacter ubique	73956

EU804445.1 gg_id:310572 It's all ranking aquatic 250 miles Panama City clone 6C232373
EF572751.1 gg_id:234005 Coco's Island site 23 marine clone S23_850
EU805034.1 gg_id:325083 It's all ranking aquatic 250 miles Panama City clone 6C233016
EU805307.1 gg_id:349966 It's all ranking aquatic 250 miles Panama City clone 6C233309
GU230237.1 gg_id:589643 Multilevel approach along Rio de la Plata-South Atlantic Ocean coastal water clone A
L10935.1 gg_id:5908 marine clone FL11
EF573024.1 gg_id:227598 Coco's Island site 23 marine clone S23_1123
EU802266.1 gg_id:305764 It's all ranking aquatic Northeast Colon Panama clone 4C229568
EF574501.1 gg_id:229394 site S25 near Coco's Island marine clone S25_845
GQ349360.1 gg_id:562690 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
EU800659.1 gg_id:353974 It's all ranking aquatic Delaware Bay NJ clone 2C228821
EU804959.1 gg_id:342655 It's all ranking aquatic 250 miles Panama City clone 6C232937
EU803180.1 gg_id:336030 It's all ranking aquatic Northeast Colon Panama clone 4C230617
EU804468.1 gg_id:326529 It's all ranking aquatic 250 miles Panama City clone 6C232399
EF572776.1 gg_id:234022 Coco's Island site 23 marine clone S23_875
GU230215.1 gg_id:545228 Multilevel approach along Rio de la Plata-South Atlantic Ocean coastal water clone A
EU802388.1 gg_id:352099 It's all ranking aquatic Northeast Colon Panama clone 4C229710
EU804553.1 gg_id:317436 It's all ranking aquatic 250 miles Panama City clone 6C232500
EF571925.1 gg_id:232961 Coco's Island site 23 marine clone S23_24
AB186970.1 gg_id:105858 Mariana trough hydrothermal vent water 0.2micro-m filterable fraction clone MT-NE
GU061794.1 gg_id:586928 and function microbial mesoscale eddy perturbations South China Sea clone CEP-DC
EU638843.1 gg_id:329172 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n
GU061451.1 gg_id:562584 and function microbial mesoscale eddy perturbations South China Sea clone CE1-DC
GU061695.1 gg_id:581190 and function microbial mesoscale eddy perturbations South China Sea clone CEP-5m
EU802853.1 gg_id:324621 It's all ranking aquatic Northeast Colon Panama clone 4C230237
EU801758.1 gg_id:345184 It's all ranking aquatic Chesapeake Bay MD clone 3C003127
FJ744964.1 gg_id:558120 Transporter genes expressed coastal response dissolved organic carbon surface wate
GQ351154.1 gg_id:554776 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Eastern
EU800851.1 gg_id:336634 It's all ranking aquatic Delaware Bay NJ clone 2C229079
FJ745165.1 gg_id:561678 Transporter genes expressed coastal response dissolved organic carbon surface wate
EU805345.1 gg_id:342433 It's all ranking aquatic 250 miles Panama City clone 6C233349
EF573040.1 gg_id:234332 Coco's Island site 23 marine clone S23_1139
DQ071171.1 gg_id:130137 marine surface water clone Surf1.8
GQ348102.1 gg_id:590363 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
GQ348021.1 gg_id:590277 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
GU061790.1 gg_id:571620 and function microbial mesoscale eddy perturbations South China Sea clone CEP-DC
GU230229.1 gg_id:575529 Multilevel approach along Rio de la Plata-South Atlantic Ocean coastal water clone A
EU804396.1 gg_id:344788 It's all ranking aquatic 250 miles Panama City clone 6C232311
GU119384.1 gg_id:576863 Threatened Corals Provide Microbial Habitats reef water clone Reef_H22
EU803151.1 gg_id:308243 It's all ranking aquatic Northeast Colon Panama clone 4C230583
GU230235.1 gg_id:546752 Multilevel approach along Rio de la Plata-South Atlantic Ocean coastal water clone A

EU804445.1	310572	3215.2	1805.0	1414.2	2345.9	3632.9	3131.9
EF572751.1	234005	4657.6	2749.0	3689.2	3151.8	4836.6	5198.1
EU805034.1	325083	1985.4	1308.7	1029.1	1872.4	3009.2	2608.9
EU805307.1	349966	2380.1	1723.1	1826.5	2601.1	2989.5	2950.5
GU230237.1	589643	4407.5	3761.7	2893.2	3745.0	5729.6	4548.3
L10935.1	5908	6139.6	4788.7	4663.5	5536.9	6167.5	6362.0
EF573024.1	227598	1534.1	1383.7	1147.9	1875.7	2810.0	2783.5
EU802266.1	305764	5916.8	3960.2	3697.1	4381.0	6675.9	5907.3
EF574501.1	229394	3342.1	3023.3	2832.3	3515.4	4641.5	4702.4
GQ349360.1	562690	5236.4	3923.2	5263.3	4748.0	6855.3	8022.2
EU800659.1	353974	1932.6	1054.0	499.3	924.9	173.9	135.1
EU804959.1	342655	4197.8	2857.5	3432.2	2998.4	5294.0	5242.2
EU803180.1	336030	4655.3	2923.5	3552.2	3282.6	5021.8	4851.1
EU804468.1	326529	1523.4	1308.1	1050.9	1809.0	2878.2	2741.5
EF572776.1	234022	5447.3	2971.4	4451.8	3635.5	4540.2	5029.0
GU230215.1	545228	2876.9	1154.6	1132.2	1297.7	980.1	689.7
EU802388.1	352099	6888.4	5006.2	5414.0	5311.0	7743.0	6678.8
EU804553.1	317436	6075.4	4177.3	5073.4	3805.8	5184.7	5936.5
EF571925.1	232961	1060.1	844.9	1156.8	878.8	1790.4	1871.3
AB186970.1	105858	10999.0	10736.0	14128.7	10623.2	15164.3	13997.7
GU061794.1	586928	228.9	256.6	694.2	217.5	505.0	747.8
EU638843.1	329172	3927.3	2157.5	1939.7	2773.4	3533.1	3033.8
GU061451.1	562584	3006.0	1657.3	1571.2	2364.4	2867.3	2461.1
GU061695.1	581190	2301.2	555.8	420.7	463.7	288.5	165.2
EU802853.1	324621	1929.2	1162.9	1944.5	1935.8	1723.2	2165.9
EU801758.1	345184	2888.6	3490.9	796.2	756.1	2053.4	2414.2
FJ744964.1	558120	1307.8	1097.4	710.5	1373.6	2464.4	2353.8
GQ351154.1	554776	9340.3	8801.4	8099.0	9219.5	12847.2	6872.9
EU800851.1	336634	380.1	276.7	195.7	153.4	342.5	220.3
FJ745165.1	561678	1327.0	2037.5	2340.8	1501.5	841.7	1725.1
EU805345.1	342433	2678.3	1680.5	1085.8	2052.4	3091.0	2464.8
EF573040.1	234332	1065.0	818.7	1515.9	797.1	1750.7	2006.9
DQ071171.1	130137	3448.6	1588.8	1475.2	2334.1	2406.6	2214.6
GQ348102.1	590363	8210.7	6728.9	6860.1	7222.3	8571.1	7604.8
GQ348021.1	590277	128.1	768.0	616.2	535.4	181.4	132.3
GU061790.1	571620	2050.5	1545.5	1875.0	1490.8	2871.1	3336.1
GU230229.1	575529	4573.5	5549.6	3788.3	3371.8	4265.8	6942.9
EU804396.1	344788	4436.0	2654.7	3162.3	3076.8	5086.0	5841.0
GU119384.1	576863	384.0	162.7	178.6	146.8	68.4	37.0
EU803151.1	308243	4205.0	4154.5	1802.1	3282.4	5739.3	6593.1
GU230235.1	546752	4665.1	2752.0	3685.6	3148.8	4792.9	5204.6

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AY907723.1 gg_id:136391 identification picoplankton contrasting waters Arabian Sea water clone A312016
GU061320.1 gg_id:581682 Evaluation culturing methods cultivate previously Yel Sea intertidal beach seawater
EF646133.1 gg_id:236718 Potential interactions particle- anammox and archaeal partners namibian Namibian u
EU801782.1 gg_id:319174 It's all ranking aquatic Chesapeake Bay MD clone 3C003154
EU799608.1 gg_id:338826 It's all ranking aquatic Newport Harbour RI clone 1C227227
EU803146.1 gg_id:356204 It's all ranking aquatic Northeast Colon Panama clone 4C230578
GQ350235.1 gg_id:592248 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
GU119470.1 gg_id:571275 Threatened Corals Provide Microbial Habitats reef water clone Reef_G05
EF573467.1 gg_id:230749 Coco's Island site 23 marine clone S23_1566
EU800773.1 gg_id:342165 It's all ranking aquatic Delaware Bay NJ clone 2C228970
EU802549.1 gg_id:343006 It's all ranking aquatic Northeast Colon Panama clone 4C229892
EU800179.1 gg_id:352754 It's all ranking aquatic Delaware Bay NJ clone 2C228183
FJ545605.1 gg_id:571079 Diveristy Seawater and Sediment Northern North Yel Sea seawater clone W2-20
GQ346837.1 gg_id:585543 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
GQ348739.1 gg_id:537683 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
GQ350198.1 gg_id:548268 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
EF573286.1 gg_id:233612 Coco's Island site 23 marine clone S23_1385
EF572914.1 gg_id:229690 Coco's Island site 23 marine clone S23_1013
GU230234.1 gg_id:582241 Multilevel approach along Rio de la Plata-South Atlantic Ocean coastal water clone A
EU804337.1 gg_id:331996 It's all ranking aquatic 250 miles Panama City clone 6C232242
EU800264.1 gg_id:331734 It's all ranking aquatic Delaware Bay NJ clone 2C228304
EU804878.1 gg_id:325227 It's all ranking aquatic 250 miles Panama City clone 6C232849
EU592389.1 gg_id:577168 Seasonal changes Salton Sea hypersaline water clone SSW78Ap
EU804831.1 gg_id:336773 It's all ranking aquatic 250 miles Panama City clone 6C232796
GU061707.1 gg_id:544545 and function microbial mesoscale eddy perturbations South China Sea clone CEP-5m
GQ348024.1 gg_id:568072 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
FJ155041.1 gg_id:309414 seasonal fluctuation coastal Bohai Bay sequencing and RFLP ocean water clone G
AY697876.1 gg_id:100107 Antarctica clone F2CB7
EF571998.1 gg_id:232340 Coco's Island site 23 marine clone S23_97
GU061376.1 gg_id:582403 and function microbial mesoscale eddy perturbations South China Sea clone CE1-5m
GQ348097.1 gg_id:548057 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
FJ745256.1 gg_id:559049 Transporter genes expressed coastal response dissolved organic carbon surface wate
EF572775.1 gg_id:230717 Coco's Island site 23 marine clone S23_874
GU119216.1 gg_id:547572 Threatened Corals Provide Microbial Habitats reef water clone Reef_P13
EF572805.1 gg_id:233186 Coco's Island site 23 marine clone S23_904
EF571996.1 gg_id:227935 Coco's Island site 23 marine clone S23_95
EF573444.1 gg_id:230013 Coco's Island site 23 marine clone S23_1543
GQ350155.1 gg_id:567509 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
EF575211.1 gg_id:229546 site S25 near Coco's Island marine clone S25_1555
EF572864.1 gg_id:231051 Coco's Island site 23 marine clone S23_963
EU802719.1 gg_id:337956 It's all ranking aquatic Northeast Colon Panama clone 4C230082

AY907723.1	136391	1485.6	2839.6	1392.7	1147.7	9900.2	6377.1
GU061320.1	581682	3514.2	2306.7	3007.6	2643.2	4463.9	4509.1
EF646133.1	236718	4349.9	3418.4	3416.3	3383.2	5028.6	4853.2
EU801782.1	319174	1270.0	499.5	69.5	362.2	51.1	38.3
EU799608.1	338826	2046.7	1447.4	1341.5	1965.0	2820.6	2396.8
EU803146.1	356204	2706.5	1646.8	1365.6	2108.6	2855.5	2815.9
GQ350235.1	592248	4078.9	2840.4	4262.3	3106.7	4756.1	5350.8
GU119470.1	571275	2388.0	1183.2	1685.7	1918.6	1984.0	2916.5
EF573467.1	230749	3720.5	2742.7	3210.5	2731.5	5275.9	5621.3
EU800773.1	342165	4938.0	4690.9	3278.8	3963.7	4110.3	5751.6
EU802549.1	343006	4506.0	4343.8	3877.5	2953.1	5743.4	6574.5
EU800179.1	352754	1612.4	1278.1	1011.4	1609.9	2816.9	2995.5
FJ545605.1	571079	583.5	686.0	1318.8	591.0	415.4	900.3
GQ346837.1	585543	6035.0	4075.1	5695.7	4998.3	6310.5	6596.1
GQ348739.1	537683	378.3	881.3	617.4	581.7	250.0	146.5
GQ350198.1	548268	2493.4	991.7	799.2	1151.2	1464.4	1150.8
EF573286.1	233612	5632.1	3639.0	3848.9	3938.8	6448.0	6485.3
EF572914.1	229690	605.9	483.8	2985.0	431.7	1273.4	2620.6
GU230234.1	582241	5264.6	4234.0	4514.4	5905.9	7228.1	7517.3
EU804337.1	331996	1735.7	1026.4	1330.3	1551.0	2386.3	1929.1
EU800264.1	331734	3431.6	4152.0	10507.8	8453.7	3462.3	2820.5
EU804878.1	325227	4418.4	2717.6	3608.7	3271.7	4833.4	5163.0
EU592389.1	577168	43.7	72.8	74.8	88.3	77.6	33.9
EU804831.1	336773	4470.2	2736.3	3601.0	3274.3	4827.4	4821.2
GU061707.1	544545	6758.2	4681.1	5042.3	4807.1	6866.7	7137.7
GQ348024.1	568072	3211.5	2031.0	1829.9	2532.4	2877.0	2633.0
FJ155041.1	309414	1576.8	1217.8	888.5	1625.7	3004.2	3019.4
AY697876.1	100107	3216.4	2160.3	1741.3	2554.8	3032.9	2534.4
EF571998.1	232340	5078.1	2252.9	2038.2	3204.8	3784.0	2771.0
GU061376.1	582403	13346.9	14195.8	8131.6	11284.0	13431.3	11171.9
GQ348097.1	548057	4302.3	2596.2	3091.9	2449.2	4413.0	5507.7
FJ745256.1	559049	5025.8	4263.9	3876.8	4423.0	5954.5	5585.2
EF572775.1	230717	86.2	82.7	82.4	81.9	56.5	21.1
GU119216.1	547572	1844.6	1463.6	1957.4	2151.7	1987.1	2512.2
EF572805.1	233186	4829.2	2095.5	2533.2	2250.0	3437.3	3812.3
EF571996.1	227935	1896.0	1230.4	723.7	1570.4	3134.6	2716.9
EF573444.1	230013	5724.4	3811.0	3741.1	4850.1	4741.7	4493.4
GQ350155.1	567509	13195.3	17523.2	13294.9	12358.0	15264.1	17033.7
EF575211.1	229546	1715.3	1334.6	1100.2	1675.5	3086.2	2955.0
EF572864.1	231051	2597.6	1670.4	1372.8	2119.2	2857.5	3016.0
EU802719.1	337956	1622.1	1291.9	1730.2	2024.7	1515.7	2094.8

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GQ349440.1 gg_id:541444 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
EF572356.1 gg_id:230117 Coco's Island site 23 marine clone S23_455
GU119458.1 gg_id:538125 Threatened Corals Provide Microbial Habitats reef water clone Reef_O05
GU061332.1 gg_id:569420 and function microbial mesoscale eddy perturbations South China Sea clone CE1-5m
GQ346735.1 gg_id:589317 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
AY907725.1 gg_id:136383 identification picoplankton contrasting waters Arabian Sea water clone A312018
EU801049.1 gg_id:331948 It's all ranking aquatic Delaware Bay NJ clone 2C229348
EU799135.1 gg_id:317800 It's all ranking aquatic Newport Harbour RI clone 1C226699
EU804369.1 gg_id:341897 It's all ranking aquatic 250 miles Panama City clone 6C232281
GU061709.1 gg_id:534335 and function microbial mesoscale eddy perturbations South China Sea clone CEP-5m
GU061714.1 gg_id:582991 and function microbial mesoscale eddy perturbations South China Sea clone CEP-5m
EF573016.1 gg_id:234359 Coco's Island site 23 marine clone S23_1115
GQ347968.1 gg_id:582234 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
GQ349905.1 gg_id:554098 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
EU801284.1 gg_id:305596 It's all ranking aquatic Chesapeake Bay MD clone 3C002538
EU802428.1 gg_id:333447 It's all ranking aquatic Northeast Colon Panama clone 4C229755
GU061338.1 gg_id:564801 and function microbial mesoscale eddy perturbations South China Sea clone CE1-5m
GU061507.1 gg_id:571143 and function microbial mesoscale eddy perturbations South China Sea clone CE2-5m
GQ348152.1 gg_id:543428 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
EU802674.1 gg_id:345739 It's all ranking aquatic Northeast Colon Panama clone 4C230033
EF572654.1 gg_id:227884 Coco's Island site 23 marine clone S23_753
GQ349030.1 gg_id:592949 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
EU800753.1 gg_id:330543 It's all ranking aquatic Delaware Bay NJ clone 2C228941
GU061344.1 gg_id:593116 and function microbial mesoscale eddy perturbations South China Sea clone CE1-5m
GQ350567.1 gg_id:573588 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
AB193929.1 gg_id:108889 deep-sea vent clone MabScd-NB
EF572230.1 gg_id:233341 Coco's Island site 23 marine clone S23_329
GU119310.1 gg_id:593014 Threatened Corals Provide Microbial Habitats reef water clone Reef_P08
FJ826405.1 gg_id:551570 Succession during spring diatom bloom Sea filtered surface sea water contrasting nor
GU119456.1 gg_id:561610 Threatened Corals Provide Microbial Habitats reef water clone Reef_A07
GU119421.1 gg_id:586285 Threatened Corals Provide Microbial Habitats reef water clone Reef_I03
EU805029.1 gg_id:322492 It's all ranking aquatic 250 miles Panama City clone 6C233011
GU061701.1 gg_id:573467 and function microbial mesoscale eddy perturbations South China Sea clone CEP-5m
EF572907.1 gg_id:230670 Coco's Island site 23 marine clone S23_1006
DQ071055.1 gg_id:133857 marine surface water clone Chl1.42
EF572304.1 gg_id:234195 Coco's Island site 23 marine clone S23_403
EU800672.1 gg_id:356107 It's all ranking aquatic Delaware Bay NJ clone 2C228836
EU268069.1 gg_id:239902 summer Dalian and Liaodong bay determined sea water clone D4758
EF572266.1 gg_id:231018 Coco's Island site 23 marine clone S23_365
GU230227.1 gg_id:575839 Multilevel approach along Rio de la Plata-South Atlantic Ocean coastal water clone A

EF573088.1	230406	6332.5	4675.0	4860.2	5809.2	7284.3	7026.1
GQ349440.1	541444	5239.1	3528.7	4185.4	3579.8	4442.7	5426.5
EF572356.1	230117	9565.5	12399.1	5922.4	10515.0	13172.2	11241.0
GU119458.1	538125	271.8	198.9	210.1	150.3	168.4	78.4
GU061332.1	569420	2242.4	914.8	931.1	1029.6	936.8	1058.6
GQ346735.1	589317	4368.0	3133.4	3691.9	3366.1	4839.2	5565.4
AY907725.1	136383	1610.5	1140.4	1247.0	847.7	3676.7	3468.6
EU801049.1	331948	5931.3	4294.9	5246.9	4635.4	6720.1	6751.8
EU799135.1	317800	4929.6	4015.4	940.7	2205.8	2047.9	2085.4
EU804369.1	341897	2692.6	3384.8	2754.1	3171.3	2679.0	2923.6
GU061709.1	534335	915.7	813.3	1051.8	866.5	1181.8	1296.7
GU061714.1	582991	6476.3	4285.8	5329.2	4589.6	6575.4	7200.8
EF573016.1	234359	5551.1	2837.4	3919.5	3524.0	4473.3	5745.4
GQ347968.1	582234	2711.7	1893.4	1582.1	2253.6	2865.6	3013.6
GQ349905.1	554098	1492.8	1237.2	1191.9	1552.4	3009.8	2161.5
EU801284.1	305596	478.4	476.7	1500.9	877.2	492.5	900.9
EU802428.1	333447	1748.8	1599.2	2619.0	1687.4	1800.1	2026.4
GU061338.1	564801	16078.7	17340.3	11823.0	12159.8	17264.4	14742.2
GU061507.1	571143	469.3	224.5	204.7	181.2	254.0	144.3
GQ348152.1	543428	212.3	233.8	250.1	105.0	328.1	344.1
EU802674.1	345739	6273.5	2946.0	4155.1	3626.7	4534.7	5385.3
EF572654.1	227884	5733.0	3806.3	5367.0	4915.7	6223.5	6099.5
GQ349030.1	592949	88.8	258.1	204.2	164.2	47.9	22.9
EU800753.1	330543	3727.0	3376.3	5273.2	4474.7	7079.9	5796.5
GU061344.1	593116	2397.3	2007.3	1775.0	3131.5	3283.3	3167.9
GQ350567.1	573588	3202.9	1884.1	1972.6	2701.4	2867.7	3056.5
AB193929.1	108889	3226.9	1761.1	1822.2	1387.1	1866.2	2806.7
EF572230.1	233341	1764.2	1546.5	1863.4	1536.0	2816.1	3627.6
GU119310.1	593014	78.0	102.3	162.9	84.7	114.5	58.1
FJ826405.1	551570	5847.6	3998.6	5105.9	3812.9	5211.2	4973.8
GU119456.1	561610	5251.8	3539.1	2521.1	2010.1	4040.2	4863.5
GU119421.1	586285	5327.9	4086.3	4972.2	4224.0	6501.8	7651.1
EU805029.1	322492	554.2	473.4	799.2	341.7	584.5	1005.1
GU061701.1	573467	5706.6	4373.7	4874.4	6585.8	8247.9	7797.2
EF572907.1	230670	2046.5	1475.4	1520.6	2052.8	3086.9	2689.9
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EF572304.1	234195	4823.1	4077.4	2296.6	4431.5	6318.2	5662.5
EU800672.1	356107	6248.8	3926.8	6044.6	5249.7	7470.3	8401.5
EU268069.1	239902	4387.7	2749.4	3058.6	4228.2	3902.6	4337.9
EF572266.1	231018	2052.1	1471.8	900.9	1289.4	1321.6	1583.1
GU230227.1	575839	3636.3	3717.2	2112.4	3708.8	3403.9	3465.8

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GQ349927.1 gg_id:559135 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
EU237291.1 gg_id:252418 Genes transcripts Eastern and Western Equatorial North Atlantic Ocean microbial as:
GU119329.1 gg_id:537039 Threatened Corals Provide Microbial Habitats reef water clone Reef_N05
DQ071149.1 gg_id:136073 marine surface water clone Surf1.23
EU804835.1 gg_id:328677 It's all ranking aquatic 250 miles Panama City clone 6C232800
AJ400350.1 gg_id:71838 dominates and dimethylsulphoniopropionate uptake after algal bloom North Sea f cyt
EF572090.1 gg_id:233599 Coco's Island site 23 marine clone S23_189
EF572828.1 gg_id:228464 Coco's Island site 23 marine clone S23_927
EU800463.1 gg_id:310712 It's all ranking aquatic Delaware Bay NJ clone 2C228574
EU544717.1 gg_id:262536 free-living particle- aggregate- archaeal and Laptev Sea 0.22-1.0 um size fraction (fre
EF574586.1 gg_id:235137 site S25 near Coco's Island marine clone S25_930
GU061508.1 gg_id:552249 and function microbial mesoscale eddy perturbations South China Sea clone CE2-5m
EU802748.1 gg_id:340698 It's all ranking aquatic Northeast Colon Panama clone 4C230118
GU061812.1 gg_id:592029 and function microbial mesoscale eddy perturbations South China Sea clone CEP-DC
EU804885.1 gg_id:310744 It's all ranking aquatic 250 miles Panama City clone 6C232857
EU800228.1 gg_id:347716 It's all ranking aquatic Delaware Bay NJ clone 2C228250
EF572698.1 gg_id:233393 Coco's Island site 23 marine clone S23_797
EU800767.1 gg_id:336527 It's all ranking aquatic Delaware Bay NJ clone 2C228961
GU230210.1 gg_id:576779 Multilevel approach along Rio de la Plata-South Atlantic Ocean coastal water clone A
EF573605.1 gg_id:230554 Coco's Island site 23 marine clone S23_1704
EU805370.1 gg_id:355973 It's all ranking aquatic 250 miles Panama City clone 6C233377
GQ348121.1 gg_id:574611 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
EU800573.1 gg_id:336168 It's all ranking aquatic Delaware Bay NJ clone 2C228719
GQ347984.1 gg_id:535016 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
FJ826463.1 gg_id:552472 Succession during spring diatom bloom Sea filtered surface sea water contrasting nor
EU805242.1 gg_id:334464 It's all ranking aquatic 250 miles Panama City clone 6C233239
GU230241.1 gg_id:548888 Multilevel approach along Rio de la Plata-South Atlantic Ocean coastal water clone A
GU061807.1 gg_id:554292 and function microbial mesoscale eddy perturbations South China Sea clone CEP-DC
EF572202.1 gg_id:228993 Coco's Island site 23 marine clone S23_301
EF571907.1 gg_id:233932 Coco's Island site 23 marine clone S23_6
EU804502.1 gg_id:348475 It's all ranking aquatic 250 miles Panama City clone 6C232440
EU800005.1 gg_id:322498 It's all ranking aquatic Newport Harbour RI clone 1C227685
EF572463.1 gg_id:232144 Coco's Island site 23 marine clone S23_562
EF572449.1 gg_id:232239 Coco's Island site 23 marine clone S23_548
GU230236.1 gg_id:555992 Multilevel approach along Rio de la Plata-South Atlantic Ocean coastal water clone A
GQ347181.1 gg_id:591181 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
EU804475.1 gg_id:348011 It's all ranking aquatic 250 miles Panama City clone 6C232409
EF572912.1 gg_id:233011 Coco's Island site 23 marine clone S23_1011
EU802138.1 gg_id:312524 It's all ranking aquatic Chesapeake Bay MD clone 3C003551
EU394584.1 gg_id:343762 Coccolithophore bloom dynamics shape (NE-Atl) northern Bay Biscay pelagic particle
GU061702.1 gg_id:536611 and function microbial mesoscale eddy perturbations South China Sea clone CEP-5m

GQ349927.1	559135	2844.1	1739.2	1482.5	2242.9	3484.3	2805.4
EU237291.1	252418	7847.2	6267.3	4571.6	6974.5	10444.9	9216.3
GU119329.1	537039	814.4	296.9	318.4	406.5	175.6	122.2
DQ071149.1	136073	4602.9	3546.2	3021.5	4102.5	5431.3	4699.7
EU804835.1	328677	4014.5	1900.3	1643.9	2897.4	2955.8	2875.9
AJ400350.1	71838	12932.5	14415.0	11087.6	11283.7	11438.9	11677.9
EF572090.1	233599	4984.5	4083.7	3281.2	4407.9	6223.2	6585.8
EF572828.1	228464	2803.0	2322.8	1488.6	2519.0	4465.3	4582.2
EU800463.1	310712	2427.8	1481.0	1493.6	2210.3	2032.0	2370.4
EU544717.1	262536	16.3	29.9	39.8	29.1	34.8	16.4
EF574586.1	235137	74.2	156.2	269.5	133.6	251.9	143.7
GU061508.1	552249	5850.7	5449.6	5277.1	5582.3	7913.4	7366.6
EU802748.1	340698	2462.6	1718.0	2111.6	2414.6	4098.3	3688.3
GU061812.1	592029	423.5	179.9	132.2	153.1	305.0	111.0
EU804885.1	310744	5650.7	3500.5	3725.9	4248.9	4640.5	4780.6
EU800228.1	347716	5470.1	3591.2	4841.4	4356.7	6138.4	6198.8
EF572698.1	233393	1328.3	744.0	696.6	694.8	1751.6	1379.1
EU800767.1	336527	1303.6	523.9	210.7	395.9	405.1	235.6
GU230210.1	576779	12699.8	10871.1	8393.7	9424.9	13070.0	13619.9
EF573605.1	230554	3496.0	2544.7	3474.2	2714.5	4947.5	5205.5
EU805370.1	355973	4704.1	2759.5	3478.6	3156.9	4958.4	4702.5
GQ348121.1	574611	6705.7	4021.7	4641.3	4928.5	6451.0	6744.0
EU800573.1	336168	2505.8	1490.4	1360.1	1989.6	3042.3	2954.7
GQ347984.1	535016	6004.6	4514.9	7795.5	4197.9	6104.2	6918.3
FJ826463.1	552472	3980.7	3945.9	1333.7	2404.2	5956.3	5246.1
EU805242.1	334464	2088.5	1518.9	1984.6	1514.7	2808.5	3625.6
GU230241.1	548888	3766.3	1804.0	1746.2	2622.6	2946.2	2827.1
GU061807.1	554292	438.0	349.0	854.7	262.6	782.0	1019.0
EF572202.1	228993	2643.9	1844.2	1788.6	2774.7	4387.5	3747.2
EF571907.1	233932	2012.3	1501.5	1350.5	1767.8	3214.7	3608.9
EU804502.1	348475	4210.8	3212.9	3638.8	4023.0	4750.8	4711.0
EU800005.1	322498	3964.7	5036.6	3099.2	5890.2	7151.4	7097.5
EF572463.1	232144	5576.9	3667.3	4983.5	3534.3	4553.3	5653.2
EF572449.1	232239	2392.0	1497.6	1730.1	2423.3	2987.6	2749.5
GU230236.1	555992	2690.5	1495.3	1273.8	2127.5	2835.4	2450.3
GQ347181.1	591181	2324.5	2089.1	2170.5	3010.9	4345.0	4640.6
EU804475.1	348011	4184.6	2718.5	3210.3	2722.8	5274.3	6049.8
EF572912.1	233011	4029.2	2709.6	3200.0	3084.7	2793.4	3487.8
EU802138.1	312524	2080.3	949.6	208.1	633.6	1322.7	378.5
EU394584.1	343762	3580.3	3215.1	2740.9	3306.1	4761.1	4937.9
GU061702.1	536611	8853.0	10927.8	8304.8	7223.6	10885.2	9907.5

k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
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o__Rickettsiales	f__Pelagibacteraceae
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g__Candidatus Pelagibacter
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s__Candidatus Pelagibacter ubique	74515
s__Candidatus Pelagibacter ubique	74518
s__Candidatus Pelagibacter ubique	74522
s__Candidatus Pelagibacter ubique	74523
s__Candidatus Pelagibacter ubique	74528
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EU802440.1 gg_id:304430 It's all ranking aquatic Northeast Colon Panama clone 4C229770
EF573095.1 gg_id:230831 Coco's Island site 23 marine clone S23_1194
EU800405.1 gg_id:347665 It's all ranking aquatic Delaware Bay NJ clone 2C228495
AB193898.1 gg_id:108822 deep-sea vent clone MT797-NB06
GQ347809.1 gg_id:581936 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
GQ346920.1 gg_id:546028 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
GQ350110.1 gg_id:557752 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
EU800275.1 gg_id:332963 It's all ranking aquatic Delaware Bay NJ clone 2C228315
EU802779.1 gg_id:317970 It's all ranking aquatic Northeast Colon Panama clone 4C230154
EF573478.1 gg_id:233480 Coco's Island site 23 marine clone S23_1577
EU800496.1 gg_id:354542 It's all ranking aquatic Delaware Bay NJ clone 2C228617
EU805076.1 gg_id:303685 It's all ranking aquatic 250 miles Panama City clone 6C233059
GQ347932.1 gg_id:579167 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
DQ071040.1 gg_id:133968 marine surface water clone Chl1.22
EU805407.1 gg_id:349492 It's all ranking aquatic 250 miles Panama City clone 6C233418
EU802293.1 gg_id:335921 It's all ranking aquatic Northeast Colon Panama clone 4C229602
EF572302.1 gg_id:231569 Coco's Island site 23 marine clone S23_401
GQ348074.1 gg_id:557720 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
EF572986.1 gg_id:228647 Coco's Island site 23 marine clone S23_1085
EU802488.1 gg_id:322048 It's all ranking aquatic Northeast Colon Panama clone 4C229822
EF573272.1 gg_id:233281 Coco's Island site 23 marine clone S23_1371
EU805105.1 gg_id:323335 It's all ranking aquatic 250 miles Panama City clone 6C233091
EU802646.1 gg_id:354371 It's all ranking aquatic Northeast Colon Panama clone 4C230004
AY907729.1 gg_id:136369 identification picoplankton contrasting waters Arabian Sea water clone A312033
GU061948.1 gg_id:553625 and function microbial mesoscale eddy perturbations South China Sea clone S-DCM-
EU237270.1 gg_id:255537 Genes transcripts Eastern and Western Equatorial North Atlantic Ocean microbial as:
AF406514.1 gg_id:60660 bacterioplankton clone AEGEAN_107
EU804202.1 gg_id:335668 It's all ranking aquatic 250 miles Panama City clone 6C232099
EF572982.1 gg_id:231734 Coco's Island site 23 marine clone S23_1081
AY907756.1 gg_id:136700 identification picoplankton contrasting waters Arabian Sea water clone A314007
EU799107.1 gg_id:330866 It's all ranking aquatic Newport Harbour RI clone 1C226669
EU805315.1 gg_id:305656 It's all ranking aquatic 250 miles Panama City clone 6C233318
EU010187.1 gg_id:253778 Biogeography Singapore seawaters seawater clone C36
GQ350009.1 gg_id:592350 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
EU010177.1 gg_id:252942 Biogeography Singapore seawaters seawater clone C19
EU394549.1 gg_id:336437 Coccolithophore bloom dynamics shape (NE-Atl) northern Bay Biscay pelagic free-livi
GQ351239.1 gg_id:547409 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Eastern
AF406553.1 gg_id:60623 bacterioplankton clone AEGEAN_248
DQ009258.1 gg_id:120203 bacterioplankton clone SPOTSAPR01_5m130
GU061443.1 gg_id:589819 and function microbial mesoscale eddy perturbations South China Sea clone CE1-DC
GQ348599.1 gg_id:568494 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich

EU802440.1	304430	2616.1	2462.9	2282.2	3130.6	4439.6	4281.8
EF573095.1	230831	2150.7	1535.1	879.6	1688.1	3337.4	3296.6
EU800405.1	347665	2949.3	4576.5	2364.5	564.1	1335.5	2264.8
AB193898.1	108822	607.0	618.3	600.4	582.1	739.6	791.5
GQ347809.1	581936	2265.1	867.7	1123.2	1129.4	388.7	434.3
GQ346920.1	546028	1800.5	767.9	1051.8	594.8	1034.0	591.4
GQ350110.1	557752	13402.1	14479.0	14245.5	12231.6	14675.7	13841.2
EU800275.1	332963	5243.1	4341.3	6082.5	6582.6	10205.8	7406.7
EU802779.1	317970	3351.5	1724.4	2082.1	1895.0	2723.4	3152.2
EF573478.1	233480	2899.2	1555.3	1033.5	2110.0	3012.7	2450.4
EU800496.1	354542	6539.9	6987.1	6338.2	5137.0	3434.4	210.4
EU805076.1	303685	7224.0	6119.2	5297.1	7250.8	9069.5	7054.1
GQ347932.1	579167	475.4	665.0	1370.2	565.9	733.4	659.7
DQ071040.1	133968	5957.0	4444.3	3698.9	6002.1	7038.9	6328.7
EU805407.1	349492	5021.6	3116.0	3700.5	3488.1	5453.7	5766.2
EU802293.1	335921	3988.2	2693.0	3157.1	3101.3	5084.3	5010.6
EF572302.1	231569	2071.6	1426.7	1168.9	1888.9	2968.1	2424.3
GQ348074.1	557720	588.2	682.5	1319.7	680.4	422.4	754.0
EF572986.1	228647	8568.5	5902.4	5296.5	5817.6	8292.4	7106.1
EU802488.1	322048	4452.1	3235.6	4483.3	4269.9	5823.4	6142.0
EF573272.1	233281	2140.7	1501.8	1199.9	1889.2	3746.1	3267.9
EU805105.1	323335	727.9	469.6	675.5	451.0	1037.6	1265.5
EU802646.1	354371	10323.2	10705.1	8284.2	9289.5	13970.9	10729.4
AY907729.1	136369	9847.9	9664.4	9688.1	7594.4	11050.7	12135.6
GU061948.1	553625	4128.8	4061.9	6088.2	6896.9	18006.1	10998.4
EU237270.1	255537	2559.4	3345.5	2628.1	2107.1	4148.8	3633.7
AF406514.1	60660	6314.7	6502.6	7133.0	5359.0	7896.8	8367.1
EU804202.1	335668	6598.0	7019.4	4737.1	4614.3	9505.0	5119.4
EF572982.1	231734	4185.2	5124.8	5095.5	3665.7	7014.2	4432.2
AY907756.1	136700	1428.8	1978.7	4135.4	1673.1	5956.2	5531.0
EU799107.1	330866	612.9	611.0	1800.3	1033.6	2613.9	4606.3
EU805315.1	305656	1309.4	2036.4	1460.1	1705.8	3337.5	3419.0
EU010187.1	253778	1142.3	1587.8	2147.6	1670.7	1962.7	2667.7
GQ350009.1	592350	7316.9	6978.8	7350.2	9136.7	6700.8	7668.3
EU010177.1	252942	7979.7	10782.1	5340.7	6373.3	14712.9	7881.8
EU394549.1	336437	50.2	53.7	62.1	103.1	99.0	52.8
GQ351239.1	547409	7365.7	8396.3	7267.8	6343.4	8899.5	6582.5
AF406553.1	60623	13286.7	15954.3	15431.4	11216.8	17923.4	13396.9
DQ009258.1	120203	4538.6	3070.8	3216.4	5252.1	6854.7	3544.4
GU061443.1	589819	1661.2	2276.2	2791.7	1427.4	3447.3	3375.5
GQ348599.1	568494	7472.3	8099.8	6713.6	6765.5	14404.7	9609.4

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AB186991.1 gg_id:107205 Suiyo seamount hydrothermal vent water 0.2micro-m filterable fraction clone SSM-N
EU805060.1 gg_id:306417 It's all ranking aquatic 250 miles Panama City clone 6C233042
AY274843.1 gg_id:82782 Delaware River estuary clone 3G9
GQ340185.1 gg_id:581266 Prokaryotic Marathonas Reservoir Greece water column clone K07-79-BAC
EU802303.1 gg_id:306827 It's all ranking aquatic Northeast Colon Panama clone 4C229613
EU259796.1 gg_id:242575 summer sea Dalian and Liaodong determined bay water clone D2893
EU237308.1 gg_id:241412 Genes transcripts Eastern and Western Equatorial North Atlantic Ocean microbial as
GQ337312.1 gg_id:553107 Hydrography shapes biogeography deep Arctic Ocean water depth 252m clone NB2
AACY01057101.1 gg_id:106333 Sargasso Sea
GQ337233.1 gg_id:534129 Hydrography shapes biogeography deep Arctic Ocean water depth 1000m clone CB
DQ396217.1 gg_id:153914 deep-sea octacoral clone ctg_NISAA48
EF573474.1 gg_id:235226 Coco's Island site 23 marine clone S23_1573
EU803100.1 gg_id:304953 It's all ranking aquatic Northeast Colon Panama clone 4C230523
EU802263.1 gg_id:306624 It's all ranking aquatic Northeast Colon Panama clone 4C229565
AY033303.1 gg_id:68988 marine bacterioplankton clone MB11D08
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EF572228.1 gg_id:227567 Coco's Island site 23 marine clone S23_327
AF353226.1 gg_id:50807 marine clone Arctic96A-7
DQ906738.1 gg_id:171294 and marine microorganisms Antarctic sea water 20 m clone AntCL1H3
GQ348746.1 gg_id:578821 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
GQ347999.1 gg_id:593858 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
EF573142.1 gg_id:232227 Coco's Island site 23 marine clone S23_1241
GQ337106.1 gg_id:573002 Hydrography shapes biogeography deep Arctic Ocean water depth 1000m clone CB
GU119433.1 gg_id:579477 Threatened Corals Provide Microbial Habitats reef water clone Reef_C06
AY921813.1 gg_id:113622 farm soil clone AKYH1091
EU802363.1 gg_id:354980 It's all ranking aquatic Northeast Colon Panama clone 4C229680
EF573485.1 gg_id:231006 Coco's Island site 23 marine clone S23_1584
AB193924.1 gg_id:108885 deep-sea vent clone Sc-NB08
EU802142.1 gg_id:330438 It's all ranking aquatic Chesapeake Bay MD clone 3C003555
EU802938.1 gg_id:312639 It's all ranking aquatic Northeast Colon Panama clone 4C230334
FJ545616.1 gg_id:560900 Diveristy Seawater and Sediment Northern North Yel Sea seawater clone W2-33
DQ906712.1 gg_id:171482 and marine microorganisms Antarctic sea water 20 m clone AntCL1B7
FJ612305.1 gg_id:510517 and Biogeochemistry Dongping Lake Ecosystems lake water clone DP7.5.89
EF573216.1 gg_id:230136 Coco's Island site 23 marine clone S23_1315
AB193906.1 gg_id:108863 deep-sea vent clone Mb-NB10
GQ348295.1 gg_id:582171 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
GQ347833.1 gg_id:579810 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
AF353209.1 gg_id:40986 marine clone Arctic96B-3
EU802246.1 gg_id:337290 It's all ranking aquatic Northeast Colon Panama clone 4C229547

FN435239.1	561168	878.3	694.9	640.6	301.8	936.4	527.0
AB186991.1	107205	13481.0	10727.5	12389.4	10746.5	17309.3	14866.5
EU805060.1	306417	6003.9	3495.5	5389.5	4607.3	5838.2	6193.2
AY274843.1	82782	2387.2	863.0	1199.0	1027.0	566.8	860.5
GQ340185.1	581266	11765.3	6437.6	5087.4	8199.8	6340.4	7839.7
EU802303.1	306827	3883.5	2952.6	5006.8	3598.0	3150.3	3171.0
EU259796.1	242575	4871.9	3505.7	3226.7	3675.5	5404.9	5282.4
EU237308.1	241412	1760.9	1999.9	2248.8	3502.4	3207.1	4036.7
GQ337312.1	553107	2581.4	6426.3	2939.7	1664.7	1859.2	2336.1
AACY01057101.1	106333	3373.5	1546.5	1960.0	2508.3	1630.5	2354.7
GQ337233.1	534129	5706.4	6643.8	4978.6	5897.4	12169.8	6636.5
DQ396217.1	153914	912.4	625.1	726.9	671.0	1387.7	1600.1
EF573474.1	235226	7064.9	6383.5	6334.4	7447.9	9416.0	8146.2
EU803100.1	304953	6395.4	4336.7	5417.0	5758.8	7904.9	7741.6
EU802263.1	306624	3714.7	2394.0	2546.1	3487.5	2738.0	3000.7
AY033303.1	68988	5896.9	6704.1	5074.7	7198.4	8636.8	7835.6
GU230256.1	581578	8070.0	6101.5	4724.6	7260.9	6565.7	6972.4
EU802760.1	355191	2460.0	1892.7	1307.1	2953.1	3566.5	3464.7
EF572228.1	227567	3249.9	1514.4	1826.3	2472.1	1629.6	2343.9
AF353226.1	50807	349.8	308.5	1327.5	644.1	689.9	396.0
DQ906738.1	171294	6085.1	3791.7	6290.5	5302.5	7111.7	8068.5
GQ348746.1	578821	3184.6	2988.3	2907.3	4676.6	2874.7	4018.0
GQ347999.1	593858	224.7	140.7	238.3	115.2	265.3	90.0
EF573142.1	232227	6185.3	5022.4	6076.4	6208.5	6989.9	6125.9
GQ337106.1	573002	7027.4	7062.6	7762.4	7459.8	11134.4	8971.7
GU119433.1	579477	3136.4	3483.3	2433.1	3513.8	8599.5	8173.6
AY921813.1	113622	6211.9	5228.4	4671.4	6626.7	9364.4	10131.9
EU802363.1	354980	5102.0	3121.9	3814.5	4426.5	5154.0	5665.0
EF573485.1	231006	3468.0	1856.9	3513.7	2840.4	1087.7	1732.2
AB193924.1	108885	28.0	33.6	16.0	50.9	54.0	28.6
EU802142.1	330438	2359.1	2958.4	4513.3	3594.3	1014.1	1673.9
EU802938.1	312639	7604.4	6320.5	4994.6	6847.5	9305.7	9292.1
FJ545616.1	560900	5706.4	3522.5	5056.4	4636.0	6195.6	6251.8
DQ906712.1	171482	23.1	24.8	19.5	57.6	65.7	23.0
FJ612305.1	510517	15387.3	11032.2	9413.1	10377.0	9872.8	10014.8
EF573216.1	230136	16060.5	16242.6	5202.1	14144.6	19687.3	17115.0
AB193906.1	108863	6575.3	8867.4	8764.6	4925.4	4057.0	5243.6
GQ348295.1	582171	1426.4	1217.3	1119.3	1535.2	3002.5	2340.0
GQ347833.1	579810	686.5	601.8	891.4	578.4	960.1	1262.6
AF353209.1	40986	4525.9	3508.1	3211.1	3680.4	5410.3	6332.0
EU802246.1	337290	5163.6	4242.8	5542.9	5399.9	6344.7	6146.6

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GQ337109.1 gg_id:532709 Hydrography shapes biogeography deep Arctic Ocean water depth 1000m clone CB(
EU804389.1 gg_id:324100 It's all ranking aquatic 250 miles Panama City clone 6C232301
EU802660.1 gg_id:306741 It's all ranking aquatic Northeast Colon Panama clone 4C230018
U75258.1 gg_id:5904 marine planktonic clone SAR241
GQ337209.1 gg_id:583381 Hydrography shapes biogeography deep Arctic Ocean water depth 400m clone CB1:
FJ545627.1 gg_id:571962 Diveristy Seawater and Sediment Northern North Yel Sea seawater clone W2-52
GU230232.1 gg_id:550223 Multilevel approach along Rio de la Plata-South Atlantic Ocean coastal water clone A
EU802776.1 gg_id:339096 It's all ranking aquatic Northeast Colon Panama clone 4C230151
EU799116.1 gg_id:308445 It's all ranking aquatic Newport Harbour RI clone 1C226678
DQ009163.1 gg_id:126283 bacterioplankton clone SPOTSAPR01_5m40
GU061715.1 gg_id:580262 and function microbial mesoscale eddy perturbations South China Sea clone CEP-5m
EU804225.1 gg_id:318608 It's all ranking aquatic 250 miles Panama City clone 6C232125
GU061813.1 gg_id:539918 and function microbial mesoscale eddy perturbations South China Sea clone CEP-DC
EU802664.1 gg_id:336767 It's all ranking aquatic Northeast Colon Panama clone 4C230022
EU802586.1 gg_id:317606 It's all ranking aquatic Northeast Colon Panama clone 4C229937
GQ337266.1 gg_id:588790 Hydrography shapes biogeography deep Arctic Ocean water depth 428m clone CB1!
EU801793.1 gg_id:355198 It's all ranking aquatic Chesapeake Bay MD clone 3C003170
EU801908.1 gg_id:314611 It's all ranking aquatic Chesapeake Bay MD clone 3C003287
EU804890.1 gg_id:324490 It's all ranking aquatic 250 miles Panama City clone 6C232862
GQ351203.1 gg_id:582145 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Eastern
EF575159.1 gg_id:233031 site S25 near Coco's Island marine clone S25_1503
GU061792.1 gg_id:582928 and function microbial mesoscale eddy perturbations South China Sea clone CEP-DC
EF572150.1 gg_id:229222 Coco's Island site 23 marine clone S23_249
EU802828.1 gg_id:312388 It's all ranking aquatic Northeast Colon Panama clone 4C230207
EU803133.1 gg_id:349290 It's all ranking aquatic Northeast Colon Panama clone 4C230561
EU802309.1 gg_id:328726 It's all ranking aquatic Northeast Colon Panama clone 4C229620
GQ259214.1 gg_id:548664 Microbial activities coastal marine sediments and column Svalbard deep water clone
DQ396078.1 gg_id:155140 deep-sea octacoral clone ctg_NISAA12
AF353223.1 gg_id:22763 marine clone Arctic95D-8
GU061818.1 gg_id:582665 and function microbial mesoscale eddy perturbations South China Sea clone CEP-DC
EU803539.1 gg_id:341222 It's all ranking aquatic Lake Gatun clone 5C231125
EU005952.1 gg_id:261438 Major activity inside and outside natural iron-fertilized phytoplankton bloom 3 micro
GQ351188.1 gg_id:542603 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Eastern
GQ337278.1 gg_id:551848 Hydrography shapes biogeography deep Arctic Ocean water depth 996m clone NB0(
EU801227.1 gg_id:335684 It's all ranking aquatic Chesapeake Bay MD clone 3C002474
EU804559.1 gg_id:305051 It's all ranking aquatic 250 miles Panama City clone 6C232506
GU061450.1 gg_id:579714 and function microbial mesoscale eddy perturbations South China Sea clone CE1-DC
AM259853.1 gg_id:209588 Spatial sponge- Mediterranean Tethya aurantium sponge cortex clone TAA-10-18
DQ906754.1 gg_id:170374 and marine microorganisms Antarctic sea water 20 m clone AntCL2H12
EU919824.1 gg_id:340376 Kongsfjorden western Spitsbergen Svalbard ocean water clone s3
EU803466.1 gg_id:320839 It's all ranking aquatic Lake Gatun clone 5C231039

GQ337109.1	532709	10328.9	10771.8	8223.8	9934.1	13968.4	14505.3
EU804389.1	324100	4474.8	3243.6	4197.6	4314.5	3999.1	4120.0
EU802660.1	306741	2897.8	2597.1	2952.0	3549.5	5087.6	4354.3
U75258.1	5904	1688.8	2215.3	1236.4	1291.7	6938.3	5179.3
GQ337209.1	583381	32.1	46.5	32.5	77.5	74.8	92.8
FJ545627.1	571962	6234.0	7641.0	5171.2	6368.6	7963.4	5076.7
GU230232.1	550223	100.2	113.2	238.4	136.3	97.2	148.3
EU802776.1	339096	4177.9	2295.8	2054.9	5037.0	1456.2	2346.1
EU799116.1	308445	2706.5	7174.3	3311.8	3006.8	2441.4	4130.2
DQ009163.1	126283	127.0	271.0	594.7	454.6	805.8	668.7
GU061715.1	580262	8271.3	7295.4	3965.9	5649.6	5420.5	6362.9
EU804225.1	318608	4315.9	2777.4	2842.0	3965.7	3438.6	3529.9
GU061813.1	539918	6340.1	3864.3	3767.8	5463.9	5170.8	5177.8
EU802664.1	336767	5108.4	5945.3	4320.6	6575.7	9086.6	6995.2
EU802586.1	317606	6675.0	4579.7	5179.2	5987.6	8566.3	7923.7
GQ337266.1	588790	8136.7	8743.3	8308.1	9334.7	10987.2	10626.8
EU801793.1	355198	1598.9	907.0	1145.9	990.4	426.7	784.9
EU801908.1	314611	1384.0	856.3	674.1	871.2	193.3	342.8
EU804890.1	324490	6095.6	4155.3	3880.9	4669.0	5532.6	5282.7
GQ351203.1	582145	6210.9	7273.8	4923.3	4739.4	9029.0	7026.1
EF575159.1	233031	3434.6	3052.3	2485.6	4027.2	5467.6	5245.6
GU061792.1	582928	6102.2	4589.7	3666.0	6089.7	6731.0	6705.5
EF572150.1	229222	3311.4	1886.1	2510.0	2770.2	2729.4	2693.1
EU802828.1	312388	583.8	750.0	1563.7	390.6	330.5	335.2
EU803133.1	349290	5141.3	4103.6	4782.0	4613.3	6500.6	6053.7
EU802309.1	328726	5101.5	3123.6	3814.6	4153.1	5153.3	5670.6
GQ259214.1	548664	3849.7	1798.1	1921.6	2466.1	2823.2	3244.3
DQ396078.1	155140	7367.6	5586.8	6380.0	7199.1	9123.7	9929.4
AF353223.1	22763	1547.7	745.4	863.0	2260.1	603.3	412.7
GU061818.1	582665	725.8	643.2	802.2	657.9	2079.9	1402.8
EU803539.1	341222	10527.0	7206.1	6582.6	11076.6	6693.0	8173.0
EU005952.1	261438	30.5	33.5	87.3	36.9	53.2	13.0
GQ351188.1	542603	5938.5	6829.7	6117.5	9331.2	8807.2	9898.6
GQ337278.1	551848	8049.0	8287.5	8269.3	9409.0	14076.4	11651.5
EU801227.1	335684	4609.7	3707.1	6825.7	4373.7	7288.3	5316.0
EU804559.1	305051	4676.5	2830.0	3809.6	3280.1	4396.5	4286.7
GU061450.1	579714	6496.8	6478.8	5065.3	6052.4	12204.5	10059.5
AM259853.1	209588	11790.4	15045.8	4928.7	7504.9	11225.8	12755.2
DQ906754.1	170374	220.7	405.6	888.0	304.0	1112.5	723.0
EU919824.1	340376	5941.6	3073.6	4238.8	3496.8	4886.2	5691.8
EU803466.1	320839	10233.4	6712.4	4733.1	8559.6	5078.7	7120.6

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AF534425.1 gg_id:85388 Toolik Lake main station at 3 m depth clone TLM01/TLMdgge14 proteobacterium
GQ349786.1 gg_id:593932 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
EU803037.1 gg_id:343789 It's all ranking aquatic Northeast Colon Panama clone 4C230445
EU010144.1 gg_id:245665 Biogeography Singapore seawaters seawater clone B55
EU802276.1 gg_id:354196 It's all ranking aquatic Northeast Colon Panama clone 4C229581
GQ351241.1 gg_id:585642 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Eastern
EU802321.1 gg_id:346262 It's all ranking aquatic Northeast Colon Panama clone 4C229633
EF572632.1 gg_id:227854 Coco's Island site 23 marine clone S23_731
EU802028.1 gg_id:317489 It's all ranking aquatic Chesapeake Bay MD clone 3C003417
EU800327.1 gg_id:326805 It's all ranking aquatic Delaware Bay NJ clone 2C228380
U75256.1 gg_id:5902 marine planktonic clone SAR211
GQ346815.1 gg_id:551062 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
DQ071172.1 gg_id:128312 marine surface water clone Surf1.9
EU703194.1 gg_id:572065 taxon richness -altitude lakes eastern tin plateau predominance Bacteroidetes and S
GQ337168.1 gg_id:544967 Hydrography shapes biogeography deep Arctic Ocean water depth 410m clone CB1
EU804826.1 gg_id:307486 It's all ranking aquatic 250 miles Panama City clone 6C232791
EU805084.1 gg_id:309659 It's all ranking aquatic 250 miles Panama City clone 6C233069
DQ071046.1 gg_id:131757 marine surface water clone Chl1.32
GQ351217.1 gg_id:593777 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Eastern
GQ337299.1 gg_id:555674 Hydrography shapes biogeography deep Arctic Ocean water depth 252m clone NB2
EU802668.1 gg_id:308130 It's all ranking aquatic Northeast Colon Panama clone 4C230026
EU802856.1 gg_id:316482 It's all ranking aquatic Northeast Colon Panama clone 4C230240
EU801709.1 gg_id:307941 It's all ranking aquatic Chesapeake Bay MD clone 3C003069
AB187007.1 gg_id:106132 Suiyo seamount hydrothermal vent water 0.2micro-m filterable fraction clone SSM-N
EU804121.1 gg_id:323752 It's all ranking aquatic 250 miles Panama City clone 6C232013
GQ337208.1 gg_id:571518 Hydrography shapes biogeography deep Arctic Ocean water depth 400m clone CB1
GQ337194.1 gg_id:557396 Hydrography shapes biogeography deep Arctic Ocean water depth 1000m clone CB
GQ337176.1 gg_id:568404 Hydrography shapes biogeography deep Arctic Ocean water depth 1000m clone CB
EU802580.1 gg_id:332667 It's all ranking aquatic Northeast Colon Panama clone 4C229928
GQ347006.1 gg_id:538870 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
EU802269.1 gg_id:318647 It's all ranking aquatic Northeast Colon Panama clone 4C229571
EU801648.1 gg_id:348015 It's all ranking aquatic Chesapeake Bay MD clone 3C002994
GU061225.1 gg_id:587129 Evaluation culturing methods cultivate previously Yel Sea intertidal beach seawater
EU803197.1 gg_id:355010 It's all ranking aquatic Northeast Colon Panama clone 4C230639
GU061335.1 gg_id:545379 and function microbial mesoscale eddy perturbations South China Sea clone CE1-5m
EU802749.1 gg_id:323099 It's all ranking aquatic Northeast Colon Panama clone 4C230121
EF572257.1 gg_id:234083 Coco's Island site 23 marine clone S23_356
EU802486.1 gg_id:346488 It's all ranking aquatic Northeast Colon Panama clone 4C229820
U75255.1 gg_id:5901 marine planktonic clone SAR203
GU061422.1 gg_id:560097 and function microbial mesoscale eddy perturbations South China Sea clone CE1-DC

EU802637.1	311063	5236.8	3952.1	6652.9	4697.5	7512.8	7361.5
AF534425.1	85388	13878.4	9893.9	8543.3	10625.3	10543.5	10571.4
GQ349786.1	593932	4063.2	1807.3	1449.7	2380.4	2953.1	3194.4
EU803037.1	343789	3710.6	2493.3	4252.4	2872.8	3055.4	3112.2
EU010144.1	245665	4279.6	4668.8	2227.2	3210.9	3377.6	4172.6
EU802276.1	354196	1221.3	898.1	1596.6	954.7	889.8	825.9
GQ351241.1	585642	9818.9	7924.2	8074.7	8500.8	12940.4	11360.0
EU802321.1	346262	3370.9	2253.4	2313.5	2988.2	3762.8	4693.7
EF572632.1	227854	4812.5	3728.1	3589.6	4168.5	5638.1	5004.7
EU802028.1	317489	5105.5	3544.2	5458.3	2958.1	4130.5	4776.7
EU800327.1	326805	9059.1	6638.2	5241.2	7314.2	2942.4	4537.3
U75256.1	5902	46.6	47.7	35.0	58.2	90.8	64.4
GQ346815.1	551062	1162.3	850.3	884.3	1029.2	1667.1	2434.0
DQ071172.1	128312	9830.4	7381.7	12375.2	6655.4	12049.7	10478.3
EU703194.1	572065	11172.8	8841.6	5948.7	8252.5	6697.1	7880.3
GQ337168.1	544967	1034.1	1105.1	889.3	1200.2	1079.1	1407.0
EU804826.1	307486	5065.6	4208.0	5238.2	5384.2	5894.6	5958.6
EU805084.1	309659	8355.4	9959.1	8604.6	8600.8	15664.8	12921.7
DQ071046.1	131757	5385.7	5752.8	6290.7	6902.4	10073.8	9240.5
GQ351217.1	593777	4041.2	2900.3	3003.4	4007.7	4827.4	4314.9
GQ337299.1	555674	3330.0	2391.1	3375.7	3206.5	1842.6	2290.3
EU802668.1	308130	2992.6	1987.3	2677.1	3007.7	3800.0	4022.2
EU802856.1	316482	2101.7	1276.6	2367.2	1219.4	852.7	740.8
EU801709.1	307941	1992.0	938.6	1102.5	1163.5	744.6	834.9
AB187007.1	106132	6841.3	7366.9	6024.4	5622.0	8671.9	7090.7
EU804121.1	323752	6789.9	4291.3	5936.9	5659.9	7444.2	7644.3
GQ337208.1	571518	5191.3	4247.0	4429.5	5375.6	6593.9	6072.1
GQ337194.1	557396	1663.9	1387.1	4137.9	1831.2	2787.7	2177.1
GQ337176.1	568404	3404.5	4242.9	3630.9	3042.2	4942.3	4492.7
EU802580.1	332667	1832.7	1845.8	1786.5	2560.0	4449.7	3674.3
GQ347006.1	538870	3626.9	1991.1	1981.4	2567.3	3041.8	3245.1
EU802269.1	318647	4006.3	2732.9	3234.7	3695.3	4187.2	4750.6
EU801648.1	348015	5279.4	2881.1	3032.3	3067.9	1522.7	2652.4
GU061225.1	587129	4805.9	3494.2	3031.6	3672.8	5402.1	5760.8
EU803197.1	355010	4882.8	3493.0	5945.3	3230.1	4562.7	5039.5
GU061335.1	545379	5176.5	4972.7	2242.3	6895.0	8077.1	7792.0
EU802749.1	323099	2210.4	1659.2	2781.1	2554.4	3643.4	4571.0
EF572257.1	234083	7984.1	5766.2	6195.8	5531.7	9098.4	8886.3
EU802486.1	346488	2495.8	2179.6	1544.1	3188.0	3557.4	3474.0
U75255.1	5901	6520.1	5869.5	4853.0	6826.4	9106.6	10346.8
GU061422.1	560097	2512.1	1390.9	1253.1	1884.1	2579.1	2562.6

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EU804185.1 gg_id:322364 It's all ranking aquatic 250 miles Panama City clone 6C232081
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AY033322.1 gg_id:68975 marine bacterioplankton clone MB21A02
GQ350463.1 gg_id:553931 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
GU061331.1 gg_id:576730 and function microbial mesoscale eddy perturbations South China Sea clone CE1-5m
EU802844.1 gg_id:308027 It's all ranking aquatic Northeast Colon Panama clone 4C230228
GQ346794.1 gg_id:554239 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
EU802334.1 gg_id:350605 It's all ranking aquatic Northeast Colon Panama clone 4C229646
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GQ351212.1 gg_id:557820 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Eastern
EU804375.1 gg_id:308733 It's all ranking aquatic 250 miles Panama City clone 6C232287
EU801132.1 gg_id:356060 It's all ranking aquatic Delaware Bay NJ clone 2C229469
GQ337177.1 gg_id:580656 Hydrography shapes biogeography deep Arctic Ocean water depth 1000m clone CB1
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GQ348793.1 gg_id:546554 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
GQ337163.1 gg_id:583834 Hydrography shapes biogeography deep Arctic Ocean water depth 410m clone CB1
FJ545588.1 gg_id:535511 Diveristy Seawater and Sediment Northern North Yel Sea seawater clone W2-1
DQ396175.1 gg_id:151130 deep-sea octacoral clone ctg_NISA034
AB193887.1 gg_id:108804 deep-sea vent clone Ma-NB07
FJ745027.1 gg_id:562372 Transporter genes expressed coastal response dissolved organic carbon surface wate
EU802493.1 gg_id:321420 It's all ranking aquatic Northeast Colon Panama clone 4C229828
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GQ337130.1 gg_id:558072 Hydrography shapes biogeography deep Arctic Ocean water depth 395m clone CB5(
EF573593.1 gg_id:234950 Coco's Island site 23 marine clone S23_1692
AB186966.1 gg_id:101793 Mariana trough hydrothermal vent water 0.2micro-m filterable fraction clone MT-NE
GU061700.1 gg_id:583930 and function microbial mesoscale eddy perturbations South China Sea clone CEP-5m
GQ337179.1 gg_id:543492 Hydrography shapes biogeography deep Arctic Ocean water depth 1000m clone CB1
GU061788.1 gg_id:538087 and function microbial mesoscale eddy perturbations South China Sea clone CEP-DC
FJ612222.1 gg_id:513317 and Biogeochemistry Dongping Lake Ecosystems lake water clone DP7.3.77
U13159.1 gg_id:5889 marine clone PLY43
GU061793.1 gg_id:586737 and function microbial mesoscale eddy perturbations South China Sea clone CEP-DC
GQ337293.1 gg_id:584441 Hydrography shapes biogeography deep Arctic Ocean water depth 996m clone NB0(
EU799110.1 gg_id:317571 It's all ranking aquatic Newport Harbour RI clone 1C226672

EU805399.1	309488	13365.2	11369.6	6542.0	10755.9	14238.2	12600.8
EU804185.1	322364	1082.1	1015.8	1329.1	1023.2	1496.1	1791.4
DQ906711.1	166129	8240.6	8180.0	6898.4	8271.4	10453.2	11831.0
AF406519.1	60652	3636.6	3901.0	3666.8	4702.9	8111.5	4619.7
AY033322.1	68975	6813.0	5918.5	6871.6	5325.4	12206.6	8876.3
GQ350463.1	553931	1613.7	808.4	1030.8	821.6	1425.6	1734.5
GU061331.1	576730	8399.0	5415.3	6705.3	6966.2	9291.4	7723.7
EU802844.1	308027	1056.8	1298.4	4459.1	1912.6	4283.1	5809.4
GQ346794.1	554239	235.6	215.8	289.9	139.6	456.1	352.8
EU802334.1	350605	3195.2	2279.6	2353.6	4148.8	4013.8	4555.3
DQ071063.1	133992	2154.8	1652.5	2458.6	2445.2	4677.6	3707.6
GQ351212.1	557820	3374.0	1690.8	1964.1	2595.2	1623.2	2008.5
EU804375.1	308733	4155.4	3212.8	3623.5	4107.1	5283.1	5137.1
EU801132.1	356060	876.0	730.2	957.6	1053.7	1909.5	1896.0
GQ337177.1	580656	4115.5	3942.6	3819.0	6235.8	7475.4	8364.7
DQ009440.1	119480	1090.7	1069.7	2922.8	1717.2	1932.9	4046.1
GU061426.1	539698	1668.7	1500.8	1883.1	1790.9	2350.6	2110.3
EU805303.1	316921	5695.2	4763.8	5742.2	5829.8	7022.0	6735.0
GQ348126.1	584741	377.2	416.9	1410.1	867.5	1328.9	1659.4
AF353224.1	31458	2108.8	1844.6	3352.9	1560.7	1369.9	1714.0
GQ337101.1	571844	4524.9	3587.0	4674.9	3930.6	5551.0	5348.3
GQ348793.1	546554	5582.0	4234.6	7430.1	5947.4	3226.2	6355.4
GQ337163.1	583834	806.3	319.1	1009.3	224.7	1585.7	1274.6
FJ545588.1	535511	380.7	388.0	652.7	312.0	412.1	539.0
DQ396175.1	151130	6630.5	5672.4	5729.7	10031.9	7538.1	6806.3
AB193887.1	108804	1516.1	1752.3	2334.2	1547.4	5919.5	8438.7
FJ745027.1	562372	10625.4	10899.9	10683.9	10027.1	15038.3	13273.0
EU802493.1	321420	2192.2	2618.4	502.4	882.6	1376.4	1969.0
GU061438.1	548183	2960.4	1496.9	2111.1	2278.1	1783.0	2496.8
EU802848.1	349307	3705.3	4604.8	4865.2	1795.9	8129.3	8047.8
GQ337130.1	558072	12657.6	10805.4	15112.4	11346.5	14369.7	14397.1
EF573593.1	234950	5159.8	3834.2	3760.4	4336.9	5472.2	5176.5
AB186966.1	101793	3623.7	1323.6	2076.3	1939.8	647.3	1427.8
GU061700.1	583930	1492.8	1151.6	936.8	1683.8	2811.5	2988.9
GQ337179.1	543492	6377.9	6022.7	6514.0	4646.4	5868.9	5607.8
GU061788.1	538087	2543.2	1560.2	1686.6	2410.5	1583.9	2114.5
FJ612222.1	513317	11127.9	6747.9	4063.1	7152.1	5534.7	7023.0
U13159.1	5889	3050.4	2044.0	1469.4	4325.8	3298.5	3703.1
GU061793.1	586737	3532.4	1511.5	1911.9	2491.2	1562.4	2068.5
GQ337293.1	584441	4069.9	1956.5	1967.1	2550.7	2887.8	3216.1
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AB193876.1 gg_id:108793 deep-sea vent clone Ma-NB01
EU800253.1 gg_id:345461 It's all ranking aquatic Delaware Bay NJ clone 2C228289
EU237461.1 gg_id:257016 Genes transcripts Eastern and Western Equatorial North Atlantic Ocean microbial as
EU804682.1 gg_id:319166 It's all ranking aquatic 250 miles Panama City clone 6C232636
EU803131.1 gg_id:308364 It's all ranking aquatic Northeast Colon Panama clone 4C230559
Z99997.1 gg_id:31774 freshwater clone LD12
EU803190.1 gg_id:346064 It's all ranking aquatic Northeast Colon Panama clone 4C230631
EU800834.1 gg_id:332205 It's all ranking aquatic Delaware Bay NJ clone 2C229054
EU802984.1 gg_id:330709 It's all ranking aquatic Northeast Colon Panama clone 4C230385
GQ350111.1 gg_id:563267 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
EU802475.1 gg_id:308475 It's all ranking aquatic Northeast Colon Panama clone 4C229808
EU802797.1 gg_id:303971 It's all ranking aquatic Northeast Colon Panama clone 4C230173
GQ337280.1 gg_id:588922 Hydrography shapes biogeography deep Arctic Ocean water depth 996m clone NB0
AB193896.1 gg_id:108820 deep-sea vent clone Mb-NB03
EU802368.1 gg_id:307148 It's all ranking aquatic Northeast Colon Panama clone 4C229685
GQ337146.1 gg_id:589669 Hydrography shapes biogeography deep Arctic Ocean water depth 1000m clone CB
GU061430.1 gg_id:540815 and function microbial mesoscale eddy perturbations South China Sea clone CE1-DC
EU799917.1 gg_id:351848 It's all ranking aquatic Newport Harbour RI clone 1C227590
EU803033.1 gg_id:355302 It's all ranking aquatic Northeast Colon Panama clone 4C230441
GQ337304.1 gg_id:545562 Hydrography shapes biogeography deep Arctic Ocean water depth 252m clone NB2
GQ351208.1 gg_id:565272 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Eastern
EF573375.1 gg_id:234504 Coco's Island site 23 marine clone S23_1474
U75254.1 gg_id:5900 marine planktonic clone SAR464
AY274867.1 gg_id:86470 Delaware River estuary clone 1A3
EF573087.1 gg_id:232249 Coco's Island site 23 marine clone S23_1186
GU061778.1 gg_id:564836 and function microbial mesoscale eddy perturbations South China Sea clone CEP-DC
GQ337200.1 gg_id:564901 Hydrography shapes biogeography deep Arctic Ocean water depth 1000m clone CB
GQ337245.1 gg_id:550273 Hydrography shapes biogeography deep Arctic Ocean water depth 1000m clone CB
EU804245.1 gg_id:308914 It's all ranking aquatic 250 miles Panama City clone 6C232147
GQ337191.1 gg_id:571241 Hydrography shapes biogeography deep Arctic Ocean water depth 1000m clone CB
FJ545590.1 gg_id:537023 Diveristy Seawater and Sediment Northern North Yel Sea seawater clone W2-4
GQ347972.1 gg_id:585433 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
EU802803.1 gg_id:350422 It's all ranking aquatic Northeast Colon Panama clone 4C230180
EF571950.1 gg_id:232891 Coco's Island site 23 marine clone S23_49
GU061817.1 gg_id:536017 and function microbial mesoscale eddy perturbations South China Sea clone CEP-DC
EF572033.1 gg_id:228764 Coco's Island site 23 marine clone S23_132
GQ350261.1 gg_id:591120 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
EU802256.1 gg_id:335505 It's all ranking aquatic Northeast Colon Panama clone 4C229558
GQ351199.1 gg_id:584009 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Eastern
EU804444.1 gg_id:307511 It's all ranking aquatic 250 miles Panama City clone 6C232372

GQ348609.1	586571	4544.7	3490.4	4059.8	6001.8	7123.3	7288.6
AB193876.1	108793	4530.9	2144.8	2445.0	2897.3	4046.8	3657.4
EU800253.1	345461	8397.0	6694.4	5815.4	5900.6	7462.9	6538.5
EU237461.1	257016	3818.6	1881.8	1808.2	3305.2	2919.3	2864.7
EU804682.1	319166	2971.5	4426.4	2101.6	2603.5	6814.4	1288.3
EU803131.1	308364	4522.3	3153.6	4308.2	3738.5	5536.2	6493.8
Z99997.1	31774	5790.5	2813.9	1656.9	4134.9	3119.3	3519.4
EU803190.1	346064	4643.8	4429.3	2909.7	4813.2	5761.5	6058.3
EU800834.1	332205	37.2	48.7	87.0	73.7	64.6	14.9
EU802984.1	330709	2451.4	1956.1	1596.1	2834.3	3877.1	3364.2
GQ350111.1	563267	3659.8	3125.3	1927.1	5599.5	6878.6	6920.8
EU802475.1	308475	7786.2	7793.8	7270.1	6592.9	11138.9	8831.8
EU802797.1	303971	1770.2	1909.0	2107.7	1292.3	1342.8	1576.4
GQ337280.1	588922	3996.7	2864.8	4077.6	3780.2	6841.8	5226.9
AB193896.1	108820	2951.4	1404.3	1784.4	2217.1	1554.8	2151.1
EU802368.1	307148	4181.4	4048.7	1918.5	2864.3	3647.2	4166.4
GQ337146.1	589669	308.6	731.1	1121.2	1941.5	1664.6	2349.5
GU061430.1	540815	4755.5	3393.3	2764.7	3695.3	5711.1	4902.1
EU799917.1	351848	2138.8	3739.9	2507.0	2003.0	8534.3	5623.3
EU803033.1	355302	7638.6	6697.1	3678.1	6745.6	12322.3	9349.9
GQ337304.1	545562	2447.3	1430.7	3410.2	4838.2	4013.8	7047.9
GQ351208.1	565272	6837.4	7885.1	7240.8	6051.9	6228.8	7074.7
EF573375.1	234504	167.3	222.1	268.3	256.3	461.7	2348.8
U75254.1	5900	43.7	39.4	26.5	55.2	65.1	27.2
AY274867.1	86470	2172.2	709.2	1660.2	721.1	56.2	409.7
EF573087.1	232249	3767.2	2863.3	4768.9	6601.0	1553.9	3941.2
GU061778.1	564836	45.3	43.6	20.5	54.7	53.8	17.7
GQ337200.1	564901	4767.0	6427.4	4803.5	3919.0	10458.6	7469.5
GQ337245.1	550273	23610.3	19005.6	10171.0	14788.6	18677.9	18458.7
EU804245.1	308914	4574.9	4177.4	2075.7	4979.0	8425.7	5823.9
GQ337191.1	571241	6719.5	4567.0	5557.4	6353.8	7607.8	6878.8
FJ545590.1	537023	2125.0	1064.2	816.1	4121.9	2069.2	6692.7
GQ347972.1	585433	4075.1	4812.2	3178.2	4572.4	4662.7	4650.5
EU802803.1	350422	9281.3	9213.2	6584.4	8811.8	11442.9	9504.4
EF571950.1	232891	3512.9	2142.4	2063.4	3440.1	3220.9	3193.0
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EF572033.1	228764	2575.2	4780.2	4749.2	4713.1	7099.5	6389.8
GQ350261.1	591120	3195.4	2164.0	5183.3	2423.6	6316.9	5071.3
EU802256.1	335505	2603.3	2178.4	4312.1	3570.4	4133.1	4765.7
GQ351199.1	584009	6832.0	5207.5	4881.1	5397.7	6688.2	5567.5
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GQ337316.1 gg_id:532828 Hydrography shapes biogeography deep Arctic Ocean water depth 252m clone NB2
DQ396170.1 gg_id:153164 deep-sea octacoral clone ctg_NISA187
GQ337164.1 gg_id:541009 Hydrography shapes biogeography deep Arctic Ocean water depth 410m clone CB1
EU804177.1 gg_id:335458 It's all ranking aquatic 250 miles Panama City clone 6C232073
AB193901.1 gg_id:108825 deep-sea vent clone MbSd-NB
EU801907.1 gg_id:324916 It's all ranking aquatic Chesapeake Bay MD clone 3C003286
EU800742.1 gg_id:329304 It's all ranking aquatic Delaware Bay NJ clone 2C228929
AF353227.1 gg_id:23331 marine clone Arctic95A-16
GQ348698.1 gg_id:537980 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
EU804847.1 gg_id:318621 It's all ranking aquatic 250 miles Panama City clone 6C232813
EU805329.1 gg_id:322488 It's all ranking aquatic 250 miles Panama City clone 6C233332
DQ071146.1 gg_id:131395 marine surface water clone Surf1.20
GU061690.1 gg_id:555280 and function microbial mesoscale eddy perturbations South China Sea clone CEP-5m
GQ337272.1 gg_id:564999 Hydrography shapes biogeography deep Arctic Ocean water depth 428m clone CB1
EU919806.1 gg_id:311134 Kongsfjorden western Spitsbergen Svalbard ocean water clone b107
EF572259.1 gg_id:232682 Coco's Island site 23 marine clone S23_358
GU061816.1 gg_id:579131 and function microbial mesoscale eddy perturbations South China Sea clone CEP-DC
EU803155.1 gg_id:331745 It's all ranking aquatic Northeast Colon Panama clone 4C230588
GQ340070.1 gg_id:587437 Prokaryotic Marathonas Reservoir Greece water column clone A07-14-BAC
GQ337262.1 gg_id:564936 Hydrography shapes biogeography deep Arctic Ocean water depth 428m clone CB1
EU803109.1 gg_id:344462 It's all ranking aquatic Northeast Colon Panama clone 4C230532
GQ452886.1 gg_id:513339 Biodiversity planktonic surface water Northern Bering Sea clone s27
GQ337131.1 gg_id:594118 Hydrography shapes biogeography deep Arctic Ocean water depth 395m clone CB5
EU802530.1 gg_id:343807 It's all ranking aquatic Northeast Colon Panama clone 4C229870
AY907726.1 gg_id:136412 identification picoplankton contrasting waters Arabian Sea water clone A312002
AF327027.1 gg_id:40239 arctic bacterioplankton clone AWS98-19a
EU237435.1 gg_id:241493 Genes transcripts Eastern and Western Equatorial North Atlantic Ocean microbial as
EU801599.1 gg_id:331801 It's all ranking aquatic Chesapeake Bay MD clone 3C002936
DQ071144.1 gg_id:129333 marine surface water clone Surf1.19
EU801116.1 gg_id:353623 It's all ranking aquatic Delaware Bay NJ clone 2C229441
EU803848.1 gg_id:323987 It's all ranking aquatic Lake Gatun clone 5C231485
EU802887.1 gg_id:323030 It's all ranking aquatic Northeast Colon Panama clone 4C230278
DQ513056.1 gg_id:160119 Microbial life fluids ridge flank crustal fluid clone CTD005-4B-02
DQ396295.1 gg_id:156116 deep-sea octacoral clone ctg_NISA056
EU801575.1 gg_id:337416 It's all ranking aquatic Chesapeake Bay MD clone 3C002902
DQ009454.1 gg_id:116109 bacterioplankton clone SPOTSMAY03_150m16
EU804865.1 gg_id:337774 It's all ranking aquatic 250 miles Panama City clone 6C232832
EF572440.1 gg_id:228191 Coco's Island site 23 marine clone S23_539
GQ349613.1 gg_id:542775 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
GQ337083.1 gg_id:553977 Hydrography shapes biogeography deep Arctic Ocean water depth 1191m clone NB

EF471704.1	267911	1433.3	2605.4	3069.6	1042.3	4301.5	3739.3
GQ337316.1	532828	616.6	329.1	434.7	206.4	1459.0	881.4
DQ396170.1	153164	111.0	199.4	487.3	302.6	568.1	553.8
GQ337164.1	541009	315.8	623.2	425.2	338.7	184.4	240.7
EU804177.1	335458	5534.4	4994.3	5258.3	5266.4	4853.9	5800.8
AB193901.1	108825	2243.4	2275.6	2097.9	2476.5	1806.0	2237.1
EU801907.1	324916	2638.4	2070.8	982.7	918.0	2183.8	2161.6
EU800742.1	329304	4144.9	4477.2	5918.2	3835.6	10987.4	7506.9
AF353227.1	23331	43.1	50.8	74.8	69.0	52.4	11.4
GQ348698.1	537980	2347.3	2961.0	2178.0	1625.0	1787.8	2414.8
EU804847.1	318621	3615.8	3507.5	1019.6	1684.9	2093.0	2711.0
EU805329.1	322488	3398.7	3232.9	2419.9	3835.8	4898.2	4654.6
DQ071146.1	131395	11503.0	13529.4	15059.0	9288.8	15798.0	15329.0
GU061690.1	555280	6081.6	6197.5	3460.5	5794.4	10257.1	9782.1
GQ337272.1	564999	1171.9	1455.0	2463.9	1112.6	3552.9	4328.2
EU919806.1	311134	3073.4	2069.7	2856.0	3299.5	2314.2	3984.3
EF572259.1	232682	2346.9	1578.8	2708.6	1666.3	1796.8	1779.4
GU061816.1	579131	4842.1	3429.0	3607.4	4022.8	5706.4	4875.5
EU803155.1	331745	8506.7	7923.2	8394.9	7419.2	9834.3	8565.2
GQ340070.1	587437	12372.9	7954.9	7021.5	8492.5	7563.4	7906.9
GQ337262.1	564936	8116.3	8033.1	6776.0	7592.0	11021.0	9260.6
EU803109.1	344462	466.6	449.5	398.1	164.6	186.4	841.4
GQ452886.1	513339	4177.2	3074.0	3233.3	4365.3	5185.3	5195.3
GQ337131.1	594118	3061.3	1835.3	2728.9	4816.8	3054.4	4783.3
EU802530.1	343807	5167.2	4295.9	4325.2	4127.4	11557.8	7699.1
AY907726.1	136412	18.5	30.1	75.8	64.0	51.2	14.2
AF327027.1	40239	2088.6	1245.1	1426.3	1778.5	2493.1	2883.4
EU237435.1	241493	3566.8	2902.9	4014.9	2385.0	9193.4	9151.0
EU801599.1	331801	9662.4	8537.6	11111.1	9451.2	7146.3	10512.4
DQ071144.1	129333	5445.8	2660.3	3331.5	3354.3	3674.9	4008.6
EU801116.1	353623	3146.8	2357.1	3026.8	2881.5	3276.8	3106.6
EU803848.1	323987	8732.0	4557.7	4040.8	5290.2	3777.3	6126.9
EU802887.1	323030	7623.5	6472.1	8162.1	8319.7	11520.1	9884.6
DQ513056.1	160119	42.2	66.4	81.9	74.8	65.1	34.0
DQ396295.1	156116	644.4	1324.3	892.0	1016.7	271.3	791.9
EU801575.1	337416	1851.1	992.4	1146.5	1004.6	598.0	959.2
DQ009454.1	116109	499.5	367.1	670.2	700.8	240.6	550.2
EU804865.1	337774	3956.9	4182.8	2604.4	4420.3	6191.7	6012.6
EF572440.1	228191	2617.3	2287.6	1627.9	3231.1	3734.7	3688.2
GQ349613.1	542775	1197.5	1290.2	1506.5	2537.3	3562.9	3522.5
GQ337083.1	553977	263.8	165.1	483.6	245.1	366.1	192.2

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EU802583.1	339982	1034.0	582.6	635.6	671.0	1175.6	1292.8
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o__Rickettsiales	f__Rickettsiaceae

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s__Rickettsia akari	72592
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s__Rickettsia australis	72061
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s__Rickettsia conorii	72114
s__Rickettsia endosymbiont of Deronectes platynotus	73039
s__Rickettsia montanensis	72101
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s__Rickettsia rickettsii	72874
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GU061708.1 gg_id:550515 and function microbial mesoscale eddy perturbations South China Sea clone CEP-5m
EF572364.1 gg_id:233869 Coco's Island site 23 marine clone S23_463
GU061435.1 gg_id:578594 and function microbial mesoscale eddy perturbations South China Sea clone CE1-DC
U17257.1 gg_id:5983 Orientia tsutsugamushi str. Karp
AF479301.1 gg_id:111855 Orientia tsutsugamushi str. TA678
AF479300.1 gg_id:111655 Orientia tsutsugamushi str. TH1817
U12458.1 gg_id:5969 Rickettsia akari str. Hartford
L36099.1 gg_id:5943 Rickettsia akari str. MK (Kaplan)
U17644.1 gg_id:5947 Rickettsia australis str. PHS
L36101.1 gg_id:5923 Rickettsia australis str. Phillips
U25042.1 gg_id:5927 Rickettsia sp str. S unnamed isolate spotted fever group
AF322442.1 gg_id:111884 Rickettsia limoniae str. Gent
L36215.1 gg_id:5973 Rickettsia montana
DQ150682.1 gg_id:138092 Rickettsia rickettsii str. 1989CO1
AY737685.1 gg_id:107037 Rickettsia marmionii str. KB
U12462.1 gg_id:5956 Rickettsia sibirica str. 246
L36221.1 gg_id:5932 Rickettsia typhi str. Wilmington
AF060705.2 gg_id:5958 Rickettsia honei str. RB
AB021128.1 gg_id:5952 Rickettsia sp
U15162.1 gg_id:5968 Rickettsia canadensis str. McKeil
EU036982.1 gg_id:345789 Rickettsia raoultii str. Elanda-23/95
L36673.1 gg_id:5976 Rickettsia parkeri str. Maculatum 20
U11019.1 gg_id:5944 Rickettsia rhipicephali
DQ102712.1 gg_id:139382 Rickettsia felis scc50
U12461.1 gg_id:5953 Rickettsia parkeri str. Maculatum-20
NR_026042.1 gg_id:562771 Rickettsia aeschlimannii str. Mc16
U04163.1 gg_id:5922 Rickettsia species
L36212.1 gg_id:5938 Rickettsia helvetica str. C9P9
L36103.1 gg_id:5961 Rickettsia bellii str. 369L42-1
AJ429500.1 gg_id:45652 Wolbachia pipientis
U11012.1 gg_id:5940 Rickettsia amblyommii str. MO 85-1084
L36213.1 gg_id:5948 Rickettsia japonica str. YM
AF172942.1 gg_id:112194 Rickettsia hulinii str. HL-93
DQ100164.1 gg_id:145296 Rickettsia monacensis str. IrR/Munich
CU466797.1 gg_id:352699 Evry wastewater treatment plant anoxic basin clone
U23709.1 gg_id:6128 Wolbachia pipientis
AJ548801.1 gg_id:105908 Wolbachia pipientis
AJ628417.1 gg_id:112673 Wolbachia pipientis
AJ548799.1 gg_id:102098 Wolbachia pipientis
AJ548802.1 gg_id:106063 Wolbachia pipientis
L02884.1 gg_id:6105 Trichogramma deion symbiont

GU061708.1	550515	1581.5	1078.0	844.2	2447.9	546.2	509.1
EF572364.1	233869	13682.8	14892.7	17438.4	10633.8	15631.2	15745.8
GU061435.1	578594	1958.9	825.5	1418.9	1299.6	814.6	1000.3
U17257.1	5983	60.8	133.6	67.7	120.3	114.6	97.1
AF479301.1	111855	179.1	219.2	408.1	979.0	312.8	144.7
AF479300.1	111655	6651.8	6581.6	3682.4	6733.0	6550.2	7342.6
U12458.1	5969	6820.9	7546.2	11376.7	7891.3	7400.0	9193.3
L36099.1	5943	5304.4	7367.1	8603.7	6119.4	11242.5	9160.0
U17644.1	5947	7700.9	9136.2	7844.3	8558.2	9831.8	10937.0
L36101.1	5923	8897.8	11463.4	6672.1	7115.9	10615.0	8621.4
U25042.1	5927	4412.1	5243.0	6508.1	5361.9	7268.7	7572.6
AF322442.1	111884	95.4	163.8	208.3	213.4	135.6	227.9
L36215.1	5973	6726.0	7788.5	10175.1	8161.2	12188.6	12350.5
DQ150682.1	138092	4033.4	4515.4	6376.4	6063.3	5796.6	5727.9
AY737685.1	107037	4880.1	5560.2	8626.1	6458.3	7819.0	7577.2
U12462.1	5956	4886.5	5554.8	8627.0	6474.2	7818.9	7558.0
L36221.1	5932	2682.5	4004.5	4674.3	3941.9	8796.0	9044.8
AF060705.2	5958	5383.5	6455.1	9284.0	7623.8	7840.7	7639.1
AB021128.1	5952	492.9	818.0	3464.4	1035.2	2256.3	1665.8
U15162.1	5968	4064.6	3154.1	8997.0	4873.2	5734.8	6420.1
EU036982.1	345789	6949.1	8246.0	10314.8	8586.3	13480.9	13487.5
L36673.1	5976	3631.7	4584.9	7400.1	5551.5	5561.6	5393.9
U11019.1	5944	7308.7	8615.7	10957.6	9065.3	14039.4	13979.9
DQ102712.1	139382	2661.9	3871.0	5348.5	3431.7	5147.0	5918.9
U12461.1	5953	3853.5	3183.9	6752.3	5457.5	4255.0	3609.0
NR_026042.1	562771	7130.1	8207.7	10479.5	8757.8	13127.3	13025.4
U04163.1	5922	3390.0	2442.8	6968.4	2681.2	4805.7	5987.5
L36212.1	5938	5372.5	6631.7	8590.0	6634.1	10821.7	10894.9
L36103.1	5961	2198.5	2068.3	2713.4	2442.2	3516.5	3391.6
AJ429500.1	45652	6337.4	7425.0	2640.3	7841.8	9149.7	8744.9
U11012.1	5940	5020.3	6403.0	7658.7	6664.9	11556.2	12101.0
L36213.1	5948	6907.8	8167.0	10126.3	8437.3	13090.2	13302.3
AF172942.1	112194	10401.1	11383.4	9668.9	11278.0	16334.0	15624.0
DQ100164.1	145296	2239.6	4142.8	7015.5	3465.7	11376.1	8638.5
CU466797.1	352699	1829.4	2975.8	5180.2	2671.0	4453.4	2447.2
U23709.1	6128	4886.1	4567.2	4075.4	3846.3	5078.6	3705.8
AJ548801.1	105908	303.7	202.2	146.3	457.3	123.1	139.8
AJ628417.1	112673	8158.3	9632.4	8700.2	7666.1	12719.8	9451.4
AJ548799.1	102098	631.2	1391.5	2779.5	353.3	1626.6	1301.6
AJ548802.1	106063	6809.2	8551.6	8046.4	7228.4	12673.5	9510.0
L02884.1	6105	8905.1	7190.0	4186.6	7711.9	11316.7	9529.7

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s__Wolbachia endosymbiont of Culex quinquefasciatus	72911
s__Wolbachia endosymbiont of Dirofilaria immitis	72016
s__Wolbachia endosymbiont of Dirofilaria immitis	72397
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s__Erythrobacter citreus	60282
s__Erythrobacter flavus	61226
s__Erythrobacter longus	60643
s__Erythrobacter longus	60648
s__Erythrobacter vulgaris	61220
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s__Erythromicrobium ramosum	60457
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s__unclassified	60419

AJ548800.1 gg_id:105759 Wolbachia pipientis
AJ548798.1 gg_id:101940 Wolbachia pipientis
U83091.1 gg_id:6095 Wolbachia sp
L02888.1 gg_id:6104 Trichogramma deion symbiont
AJ628416.1 gg_id:112509 Wolbachia pipientis
FJ152094.1 gg_id:308082 Inherited Fungal Endosymbionts Parasitic Wasp and Its Cockroach Host clone b6
L02882.1 gg_id:6082 Muscifidurax uniraptor symbiont
EU833482.1 gg_id:434746 symbiont
U83092.1 gg_id:6096 Wolbachia sp
FJ152096.1 gg_id:310108 Inherited Fungal Endosymbionts Parasitic Wasp and Its Cockroach Host clone cb5
AF035160.1 gg_id:6093 Wolbachia sp
AJ010275.1 gg_id:6124 Wolbachia endosymbiont of Brugia malayi
AB475124.1 gg_id:525041 Wolbachia pipientis str. TUA
AM999887.1 gg_id:308581 Wolbachia pipientis str. wPip
AF304445.1 gg_id:43030 Wolbachia sp. Okinawa-RS32
AJ276500.1 gg_id:23566 filarial nematode Dirofilaria repens symbiont of
AM990908.1 gg_id:279145 Citromicrobium sp. MOLA 134
AY461442.1 gg_id:106575 Erythrobacter aquimaris str. SW-116
AM990822.1 gg_id:279411 Erythrobacter sp. MOLA 47
AF500005.1 gg_id:64083 Erythrobacter flavus str. SW-52
L01786.1 gg_id:6333 Erythrobacter longus str. OCh101
AF465835.1 gg_id:107785 Erythrobacter longus str. DSM 6997
AY706937.1 gg_id:99838 Erythrobacter vulgaris str. 022 2-12
AF432339.1 gg_id:31853 template extracted sediment oil-contaminated nutrient amended beach microcosms;
EU935322.1 gg_id:539587 str. daSW.23
FJ843590.1 gg_id:550126 Sphingomonas phyllosphaerae str. FA2
AM990791.1 gg_id:277841 Erythrobacter sp. MOLA 15
EU440989.1 gg_id:326335 Erythrobacter flavus str. 2PR56-3
EU488295.1 gg_id:575919 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and
DQ985049.1 gg_id:179170 Erythrobacter sp. str. JL993
DQ480144.1 gg_id:157107 Erythrobacter sp. D3043
FJ607439.1 gg_id:534887 Erythrobacter citreus str. 107
EF512708.1 gg_id:224600 Erythrobacter vulgaris str. JL271
FN431786.1 gg_id:562499 Erythrobacter gaetbuli str. AMV3 AMV17
FM180516.1 gg_id:335238 Erythrobacter sp. ZZ-2008 str. B2
FJ999661.1 gg_id:415733 Sphingomonas phyllosphaerae str. FA2
FN668376.1 gg_id:519549 Erythromicrobium sp. str. BF8
GQ284449.1 gg_id:541199 Erythromicrobium ramosum str. THWCS10
AB013355.1 gg_id:6348 Erythromicrobium ramosum str. DSM8510T
GQ472116.1 gg_id:563240 Microcystis aeruginosa freshwater lake clone C-71
GU321359.1 gg_id:546220 Porphyrobacter sp. str. NMC22

AJ548800.1	105759	289.0	577.2	1864.5	253.8	518.5	1218.6
AJ548798.1	101940	210.7	376.4	1716.7	205.1	313.8	893.1
U83091.1	6095	1539.7	1985.7	1493.3	2803.0	7417.5	5631.4
L02888.1	6104	786.1	770.8	468.9	203.8	311.1	602.9
AJ628416.1	112509	4482.0	4921.8	4045.4	4750.5	5350.8	2997.5
FJ152094.1	308082	4181.4	6362.9	1177.3	3947.5	2298.0	2329.4
L02882.1	6082	1021.9	1133.6	585.0	218.9	239.4	191.3
EU833482.1	434746	8415.3	7989.3	12891.6	9921.4	12867.9	10194.7
U83092.1	6096	3490.7	3629.3	2831.3	2556.3	4840.4	3640.3
FJ152096.1	310108	39.5	51.0	93.6	67.1	73.3	40.8
AF035160.1	6093	4118.7	4828.0	6022.6	4233.9	6734.4	6179.3
AJ010275.1	6124	167.1	231.2	794.9	216.4	134.4	662.5
AB475124.1	525041	4699.7	4684.6	3736.6	4109.8	2815.4	4342.2
AM999887.1	308581	5289.6	5131.2	4771.5	4091.4	6270.7	4770.1
AF304445.1	43030	5220.3	6715.4	3138.5	6234.7	5188.3	4323.7
AJ276500.1	23566	1265.3	2604.9	2102.2	824.8	1064.1	1446.9
AM990908.1	279145	2016.3	2081.5	1054.2	3314.0	7096.5	2595.0
AY461442.1	106575	1389.0	1399.6	1580.5	1847.5	3883.5	2021.2
AM990822.1	279411	2261.3	3355.9	5494.6	4415.7	8980.0	4900.8
AF500005.1	64083	1948.0	2491.6	2579.4	3028.0	7224.2	3798.5
L01786.1	6333	2703.6	3307.1	3143.3	2681.5	5000.7	3750.4
AF465835.1	107785	1834.1	2283.7	1831.7	1868.7	3274.7	2513.7
AY706937.1	99838	1000.7	1856.1	3775.3	3414.9	1601.4	3175.1
AF432339.1	31853	1738.3	2005.0	3926.4	2720.0	9892.9	4558.3
EU935322.1	539587	13205.5	13441.2	7966.2	13784.2	17879.0	16035.5
FJ843590.1	550126	1694.4	1960.8	2811.7	2531.0	7660.5	3779.3
AM990791.1	277841	1355.6	2022.9	3167.7	1108.3	7093.3	3007.1
EU440989.1	326335	2019.5	2474.3	3497.9	3098.1	9012.6	4534.3
EU488295.1	575919	521.4	658.5	1364.2	613.7	2594.2	2361.0
DQ985049.1	179170	1877.4	1877.8	2287.1	2163.8	11028.9	2561.8
DQ480144.1	157107	1128.5	1233.0	1909.4	1148.9	4252.5	3340.8
FJ607439.1	534887	5285.5	6170.9	6250.0	3692.3	11514.2	8129.8
EF512708.1	224600	819.3	835.5	1110.9	428.8	1290.6	730.2
FN431786.1	562499	697.1	632.7	2791.3	1083.3	2452.7	841.4
FM180516.1	335238	2018.4	2492.8	5462.6	3186.3	7534.6	4504.9
FJ999661.1	415733	1994.8	2383.0	2400.6	2746.1	6086.8	3768.7
FN668376.1	519549	850.6	1562.0	2401.4	998.4	2169.1	2596.1
GQ284449.1	541199	1821.7	3210.5	3588.2	2420.3	15822.5	8660.7
AB013355.1	6348	277.1	505.9	740.3	573.4	4246.9	1930.1
GQ472116.1	563240	868.2	712.4	1461.0	971.8	6007.2	1662.3
GU321359.1	546220	2432.8	3353.8	7457.3	5796.8	14104.6	4868.4

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EF157133.1 gg_id:235560 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon
DQ001633.1 gg_id:158572 Microbial seeps asphalt seep clone E91-43
FJ997597.1 gg_id:421125 Altererythrobacter sp. str. KYW147
GQ264058.1 gg_id:588310 Structure Simulated Level Waste Site simulated level waste site clone WC3_156
DQ676427.1 gg_id:219175 Archaeal and plankton freshwater pond suboxic freshwater-pond sediment clone M
DQ811848.1 gg_id:162725 mangrove soil clone MSB-3A6
EU440968.1 gg_id:312240 Lutibacterium anuloederans str. PR54-13
NR_025816.1 gg_id:536261 Porphyrobacter donghaensis str. SW-132; KCTC 12229
AB033328.1 gg_id:6344 Porphyrobacter tepidarius str. DSM 10594
AF465839.1 gg_id:99433 Porphyrobacter tepidarius str. DSM 10594
AM691106.1 gg_id:221235 Erythrobacter longus str. EG6
EU770257.1 gg_id:346240 Porphyrobacter sp. str. A2
FJ516793.1 gg_id:539522 semiarid 'Tablas de Daimiel National Park' wetland (Central Spain) unravelled biofilm
EU276570.1 gg_id:362799 -DGGE and Approaches Analyze Effect Agricultural Practices on Soil agricultural soil c
GQ016328.1 gg_id:493339 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
DQ399262.2 gg_id:156567 Erythrobacter indica str. YPM1
DQ448852.1 gg_id:164787 Novosphingobium nitrogenifigens str. Y88
AF465836.1 gg_id:79367 Erythrobacter litoralis str. DSM 8509
EF424398.1 gg_id:205122 Erythrobacter sp. str. SM115
DQ985038.1 gg_id:181578 Erythrobacter sp. str. JL1020
FJ674974.1 gg_id:516226 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
AF407713.1 gg_id:60586 Great Artesian Basin clone B10
AM176884.1 gg_id:161637 Recovery mangrove sediment clone SZB32
GQ476825.2 gg_id:534168 Altererythrobacter sp. str. R83-1
FJ672518.1 gg_id:531645 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
EU118985.1 gg_id:243523 Novosphingobium yangbajingensis str. YBSY-12-2
EF520398.1 gg_id:231088 structure lakes: what controls ? acid-impacted lake clone ADK-BTh02-25
DQ520195.1 gg_id:160939 shal China sequences hypertrophic freshwater lake clone ML-9-79.2
AY576736.1 gg_id:139435 Erythrobacter sp. str. 5IX/A01/140
DQ304436.1 gg_id:147665 Alterierythrobacter epoxidivorans str. JCS350
DQ532296.1 gg_id:171201 Geographical Variation Microbial Burden and Spacecraft Assembly Kennedy Space C
AM936339.1 gg_id:547624 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
AY922042.1 gg_id:114156 farm soil clone AKYG623
AM746688.1 gg_id:256823 etiology rosy discoloration ancient wall paintings rosy-discoloured mural clone A10
EU328097.1 gg_id:278897 dynamics during bioremediation crude oil contaminated moderate saline soil clone Y
EF157081.1 gg_id:256321 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon
GQ048646.1 gg_id:445570 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu4
FJ675449.1 gg_id:518998 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
AB012062.1 gg_id:6337 Erythrobacter sp. str. MBIC3019 D1215
EU104298.1 gg_id:345528 Evidence Comamonadaceae determinants settling performance activated sludge clo
CU914890.1 gg_id:445733 and dynamics adapted microbiota during degradation Tunisian zarzatine enriched se

EF157133.1	235560	569.2	641.8	2042.2	857.0	2667.0	1324.0
DQ001633.1	158572	33.8	79.0	143.3	106.2	400.1	136.7
FJ997597.1	421125	3414.2	3633.4	3222.8	1945.5	7728.9	4399.3
GQ264058.1	588310	2473.8	3305.2	5996.1	4277.4	13695.5	4117.0
DQ676427.1	219175	1135.2	1220.3	1318.4	2155.7	7094.3	3597.5
DQ811848.1	162725	1542.0	1938.7	3708.4	2365.3	10953.8	4558.6
EU440968.1	312240	1323.7	1345.9	515.9	258.5	1825.7	1057.6
NR_025816.1	536261	2955.0	3036.3	3797.8	3776.7	16630.6	4681.5
AB033328.1	6344	10914.9	9601.0	8406.5	8542.8	18866.8	11605.4
AF465839.1	99433	2589.0	2410.7	4409.1	3735.6	11955.2	4508.1
AM691106.1	221235	2338.9	2615.6	2394.5	1533.2	3413.0	2279.6
EU770257.1	346240	1862.3	1942.4	6242.3	5432.4	13287.0	3172.5
FJ516793.1	539522	4873.2	4429.6	4198.8	4247.3	11875.7	5528.3
EU276570.1	362799	1593.5	2324.8	3102.1	2047.6	8657.3	3063.9
GQ016328.1	493339	1480.0	1894.6	2431.7	2175.1	8631.8	2754.2
DQ399262.2	156567	2110.4	2437.3	7976.6	5159.4	10911.9	6188.5
DQ448852.1	164787	4265.8	3959.2	3696.5	3994.4	6981.7	5703.8
AF465836.1	79367	1654.6	2417.8	4464.9	2208.4	6641.2	3238.6
EF424398.1	205122	43.0	92.6	1199.7	653.8	569.0	143.8
DQ985038.1	181578	2828.7	3404.6	6069.4	2891.0	11673.5	6105.8
FJ674974.1	516226	1583.6	2382.4	3007.0	2154.8	7138.6	4784.0
AF407713.1	60586	3009.3	2713.8	7255.6	5012.9	11535.1	4776.5
AM176884.1	161637	1039.5	1261.3	2682.1	2057.9	5648.0	1878.4
GQ476825.2	534168	1997.0	2615.1	1828.1	1701.8	11619.9	4869.7
FJ672518.1	531645	2022.7	2814.4	10795.4	3913.7	12867.5	9652.0
EU118985.1	243523	1850.9	2341.9	1541.6	1990.8	4731.5	1922.3
EF520398.1	231088	5243.7	4653.8	6272.7	5424.7	16192.7	5444.6
DQ520195.1	160939	93.8	105.2	482.6	1254.3	98.5	29.5
AY576736.1	139435	1483.0	1930.5	2449.9	3253.7	8164.8	3071.7
DQ304436.1	147665	4440.4	5073.2	4606.7	3967.6	9718.5	5666.4
DQ532296.1	171201	4149.0	4987.8	5765.2	2840.0	6995.2	3618.9
AM936339.1	547624	2641.6	3775.2	4093.2	3847.1	12680.9	5535.6
AY922042.1	114156	4104.1	4074.8	3532.0	3605.1	8042.1	4787.6
AM746688.1	256823	3104.0	4686.0	5896.8	2876.8	8274.7	4857.4
EU328097.1	278897	1733.2	2320.8	3140.7	3737.0	9904.3	7771.3
EF157081.1	256321	1656.8	1145.4	2365.4	1909.8	5728.1	2056.9
GQ048646.1	445570	4501.1	5955.9	9940.7	4681.1	20499.1	8261.8
FJ675449.1	518998	5065.3	7550.2	8061.7	5798.9	18131.3	13795.0
AB012062.1	6337	294.1	379.9	305.8	181.0	2697.0	448.0
EU104298.1	345528	3077.6	3367.5	10135.0	6137.3	15727.9	5175.1
CU914890.1	445733	3385.7	4657.8	7174.5	3417.6	10873.6	4809.6

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AJ565420.1 gg_id:90664 Sphingomonadaceae MWH-CaK2
DQ298332.1 gg_id:153621 studies on and nifH Lasiurus sindicus Sewan grass Thar Desert Rajasthan India rhizos
AJ000920.2 gg_id:37092 Novosphingobium sp. str. K16
DQ416556.1 gg_id:154250 s1cb26
AY921774.1 gg_id:113287 farm soil clone AKYG900
EF433552.1 gg_id:211658 Sphingomonas sp. str. WW11
DQ396158.1 gg_id:151573 deep-sea octacoral clone ctg_NISA006
EF157121.1 gg_id:257302 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon
AB219359.1 gg_id:157745 Sphingomonas sp. str. JEM-1
EU571151.1 gg_id:266620 eubacterium sp. str. 7-22
DQ011529.1 gg_id:122133 Porphyrobacter dokdonensis str. DSW-74
AF361178.2 gg_id:31470 Sphingomonas sp. Pee Shoal
DQ860069.1 gg_id:166645 Symbiotic aerobic anoxygenic phototrophic colonial tunicate clone L30
AF407721.1 gg_id:56491 Great Artesian Basin clone B37
DQ856560.1 gg_id:240257 intestinal microflora Chinese mitten crab (Eriocheir sinensis) clone C3X
EU784670.1 gg_id:341576 Sphingomonas sp. str. FG03
CU466791.1 gg_id:328857 Evry wastewater treatment plant anoxic basin clone
EU131005.1 gg_id:251580 Sphingomonas sp. BAC151
DQ860058.1 gg_id:164190 Symbiotic aerobic anoxygenic phototrophic colonial tunicate clone C1
EF516627.1 gg_id:225426 grassland soil clone FCPS560
DQ985034.1 gg_id:182499 Erythrobacter sp. str. JL990
DQ898300.1 gg_id:162144 Sphingomonas sp. str. MTR-71
EU360289.1 gg_id:263034 Pyrene-Degrading Consortium Deep-Sea Sediment West Pacific and its Key Member
AY792292.1 gg_id:123759 Humic Lake clone CrystalBog5F2
DQ454121.1 gg_id:156628 Porphyrobacter sp. str. J3-AN66
FN397674.1 gg_id:460604 Erythromicrobium sp. str. AMV10
EU283461.1 gg_id:277643 Model Early Earth Harbors Deeply Divergent Divisions Anderson Lake clone A553
EU327998.1 gg_id:277975 dynamics during bioremediation crude oil contaminated moderate saline soil clone B
GQ060166.1 gg_id:459373 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
Y10678.1 gg_id:6365 Sandaracinobacter sibiricus
CU920729.1 gg_id:533603 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
FJ444668.1 gg_id:569696 Cotton Rhizosphere cotton rhizosphere clone 2y-17
AB094461.1 gg_id:78562 Erythrobacter sp. str. 2216.25.25
EF173348.1 gg_id:191991 Options situ remediation contaminated mixture chlorinated hydrocarbons hydrocarb
FM873313.1 gg_id:367391 occupant source house floor dust clone FD01E08
GQ169059.1 gg_id:543056 Novosphingobium sp. str. CTDB1
AB033327.1 gg_id:6350 Porphyrobacter neustonensis str. DSM 9434
AF468357.1 gg_id:79915 Arctic sea ice ARK10031
AF468353.1 gg_id:79611 Arctic sea ice ARK10016
AB363004.1 gg_id:269458 Erythrobacter ishigakiensis str. NITE-AP48
DQ453142.1 gg_id:157567 Erythrobacter sp. str. CNU001

AJ565420.1	90664	369.2	797.9	1850.9	742.9	3443.0	714.6
DQ298332.1	153621	1795.5	3102.6	5143.1	4643.5	12190.9	3358.0
AJ000920.2	37092	3510.1	1979.8	4370.8	2855.8	5679.1	4043.3
DQ416556.1	154250	3163.1	4716.7	4399.6	3343.0	9289.8	5080.2
AY921774.1	113287	3681.7	4455.0	7921.4	6957.2	9980.2	4981.7
EF433552.1	211658	1105.8	1127.7	3220.4	1493.0	9752.2	3648.5
DQ396158.1	151573	1618.6	2143.3	5323.1	4379.9	6020.6	3645.4
EF157121.1	257302	2401.9	1731.9	2043.3	1425.3	12928.7	4974.7
AB219359.1	157745	4051.3	3333.2	7071.3	5878.4	12179.1	2979.6
EU571151.1	266620	523.5	617.2	1125.3	776.9	6051.0	2809.0
DQ011529.1	122133	1575.8	1495.5	5175.9	3277.9	13704.7	5096.1
AF361178.2	31470	4129.4	6500.6	5806.1	3135.8	10031.7	4718.5
DQ860069.1	166645	7101.8	7501.0	7064.6	7015.8	14268.6	9893.9
AF407721.1	56491	1414.9	2333.3	2742.2	940.8	4717.8	2458.2
DQ856560.1	240257	7191.3	9564.2	13055.0	7033.8	20148.1	16452.2
EU784670.1	341576	4313.3	4210.5	4104.1	3882.6	15517.3	4365.0
CU466791.1	328857	2054.7	1941.3	4958.5	4462.0	10722.6	4645.9
EU131005.1	251580	2582.3	3199.7	5861.6	4395.6	14785.4	6173.9
DQ860058.1	164190	4472.7	4841.6	4272.2	4654.3	6990.2	4763.6
EF516627.1	225426	1885.7	3269.2	5135.1	4521.2	10957.4	4245.8
DQ985034.1	182499	703.4	867.0	2084.6	1059.3	6445.1	2134.4
DQ898300.1	162144	1270.1	2319.8	4230.4	2781.3	9139.5	5071.4
EU360289.1	263034	3117.9	4300.0	3867.1	3184.1	7193.6	3149.1
AY792292.1	123759	3701.2	2578.1	2098.8	4798.6	3140.3	3540.0
DQ454121.1	156628	3600.6	3645.2	5056.5	3660.1	12356.6	6649.0
FN397674.1	460604	2843.4	2440.6	3121.9	2817.9	6871.0	3295.1
EU283461.1	277643	2221.8	2778.6	6225.6	3997.9	16633.9	4383.1
EU327998.1	277975	4311.8	4465.6	4221.0	5723.1	12916.6	9499.3
GQ060166.1	459373	3701.4	4254.1	5004.6	2903.0	8690.6	5084.0
Y10678.1	6365	625.9	626.9	803.3	821.6	4752.2	1653.6
CU920729.1	533603	3331.7	4037.7	8561.7	5557.2	16273.4	7776.9
FJ444668.1	569696	2249.3	2476.6	8304.1	3387.3	8333.0	4532.5
AB094461.1	78562	1451.2	1958.3	4258.8	3864.3	8824.1	3969.1
EF173348.1	191991	3325.3	3841.3	7639.0	2790.4	11489.0	10979.8
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GQ169059.1	543056	4874.8	7063.0	7389.4	6008.9	8962.2	8281.9
AB033327.1	6350	1617.2	2418.4	3001.5	1512.5	9734.7	4843.9
AF468357.1	79915	6383.6	4859.4	2071.2	1399.4	5927.8	2718.3
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AB363004.1	269458	684.7	973.4	1975.8	1704.5	5385.7	2856.6
DQ453142.1	157567	2128.7	2097.4	4124.0	3552.5	6629.2	3525.6

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s__Novosphingobium resinovorum	60586

DQ856526.1 gg_id:246512 intestinal microflora Chinese mitten crab (Eriocheir sinensis) clone C2F
EF157278.1 gg_id:258039 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon
U90216.1 gg_id:6294 Sphingomonas sp. 2MPII
EU682685.1 gg_id:342749 Sphingomonas sp. str. V2M44
GQ020378.1 gg_id:489291 Topographical and Temporal Human Skin Microbiome skin glabella clone nbu268d11
U20775.2 gg_id:44107 Novosphingobium stygium str. SMCC B0712
EU335142.1 gg_id:257791 Changes microbial metabolic and along hydrogeochemically variable profile saturate
DQ906835.1 gg_id:256780 Oman subsurface soil clone 7B-8
GU166344.1 gg_id:582973 Altererythrobacter sp. str. JM27
EU707558.1 gg_id:352352 Novosphingobium sp. str. YC6720
AJ746092.1 gg_id:113876 Novosphingobium sp. MG35
EU726272.1 gg_id:349727 Alterierythrobacter sp. str. H32
FJ542890.1 gg_id:525932 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone A
DQ497759.1 gg_id:161477 Sphingomonas sp. str. M80C3
DQ295907.1 gg_id:147648 Cohn's Crenothrix filamentous oxidizer unusual methane monooxygenase physical e
GU180153.1 gg_id:555283 Impact coplanar PCBs on microbial activity anaerobic estuarine sediments sediment
Y13774.1 gg_id:6269 Blastomonas natatoria str. DSM 3183
AM940945.1 gg_id:282135 Sphingomonas sp. ECN-2008
D13737.1 gg_id:6255 Sphingomonas suberifaciens str. IFO 15211
EU202871.1 gg_id:340768 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo
EF516033.1 gg_id:222080 grassland soil clone FCPS756
EF580938.1 gg_id:278358 Survey Microbial Freshwater Calcareous Mats freshwater calcareous mat clone CM4
GQ008488.1 gg_id:501177 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
FJ478827.1 gg_id:591215 species richness estimates obtained nearly and simulated pyrosequencing-generated
EU202876.1 gg_id:304392 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo
DQ248234.1 gg_id:143386 carbon tetrachloride contaminated soil clone UE1
EU223953.1 gg_id:249385 -RFLP microbes Qinghai-Tin rail soil clone 120
EU193103.1 gg_id:367223 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo
AY922159.1 gg_id:114292 farm soil clone AKYH831
EU193101.1 gg_id:367335 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo
AY850294.1 gg_id:136384 depending on what microbial treatment present soil clone w4
EU193107.1 gg_id:364127 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo
AB258386.1 gg_id:159768 Kaistobacter terrae str. KCTC12630
EU202894.1 gg_id:344045 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo
AY769084.1 gg_id:108378 Kaistobacter koreensis str. PB180
EU202882.1 gg_id:340856 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo
AM935913.1 gg_id:563989 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
EU133392.1 gg_id:242675 tallgrass prarie soil clone FFCH13278
GQ051344.1 gg_id:414905 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu4
FJ266331.1 gg_id:549411 Novosphingobium capsulatum str. RFNB21
AB196250.1 gg_id:115182 Sphingomonas sp. str. IC081

DQ856526.1	246512	943.8	1124.9	4471.3	1756.8	12570.9	2487.0
EF157278.1	258039	2740.3	3302.1	11060.7	4450.4	11839.4	14496.4
U90216.1	6294	7063.2	8713.8	10240.7	7354.3	20343.3	11884.2
EU682685.1	342749	1622.0	2616.1	3401.5	2194.1	10472.9	7018.9
GQ020378.1	489291	1166.2	1899.6	3332.2	2226.7	12563.5	2321.8
U20775.2	44107	4549.2	4630.6	9778.4	5465.1	11639.9	4281.6
EU335142.1	257791	1800.3	3056.0	2991.1	2414.5	8930.0	8015.2
DQ906835.1	256780	1733.2	1494.6	1628.8	1743.5	10822.2	3305.0
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EU707558.1	352352	6206.3	7146.5	10791.3	6211.5	18166.3	8341.7
AJ746092.1	113876	757.8	3411.1	3644.8	3116.1	6325.4	3798.8
EU726272.1	349727	3065.9	3782.8	7846.7	4628.1	7790.1	3081.4
FJ542890.1	525932	1680.4	2473.5	7516.8	2520.3	13681.7	4733.9
DQ497759.1	161477	187.1	337.0	817.5	689.6	4972.2	4414.6
DQ295907.1	147648	589.8	1216.1	571.1	722.0	4002.7	1183.4
GU180153.1	555283	1884.6	2278.7	2785.2	1650.5	5516.9	2807.8
Y13774.1	6269	2698.3	3104.4	5215.0	1780.2	7698.0	2041.2
AM940945.1	282135	1213.8	2369.8	3581.4	2215.4	9005.1	2336.6
D13737.1	6255	1303.4	2781.3	4872.7	2993.3	11278.3	3809.1
EU202871.1	340768	8551.3	8819.9	5562.3	2771.7	9263.8	3880.1
EF516033.1	222080	9459.7	10784.1	6944.2	7155.8	15704.2	9638.3
EF580938.1	278358	5101.4	7476.8	4250.2	5067.8	14223.7	7448.0
GQ008488.1	501177	8150.3	9169.1	7515.4	7369.3	19534.5	8303.0
FJ478827.1	591215	4875.1	3620.4	5014.0	4556.4	15915.5	4825.1
EU202876.1	304392	4539.1	4625.1	3799.3	4097.5	14172.0	6750.1
DQ248234.1	143386	2548.3	1825.8	3468.0	1806.7	5596.7	1397.2
EU223953.1	249385	4065.5	4047.2	5731.8	3158.2	13404.2	7168.4
EU193103.1	367223	8268.6	8355.0	5917.8	3999.5	8861.0	7096.0
AY922159.1	114292	8412.8	10996.8	9451.0	7807.4	14174.4	12099.5
EU193101.1	367335	3498.9	3893.1	2089.5	4026.5	10858.5	3851.7
AY850294.1	136384	672.4	958.6	1259.6	1160.7	4491.6	2197.1
EU193107.1	364127	8483.1	8951.8	8216.5	9014.1	18958.7	10927.8
AB258386.1	159768	4087.9	3406.4	6267.3	5847.7	18562.5	5934.1
EU202894.1	344045	1951.1	3896.4	3785.3	4533.7	14271.3	7751.1
AY769084.1	108378	3341.0	3838.2	3747.2	3795.9	7408.0	3402.0
EU202882.1	340856	7374.7	6228.4	4385.9	1393.1	7659.4	2519.4
AM935913.1	563989	6452.2	6820.5	6412.4	5882.3	11617.3	6003.2
EU133392.1	242675	6161.6	6700.7	10564.6	5005.8	8399.6	5540.5
GQ051344.1	414905	2674.2	3187.5	8841.6	4810.8	12603.2	3182.3
FJ266331.1	549411	2574.2	4114.1	10891.4	6330.9	13407.7	6994.0
AB196250.1	115182	584.7	543.7	1200.4	689.7	6818.2	1095.1

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FN421972.1 gg_id:577344 proteogenomics physiology phyllosphere clover clone 5_D06
AB275605.1 gg_id:214353 Sphingomonas bosoensis str. WF3
AB360760.1 gg_id:240554 Novosphingobium sp. str. NIY3
AB088760.1 gg_id:78821 Novosphingobium sp. str. J30
EU304250.1 gg_id:248028 Novosphingobium str. Hg4-04
AB453304.1 gg_id:514645 Sphingomonas sp. str. SO11
GQ388869.1 gg_id:511687 quality deterioration drinking system during serious red water outbreak clone Z28
EU730906.1 gg_id:332390 Novosphingobium stygium str. 159
DQ137853.2 gg_id:138108 Novosphingobium sp. str. Geo25
GQ388914.1 gg_id:580916 quality deterioration drinking system during serious red water outbreak clone Z76
FJ425737.1 gg_id:364924 Novosphingobium sp. str. CC-TPE-1
DQ337059.1 gg_id:149880 subsurface water clone EV818SWSAP5
GQ264150.1 gg_id:579694 Structure Simulated Level Waste Site simulated level waste site clone WC3_91
GQ023414.1 gg_id:486255 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu318b1(
U20755.2 gg_id:73612 Novosphingobium aromaticivorans str. SMCC B0695
AB362778.1 gg_id:256401 Sphingomonas sp. str. YT0136
GQ103626.1 gg_id:438411 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
GQ069267.1 gg_id:374280 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw241e0
AY571829.1 gg_id:102884 Sphingomonas sp. 44/40
AY792290.1 gg_id:127870 Humic Lake clone CrystalBog2A11
FJ377543.1 gg_id:369876 Novosphingobium sp. str. F2
GQ038636.1 gg_id:412772 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu4
GQ020999.1 gg_id:488670 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu2
EU937904.1 gg_id:334944 Biogeochemistry Iron Oxidation Circumneutral Freshwater Habitat riparian iron oxidi
GQ021683.1 gg_id:487986 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ472779.1 gg_id:576436 Biodiversity planktonic Northern surface water northern Bering Sea clone u3
FJ459983.1 gg_id:453127 Novosphingobium subterraneum str. C1-3-2; IMER-A3-1
GQ038752.1 gg_id:378163 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu522f03
AB331237.1 gg_id:239753 Novosphingobium aromaticivorans str. FM-1
AJ617857.1 gg_id:111304 oxic-anoxic interphase flooded paddy soil clone D28217
EU937862.1 gg_id:313934 Biogeochemistry Iron Oxidation Circumneutral Freshwater Habitat riparian iron oxidi
AY921998.1 gg_id:113391 farm soil clone AKYG1872
EU644200.1 gg_id:281742 and Samoylov Island Lena active layer -centred polygon near surface horizon; Rim_T
AJ416411.1 gg_id:38548 Novosphingobium hassiacum W-51
AB177224.1 gg_id:133463 seafloor methane hydrate clone ODP1230B9.15
EF127604.1 gg_id:208477 Fossil Genes and Microbes Entombed Oldest Ice on Earth ice clone EME109
GQ083294.1 gg_id:403709 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
AF411072.1 gg_id:39863 Sphingomonas sp. str. ACM-3962
GQ038964.1 gg_id:371390 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu4
GQ102705.1 gg_id:382549 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw(

AY914073.1	112989	3184.3	3381.1	3911.1	2885.0	5174.7	1125.6
FN421972.1	577344	6209.5	6762.8	7903.5	6503.6	16902.4	9194.6
AB275605.1	214353	30.0	33.6	53.8	634.3	1899.5	82.4
AB360760.1	240554	326.6	677.1	3263.3	2430.9	12651.6	1717.1
AB088760.1	78821	3988.5	5378.4	6873.2	4886.9	14090.4	6554.4
EU304250.1	248028	2842.8	2902.3	10300.3	5073.4	16275.0	3493.9
AB453304.1	514645	5211.2	5294.1	6608.8	5683.5	13239.0	6598.2
GQ388869.1	511687	4932.6	5669.6	5067.8	6207.0	10585.8	3797.3
EU730906.1	332390	3976.0	4313.4	10685.3	5883.7	12166.2	3396.7
DQ137853.2	138108	5558.2	5494.0	10289.9	5463.8	10294.3	4857.3
GQ388914.1	580916	7478.7	8246.5	9571.5	8740.1	15765.6	10103.9
FJ425737.1	364924	1756.5	1845.3	7519.8	4084.9	9965.4	2187.2
DQ337059.1	149880	1833.4	2337.9	984.2	1069.6	585.6	965.4
GQ264150.1	579694	5058.4	6531.3	8355.8	7159.3	14964.6	9368.0
GQ023414.1	486255	6621.5	8683.7	9641.6	6436.0	18016.9	13328.9
U20755.2	73612	3002.0	3474.6	9877.4	4409.6	8672.8	2724.5
AB362778.1	256401	2493.1	1415.3	8391.1	4862.2	13801.4	2617.8
GQ103626.1	438411	4763.9	7043.5	8588.0	5583.7	18987.0	11094.6
GQ069267.1	374280	7940.1	8847.3	8037.2	9001.7	19319.4	14228.6
AY571829.1	102884	279.7	413.1	860.8	314.3	2456.2	451.5
AY792290.1	127870	6907.1	10175.0	6930.5	7334.8	18058.6	11980.6
FJ377543.1	369876	995.0	836.3	4841.9	3532.7	16451.7	1606.8
GQ038636.1	412772	8411.9	9923.0	8048.6	7841.8	16706.7	15795.2
GQ020999.1	488670	10199.0	11022.4	7819.8	10149.7	18031.0	15988.6
EU937904.1	334944	1335.0	1560.6	4824.4	1816.5	13227.1	1808.8
GQ021683.1	487986	16089.7	15964.6	10977.1	13936.4	17797.6	16491.1
GQ472779.1	576436	7726.4	7032.1	10315.4	7547.8	12425.3	7635.2
FJ459983.1	453127	2144.4	2484.1	6713.0	3067.9	10040.8	1308.5
GQ038752.1	378163	7179.4	8027.1	10852.0	7347.6	14489.7	8657.5
AB331237.1	239753	3478.6	3869.6	10676.4	4721.3	9031.4	2727.8
AJ617857.1	111304	2158.1	3008.0	5237.1	2628.5	10127.9	2530.1
EU937862.1	313934	6432.7	5693.5	11559.7	6906.7	12323.4	6477.5
AY921998.1	113391	2978.0	3143.7	9021.9	5033.1	7249.1	2874.6
EU644200.1	281742	1758.4	2504.5	2880.4	1780.7	4635.9	1619.7
AJ416411.1	38548	603.0	557.2	3726.2	1278.0	5867.1	1206.4
AB177224.1	133463	2996.3	3019.5	8915.1	5038.1	9459.4	2891.2
EF127604.1	208477	3772.1	4554.0	3738.8	3453.5	10976.2	6777.1
GQ083294.1	403709	8607.6	9439.6	8752.5	9159.6	15161.9	10860.8
AF411072.1	39863	8220.6	6116.6	7363.8	7937.1	11730.8	6709.7
GQ038964.1	371390	8656.8	11015.8	11729.0	8241.0	20372.7	17347.2
GQ102705.1	382549	2034.3	2266.7	6901.4	4703.9	11797.7	1391.4

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GQ083414.1 gg_id:402526 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
DQ327674.1 gg_id:165838 Biological filtration limits carbon availability affects downstream biofilm formation a
GQ023478.1 gg_id:486191 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu319b0
GQ092194.1 gg_id:449436 Topographical and Temporal Human Skin Microbiome skin palm clone nbw409f03c1
EF549586.1 gg_id:252275 Novosphingobium indicum str. H25
AY328849.1 gg_id:90554 drinking water MB27
FJ801185.1 gg_id:513803 Investigation Water -DGGE and Clone Library Zoige Alpine Wetland clone ZWB2-14
GQ099344.1 gg_id:439803 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw5
EU431800.1 gg_id:562657 Troglobitic (Cansiliella) on specialized feeding apparatus calcium carbonate (moonmi
AB240479.1 gg_id:142028 microbial structure rhizosphere biofilm Sapporo root-tip (0 40 mm) Phragmites Sosei
DQ463204.1 gg_id:157220 Acid Drainage Tong Lushan Copper Mine China acid mine drainage clone tls3-9
GQ022145.1 gg_id:487522 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu3
AF025352.1 gg_id:6293 Sphingomonas sp. str. D16
EF029110.1 gg_id:221739 Novosphingobium resinovorum str. NCIMB 8767
DQ450761.1 gg_id:160417 Microbial Alpine Tundra Wet Meadow Soil: Chloroflexi Cold Water-Saturated saturat
EU639137.1 gg_id:323096 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n
DQ501315.1 gg_id:189621 Seasonal dynamics free-living and particle- four lakes northeastern Germany freshw
FJ801188.1 gg_id:542132 Investigation Water -DGGE and Clone Library Zoige Alpine Wetland clone ZWB3-1
GQ020347.1 gg_id:489319 Topographical and Temporal Human Skin Microbiome skin glabella clone nbu267h11
U20756.2 gg_id:136117 Novosphingobium aromaticivorans str. SMCC F199
DQ676432.1 gg_id:224427 Archaeal and plankton freshwater pond suboxic freshwater-pond sediment clone M
FM872861.1 gg_id:360253 occupant source house floor dust clone FB03H05
FM178802.1 gg_id:311289 Monitoring abundance and expression 'dehalococcoides' species chloroethene-redu
AY792291.1 gg_id:150609 Temporal Variation and Humic Lake clone CrystalBog022E8
DQ207361.1 gg_id:139541 Sphingomonas sp. str. PF-I
EU104173.1 gg_id:341018 Evidence Comamonadaceae determinants settling performance activated sludge clo
CU917745.1 gg_id:533625 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
EU827494.1 gg_id:352634 Sphingomonas sp. tfd44 str. TFD44
AF097802.2 gg_id:21583 activated sludge clone 1958
AY212578.1 gg_id:99539 water 10 m downstream manure clone 127ds10
GQ050992.1 gg_id:435628 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
AB286635.1 gg_id:214915 Reducing production and domination comamonadaceae reducing oxygen supply was
AY922004.1 gg_id:113584 farm soil clone AKYG395
FJ177534.2 gg_id:341537 Novosphingobium sp. str. HU1-AH51
GQ069243.1 gg_id:397437 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw241b0
GQ037883.1 gg_id:464605 Topographical and Temporal Human Skin Microbiome skin interdigital web space cl
AJ292613.1 gg_id:150636 Combined use and study polychlorinated biphenyl-polluted soil clone WD2119
Z93995.1 gg_id:6292 activated sludge clone T28
U20774.2 gg_id:70401 Novosphingobium aromaticivorans str. SMCC B0522
AB237654.1 gg_id:156847 Novosphingobium subarcticum str. T7b
AB177883.1 gg_id:103401 Novosphingobium sp. str. TUT562

GQ083414.1	402526	12534.9	13933.9	10887.5	9224.0	16395.5	14206.4
DQ327674.1	165838	2308.4	2424.2	1763.8	3040.5	6267.1	3414.8
GQ023478.1	486191	8004.6	10090.2	8820.0	8226.7	17723.2	10780.2
GQ092194.1	449436	4889.7	6319.9	7853.7	5450.2	15913.9	11859.2
EF549586.1	252275	1646.0	2091.1	3067.8	2949.0	6765.6	4375.2
AY328849.1	90554	2440.0	2854.5	8876.7	4707.7	11723.6	1376.3
FJ801185.1	513803	1094.1	1126.3	4072.6	1942.4	8842.5	1111.6
GQ099344.1	439803	8788.4	9924.9	14121.0	11850.7	19372.1	16131.3
EU431800.1	562657	4568.0	3943.6	9180.5	5710.1	11214.1	5561.1
AB240479.1	142028	3268.9	3876.3	13293.1	7360.7	12645.0	7582.6
DQ463204.1	157220	2846.1	3348.9	7772.2	5348.4	11313.8	3567.6
GQ022145.1	487522	7375.4	10369.5	7729.5	9607.5	15842.5	15197.4
AF025352.1	6293	2288.1	2783.0	5438.7	4026.5	13019.1	1854.0
EF029110.1	221739	2051.5	2459.7	3211.4	1625.4	5389.1	3013.4
DQ450761.1	160417	1178.9	1472.8	6361.2	3272.9	8343.1	1299.3
EU639137.1	323096	6267.7	6888.1	10909.5	7068.6	17105.9	8987.1
DQ501315.1	189621	2219.5	2772.6	4494.8	4469.9	7108.9	3794.5
FJ801188.1	542132	2321.1	3179.8	3306.2	2308.5	9690.0	3811.7
GQ020347.1	489319	1856.4	2209.1	8821.3	3415.1	16893.6	4878.0
U20756.2	136117	2268.0	2777.4	6785.4	3351.7	7157.6	1647.7
DQ676432.1	224427	2320.5	2941.3	6962.4	3345.1	7240.1	5082.7
FM872861.1	360253	5546.1	5057.6	9210.1	5739.7	12071.0	5223.5
FM178802.1	311289	5060.4	5879.1	5073.3	6418.4	15654.8	7198.9
AY792291.1	150609	3711.1	3904.4	4955.8	4332.8	7501.4	4565.2
DQ207361.1	139541	4278.5	3826.4	7769.4	5120.7	12181.6	4084.2
EU104173.1	341018	2705.8	3014.6	7300.0	5370.2	13805.7	3742.2
CU917745.1	533625	10367.3	13966.9	8727.2	13128.5	21054.4	17038.6
EU827494.1	352634	1477.7	2374.8	12773.6	5131.1	15178.9	3319.6
AF097802.2	21583	6371.8	6434.2	16188.4	8528.7	24663.3	8716.9
AY212578.1	99539	3034.4	2859.5	4321.8	4357.8	8146.1	3451.9
GQ050992.1	435628	1378.2	1864.6	5294.5	3055.2	12477.4	1697.9
AB286635.1	214915	3718.0	3298.6	5488.0	2803.2	8286.7	3001.9
AY922004.1	113584	3575.1	7361.1	4091.0	1831.9	11341.6	4917.8
FJ177534.2	341537	4331.0	5515.7	7164.8	6811.6	14386.8	6809.8
GQ069243.1	397437	7442.5	8385.9	5788.8	6888.4	10572.7	10508.1
GQ037883.1	464605	7786.5	8487.4	8004.7	8039.0	17776.5	14116.9
AJ292613.1	150636	862.2	1302.5	2359.7	2059.4	2548.6	1312.4
Z93995.1	6292	5995.3	5506.7	9203.8	4592.7	15047.8	5925.0
U20774.2	70401	2107.0	3293.3	5706.0	3943.0	9272.8	2773.9
AB237654.1	156847	2236.0	2570.3	7314.9	3996.1	12061.7	4092.1
AB177883.1	103401	1065.6	1244.8	5161.6	3053.9	13936.7	1613.4

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AF418947.1 gg_id:19427 USA: Colorado Fort collins Horsetooth Reservoir clone HTB9
GQ093042.1 gg_id:426566 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw408d11
GQ022398.1 gg_id:487271 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbu31
GU208446.1 gg_id:563756 Study on Sediment Dongping Lake sediment clone Fr2-8
GQ008813.1 gg_id:500852 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
AY328817.1 gg_id:90016 drinking water Y14
DQ337064.1 gg_id:146133 subsurface water clone EV818SWSAP16
EU937930.1 gg_id:348236 Biogeochemistry Iron Oxidation Circumneutral Freshwater Habitat riparian iron oxidi
AY500142.1 gg_id:104274 Novosphingobium sp. T3-B9 str. T3-B9; AS 1.3432
EU907884.1 gg_id:320881 Identification hexahydro-135-trinitro-135-triazine (RDX)-degrading microorganisms v
EU431820.1 gg_id:554799 Troglobitic (Cansiliella) on specialized feeding apparatus calcium carbonate (moonmi
EU984513.1 gg_id:306710 Novosphingobium sp. str. Rr 2-17
GQ035853.1 gg_id:418017 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbu37
AJ009707.2 gg_id:31884 Novosphingobium sp. K39
GQ083357.1 gg_id:427762 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
AB074191.1 gg_id:24166 Sphingomonas sp. str. HL7
EU937960.1 gg_id:342517 Biogeochemistry Iron Oxidation Circumneutral Freshwater Habitat riparian iron oxidi
GQ007148.1 gg_id:502513 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
EU679659.1 gg_id:295118 Sphingobium chungbukense str. DJ77
AB491315.1 gg_id:546882 Sphingobium fuliginis str. TIK-1
AB042233.1 gg_id:18499 Sphingobium herbicidovorans
EF065102.1 gg_id:179619 Sphingobium herbicidovorans str. FL
FJ191952.1 gg_id:321055 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior
DQ885954.1 gg_id:162032 Sphingomonas sp. str. BSL8
AY574367.1 gg_id:106220 Sphingobium yanoikuyae str. DD109
AB331239.1 gg_id:240760 Sphingobium yanoikuyae str. FM-3
Y12803.1 gg_id:38158 Sphingomonas agrestis str. HV3
DQ374096.1 gg_id:156568 Sphingomonas agrestis str. MP5
AB025530.1 gg_id:6164 Sphingomonas sp. str. MBIC3990 Lo251
AM489507.1 gg_id:203347 Sphingomonas olei str. IMMIB HF-1
GQ025136.1 gg_id:415594 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1
EU744623.1 gg_id:349718 Sphingobium sp. str. W1
AF157490.1 gg_id:6196 Sphingomonas sp. str. JS5
EU050705.1 gg_id:238200 Microbial waters production water Daqing oil field clone DQ328-85
EU286535.1 gg_id:239979 Sphingobium sp. 2F5-2
AB112465.1 gg_id:88144 Suiyo Seamount hydrothermal plume clone SUP27-27
AY771799.1 gg_id:108045 Sphingomonas sp. 12-7
GQ096356.1 gg_id:423731 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
DQ202286.1 gg_id:139757 Sphingomonas sp. str. PF-K
AB000106.1 gg_id:6183 Sphingomonas sp. str. VT1

GQ023295.1	486374	10908.2	9778.0	9363.7	11559.0	17810.8	10258.8
AF418947.1	19427	6883.4	7939.8	8040.6	5131.4	13005.0	8222.1
GQ093042.1	426566	6254.8	6917.2	5167.9	7025.1	15967.2	11359.3
GQ022398.1	487271	13988.5	13823.5	7425.7	11499.7	16004.6	16487.9
GU208446.1	563756	459.2	627.1	410.4	469.9	161.6	308.9
GQ008813.1	500852	14308.7	17128.1	12644.6	12008.7	22884.3	19482.4
AY328817.1	90016	2504.4	3033.2	6418.0	3716.4	7301.3	3086.9
DQ337064.1	146133	6124.2	6794.3	3553.9	4665.1	11304.3	8164.6
EU937930.1	348236	2380.4	3508.2	4816.4	3195.8	5357.8	3940.3
AY500142.1	104274	3209.6	1893.2	8368.8	4044.8	3662.8	2468.6
EU907884.1	320881	2525.3	2377.8	11963.6	6308.2	15125.2	3713.8
EU431820.1	554799	1775.7	2628.9	3549.0	3563.2	11382.9	4919.2
EU984513.1	306710	1765.6	2832.6	5456.5	3780.0	9860.0	6462.4
GQ035853.1	418017	4378.5	4856.7	5393.6	9834.3	10644.9	8357.4
AJ009707.2	31884	2787.2	2811.6	7251.9	4581.0	11026.8	2337.6
GQ083357.1	427762	4285.9	5314.3	4439.8	5070.6	11573.3	9479.4
AB074191.1	24166	3053.2	2856.1	5801.6	3626.5	7296.2	2196.0
EU937960.1	342517	6345.4	6806.6	10529.6	8785.2	12269.3	6366.1
GQ007148.1	502513	6363.5	7148.4	11153.5	7561.5	20815.3	11160.9
EU679659.1	295118	1561.4	2324.5	2320.2	1442.7	9943.6	2505.8
AB491315.1	546882	2029.2	2752.0	4089.2	3693.8	11529.5	5405.1
AB042233.1	18499	12782.5	14172.8	13857.6	10700.1	22751.1	18345.5
EF065102.1	179619	6791.5	6248.2	10309.8	5856.7	16203.0	8896.7
FJ191952.1	321055	2762.5	1894.3	1724.8	1413.1	16704.3	3584.2
DQ885954.1	162032	1966.4	2511.6	4307.8	2013.1	11271.4	2806.6
AY574367.1	106220	334.5	545.4	1713.9	1227.0	8161.5	755.5
AB331239.1	240760	3844.0	4254.4	6237.9	5617.8	14824.4	5683.2
Y12803.1	38158	4172.5	3824.3	6660.2	5466.1	16150.1	5245.0
DQ374096.1	156568	17903.5	13915.8	8723.1	11122.3	18574.6	12493.2
AB025530.1	6164	1292.6	2456.8	4079.8	3113.4	15342.1	7592.2
AM489507.1	203347	581.4	1518.8	2449.4	2015.4	8863.8	2593.3
GQ025136.1	415594	3643.1	3797.4	2503.5	2670.8	16149.4	4907.2
EU744623.1	349718	2752.3	4848.8	4572.7	5151.3	11647.6	6015.9
AF157490.1	6196	662.0	714.5	1883.2	1098.5	9100.6	783.3
EU050705.1	238200	142.5	477.8	1157.8	813.7	11181.0	1044.7
EU286535.1	239979	1844.6	2123.1	3197.0	1787.3	12921.8	2023.6
AB112465.1	88144	4896.9	4088.1	3335.4	3896.8	17469.7	8473.4
AY771799.1	108045	376.4	481.7	663.3	578.2	10745.5	2366.1
GQ096356.1	423731	1845.7	3204.6	3842.1	3640.3	9102.1	6064.7
DQ202286.1	139757	6861.6	5741.1	6998.3	5053.8	14383.2	8467.7
AB000106.1	6183	646.6	757.9	2056.1	719.2	15089.9	2910.7

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GQ075940.1 gg_id:432730 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
EU440973.1 gg_id:306928 Sphingobium sp. str. PR52-27
AB299582.1 gg_id:254239 Sphingomonas sp. str. M30-VN10-1W
FJ192049.1 gg_id:315748 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior
EU159273.1 gg_id:354715 Sphingobium sp. str. YBL3
D13728.1 gg_id:6148 Sphingobium yanoikuyae str. IFO15102
EU009209.1 gg_id:255180 Sphingobium yanoikuyae str. WP01
X94098.1 gg_id:6200 Sphingomonas xenophaga str. BN6
GQ086522.1 gg_id:467619 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw29
AY367025.1 gg_id:93363 Sphingomonas sp. As1-3
X94100.1 gg_id:6163 Sphingomonas paucimobilis str. EPA 505
AF177917.1 gg_id:6193 Sphingomonas sp. str. DhA-95
AF191022.1 gg_id:6167 Sphingomonas sp. str. CD
EU183233.1 gg_id:251876 Sphingobium yanoikuyae str. XJ
EU307932.1 gg_id:239648 Sphingobium yanoikuyae str. BF-18
FJ191324.1 gg_id:310721 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior
EU375008.1 gg_id:275989 Sphingomonas sp. str. PhS5B
AM998824.1 gg_id:552210 Sphingomonas sp. VC-230 str. VC-230=CCUG 55809
X85023.1 gg_id:6161 Sphingobium yanoikuyae str. PAH-degrading
AJ011505.1 gg_id:6162 Sphingomonas sp. str. DhA-33
FJ191470.1 gg_id:332159 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior
AJ000918.2 gg_id:40332 Sphingomonas sp. str. K6
FJ191669.1 gg_id:329197 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior
EU240401.1 gg_id:252134 Sphingomonas xenophaga str. B107
AY367026.1 gg_id:93744 Sphingomonas sp. As1-5
FJ966197.1 gg_id:589286 Sphingobium sp. str. P21
FJ193541.1 gg_id:322175 Genetic inventory 'LMA-MTF' spacecraft assembly clean room during Phoenix missior
U37341.1 gg_id:6178 Sphingomonas paucimobilis
AY635898.1 gg_id:101815 Sphingomonas sp. str. AMS7
EU616621.1 gg_id:271841 Sphingomonas sp. str. JK1 soil
U37525.1 gg_id:6160 Sphingobium yanoikuyae str. Q1
EU159274.1 gg_id:313442 Sphingobium sp. str. YBL1
D16145.1 gg_id:6171 Sphingobium yanoikuyae str. GIFU9882
GQ019477.1 gg_id:490192 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu190d
GQ101175.1 gg_id:370761 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw49
AY151393.1 gg_id:73215 Sphingomonas cloacae LH227
AB299577.1 gg_id:251303 Sphingomonas sp. str. M5-VN5-4W
AB214867.1 gg_id:131055 Sphingomonas sp. str. ED8
FJ191966.1 gg_id:306789 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior
GQ087461.1 gg_id:416479 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw357g0
GQ023300.1 gg_id:486369 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu2

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EU440973.1	306928	2756.6	2357.3	3901.2	2093.6	9005.3	2669.4
AB299582.1	254239	1183.2	1680.5	1925.6	1920.8	15478.6	3377.1
FJ192049.1	315748	2865.3	2385.1	5120.1	2327.1	18040.4	2350.8
EU159273.1	354715	2122.9	4003.3	3739.3	3525.3	13021.8	9458.3
D13728.1	6148	3235.3	3827.9	4129.1	5064.8	17417.8	7257.2
EU009209.1	255180	4509.8	5970.7	7084.9	4367.1	12358.3	4421.6
X94098.1	6200	8520.3	6408.1	7347.2	7279.5	19973.0	6909.2
GQ086522.1	467619	12452.5	12454.7	15122.6	11917.7	17944.2	13120.2
AY367025.1	93363	10003.5	12508.9	9197.9	7131.4	20816.1	13795.3
X94100.1	6163	3824.2	5612.5	3729.7	5089.6	12903.3	7919.3
AF177917.1	6193	17483.2	17584.4	18225.6	15022.9	23744.6	16618.9
AF191022.1	6167	5547.6	4979.5	3308.9	3728.1	14869.9	5456.9
EU183233.1	251876	1294.9	1998.9	3908.9	3307.8	13586.1	3838.1
EU307932.1	239648	1122.1	1841.2	3761.6	3118.2	11888.2	3671.0
FJ191324.1	310721	1566.2	1190.5	2399.3	1901.2	16864.3	1871.7
EU375008.1	275989	763.2	757.8	898.3	420.8	5141.4	882.2
AM998824.1	552210	2338.7	2709.7	4251.4	3547.7	11431.2	4622.3
X85023.1	6161	1407.8	2073.4	3329.1	3620.9	12883.7	3757.6
AJ011505.1	6162	664.7	788.3	2680.6	1131.7	14205.2	2402.9
FJ191470.1	332159	2840.5	2162.1	7117.9	2626.5	16498.6	2561.1
AJ000918.2	40332	1225.8	1491.5	2809.7	2425.5	12865.8	5175.7
FJ191669.1	329197	2707.4	3173.2	4288.4	2194.9	13265.2	3377.0
EU240401.1	252134	9390.3	10475.1	8047.9	9061.7	22409.4	14673.2
AY367026.1	93744	5079.8	4677.6	4330.1	3451.5	17336.0	4357.3
FJ966197.1	589286	8664.4	9098.4	9918.2	9173.4	16668.1	12117.1
FJ193541.1	322175	2235.4	1729.0	1699.7	1500.6	16673.7	3514.0
U37341.1	6178	5104.5	5968.9	3496.1	5664.7	8977.8	7363.4
AY635898.1	101815	1466.7	1970.4	5090.7	3465.1	6957.9	4568.5
EU616621.1	271841	2234.5	3295.6	2916.5	3185.2	10760.7	7904.9
U37525.1	6160	1609.6	2574.1	3303.8	3128.3	12916.2	4229.9
EU159274.1	313442	2034.1	2938.8	3866.2	3757.4	12997.1	5963.8
D16145.1	6171	1311.5	1983.4	3258.3	2949.2	12603.7	3653.9
GQ019477.1	490192	2759.4	3084.9	2535.6	1826.0	7755.5	3133.8
GQ101175.1	370761	3959.6	4881.4	6364.0	5041.1	12884.8	8262.1
AY151393.1	73215	2184.4	3664.5	3597.9	2741.7	17051.2	6617.1
AB299577.1	251303	3175.1	1938.3	3665.6	2072.4	6211.9	1693.2
AB214867.1	131055	3072.8	3492.0	3567.3	3865.6	11697.7	3683.5
FJ191966.1	306789	10202.5	11093.3	6721.6	7855.3	21205.5	10623.0
GQ087461.1	416479	5901.5	8302.9	3868.8	6021.9	12725.2	9356.7
GQ023300.1	486369	8096.7	8153.8	4861.0	5923.5	14161.9	8538.0

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EU057882.1 gg_id:253243 Sphingomonas sp. CH30-8
AB040739.1 gg_id:41591 Sphingomonas cloacae str. S-3
EU095328.1 gg_id:250814 Sphingobium sp. str. x23
AJ009708.2 gg_id:51138 Sphingobium sp. K40
AB120764.1 gg_id:94883 Sphingobium yanoikuyae str. EC-S01
EU219973.1 gg_id:251683 Sphingomonas sp. str. KMC001
AF038030.1 gg_id:6195 Sphingomonas sp. str. Lep1
FJ191658.1 gg_id:343666 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior
GQ093336.1 gg_id:377426 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw42
GQ036338.1 gg_id:409030 Topographical and Temporal Human Skin Microbiome skin palm clone nbu363b03c1
AY921715.1 gg_id:113008 farm soil clone AKYH784
EU240418.1 gg_id:257571 Sphingobium yanoikuyae str. B166
AY151392.1 gg_id:55376 Sphingomonas chungbukensis VM0440
FJ193550.1 gg_id:307264 Genetic inventory 'LMA-MTF' spacecraft assembly clean room during Phoenix missior
AB214868.1 gg_id:131403 Sphingomonas sp. str. ED9
AF494538.1 gg_id:67345 Sphingomonas sp. str. BPC4
AY328789.1 gg_id:90697 drinking water system simulator clone DSSD92
AY519129.1 gg_id:99094 Sphingomonas paucimobilis str. B90A
AB288318.1 gg_id:212603 Sphingomonas sp. str. SY-17
AY921943.1 gg_id:113573 farm soil clone AKYG1014
AY026948.1 gg_id:32571 Sphingomonas sp. str. ML1
GQ087010.1 gg_id:432007 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw3!
EU580697.1 gg_id:261294 Sphingobium sp. str. NP22b
DQ238831.1 gg_id:142891 Sphingobium sp. VM2
AM935351.1 gg_id:534250 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
GQ022171.1 gg_id:487497 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu3
FJ192016.1 gg_id:324267 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior
FJ192036.1 gg_id:350560 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior
AY646154.1 gg_id:136602 Sphingomonas sp. str. 3Y
GQ091495.1 gg_id:456287 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw346h1
FJ796422.1 gg_id:462836 Sphingomonas sp. str. S-II-13
AJ007800.1 gg_id:6234 Asticcacaulis excentricus str. ACM 1263 (T)
AF331660.1 gg_id:136175 Caulobacter leidyia
FN421869.1 gg_id:593077 proteogenomics physiology phyllosphere clover clone 2_E01
AY571825.1 gg_id:102263 hydrocarbon-contaminated soil clone 433E
FJ605269.1 gg_id:560773 Sphingomonas sp. str. DCY44
AM229669.1 gg_id:152429 Sphingomonas mucosissima str. CP173-2
AF409011.1 gg_id:102915 Sphingomonas sp. str. Ellin169
GU377113.1 gg_id:523159 Sphingomonas sp. str. sptzw24
FN421984.1 gg_id:585288 proteogenomics physiology phyllosphere clover clone 5_F05

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AB040739.1	41591	2366.2	4691.9	5518.3	4219.4	14190.2	8707.5
EU095328.1	250814	2779.9	3079.5	6747.2	3844.4	20618.4	7030.7
AJ009708.2	51138	1504.6	2332.3	5003.6	3097.8	10455.8	4163.7
AB120764.1	94883	6311.8	5432.9	9491.3	7658.9	15252.5	8428.1
EU219973.1	251683	3862.5	3434.6	6225.4	4488.1	15529.9	5352.1
AF038030.1	6195	11034.7	11518.1	9672.6	9872.3	19353.0	14875.6
FJ191658.1	343666	1398.8	939.0	2370.0	1482.6	17652.1	1563.1
GQ093336.1	377426	1964.4	2436.7	5546.7	2338.3	11052.7	5513.4
GQ036338.1	409030	5948.9	7182.2	3794.0	6437.1	19194.1	11629.7
AY921715.1	113008	3213.0	2962.3	1014.4	3857.4	8707.3	3384.8
EU240418.1	257571	1012.3	2242.0	4083.9	2962.0	9571.3	2410.8
AY151392.1	55376	1635.7	2246.1	3110.8	2028.4	9426.2	3093.2
FJ193550.1	307264	1213.3	735.3	855.1	941.1	11238.6	2012.3
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AF494538.1	67345	1785.0	2605.5	5597.0	3520.1	15086.2	4408.2
AY328789.1	90697	2929.6	2283.2	2467.2	3386.0	10075.2	2664.1
AY519129.1	99094	1283.0	1736.5	956.7	1602.2	6623.4	6830.3
AB288318.1	212603	4918.0	5015.8	4275.5	6736.7	15420.4	8361.9
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AY026948.1	32571	1948.5	1804.4	1625.1	2010.5	7267.5	3487.1
GQ087010.1	432007	1961.8	2349.8	3332.0	2050.4	13018.5	6088.7
EU580697.1	261294	12059.3	11967.5	8226.6	6230.4	22891.7	12223.7
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AY646154.1	136602	1276.0	2072.5	4186.6	2141.6	12649.4	4405.9
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AJ007800.1	6234	5010.3	6104.6	7619.9	3843.0	11695.8	6346.1
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FN421984.1	585288	3254.0	5119.5	5798.6	2760.3	14323.8	5889.3

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FJ603029.1 gg_id:555265 Sphingomonas sp. str. RJ5
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FJ605410.1 gg_id:465125 Sphingomonas melonis str. PL-3
FN421496.1 gg_id:555334 proteogenomics physiology phyllosphere Arabidopsis thaliana clone 12_C10
EU652483.1 gg_id:278777 Sphingomonas sp. str. JPB-3.12
EF188427.1 gg_id:331282 Microbial Altamira Cave clone 233
DQ917254.1 gg_id:168642 and functional genes 24-D degrading clone 57-39
DQ532256.1 gg_id:165325 Geographical Variation Microbial Burden and Spacecraft Assembly Johnson Space Ce
EU037946.1 gg_id:238730 Metabolic Profiles Microbial Chlorinated Pesticides Contaminated Sites Three Geogr
AM697454.1 gg_id:222699 sequencing libraries indoor dust clone BF0001D069
AJ292605.1 gg_id:31402 PCB-polluted soil clone WD286
AB105809.1 gg_id:99195 Sphingomonas sp. str. D12
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EU133434.1 gg_id:238508 tallgrass prarie soil clone FFCH14971
EU528244.1 gg_id:285960 Seasonal Dynamics Mudflat Mouth Major Kentucky Lake Reservoir Tributary sedime
X94101.1 gg_id:6204 Sphingomonas sp str. A175
EU741034.1 gg_id:336829 Sphingomonas sp. str. FeL01
NR_028634.1 gg_id:577486 Sphingomonas yabuuchiae str. A1-18; GTC 868
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GU086447.1 gg_id:581377 Sphingomonas sp. str. G12
GQ388898.1 gg_id:548051 quality deterioration drinking system during serious red water outbreak clone Z6
GQ031784.1 gg_id:423523 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
DQ218322.1 gg_id:139745 Sphingomonas sp. str. Camargue
DQ178975.1 gg_id:139465 Sphingomonas dokdonensis str. DS-4
DQ129612.1 gg_id:137871 microarray level air two cities Texas urban aerosol clone AKIW723
EU753665.1 gg_id:316463 modern freshwater stromatolites Ruidera Pools Natural Park Spain dry stromatolite
GQ264140.1 gg_id:509815 Structure Simulated Level Waste Site simulated level waste site clone WC3_80
AF395038.1 gg_id:49435 Sphingomonas sp. str. CanClear1
GQ340201.1 gg_id:541929 Prokaryotic Marathonas Reservoir Greece water column clone VE07-03-BAC
AY328839.1 gg_id:104964 drinking water MB6
EU337119.1 gg_id:510578 Sphingomonas sp. str. 3B3
DQ532255.1 gg_id:173459 Geographical Variation Microbial Burden and Spacecraft Assembly Johnson Space Ce
EU707561.1 gg_id:319666 Sphingomonas sp. str. YC6723
GU084122.1 gg_id:579774 Sphingomonas sp. str. F5
FJ192534.1 gg_id:350117 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior
DQ855091.1 gg_id:164040 Sphingomonas sp. str. EBD
EF099342.1 gg_id:176680 mouse cecum clone SWPT3_aaa02a01

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FJ603029.1	555265	1003.9	1321.7	1008.7	1480.8	10796.4	2754.2
AB217471.1	149563	8811.7	9862.3	10199.9	8772.0	19531.2	9125.2
FJ455061.1	532603	5890.5	6445.1	4467.4	9270.1	20057.8	9030.6
EU730918.1	320669	504.1	487.0	2244.9	594.8	9074.7	1586.7
AF502400.2	91326	10552.7	11920.4	16268.7	10482.9	25379.7	11859.8
FJ605410.1	465125	1986.9	2424.5	5144.0	2129.0	12499.5	6224.1
FN421496.1	555334	2609.9	3587.0	6671.4	4131.4	17293.5	5285.7
EU652483.1	278777	1764.3	2635.3	1649.1	1412.1	14363.1	4251.3
EF188427.1	331282	2429.9	2150.9	4234.8	2693.9	14996.6	5526.2
DQ917254.1	168642	542.3	1210.1	4556.1	3368.5	20379.4	6753.2
DQ532256.1	165325	50.7	108.3	163.0	87.7	401.2	123.0
EU037946.1	238730	10569.1	9081.3	8645.0	9261.6	14544.2	10029.5
AM697454.1	222699	4861.3	5097.9	3292.2	4128.0	19500.7	7286.8
AJ292605.1	31402	80.9	118.4	622.4	124.9	1964.8	306.4
AB105809.1	99195	2117.2	2407.2	3984.0	3476.4	19065.7	8455.9
AY771797.1	108043	9716.1	6809.6	1835.2	6694.0	14310.7	6535.8
EU133434.1	238508	3495.9	3354.0	5388.1	2927.8	9257.8	4005.7
EU528244.1	285960	5048.8	6142.3	6890.0	4856.3	18332.6	7765.3
X94101.1	6204	3600.2	4086.0	7002.0	4259.0	22141.6	6604.5
EU741034.1	336829	3009.0	3142.0	3321.0	1844.6	9692.0	1953.4
NR_028634.1	577486	1062.3	1228.9	1428.2	907.4	11752.2	1619.6
EF540853.1	220197	8711.4	11826.1	5094.5	8317.2	18978.2	10228.5
GU086447.1	581377	1336.9	1243.6	632.0	773.5	5122.0	992.9
GQ388898.1	548051	2676.7	5102.9	6414.0	3574.2	15470.1	7746.5
GQ031784.1	423523	1818.2	2163.1	1843.8	2088.7	8778.4	4598.7
DQ218322.1	139745	2355.8	3047.8	6407.8	2735.9	12761.0	6642.1
DQ178975.1	139465	1974.8	2302.3	2161.4	1017.6	20226.0	1878.9
DQ129612.1	137871	1577.3	1879.2	3767.9	2090.8	10925.4	4810.8
EU753665.1	316463	7526.3	6779.7	4574.3	5226.9	13182.4	6262.8
GQ264140.1	509815	2085.8	2628.0	1955.3	4127.9	10368.4	3319.3
AF395038.1	49435	1722.9	1827.1	2793.9	1238.5	7277.7	1214.5
GQ340201.1	541929	5715.5	5234.7	4177.6	3719.3	23939.2	4427.7
AY328839.1	104964	3799.8	3915.7	9094.1	5334.2	16479.2	8406.7
EU337119.1	510578	664.7	930.0	5142.9	2116.1	9274.3	3072.2
DQ532255.1	173459	1293.4	2091.4	3520.7	1080.9	8839.8	3850.0
EU707561.1	319666	3865.3	6114.0	5258.8	3079.7	10141.9	7541.9
GU084122.1	579774	2893.3	4005.8	6869.0	3434.6	14393.0	5722.6
FJ192534.1	350117	2894.8	2400.4	4924.4	2049.9	15535.2	3420.0
DQ855091.1	164040	8229.1	10371.8	8307.2	9332.6	18412.0	14096.3
EF099342.1	176680	1363.9	2310.3	2885.3	2212.9	9402.8	2272.1

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AY328774.1 gg_id:90104 drinking water system simulator clone DSSD76
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EU400651.1 gg_id:263151 Sphingomonas aquatilis LBS10
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AB033944.1 gg_id:44864 Sphingomonas echinoides
FJ834325.1 gg_id:561245 Sphingomonas sp. str. BH3
EU099873.1 gg_id:243743 Sphingomonas sp. str. CJ70

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AY328774.1	90104	9426.8	10768.8	6138.9	9100.6	14184.1	10630.6
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AJ746106.1	114124	919.5	1591.4	5132.2	2243.1	18707.7	5523.1
EF540475.1	222326	26.7	40.2	180.8	145.2	534.7	346.7
FN421996.1	580312	3992.3	3639.8	5456.7	4508.4	13616.8	5858.9
EU130953.1	256074	646.5	838.3	2082.7	3073.9	8459.6	1874.3
AB261013.1	169656	845.2	1145.2	3713.7	1886.3	23380.9	2489.6
DQ314734.1	146007	3639.8	3997.9	4313.2	2817.3	11216.7	3979.2
EU133536.1	252977	2324.8	3388.5	4438.9	3265.7	15645.1	6180.7
FN421893.1	583217	12674.6	13260.6	16646.1	11388.7	25289.8	14720.0
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AF227857.1	70529	7339.9	6988.7	4438.3	4941.5	17669.4	6162.3
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AB288312.1	210631	2463.9	2368.1	5065.3	2326.8	13502.6	3092.0
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DQ463724.2	163899	358.5	438.0	1111.6	537.1	11642.2	984.2
AF408976.1	99326	2658.4	3236.3	3625.5	4534.0	15453.9	6925.0
AB288314.1	210873	11284.7	9789.2	7192.3	11669.7	15240.6	13698.4
GQ108149.1	446302	993.2	1272.0	3373.0	1636.3	14225.2	991.3
DQ129623.1	189882	501.7	570.8	1287.4	793.2	12069.6	2230.9
AM697355.1	217266	1587.8	1554.2	5714.7	2855.2	17289.8	4926.7
D16146.1	6222	4358.5	4982.3	8034.4	4696.6	23332.9	11303.5
EU400651.1	263151	3195.6	1973.5	2446.4	937.2	7018.1	2337.2
AB248285.2	152818	2886.4	1641.8	913.8	3035.5	12329.7	4547.1
EF693741.1	240698	2112.7	1579.7	3260.0	1408.8	12077.3	4414.8
DQ855413.1	169604	287.5	494.0	3348.8	804.2	14360.9	2070.6
EF423364.1	204002	3816.4	5380.8	6613.1	3731.2	15693.7	7167.2
AM697239.1	225362	2213.0	1804.3	797.9	1634.5	5905.4	1831.5
FN421879.1	591751	434.9	782.1	1843.0	1075.8	13108.0	1235.7
FN421908.1	582921	279.4	285.2	805.7	396.0	6830.7	3629.6
GQ129861.1	454787	3940.3	5001.6	4855.4	4619.8	20184.6	7650.9
AF184221.1	6221	4074.3	4438.2	6485.0	4898.2	18833.0	5838.8
AB033944.1	44864	1140.0	1279.2	2223.0	924.9	8625.1	1422.1
FJ834325.1	561245	413.5	888.0	4037.7	535.7	12622.7	3653.3
EU099873.1	243743	2479.6	3483.0	4906.3	3910.0	9016.3	5703.3

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EU488323.1 gg_id:565623 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and
FJ191372.1 gg_id:309734 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior
FN421922.1 gg_id:584046 proteogenomics physiology phyllosphere clover clone 10_D11
AM237364.1 gg_id:155666 Sphingomonas paucimobilis str. ATCC 29837 OS-64
EU977752.1 gg_id:569290 Sphingomonas sp. str. 1P08PE
GQ850582.1 gg_id:555266 bottom water northern Bering Sea clone d143
FJ193761.1 gg_id:344395 Genetic inventory 'KSC-Astrotek' spacecraft assembly clean room during DAWN missi
FJ958329.1 gg_id:459360 Sphingomonas sp. str. Tibet-YD4600-2
AB257634.1 gg_id:269203 Microbial few millimeters be surface dolomite rock 'Val Piora' Alps 1965 meters abov
DQ789172.1 gg_id:248044 Sphingomonas sp. str. nk02
AB166883.1 gg_id:104462 Sphingomonas sp. str. T5-04
AJ575817.1 gg_id:90538 Sphingomonas sp. str. C42
FJ382671.1 gg_id:590918 Potentially pathogenic and air stem cell transplant summer hospital shower water BM
X89903.1 gg_id:31767 Sphingomonas sp. str. PC5.2 (bright yel group 1 colony type) PC5.2
EU289447.1 gg_id:257439 metagenomic approach biosynthesis ansamycin endophytes or symbionts enriched s
EU400649.1 gg_id:266787 Sphingomonas sp. LBS8
DQ129624.1 gg_id:137761 microarray level air two cities Texas urban aerosol clone AKIW946
AM412238.1 gg_id:186959 Sphingomonas intermedia str. G1-2
GQ389119.1 gg_id:584563 quality deterioration drinking system during serious red water outbreak clone S72
FJ525442.1 gg_id:536944 Chlorophyll-containing deep-sea deep sea water 500 m depth clone Pac500QII-10
FJ382620.1 gg_id:589104 Potentially pathogenic and air stem cell transplant summer hospital shower water BM
EF512739.1 gg_id:225933 Novosphingobium sp. str. JL832
Y09638.1 gg_id:6244 Sphingomonas mali str. IFO 10550-T
AF128870.1 gg_id:105477 Sphingomonas sp. str. B26
EU834796.1 gg_id:579177 Microbiology Aerobic Phosphorus Removal Process aerobic phosphorus-removing se
GQ161989.1 gg_id:588949 Sphingomonas sp. str. S8-3
EU133552.1 gg_id:236646 tallgrass prarie soil clone FFCH3058
EU730903.1 gg_id:356103 Sphingomonas melonis str. 150
GQ169802.1 gg_id:533431 Sphingomonas sp. str. B1709
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AY453855.1 gg_id:105178 Sphingomonas phyllosphaerae str. FA2
FJ193525.1 gg_id:347975 Genetic inventory 'LMA-MTF' spacecraft assembly clean room during Phoenix missior
EU071479.1 gg_id:251041 and resistance microorganisms European clean room ESTEC HYDRA facility clone EHF
DQ532204.1 gg_id:162721 Geographical Variation Microbial Burden and Spacecraft Assembly Johnson Space Ce
AM697187.1 gg_id:226138 sequencing libraries indoor dust clone BF0001C028

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GQ850582.1	555266	4447.4	5030.2	4280.7	7155.0	12579.1	4952.8
FJ193761.1	344395	352.3	378.0	915.0	541.0	11422.7	1259.0
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X89903.1	31767	4524.9	4301.8	6135.0	4417.1	14869.1	7671.0
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FJ525442.1	536944	3759.6	4741.7	7805.3	3983.3	14965.1	9878.5
FJ382620.1	589104	6291.0	5553.9	4046.8	6250.1	24653.4	9148.8
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EU730903.1	356103	1912.1	2164.8	4192.8	1764.0	12627.7	4346.4
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FN421585.1 gg_id:580992 proteogenomics physiology phyllosphere Arabidopsis thaliana clone 1_C09
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U37337.1 gg_id:6229 Sphingomonas paucimobilis str. ATCC 29837
EU509065.1 gg_id:266499 cecal contents Mus musculus strain C57BL/6J; MD7 clone MD7_aap43a04
GQ007389.1 gg_id:502275 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
FN421549.1 gg_id:549986 proteogenomics physiology phyllosphere Arabidopsis thaliana clone 14_B08
FJ382733.1 gg_id:509865 Potentially pathogenic and air stem cell transplant summer hospital shower water BM
GQ129915.1 gg_id:430097 Genetic inventory 'JPL-SAF' during MSL mission spacecraft assembly clean room floc
EF363714.1 gg_id:216270 Sphingomonas insulae str. DS-28
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DQ137852.2 gg_id:138171 Sphingopyxis sp. str. Geo24
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AM697313.1	223117	4876.0	5984.9	8557.3	6698.4	22551.1	10006.4
EU332828.1	243129	865.5	1121.6	1301.0	959.2	11184.8	2152.6
EF154145.1	199504	974.1	1218.5	1803.3	1463.1	6113.8	2831.1
EU730917.1	335583	3467.3	4080.5	6407.8	5572.1	13566.5	7457.8
FN421904.1	583102	2671.9	1478.5	5676.5	3404.3	9388.7	5298.7
FJ754464.2	580805	921.8	1272.0	3653.7	2168.3	14929.5	2167.3
GQ098508.1	454324	691.1	819.8	3877.3	1935.0	13867.2	3939.8
FJ382695.1	570817	4193.3	4458.8	7523.8	5788.1	18481.8	5831.5
EF660755.1	235483	1626.3	1860.5	3526.8	3043.3	15065.7	4040.8
EF154144.1	181647	5008.3	4546.5	5083.5	4158.5	22154.9	6280.5
GQ008274.1	501391	2356.2	1977.3	4816.1	1479.7	13745.6	3212.5
EU636064.1	278497	417.9	613.5	1642.1	569.1	4398.6	1166.7
FJ382729.1	564701	3292.7	2870.2	2517.9	3045.1	10647.1	5628.1
AF378795.1	42377	5603.7	6078.8	4649.0	6015.1	16956.2	6191.1
FJ382750.1	511760	1193.3	1686.8	4806.4	2521.8	12351.9	4687.7
AF145753.1	19973	864.1	906.5	2406.0	1749.8	15116.1	2492.4
FJ263377.1	332699	4602.7	4354.5	5011.3	5633.1	11078.3	4814.4
AB245354.1	147544	1736.7	1968.8	3838.6	3824.1	10223.7	4129.6
AB015049.1	6329	613.3	799.2	1490.6	871.8	10371.8	2414.5
AB033950.1	44192	345.2	622.2	1278.9	390.1	8560.5	1465.6
AJ416410.1	45857	4912.5	5768.3	3875.8	4766.7	14433.1	10484.8
AY563034.1	100783	3575.6	4200.4	4924.7	4781.4	13236.1	8670.9
DQ376581.1	154381	5493.0	3603.6	2151.0	3811.8	16698.3	7345.5
DQ137852.2	138171	7325.8	6222.8	5859.7	6769.6	11560.7	6629.8
AB372254.1	245742	1037.2	1284.9	3690.5	2364.2	13204.1	3274.1

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FJ382563.1 gg_id:575538 Potentially pathogenic water and air stem cell transplant summer hospital shower ae
FJ382527.1 gg_id:548468 Potentially pathogenic water and air stem cell transplant summer hospital shower ae
FJ382548.1 gg_id:567426 Potentially pathogenic water and air stem cell transplant summer hospital shower ae
AY509242.1 gg_id:104644 Sphingopyxis alaskensis str. S23
EF028689.1 gg_id:197687 Sphingomonas sp. str. BCL-98
GU201847.1 gg_id:515215 Sphingopyxis alaskensis str. Guashi-1
AF131297.1 gg_id:6328 Sphingomonas taejonensis str. JSS-54
EU464953.1 gg_id:292322 African elephant feces clone AFYEL_aaj65g04
AJ871278.1 gg_id:114482 Sphingomonas sp. str. DS3-1
EU816422.1 gg_id:346880 Sphingopyxis sp. str. Geo48
DQ112242.1 gg_id:130329 Sphingopyxis sp. str. LH21
FJ382493.1 gg_id:549471 Potentially pathogenic water and air stem cell transplant summer hospital shower ae
EF523589.1 gg_id:222242 Sphingopyxis sp. str. Ds26
AY212804.1 gg_id:81691 Sphingomonas sp. str. EVA17
EU075217.1 gg_id:242041 Sphingopyxis soli DCY34
FJ382554.1 gg_id:514081 Potentially pathogenic water and air stem cell transplant summer hospital shower ae
EU143356.1 gg_id:248554 Sphingopyxis sp. str. J24
FJ382356.1 gg_id:539068 Potentially pathogenic water and air stem cell transplant summer hospital shower ae
FJ382353.1 gg_id:510825 Potentially pathogenic water and air stem cell transplant summer hospital shower ae
Z73631.1 gg_id:6327 Sphingomonas sp str. RB2256
AB245343.1 gg_id:147540 Sphingopyxis ginsengisoli str. Gsoil 250
AB219940.1 gg_id:132488 Sphingosinicella microcystinivorans str. MDB2
EU703332.1 gg_id:384499 lakes on Eastern Tin Plateau freshwater lake altitude 4298 masl clone XZTSH2
EU431722.1 gg_id:559317 Troglobitic (Cansiliella) on specialized feeding apparatus calcium carbonate (moonmi
DQ087403.1 gg_id:128144 Alisphingobium solum str. KSL-125
AJ620201.1 gg_id:99158 Sphingomonas sp. str. PlS5
EU403958.1 gg_id:305626 Microbial septic tank effluent and soil biozone infiltrative surface clean water clone (
AJ303009.1 gg_id:52593 Novosphingobium lentum str. MT1
EU016180.1 gg_id:239608 Sphingomonas sp. str. S11-S-9
DQ366009.1 gg_id:152371 Dominant soils Marble Point and Wright Valley Victoria Land Antarctica soil clone 20
EU937972.1 gg_id:311613 Biogeochemistry Iron Oxidation Circumneutral Freshwater Habitat riparian iron oxidi
AY608604.1 gg_id:100015 Sphingomonas baekryungensis str. SW-150
GQ389106.1 gg_id:565345 quality deterioration drinking system during serious red water outbreak clone S60
FJ675209.1 gg_id:525875 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
DQ823172.1 gg_id:171409 Techniques Microbial Studies Oregon Caves National Monument Quad 3 on trail clo
FJ478653.1 gg_id:582012 species richness estimates obtained nearly and simulated pyrosequencing-generated
GQ389029.1 gg_id:570614 quality deterioration drinking system during serious red water outbreak clone J76
AF170744.1 gg_id:6263 Sphingomonas sp. str. QSSC5-6
FN397673.1 gg_id:426622 Blastomonas sp. str. AMV5
D16149.1 gg_id:6203 Sphingomonas sp str. SYK6
FJ801196.1 gg_id:555964 Investigation Water -DGGE and Clone Library Zoige Alpine Wetland clone ZWB3-13

FJ382563.1	575538	3374.3	3446.6	2252.3	4785.2	12965.3	7090.4
FJ382527.1	548468	2896.8	2723.7	1965.0	3753.1	12557.5	3930.8
FJ382548.1	567426	2785.4	2108.3	2250.2	3331.6	15172.5	4912.1
AY509242.1	104644	649.6	483.4	878.8	841.5	6708.6	888.3
EF028689.1	197687	7922.5	8072.2	7044.2	6706.5	20571.8	7813.9
GU201847.1	515215	9982.6	8850.3	11706.0	9784.3	16735.7	7622.7
AF131297.1	6328	1786.3	2050.9	3517.3	2221.9	9206.1	4123.8
EU464953.1	292322	7158.6	6088.3	5482.0	6975.6	17127.9	6944.8
AJ871278.1	114482	2331.4	2884.3	3140.7	2220.2	9031.0	5442.5
EU816422.1	346880	4463.9	3472.6	5009.4	3537.8	11902.8	5164.0
DQ112242.1	130329	3769.0	5227.4	4891.4	5097.3	13172.2	10569.0
FJ382493.1	549471	6831.4	6374.1	2989.3	6064.1	16738.9	8404.8
EF523589.1	222242	1036.0	886.8	1556.1	326.6	3676.2	2345.3
AY212804.1	81691	2254.2	2015.9	3759.1	3415.4	11356.6	3393.9
EU075217.1	242041	388.2	791.9	3985.5	2845.2	9307.5	2818.9
FJ382554.1	514081	4494.2	3588.0	4949.4	5502.1	15121.4	4600.9
EU143356.1	248554	1928.7	2603.5	7751.2	3393.6	13191.2	5941.9
FJ382356.1	539068	952.5	5266.6	370.6	534.3	9781.9	2532.5
FJ382353.1	510825	3436.3	3502.9	3614.9	2936.7	14209.5	4250.6
Z73631.1	6327	1712.5	1659.4	3293.7	2335.6	15719.2	4474.1
AB245343.1	147540	5891.0	6523.3	8950.6	7647.1	15797.4	7764.3
AB219940.1	132488	1328.7	1454.5	1278.5	1404.5	7848.0	2045.0
EU703332.1	384499	5820.8	6153.0	5433.5	5069.0	14138.2	9913.7
EU431722.1	559317	847.8	1071.6	1785.6	1023.9	5263.8	2045.6
DQ087403.1	128144	534.8	626.4	1076.0	711.7	7902.2	1658.0
AJ620201.1	99158	8450.3	6299.5	4729.1	4441.7	13143.8	8717.0
EU403958.1	305626	2986.1	4826.4	9583.4	4669.5	16410.4	7099.8
AJ303009.1	52593	1564.0	1503.7	9247.2	4140.7	4113.8	4147.7
EU016180.1	239608	2267.2	4350.2	10258.9	1456.1	5303.7	8723.4
DQ366009.1	152371	30.6	59.1	96.0	62.9	7125.4	314.6
EU937972.1	311613	1347.5	1467.6	3769.2	1183.3	6802.1	1544.5
AY608604.1	100015	693.5	682.0	952.7	763.8	6824.6	1901.7
GQ389106.1	565345	12352.6	10229.8	5392.9	9469.8	20531.2	12519.4
FJ675209.1	525875	5892.9	3056.0	5399.3	4421.6	7790.6	4218.2
DQ823172.1	171409	240.1	432.5	604.3	681.1	1549.2	2377.4
FJ478653.1	582012	742.8	1811.1	2593.8	2154.7	5769.5	6800.7
GQ389029.1	570614	6971.6	5466.5	5895.0	5454.9	15070.8	7378.2
AF170744.1	6263	494.2	231.6	40.7	84.0	214.8	307.6
FN397673.1	426622	3865.1	3417.1	6367.0	4420.1	7548.6	2878.7
D16149.1	6203	3725.2	3954.9	5666.5	4354.7	17369.9	7520.4
FJ801196.1	555964	9557.2	9008.2	9997.3	8282.0	19417.3	12987.9

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DQ395425.1 gg_id:155841 deep-sea octacoral clone ctg_CGOAA47
GQ500778.1 gg_id:536871 Surveys Biofilms and Sediments Mammoth Cave Karst Aquifers Bio-Sep beads conta
EU800678.1 gg_id:305644 It's all ranking aquatic Delaware Bay NJ clone 2C228842
EF688392.1 gg_id:238429 soil clone F6-154
DQ781320.1 gg_id:166587 Sphingopyxis sp. str. FR1087
EU104232.1 gg_id:349315 Evidence Comamonadaceae determinants settling performance activated sludge clo
EU276573.1 gg_id:361840 -DGGE and Approaches Analyze Effect Agricultural Practices on Soil agricultural soil c
FN421536.1 gg_id:549682 proteogenomics physiology phyllosphere Arabidopsis thaliana clone 14_A04
GU208467.1 gg_id:584947 Study on Sediment Dongping Lake sediment clone Fr1-15
AY167827.2 gg_id:77547 Sphingomonas sp. str. SAFR-042
GQ263416.1 gg_id:564561 Structure Simulated Level Waste Site simulated level waste site clone FW2_09B
GQ111232.1 gg_id:436152 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
EF522271.1 gg_id:222183 Endolithic Microbial Ecosystems Rocky Mountain endolithic sandstone clone FQSS05:
EU016177.1 gg_id:236085 Sphingomonas sp. str. S11-S-6
D13727.1 gg_id:6320 Sphingopyxis terrae str. IFO15098
AY921978.1 gg_id:113153 farm soil clone AKYG1729
GQ263560.1 gg_id:586875 Structure Simulated Level Waste Site simulated level waste site clone FW3_112C
GU479372.1 gg_id:527848 Sphingomonas sp. str. Sphing1
GQ500764.1 gg_id:577484 Surveys Biofilms and Sediments Mammoth Cave Karst Aquifers Bio-Sep beads conta
DQ269104.1 gg_id:190640 marine macro-alga surface clone DPC150
AM990821.1 gg_id:277792 Structure and functions coastal NW Mediterranean ecosystem sea water
AM697063.1 gg_id:220477 sequencing libraries indoor dust clone BF0002B013
EU137618.1 gg_id:267439 Bartonella-positive fleas: and assembly patterns Oropsylla hirsuta (prairie dog flea) C
EU196323.1 gg_id:238220 Sphingomonas sp. NP32
FJ889532.1 gg_id:564413 Sphingopyxis sp. str. SC022
EU573097.1 gg_id:278193 and Dependent Microbial Oil Reservoir North Sea Ekofisk oil field Norwegian sector c
GQ103823.1 gg_id:397122 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
DQ228401.1 gg_id:141916 microbial compositions two subglacial possible role microbes chemical weathering p
GQ264328.1 gg_id:582134 Structure Simulated Level Waste Site simulated level waste site clone WW2_159
EU564841.1 gg_id:261978 Sphingosinicella sp. str. CC-TBT-3
DQ129622.1 gg_id:138630 microarray level air two cities Texas urban aerosol clone AKIW980
D84626.2 gg_id:557168 Novosphingobium sp. str. S23435
EU133364.1 gg_id:256653 tallgrass prarie soil clone FFCH11613
EU404009.1 gg_id:336188 Microbial septic tank effluent and soil biozone infiltrative surface clean water clone (
AM697055.1 gg_id:217733 sequencing libraries indoor dust clone BF0002B005
EU642848.1 gg_id:278075 Sandarakinorhabdus sp. JC2488 str. JC2488; IMSNU 14142
AF281033.1 gg_id:39861 Zymomonas mobilis
AF498741.1 gg_id:58089 soil isolate Ellin359
GQ264264.1 gg_id:555926 Structure Simulated Level Waste Site simulated level waste site clone WW1_b69
AY913375.1 gg_id:113174 forest soil clone DUNssu168 (-7A) (OTU#169)
AB081581.3 gg_id:74124 Rhizobiales str. A48

DQ395425.1	155841	10122.0	8347.3	9028.4	8364.5	9737.4	10503.5
GQ500778.1	536871	3338.3	4304.9	8734.2	4931.9	9571.2	5060.8
EU800678.1	305644	859.1	1182.8	1854.3	1372.0	692.7	1208.1
EF688392.1	238429	5301.5	4665.0	5404.6	3807.3	13723.3	5855.4
DQ781320.1	166587	2549.8	2015.2	1016.4	1203.2	4622.3	2484.8
EU104232.1	349315	7961.1	8638.5	10816.6	6975.5	15362.3	10610.5
EU276573.1	361840	1166.1	1989.8	4678.9	1948.1	12182.2	5099.9
FN421536.1	549682	3537.5	4918.4	4477.1	4950.3	15547.4	9657.8
GU208467.1	584947	11724.9	13427.6	15514.0	9729.0	17384.5	11946.7
AY167827.2	77547	15.9	48.6	366.9	104.3	2698.6	395.0
GQ263416.1	564561	9986.8	10475.9	6363.9	10656.4	22908.0	13954.4
GQ111232.1	436152	3415.8	3252.2	4819.0	2993.6	17497.5	3923.0
EF522271.1	222183	2615.8	3277.9	4122.8	2885.7	8825.9	3910.9
EU016177.1	236085	438.8	771.1	783.9	1163.7	5493.3	2782.5
D13727.1	6320	2550.4	2742.5	2320.8	2693.9	10387.9	4352.2
AY921978.1	113153	5310.6	6368.7	5797.6	6043.0	16943.1	8699.9
GQ263560.1	586875	7787.1	7747.1	5526.1	11212.9	18852.4	11811.0
GU479372.1	527848	579.7	518.2	664.5	329.0	5964.8	904.7
GQ500764.1	577484	2554.4	2303.4	5634.4	1112.8	5451.8	3622.4
DQ269104.1	190640	4698.1	4009.6	2525.6	4163.8	7158.5	2160.0
AM990821.1	277792	6989.7	6018.2	6685.0	6456.6	11583.7	7316.0
AM697063.1	220477	3389.2	2464.6	6415.4	3200.2	13652.5	5185.0
EU137618.1	267439	2448.3	2568.7	2068.2	2465.8	7368.7	2885.9
EU196323.1	238220	2204.4	1901.2	1353.2	582.4	5121.4	2022.0
FJ889532.1	564413	271.1	498.4	106.8	166.6	1143.2	1216.3
EU573097.1	278193	6269.7	5417.8	6416.2	8424.6	12319.3	9588.3
GQ103823.1	397122	1571.5	1773.1	3466.3	1845.1	14213.7	4929.4
DQ228401.1	141916	5379.7	3209.1	7219.8	3802.3	15563.9	7171.6
GQ264328.1	582134	103.8	472.8	1721.7	482.8	6995.8	2471.5
EU564841.1	261978	3771.7	3099.7	4192.4	3386.7	6063.5	3248.1
DQ129622.1	138630	1164.5	1745.0	3971.3	1893.1	14893.8	5043.4
D84626.2	557168	3744.5	4295.0	8518.5	3207.5	7033.0	4602.7
EU133364.1	256653	3074.0	5218.5	6592.2	4736.8	11399.0	12589.7
EU404009.1	336188	2407.8	2291.6	6320.8	3556.0	6758.1	7568.5
AM697055.1	217733	3640.1	5214.0	8435.4	5002.9	15329.1	7348.0
EU642848.1	278075	265.7	182.6	544.0	160.5	690.9	371.1
AF281033.1	39861	46.8	86.9	169.5	193.3	674.9	70.1
AF498741.1	58089	6338.1	5211.4	2914.9	3717.5	6863.1	3794.8
GQ264264.1	555926	2400.0	2416.1	2447.8	2024.0	5223.0	3846.8
AY913375.1	113174	4380.5	6080.4	5952.3	3218.7	9342.8	6193.8
AB081581.3	74124	1924.8	3294.0	3748.1	2746.6	7050.2	6283.6

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GQ402583.1 gg_id:561842 Accessing microbial biodiversity and metabolic potential tropical -based approach p
EF032742.1 gg_id:188408 cyanobacterial mat in lava cave clone HAVOmat78
EF516517.1 gg_id:225609 grassland soil clone FCPP475
DQ395957.1 gg_id:156154 deep-sea octacoral clone ctg_CGOGA24
DQ659210.1 gg_id:223869 acid mine drainage clone DBS-Clone35
AY921822.1 gg_id:114227 farm soil clone AKYG1082
GQ346863.1 gg_id:544302 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
GQ340112.1 gg_id:582308 Prokaryotic Marathonas Reservoir Greece water column clone B07-10-BAC
EU801969.1 gg_id:315241 It's all ranking aquatic Chesapeake Bay MD clone 3C003352
GQ264178.1 gg_id:510799 Structure Simulated Level Waste Site simulated level waste site clone WW1_a43
EF018958.1 gg_id:210397 aspen rhizosphere clone Amb_16S_1472
EU907883.1 gg_id:346206 Identification hexahydro-135-trinitro-135-triazine (RDX)-degrading microorganisms v
EF019039.1 gg_id:209880 aspen rhizosphere clone Amb_16S_1594
AY234503.1 gg_id:111561 soil isolate Ellin5086
FJ466360.1 gg_id:542729 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea
DQ001641.1 gg_id:158741 Microbial seeps asphalt seep clone E101-25
EF032743.1 gg_id:177583 cyanobacterial mat in lava cave clone HAVOmat80
AB198460.1 gg_id:135284 termite gut wall fraction clone RsW01-024
FJ371976.1 gg_id:366881 feces adult twins and mothers; TS8 clone TS8_a04d02
FJ683333.1 gg_id:518552 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
AY916278.1 gg_id:113865 human rectum biopsy clone V326
AB234520.1 gg_id:149833 termite gut homogenate clone MgMjR-055
EU460122.1 gg_id:296361 mammals their gut microbes eastern black and white colobus feces clone COL_aai15
EU767216.1 gg_id:348521 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C2
EU939387.1 gg_id:325850 Fecal wild pygmy loris feces clone WF16S_04
GQ898126.1 gg_id:581652 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do
GQ448745.1 gg_id:553416 Microbiome neonatal calves: shedding microorganisms fecal clone calf784_10wks_g
EU472130.1 gg_id:288432 francois langur feces clone FL_1aaa01a11
FJ683799.1 gg_id:518042 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
GQ396986.1 gg_id:538635 Functional unvegetated perhumid recently-deglaciated soils do not correlate shifts
EF126229.1 gg_id:262336 Phototrophic microbial build laminated Fe-formations on Sulawesi Indonesia mesoph
AF234717.1 gg_id:46308 sludge clone S7
AF418951.1 gg_id:50466 USA: Colorado Fort collins Horsetooth Reservoir clone HTC6
EF516476.1 gg_id:225263 grassland soil clone FCPP524
FJ004770.1 gg_id:548087 Acidobacteria former agricultural bulk soil clone 32C1B
AF234689.1 gg_id:29952 sludge clone H6
CU925843.1 gg_id:538971 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
FJ517070.1 gg_id:540307 semiarid 'Tablas de Daimiel National Park' wetland (Central Spain) unravelled water c
EU332804.1 gg_id:361890 FACS assist identification TFO present aerobic enhanced biological phosphorus remo
EU871355.1 gg_id:343481 Genetic Bovine (Bos taurus) Rumen Thailand clone CF45
AB009205.1 gg_id:5067 rumen clone RFN49

GQ402583.1	561842	1106.7	2103.8	1171.7	1321.9	7334.8	5472.9
EF032742.1	188408	891.5	1884.6	1879.7	350.7	3346.4	2268.7
EF516517.1	225609	5093.0	5632.9	6853.6	5457.2	7185.4	6085.9
DQ395957.1	156154	394.2	550.7	702.9	640.8	5074.6	1187.3
DQ659210.1	223869	144.0	244.1	223.2	114.0	310.6	436.9
AY921822.1	114227	2647.5	1548.0	4937.1	3211.1	5461.8	6585.0
GQ346863.1	544302	5901.3	6486.6	7271.9	6129.5	8907.8	8846.3
GQ340112.1	582308	5746.9	7773.9	10311.3	4795.0	10202.5	10211.9
EU801969.1	315241	1419.0	3556.1	3411.7	1568.5	4202.3	3602.5
GQ264178.1	510799	5237.2	6887.4	9344.2	5252.2	6770.9	5506.6
EF018958.1	210397	813.2	761.6	2491.4	723.2	2608.0	1250.0
EU907883.1	346206	2869.7	2364.9	4512.4	2631.1	4806.8	3558.8
EF019039.1	209880	2615.8	3078.8	3551.9	1974.2	6341.7	7739.1
AY234503.1	111561	1195.0	2704.7	2285.5	2041.3	5587.3	2723.7
FJ466360.1	542729	327.3	293.6	547.2	328.1	580.4	304.3
DQ001641.1	158741	55.0	68.3	131.0	96.9	262.3	87.2
EF032743.1	177583	674.6	1275.3	971.3	324.9	1035.3	295.9
AB198460.1	135284	21.2	29.7	27.3	61.6	54.7	32.5
FJ371976.1	366881	140.6	245.6	404.4	200.8	1077.7	997.3
FJ683333.1	518552	683.0	1223.3	1910.4	1243.7	4673.0	3553.2
AY916278.1	113865	20.6	33.6	379.8	62.9	70.4	37.6
AB234520.1	149833	27.1	44.2	80.0	53.6	67.7	18.0
EU460122.1	296361	1984.3	1938.4	643.0	2427.3	4350.0	4805.9
EU767216.1	348521	9845.0	9921.3	9509.6	9840.3	11714.0	11278.4
EU939387.1	325850	9531.6	11626.1	5479.6	7210.6	8366.0	6935.9
GQ898126.1	581652	35.4	53.0	77.6	69.2	71.7	31.3
GQ448745.1	553416	347.9	320.4	840.9	323.0	303.4	339.0
EU472130.1	288432	6463.8	6431.3	4292.7	6818.1	5865.7	4995.0
FJ683799.1	518042	8844.4	10133.0	8381.7	9174.8	10405.7	9969.1
GQ396986.1	538635	327.2	446.8	1960.0	280.8	4161.2	650.7
EF126229.1	262336	3046.9	6987.0	6279.7	1214.1	8364.4	7540.3
AF234717.1	46308	4672.6	6057.0	10422.7	5968.2	11145.7	10471.0
AF418951.1	50466	9330.6	8925.4	9850.1	8644.0	15227.2	11244.4
EF516476.1	225263	1844.3	2756.9	3384.1	1689.6	5264.0	3456.1
FJ004770.1	548087	1354.4	1695.7	2615.0	3436.4	3220.1	2129.7
AF234689.1	29952	257.3	665.8	817.8	227.8	1837.7	411.9
CU925843.1	538971	8778.7	9165.9	5845.3	6083.7	11206.5	7649.3
FJ517070.1	540307	5649.8	6814.7	10285.6	4575.2	7453.1	6426.6
EU332804.1	361890	1867.2	2716.5	4497.2	2115.3	7961.5	8092.7
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AB009205.1	5067	1303.9	1178.0	730.2	684.1	5178.6	1578.1

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EU463527.1 gg_id:297362 domesticated horse feces clone horsem_aai95e02
EU461472.1 gg_id:294743 black rhinoceros feces clone RH_aaj90d02
FJ202882.1 gg_id:345859 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k
EU369125.1 gg_id:324513 libraries oyster shell clone MBIOS-09
FJ792144.1 gg_id:536627 Unexpectedly archaeal species shift between rare and dominant over thousand year
EF092222.1 gg_id:265205 Persistent Axinella corrugata Rhizobiales clone B255_A3
DQ446131.2 gg_id:170743 Surface Mucopolysaccharide Layer and Band Microbial Mat Black Band-Diseased Sid
EU328098.1 gg_id:278145 dynamics during bioremediation crude oil contaminated moderate saline soil clone Y
DQ395844.1 gg_id:153717 deep-sea octacoral clone ctg_CGOF052
GQ069773.1 gg_id:439353 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
EF540429.1 gg_id:225544 oil-shale semi-coke solid waste clone MK27b
EU835405.1 gg_id:323533 structure and quorum sensing reverse osmosis RO membrane biofilm clone 1T15
AB185560.1 gg_id:105599 rumen clone F23-G08
EU473569.1 gg_id:291358 Somali wild ass feces clone WA_aaa03a04
EU463505.1 gg_id:294146 domesticated horse feces clone horsem_aai95b08
FJ497287.1 gg_id:583714 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun
FJ628338.1 gg_id:589268 transition and zone within near-shore basin: brackish water anoxic fjord Nitinat Lake
FJ497527.1 gg_id:537810 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun
EF520416.1 gg_id:233001 structure lakes: what controls ? acid-impacted lake clone ADK-MOe02-77
EU131034.1 gg_id:250742 alkaline China coal mine soil clone SIP CM16
AY945893.1 gg_id:149766 Thauera and Azoarcus functionally important genera denitrifying quinoline-removal
AM930304.1 gg_id:535965 gradual cooling stage mass and its spatial composting clone SMG103
GQ028948.1 gg_id:381203 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw85
DQ337048.1 gg_id:146004 subsurface water clone EV818EB5CPSAJJ48
EU104207.1 gg_id:325441 Evidence Comamonadaceae determinants settling performance activated sludge clo
AF255630.1 gg_id:44677 EBPR sludge clone Ebpr9
AB294314.1 gg_id:213592 Microbial structure deep coal seem groundwater stream clone SWB03
AY957891.1 gg_id:114901 drinking water biofilm clone B1NR70D6
EF648097.1 gg_id:237878 dynamics during produced water treatment aerobic activated sludge clone HB108
EU801354.1 gg_id:309146 It's all ranking aquatic Chesapeake Bay MD clone 3C002620
GQ348734.1 gg_id:541547 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
FJ745192.1 gg_id:575540 Transporter genes expressed coastal response dissolved organic carbon surface wate
AB200296.1 gg_id:113913 lab-scale sequencing batch reactor clone UTFS-OF08-d36-35
CU466788.1 gg_id:342450 Evry wastewater treatment plant anoxic basin clone
AY662029.1 gg_id:136114 uranium-contaminated groundwater clone 300G-A04
EF516974.1 gg_id:223237 grassland soil clone FCPP392
EF032738.1 gg_id:198250 cyanobacterial mat in lava cave clone HAVOmat41
AJ536878.1 gg_id:78776 uranium mining waste pile soil sample clone JG30-KF-AS50
EU982844.1 gg_id:335424 Rhodobium sp. str. 6
EU104244.1 gg_id:325439 Evidence Comamonadaceae determinants settling performance activated sludge clo

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FJ792144.1	536627	4029.7	5912.8	8247.9	5453.4	10745.2	7108.4
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FJ497287.1	583714	3581.5	2751.5	4047.6	2571.4	3287.9	4765.5
FJ628338.1	589268	45.2	78.8	162.3	70.3	82.9	106.7
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EF520416.1	233001	72.0	130.6	623.0	170.7	340.8	564.7
EU131034.1	250742	958.7	1208.2	1830.5	1146.8	3561.0	2674.9
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EU982844.1	335424	777.1	1577.5	1355.8	718.3	2007.6	3483.6
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EU283395.1 gg_id:249410 consecutively aerated submerged treating domestic wastewater activated sludge m
AY957890.1 gg_id:114903 drinking water biofilm clone B1NR70D5
DQ889887.1 gg_id:166172 natural product producing octocoral Erythropodium caribaeorum clone EC154
DQ856551.1 gg_id:255188 intestinal microflora Chinese mitten crab (Eriocheir sinensis) clone C3M
NC_010645.1 gg_id:281797 Bordetella avium str. 197N
AY946288.1 gg_id:114767 Achromobacter xylosoxidans 48
EU862292.1 gg_id:353739 Achromobacter ruhlandii str. jql-9
EF465456.1 gg_id:215887 Achromobacter xylosoxidans SF2
AY081976.1 gg_id:68623 atrazine-catabolizing microbial presence methanol clone KRA30+05
DQ414679.1 gg_id:207934 Achromobacter xylosoxidans
EU442188.1 gg_id:290452 Achromobacter xylosoxidans str. IdW
EU082170.1 gg_id:249176 Bordetella hinzii str. AU12584
AY081977.1 gg_id:68624 atrazine-catabolizing microbial presence methanol clone KRA30+06A
EF102817.1 gg_id:247706 Achromobacter xylosoxidans str. N-5-20
EU275351.1 gg_id:251976 Achromobacter xylosoxidans str. CONC18
EU308119.1 gg_id:240269 Achromobacter xylosoxidans str. WT1
AY170848.1 gg_id:78208 Achromobacter spanius str. LMG 5911
EU622534.1 gg_id:278800 Achromobacter denitrificans str. SPQ08
AY468369.1 gg_id:100569 Achromobacter xylosoxidans str. DTgA
AJ880765.1 gg_id:112594 Alcaligenes faecalis SLF4
FJ810080.1 gg_id:536139 Achromobacter denitrificans str. 22426
AJ491840.1 gg_id:78128 Achromobacter xylosoxidans str. A2
DQ104979.1 gg_id:136398 Achromobacter xylosoxidans str. JS1-1
EF555454.1 gg_id:230934 Achromobacter xylosoxidans str. GIST-NW7
EU434544.1 gg_id:268968 Achromobacter xylosoxidans str. b62
GU253989.1 gg_id:585153 Achromobacter xylosoxidans str. 2006
EU082175.1 gg_id:257320 Bordetella hinzii str. AU13283
AY170847.1 gg_id:78362 Achromobacter insolitus str. LMG 6003
AF531768.1 gg_id:55338 Achromobacter xylosoxidans
EF623840.1 gg_id:235810 Achromobacter xylosoxidans str. GIST-MRP66
EU360470.1 gg_id:268783 Achromobacter xylosoxidans str. B3A
DQ174269.1 gg_id:139258 Achromobacter xylosoxidans
DQ104980.1 gg_id:136390 Achromobacter xylosoxidans str. JS 1-2
AJ551119.1 gg_id:94243 Achromobacter xylosoxidans mp5
EU195874.1 gg_id:241186 Alcaligenes sp. str. SBW1
EF555452.1 gg_id:233948 Achromobacter xylosoxidans str. GIST-DRP2
AJ875020.1 gg_id:111930 Achromobacter xylosoxidans str. A8
EU006066.1 gg_id:246414 Achromobacter xylosoxidans str. SL06500
AF205370.1 gg_id:49793 Achromobacter ruhlandii str. QSSC3-1
EU877076.1 gg_id:311931 Achromobacter xylosoxidans str. EC3_3502

AB089085.1	77616	101.3	187.9	111.4	146.6	372.6	157.0
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AY957890.1	114903	80.6	177.0	489.7	185.2	1412.3	653.9
DQ889887.1	166172	20.7	43.7	56.3	52.4	78.7	53.8
DQ856551.1	255188	7494.3	8746.5	8821.0	8291.9	9989.5	8618.6
NC_010645.1	281797	7801.6	7045.9	11528.9	14116.6	6299.4	6192.0
AY946288.1	114767	2157.1	2099.6	4269.4	5753.0	2727.3	3651.5
EU862292.1	353739	3780.5	4464.7	5330.3	3917.9	3237.2	3858.8
EF465456.1	215887	5009.5	4789.2	4793.3	5474.9	5609.3	5165.6
AY081976.1	68623	9942.4	4035.4	11252.5	7475.3	2534.0	2445.6
DQ414679.1	207934	6921.1	4611.8	7539.9	7719.9	4342.0	3504.2
EU442188.1	290452	9534.7	3413.2	5562.8	10506.6	1909.5	3478.3
EU082170.1	249176	2379.4	2068.1	3402.5	4206.6	1199.4	2065.3
AY081977.1	68624	4947.9	2959.0	3957.7	6203.4	1534.5	3230.6
EF102817.1	247706	6614.9	6047.7	4201.9	8538.6	7162.3	6376.4
EU275351.1	251976	2677.6	2721.5	3380.6	3207.1	883.3	2396.5
EU308119.1	240269	1451.3	1528.3	1726.3	3792.4	996.6	1876.7
AY170848.1	78208	1468.8	1255.9	2944.3	2578.1	825.3	1325.9
EU622534.1	278800	827.3	706.5	1123.3	2634.1	207.2	314.8
AY468369.1	100569	4656.2	3705.2	4779.8	6023.3	2425.4	4144.9
AJ880765.1	112594	1248.2	1095.2	2272.5	2128.6	936.4	1532.2
FJ810080.1	536139	1561.6	1645.4	2430.1	4044.1	1734.2	2981.3
AJ491840.1	78128	1164.8	1436.1	1668.9	2264.3	1859.0	1972.5
DQ104979.1	136398	1725.6	1850.0	2480.8	4294.9	1376.9	2224.2
EF555454.1	230934	19644.6	17791.1	5155.3	13697.3	16898.8	19261.4
EU434544.1	268968	2443.9	2261.6	4223.8	3316.2	3619.4	2452.1
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AY170847.1	78362	3900.5	3764.3	5859.1	8165.4	4218.6	4747.9
AF531768.1	55338	1422.0	1274.6	2684.7	3875.6	809.0	826.6
EF623840.1	235810	12959.1	11112.3	3331.3	9715.4	11900.3	11041.2
EU360470.1	268783	1475.6	1553.4	1875.2	3635.3	1259.9	2294.0
DQ174269.1	139258	1285.2	1378.4	1540.0	2812.9	1023.0	1665.0
DQ104980.1	136390	2174.2	2239.2	4186.9	5152.0	2207.0	2606.1
AJ551119.1	94243	20803.0	18913.6	12654.7	14989.7	28221.9	18009.9
EU195874.1	241186	1237.4	1298.9	1597.3	2990.9	960.3	1856.8
EF555452.1	233948	1238.1	1071.6	2343.6	2489.0	586.5	1114.1
AJ875020.1	111930	324.7	355.3	431.7	1199.9	294.7	430.1
EU006066.1	246414	4558.1	3580.1	4549.2	6705.6	2708.5	4908.5
AF205370.1	49793	2093.6	2563.6	5333.4	3237.9	3555.5	3019.3
EU877076.1	311931	13745.4	14041.4	8373.2	11817.3	15106.5	12277.3

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AJ560627.1 gg_id:101164 Achromobacter xylosoxidans wp23
DQ917890.1 gg_id:226210 Microbial profiles bleached and wild-type Muricea elongata Achromobacter clone M
AY753652.1 gg_id:107787 Achromobacter xylosoxidans str. VH070857
AJ277798.1 gg_id:38214 Bordetella trematum str. DSM 11334 (T)
GQ409968.1 gg_id:558854 Achromobacter xylosoxidans
EF555458.1 gg_id:228554 Achromobacter xylosoxidans str. GIST-SW9
EU195868.1 gg_id:254902 Alcaligenes sp. str. BGW3
AJ880764.1 gg_id:112574 Achromobacter xylosoxidans SUF22
EF623832.1 gg_id:257616 Achromobacter xylosoxidans str. GIST-MRS3
AB234302.1 gg_id:139385 Alcaligenes sp. str. TS-MOSK-6
FJ169468.1 gg_id:574736 Achromobacter xylosoxidans str. adx-3
EU150134.1 gg_id:238226 Achromobacter marplatensis str. B2
AJ534850.1 gg_id:78940 Alcaligenes sp. DW104
AY866407.2 gg_id:111932 Alcaligenes faecalis str. RS-19
FJ796451.1 gg_id:538518 Achromobacter xylosoxidans str. IMER-B4-13
EF446888.1 gg_id:203950 Alcaligenes faecalis str. SRR-11
EF555457.1 gg_id:228065 Achromobacter xylosoxidans str. GIST-YK21
AB371725.1 gg_id:239536 Bordetella hinzii str. 3224
AJ491846.1 gg_id:78111 Achromobacter xylosoxidans str. H
EF035138.1 gg_id:182422 Achromobacter xylosoxidans str. L2-2
FN433031.1 gg_id:537770 Alcaligenes faecalis CCM5B
EU827475.1 gg_id:345476 Achromobacter xylosoxidans str. TFD47
EU195864.1 gg_id:250159 Alcaligenes sp. str. ACS1
EU221508.1 gg_id:332634 Trachelomonas armata str. ACOI 1323
AY221606.1 gg_id:89748 metal and hydrocarbon contaminated soil clone HN4-32
AJ491844.1 gg_id:77844 Achromobacter xylosoxidans str. E
EF623837.1 gg_id:256643 Achromobacter xylosoxidans str. GIST-MRS5
EF555450.1 gg_id:231036 Achromobacter xylosoxidans str. GIST-DA1
EU652103.1 gg_id:273424 Achromobacter xylosoxidans str. ybc-11
AF430122.1 gg_id:56470 Alcaligenes sp. str. VKM B-2263 dcm6
FJ224081.1 gg_id:344427 Achromobacter denitrificans str. BMB-N6
DQ466568.1 gg_id:156740 Achromobacter xylosoxidans str. B8L
EU082160.1 gg_id:242404 Bordetella avium str. AU10563
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DQ346470.1 gg_id:154579 during composting libraries compost clone 1B38
AM500784.1 gg_id:563255 proof spatial heterogeneity hot composting clone E51
FJ658470.1 gg_id:512527 Metalworking Fluids and Aerosols Metallurgy Plant metalworking aerosol clone Winte
EU931441.1 gg_id:516182 examined methods chronic venous leg ulcer clone CONR19
AJ133493.2 gg_id:6859 Alcaligenes sp. CCUG 36768
DQ346449.1 gg_id:153898 during composting libraries compost clone 1B17
EU167972.1 gg_id:273945 Pusillimonas sp. str. 21-13

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AJ277798.1	38214	3396.3	3585.1	5858.5	5218.3	2321.3	3287.6
GQ409968.1	558854	1802.2	1929.2	2482.3	4610.5	1582.6	2718.9
EF555458.1	228554	21297.0	18354.1	14303.0	17547.3	23883.3	18412.0
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EF623832.1	257616	8966.2	7875.5	7060.0	10021.7	7318.5	8484.3
AB234302.1	139385	1427.9	1557.0	2461.5	2839.3	1419.3	2474.1
FJ169468.1	574736	1736.9	1716.6	2281.1	3960.7	1687.3	2646.0
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AJ534850.1	78940	2607.9	2765.4	3167.7	3526.2	1416.7	2455.6
AY866407.2	111932	245.4	307.5	148.8	390.0	147.0	48.0
FJ796451.1	538518	758.2	823.8	447.3	1240.3	442.3	407.0
EF446888.1	203950	3841.8	3324.6	3511.9	5404.5	2241.0	3504.4
EF555457.1	228065	9712.3	5397.7	7825.6	10862.1	3661.2	5385.4
AB371725.1	239536	3511.4	3219.1	4560.8	5651.8	2189.8	3509.6
AJ491846.1	78111	9362.1	7183.8	5986.9	8957.3	8807.6	8375.8
EF035138.1	182422	3144.4	3120.3	1728.5	4866.6	1437.2	2634.2
FN433031.1	537770	3224.2	3018.8	4764.9	7141.2	1891.3	3216.5
EU827475.1	345476	374.4	431.3	299.5	770.8	133.9	103.2
EU195864.1	250159	9107.6	10378.5	23700.4	14487.8	18587.5	11823.3
EU221508.1	332634	11613.1	8004.6	8511.8	11157.9	6704.5	7745.8
AY221606.1	89748	941.2	863.5	397.0	2313.7	474.7	733.2
AJ491844.1	77844	10026.8	10063.5	6957.9	10474.0	13371.0	8298.3
EF623837.1	256643	390.7	395.2	623.7	1589.5	317.2	703.6
EF555450.1	231036	13700.4	12018.1	9170.2	12112.5	11555.6	12154.9
EU652103.1	273424	2190.4	2024.8	3697.2	4126.7	1333.2	2420.5
AF430122.1	56470	1149.8	1547.4	2291.4	3948.6	1742.2	6018.8
FJ224081.1	344427	1009.2	1832.8	1895.9	1191.4	497.4	962.6
DQ466568.1	156740	3133.5	2970.2	2921.9	6174.3	1685.9	3065.5
EU082160.1	242404	3594.6	3235.9	5219.6	8397.2	1450.8	3085.2
DQ001156.1	122410	1364.8	1626.8	5202.9	4864.6	655.3	1982.7
DQ346470.1	154579	679.9	862.6	727.3	846.3	243.2	458.2
AM500784.1	563255	9524.6	9611.9	11328.6	9358.4	9924.4	9405.0
FJ658470.1	512527	7573.2	6980.9	8746.3	9867.2	7783.2	7704.2
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AJ133493.2	6859	27.1	26.3	37.7	53.5	70.0	69.3
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o__Burkholderiales	f__Alcaligenaceae

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s__unclassified	14777
s__Pelistega europaea	15262
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s__unclassified	14740
s__unclassified	15818
s__Sutterella parvirubra	15407
s__unclassified	14519

FJ674784.1 gg_id:518282 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
AB188125.1 gg_id:132621 Alcaligenes latus str. IAM 12599
EF032746.1 gg_id:185782 cyanobacterial mat in lava cave clone HAVOmat12
AY435511.1 gg_id:107880 propane-sparged ground water well C4 clone MAFB-C4-17
FJ535109.1 gg_id:557756 microbial colonizing walls Karstic Slovenia cave wall biofilm clone 3PJM33
AB487742.1 gg_id:589854 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNSR0
AB486168.1 gg_id:579191 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC
AJ867848.1 gg_id:169526 Leptothrix sp. B2
AY493948.1 gg_id:136596 Fingerprinting aggregates soil clone 11
AB378584.1 gg_id:260565 dominate denitrification nitrate- succinate-ammended stable istope probing 13C fra
AY466115.1 gg_id:101912 Bordetella holmesii G6128
EU082165.1 gg_id:244327 Bordetella petrii str. AU11495
DQ132877.1 gg_id:137970 Bordetella sp. str. QJ9-6
EU082157.1 gg_id:251205 Bordetella sp. str. AU9919
DQ256466.1 gg_id:142658 Bordetella sp. str. 1-3
EU835434.1 gg_id:346019 structure and quorum sensing reverse osmosis RO membrane biofilm clone 2B04
EU643523.1 gg_id:280840 Bordetella bronchiseptica str. Bb5
AB255107.1 gg_id:171796 corroded concrete clone SC-127
EU603444.1 gg_id:263781 Bordetella petrii str. PTG4-17
AJ249861.1 gg_id:21781 Bordetella petrii str. DSM 12804 Se-1111R
EU082151.1 gg_id:240317 Bordetella sp. str. AU7206
AB039335.1 gg_id:37958 Bordetella sp. str. M1-6
E06073.1 gg_id:25458 Bordetella bronchiseptica
AY594190.1 gg_id:126199 Bordetella ansorpii str. SMC-8986
AF142326.1 gg_id:6889 Bordetella pertussis str. Tohama; CIP 81.32
AF366577.1 gg_id:49946 Bordetella parapertussis str. B24
GQ480840.1 gg_id:541437 Bordetella petrii str. B1
EU000383.1 gg_id:250883 Bordetella sp. str. BK-52
FJ969842.3 gg_id:445459 Bordetella parapertussis str. HT200
AJ005447.1 gg_id:6845 Alcaligenes defragrans str. 54Pin
AB195160.1 gg_id:108771 Alcaligenes defragrans str. PD-16
Y12639.1 gg_id:6856 Denitrobacter permanens
EF205259.1 gg_id:189889 Alcaligenes sp. 'TJOPY2 (-I)' str. TJOPY2 (-I)
AF227163.1 gg_id:71251 Oligella urethralis str. ATCC17960
AJ251912.1 gg_id:35834 Oligella ureolytica str. LMG 6519
AF190911.1 gg_id:6840 Pelistega europaea str. LMG15725
FN421876.1 gg_id:594220 proteogenomics physiology phyllosphere clover clone 2_F01
EU583723.1 gg_id:263890 Pigmentiphaga sp. str. JSM 061001
EU170477.1 gg_id:238547 Pigmentiphaga sp. str. Zn-d-2
AB300989.1 gg_id:272661 Sutterella parvirubra str. YIT 11816 (= JCM 14724 = DSM 19
GQ033291.1 gg_id:455791 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw

FJ674784.1	518282	2030.6	2391.7	2050.1	2522.2	354.5	711.9
AB188125.1	132621	12710.5	11586.1	11556.4	16176.9	7997.4	9984.9
EF032746.1	185782	2882.7	3571.0	3015.7	3787.7	2714.5	4137.5
AY435511.1	107880	7467.5	8343.8	5865.3	7165.7	2795.2	5698.7
FJ535109.1	557756	2856.1	2967.9	3955.9	5671.3	2997.7	2982.1
AB487742.1	589854	4622.6	4726.4	5962.1	5534.7	5665.8	6783.9
AB486168.1	579191	10456.0	11009.1	13966.7	13437.5	5422.9	8602.9
AJ867848.1	169526	2957.1	1847.3	1129.6	4535.5	1966.2	2707.5
AY493948.1	136596	8594.6	8840.3	6797.0	8487.9	9988.2	9902.2
AB378584.1	260565	9103.7	10441.8	12307.7	10220.4	5421.2	8378.0
AY466115.1	101912	4551.9	5060.4	7236.9	7699.0	4119.9	6152.5
EU082165.1	244327	5941.8	4944.4	5511.0	7969.9	3982.5	5795.5
DQ132877.1	137970	7403.1	5667.8	4324.4	8243.7	2541.2	3990.7
EU082157.1	251205	7302.5	5288.2	6506.8	8360.0	3262.0	3428.9
DQ256466.1	142658	5047.6	4302.4	8342.4	8421.9	5579.1	5029.9
EU835434.1	346019	9854.6	7235.0	12082.4	12326.5	5968.3	9894.1
EU643523.1	280840	3151.7	3173.6	4999.1	5820.4	2020.2	3789.3
AB255107.1	171796	3816.9	4495.8	8602.2	6293.6	4039.7	4720.7
EU603444.1	263781	4126.2	5340.8	8131.6	5905.1	4572.3	6412.2
AJ249861.1	21781	6040.6	4201.6	3779.7	7590.5	2046.0	2758.7
EU082151.1	240317	5021.4	3350.9	5033.9	6562.2	1626.3	2956.0
AB039335.1	37958	6331.8	5903.7	8224.6	11074.4	4596.6	6484.4
E06073.1	25458	7599.3	7287.6	6800.1	7105.9	5069.8	5291.1
AY594190.1	126199	1459.4	1564.7	2590.3	3598.8	1728.6	5073.5
AF142326.1	6889	10504.0	8564.1	6390.1	11807.9	7630.6	11916.9
AF366577.1	49946	3203.5	3212.6	4322.2	5899.0	2335.7	4003.8
GQ480840.1	541437	5489.8	4450.3	4513.2	6659.8	3270.1	4410.1
EU000383.1	250883	2526.6	2266.6	4349.9	5197.7	2309.5	3845.8
FJ969842.3	445459	11027.8	10476.9	7112.6	12276.4	7145.9	10000.4
AJ005447.1	6845	827.7	1158.1	3607.0	2536.2	723.6	589.3
AB195160.1	108771	2209.6	1692.2	4435.2	3636.1	936.4	1104.4
Y12639.1	6856	4141.0	3562.6	5879.7	4538.0	2315.8	3176.0
EF205259.1	189889	3003.9	3237.0	4278.1	4665.1	3633.9	1745.9
AF227163.1	71251	3458.6	3250.1	2255.5	4190.4	2363.9	4491.1
AJ251912.1	35834	9341.7	6159.9	6957.6	10298.6	3890.0	6883.8
AF190911.1	6840	9369.9	5363.4	7614.8	10737.4	4272.1	5231.3
FN421876.1	594220	4639.3	4294.9	3764.3	7483.6	2446.7	4212.7
EU583723.1	263890	6062.4	6191.7	6327.2	8497.5	7179.7	6853.1
EU170477.1	238547	4195.9	7041.7	8700.7	7654.1	4466.8	6971.1
AB300989.1	272661	1504.9	2608.5	3573.6	3009.6	1829.0	1833.6
GQ033291.1	455791	1228.9	2173.1	2114.6	1354.1	2799.6	1273.0

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EF400872.1 gg_id:213646 human fecal clone SJTU_D_02_65
AJ832129.1 gg_id:181656 Sutterella morbirenis str. CCUG 49335
EU532008.1 gg_id:271525 Predominant role host genetics controlling gut microbiota FMF remission stool clone
EU009806.1 gg_id:254552 intestinal microbiota domestic and wild turkeys turkey cecum clone WTB_D10
EU009787.1 gg_id:245510 intestinal microbiota domestic and wild turkeys turkey cecum clone DTB_T27
AB491209.1 gg_id:547221 Parasutterella sp. str. YIT 12071
EU767287.1 gg_id:339461 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C2
GQ011110.1 gg_id:498556 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
AJ566849.1 gg_id:104793 Sutterella stercoricanis str. CCUG 47620
GQ031994.1 gg_id:445073 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw1
EU767511.1 gg_id:322193 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C2
EU763570.1 gg_id:319660 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A4
EF071208.1 gg_id:176809 library survey and quantitative measurement major mucosa- IBD human colonic muc
AY981032.1 gg_id:126136 human rectum mucosal biopsy clone V241
FJ368987.1 gg_id:358132 feces adult twins and mothers; TS4 clone TS4_a02h09
EU767098.1 gg_id:345647 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1
DQ795867.1 gg_id:196501 human fecal clone RL245_aai83f07
NR_024915.1 gg_id:540774 Taylorella asinigenitalis str. UCD-1; ATCC 700933
AB200410.1 gg_id:112165 Taylorella equigenitalis str. Aus4
AJ864470.1 gg_id:109028 Tetrathiobacter kashmirae str. WT001
AJ864472.1 gg_id:109030 Tetrathiobacter kashmirae str. 445C
AJ864474.1 gg_id:109032 Tetrathiobacter kashmirae str. WPT
AJ864473.1 gg_id:109031 Tetrathiobacter kashmirae str. WGT
AJ864471.1 gg_id:109029 Tetrathiobacter kashmirae str. 445A
X86589.1 gg_id:6882 Alcaligenes sp str. 15-62
AY880023.1 gg_id:111634 Alcaligenes monasteriensis str. DPN7
X86584.1 gg_id:6881 Alcaligenes sp str. 05-51
AM944735.1 gg_id:323924 Advenella incenata 4
DQ469586.1 gg_id:157497 Alcaligenes monasteriensis str. Ac2-VH
X86580.1 gg_id:6833 Alcaligenes sp str. 05-36
X86590.1 gg_id:6883 Alcaligenes sp str. 30-68
AY569458.1 gg_id:107606 Advenella incenata str. R-16599
GQ203113.1 gg_id:558099 Ochrobactrum pseudogrignonense str. 21-6PIN
AM944734.1 gg_id:348042 Advenella incenata str. CCUG 45225
EU447156.1 gg_id:273668 Tetrathiobacter kashmirensis str. CA1
AY622228.1 gg_id:106744 subsurface soil clone C-CG17
FJ477679.1 gg_id:511551 Bordetella sp. HU-1 str. 1
U82826.1 gg_id:6846 Alcaligenes sp. str. NKNTAU
AY792261.1 gg_id:120103 Humic Lake clone CrystalBog1G5
EU801712.1 gg_id:309818 It's all ranking aquatic Chesapeake Bay MD clone 3C003072
EU703295.1 gg_id:466157 lakes on Eastern Tin Plateau polysaline lake altitude 3204 masl clone XZQH78

EF400872.1	213646	445.5	721.1	940.9	768.3	219.5	228.5
AJ832129.1	181656	43.2	45.5	28.9	52.0	59.9	29.8
EU532008.1	271525	4246.9	4448.0	6125.9	5626.1	4373.2	4163.2
EU009806.1	254552	12045.5	10655.3	7349.3	11523.8	11407.0	9812.4
EU009787.1	245510	4713.8	4162.6	5810.7	6245.2	3133.0	4949.8
AB491209.1	547221	37.2	69.6	56.9	91.9	107.3	69.2
EU767287.1	339461	8100.6	7167.7	11812.2	8645.1	8500.7	8846.3
GQ011110.1	498556	8149.4	7121.5	9625.3	9163.1	11279.0	11925.4
AJ566849.1	104793	4546.2	5066.7	8872.4	5712.0	5178.9	6620.4
GQ031994.1	445073	5418.4	5441.9	3744.0	5850.5	9836.8	8334.6
EU767511.1	322193	7057.4	6762.8	11643.0	7222.4	11310.2	9894.9
EU763570.1	319660	9894.7	12371.5	13939.7	9683.4	18264.6	13449.2
EF071208.1	176809	855.5	899.6	2080.3	1631.4	1132.6	2550.8
AY981032.1	126136	4760.2	3433.2	4945.3	9594.8	3484.7	4679.3
FJ368987.1	358132	5093.7	6989.3	7802.6	5767.8	10700.2	11211.7
EU767098.1	345647	8828.6	9692.0	8226.8	8930.2	8407.1	9268.1
DQ795867.1	196501	9041.1	8040.5	4670.1	9440.5	10066.1	9361.4
NR_024915.1	540774	11135.0	6989.8	12997.4	12965.9	8358.0	8263.2
AB200410.1	112165	9203.6	5213.9	14639.7	11562.6	8133.0	8587.8
AJ864470.1	109028	6327.4	6034.4	8511.6	9261.5	5108.0	6217.7
AJ864472.1	109030	16824.0	17517.8	13834.6	16360.2	16663.4	16322.6
AJ864474.1	109032	7379.7	7034.5	8373.2	10026.7	6192.8	7228.5
AJ864473.1	109031	13514.9	12249.1	8619.7	15044.2	8549.2	10175.7
AJ864471.1	109029	6603.3	6624.6	5316.8	9132.1	2702.2	5322.4
X86589.1	6882	4998.1	4773.8	6590.9	7600.9	3781.2	5271.5
AY880023.1	111634	1789.6	2228.0	5604.7	4160.8	2926.9	2509.2
X86584.1	6881	5226.2	5287.2	5932.9	7823.6	3112.1	4666.8
AM944735.1	323924	5698.1	4667.3	8302.5	7522.1	3730.6	6039.1
DQ469586.1	157497	6476.2	7169.6	6407.8	9926.2	7354.2	6052.9
X86580.1	6833	5557.9	5623.0	6438.8	8395.6	3840.1	5645.4
X86590.1	6883	6342.7	6260.3	6468.7	8656.0	4400.8	5809.2
AY569458.1	107606	6369.7	6219.9	8924.6	9255.1	5786.5	6868.4
GQ203113.1	558099	5542.3	5341.9	8283.7	8971.7	4560.7	6447.4
AM944734.1	348042	6934.7	6228.3	9573.5	9716.3	4718.0	6895.6
EU447156.1	273668	5307.5	5283.7	7293.9	8315.6	4027.8	5750.8
AY622228.1	106744	6013.3	5820.6	8558.0	7647.4	4514.1	4889.0
FJ477679.1	511551	5471.2	5022.3	6187.0	9328.2	3642.2	4444.1
U82826.1	6846	8315.9	5603.0	4941.3	8069.1	1392.5	2128.6
AY792261.1	120103	10099.4	10077.4	15459.5	15581.4	14112.3	11687.1
EU801712.1	309818	11665.0	7600.9	17915.3	17807.8	7087.5	8850.2
EU703295.1	466157	4656.2	4568.6	6419.0	7221.0	5010.4	4592.2

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AB166879.1 gg_id:100294 Alcaligenes sp. str. Ho-11
DQ346505.1 gg_id:152918 during composting libraries compost clone 2B21
EF603941.1 gg_id:230030 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
FM253637.1 gg_id:315961 Rock gold mine unusually microbial biofilm clone B01-2
EF097495.1 gg_id:194862 mouse cecum clone SWPT19_aaa03d11
AY921968.1 gg_id:112764 farm soil clone AKYG1661
AY986009.1 gg_id:127098 human stool clone D320
EF405056.1 gg_id:215097 human fecal clone SJTU_G_07_39
GQ254282.1 gg_id:540496 Bordetella sp. str. H12
AY662006.1 gg_id:137438 uranium-contaminated groundwater clone 015B-B03
DQ824015.1 gg_id:189076 human fecal clone RL204_aaj58b08
AB246799.2 gg_id:150109 Alcaligenes sp. str. R-3
EU510311.1 gg_id:273356 cecal contents Mus musculus strain C57BL/6J; WD3 clone WD3_aak04e08
AY792260.1 gg_id:119586 Humic Lake clone CrystalBog1E9
DQ905687.1 gg_id:165322 human fecal clone 014C-G4
FJ973586.1 gg_id:384641 Periodic sulfide irruptions impact microbial structure and hypersaline lake water colu
FJ477590.1 gg_id:586368 gut symbionts are tightly linked herbivory ants whole extracted single ant clone 86a
AJ005449.1 gg_id:6852 Alcaligenes defragrans str. 62Car
EF632938.1 gg_id:253486 Unique microbial contrasting aquatic altitude Andean Altiplano (northern Chile) fresh
AB259961.1 gg_id:160887 Burkholderia sp. str. Yoon-02
AJ575701.1 gg_id:95883 lake water enrichment clone NE78
FJ672653.1 gg_id:528864 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface
DQ466075.1 gg_id:160810 Pusillimonas terrae
EF405240.1 gg_id:208210 human fecal clone SJTU_G_04_82
AJ786800.1 gg_id:108077 Alcaligenes sp. R-21939
EU888003.1 gg_id:303810 Microbial structure hydrolytic stage two-stage anaerobic digestion grass silage leach
AY238499.1 gg_id:92793 Alcaligenes sp. str. 92
FJ901002.1 gg_id:547998 Polymorphism microbial reservoirs water cut stage oil field clone G-51
AY993322.1 gg_id:130981 mouse cecum clone C21_o12
EU887771.1 gg_id:339734 and RFLP anaerobes main Nisargruna biogas plant anaerobic digester clone 2SN
FJ675537.1 gg_id:526614 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface
EF096018.1 gg_id:189188 mouse cecum clone lean2_aaa02b05
FJ960346.1 gg_id:541465 bottlenose dolphin upper respiratory tract blowhole clone D9A4_244
EF175378.1 gg_id:174707 Castellaniella sp. 7.5A2
FJ880692.1 gg_id:404082 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet;
AJ318125.1 gg_id:26755 Waste-gas biofilter clone BIfciii38
EU511968.1 gg_id:273822 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_aak12a12
L29265.1 gg_id:6860 Blastocrithidia culicis Endosymbiont
EF672088.1 gg_id:256466 Pusillimonas sp. str. DCY25T
DQ799851.1 gg_id:187938 human fecal clone RL182_aah34h10
EF471693.1 gg_id:258429 Fast Screening and Estuarine Operon Libraries whole surface water Chesapeake Bay

AB166879.1	100294	3387.5	2093.8	4008.1	6609.9	1373.7	1720.6
DQ346505.1	152918	6899.7	7226.6	7475.1	9440.8	6669.7	8958.8
EF603941.1	230030	5581.1	4540.1	5049.8	2864.3	3658.0	5717.2
FM253637.1	315961	3717.6	4777.4	1042.1	3630.4	4785.2	5221.2
EF097495.1	194862	1504.2	1055.6	579.3	4492.8	872.0	1739.9
AY921968.1	112764	6072.9	4764.0	9476.7	8612.7	3553.3	4064.2
AY986009.1	127098	15149.0	12803.3	10737.9	11570.0	13106.6	16780.6
EF405056.1	215097	127.5	110.4	571.5	156.3	95.7	179.3
GQ254282.1	540496	4454.1	3598.5	6027.4	8842.1	3821.0	6908.6
AY662006.1	137438	5686.3	5848.8	6186.4	5689.4	3355.6	3990.3
DQ824015.1	189076	3489.4	3526.0	4627.8	5555.0	2385.1	4031.0
AB246799.2	150109	15471.2	14309.5	10996.9	14635.7	17646.0	17307.1
EU510311.1	273356	11618.5	9582.2	11648.6	11475.3	8536.9	9924.1
AY792260.1	119586	3192.7	3348.7	4980.2	7082.5	1627.8	2688.8
DQ905687.1	165322	7550.2	8725.4	4693.2	7327.0	3562.0	3314.0
FJ973586.1	384641	8450.5	6809.9	6725.2	9821.8	7810.8	8648.9
FJ477590.1	586368	11952.5	11503.3	20590.2	15464.1	10715.5	12938.7
AJ005449.1	6852	1907.6	1096.1	2646.1	3242.9	750.2	739.7
EF632938.1	253486	6209.0	5289.2	8278.9	7828.5	3183.6	4072.8
AB259961.1	160887	6339.9	7003.0	5911.3	7054.9	4505.6	4748.7
AJ575701.1	95883	12786.1	10857.9	8812.5	11072.4	8829.7	13025.6
FJ672653.1	528864	14328.0	13001.9	13092.5	14363.7	14065.4	14874.6
DQ466075.1	160810	2576.2	2198.9	5469.4	5101.8	2414.6	1731.4
EF405240.1	208210	1567.5	1773.2	3243.4	3305.1	1295.5	1665.0
AJ786800.1	108077	3975.7	3550.7	3956.0	6431.0	2610.5	3775.0
EU888003.1	303810	9339.5	5624.6	8549.3	10722.8	9370.8	11532.4
AY238499.1	92793	8567.4	6571.1	10079.0	10373.5	5984.7	8691.9
FJ901002.1	547998	9036.8	9808.7	9850.4	11690.0	13321.6	9428.5
AY993322.1	130981	17575.7	16562.4	15083.1	15541.3	15496.0	14584.9
EU887771.1	339734	4137.7	3534.8	6643.7	12462.5	1302.2	5018.1
FJ675537.1	526614	4731.7	4776.6	7994.2	8265.3	8113.6	9848.8
EF096018.1	189188	7080.4	7721.5	9582.7	11218.0	8557.4	8981.1
FJ960346.1	541465	9017.1	7022.1	10398.3	13898.4	8773.2	12340.7
EF175378.1	174707	2186.3	2045.3	7665.0	7787.8	1143.6	2052.6
FJ880692.1	404082	7916.2	6540.1	6711.0	7210.7	9800.0	10387.2
AJ318125.1	26755	2777.7	2766.5	6147.5	4649.1	1312.1	1792.4
EU511968.1	273822	12455.5	12209.8	5816.7	10968.3	12006.3	12060.1
L29265.1	6860	4624.4	4412.6	5207.7	5176.3	1032.5	1926.2
EF672088.1	256466	6542.6	5254.1	5445.1	9688.0	2692.4	4720.5
DQ799851.1	187938	8996.3	10863.2	11246.9	14400.3	11918.5	10329.5
EF471693.1	258429	5196.8	5859.1	6688.5	8800.2	9822.8	8962.9

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GQ263364.1 gg_id:565246 Structure Simulated Level Waste Site simulated level waste site clone FW1_b40
EF097606.1 gg_id:189120 mouse cecum clone SWPT20_aaa01b08
AY672759.1 gg_id:132213 Alcaligenes sp. 80
AM982630.1 gg_id:279278 microbial and slurry pig saw dust spent bedding clone PISD-AMH11
EF442019.1 gg_id:214423 Bordetella petrii str. PLLA-3
AY983565.1 gg_id:119964 human descending colon mucosal biopsy clone NN45
FJ755942.1 gg_id:512238 Alcaligenes sp. str. RCT1
AY770946.1 gg_id:108314 water injection well Dagang oilfield clone W6
FJ477560.1 gg_id:554733 gut symbionts are tightly linked herbivory ants whole extracted mid- and hind-gut sin
FJ959932.1 gg_id:580692 bottlenose dolphin upper respiratory tract blowhole clone D8A8_326
DQ799318.1 gg_id:187226 human fecal clone RL205_aaj20g09
DQ469227.1 gg_id:158061 Microbial and ecology water Zhong Tiaoshan mine Shanxi province China AMD clone
AY963392.1 gg_id:154501 structures and correlated ecological factors soils two evergreen broad-leaved forests
AY131213.1 gg_id:59999 Kerstersia gyiorum str. LMG 5906
EU528222.1 gg_id:282571 Seasonal Dynamics Mudflat Mouth Major Kentucky Lake Reservoir Tributary sedime
AB487629.1 gg_id:562108 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNSR0
EF097368.1 gg_id:177104 mouse cecum clone SWPT19_aaa01f07
GQ422442.1 gg_id:586902 Pusillimonas terrae str. SAG3
DQ451484.1 gg_id:156890 forest soil clone FAC45
FJ768950.1 gg_id:537405 Alcaligenes sp. str. WY200811
EF999384.1 gg_id:250119 Vertical and Methanotrophs Estuarine Sediments Pearl River Estuary sediments 22cn
AJ867907.1 gg_id:144374 Fluctuations Significantly Influence Microbial Present Nival Lakes lake water clone B4
EF471697.1 gg_id:277235 Fast Screening and Estuarine Operon Libraries whole surface water Chesapeake Bay
GQ254283.1 gg_id:574340 Castellaniella sp. str. H13
FJ477650.1 gg_id:584565 gut symbionts are tightly linked herbivory ants whole extracted single ant clone 96j
FJ152724.1 gg_id:317726 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX5A_
EF520469.1 gg_id:228829 structure lakes: what controls ? acid-impacted lake clone ADK-HDe02-53
FM873876.1 gg_id:368602 occupant source house mattress dust clone MB02C10
EF471233.1 gg_id:220259 Alcaligenes sp. str. BBTR16
X92415.1 gg_id:6857 Alcaligenes sp. str. L6
DQ802483.1 gg_id:196880 human fecal clone RL188_aah18d02
DQ799440.1 gg_id:184082 human fecal clone RL305aal86c09
AJ277742.1 gg_id:22985 Brackiella oedipodis str. LMG 1945 R8846
AF232922.1 gg_id:22530 United Kingdom: Montserrat geothermal springs clone MS8 MS8
EU133883.1 gg_id:237924 tallgrass prarie soil clone FFCH2283
EF602797.1 gg_id:228235 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
GU138383.1 gg_id:585406 Achromobacter sp. str. THG 42
DQ346507.1 gg_id:153290 during composting libraries compost clone 2B23
AY921769.1 gg_id:114410 farm soil clone AKYG1037
AY792262.1 gg_id:123064 Humic Lake clone CrystalBog5E7
EU800906.1 gg_id:330902 It's all ranking aquatic Delaware Bay NJ clone 2C229148

GQ263364.1	565246	4596.2	4315.2	5869.3	7838.3	6094.9	8190.1
EF097606.1	189120	3731.1	3669.3	4160.1	5817.5	5488.5	8027.0
AY672759.1	132213	3346.2	2739.2	5335.4	4621.4	1924.1	1774.8
AM982630.1	279278	12056.8	9869.8	9109.7	10967.5	11660.3	9041.5
EF442019.1	214423	4974.7	3966.8	3176.8	6649.7	1381.7	2934.1
AY983565.1	119964	12778.1	9470.0	8865.1	13499.6	10341.9	11440.4
FJ755942.1	512238	5752.6	5189.5	7533.3	7688.5	6471.5	8559.4
AY770946.1	108314	3455.7	4095.6	8811.5	7518.7	1399.0	2778.0
FJ477560.1	554733	12560.9	16230.8	9747.4	17678.4	15114.0	14837.4
FJ959932.1	580692	8725.2	7720.4	9327.8	10347.6	8428.1	9027.8
DQ799318.1	187226	8874.1	6695.7	6684.3	12558.0	11401.4	11314.6
DQ469227.1	158061	4439.9	3893.1	2910.1	6045.1	612.3	1491.4
AY963392.1	154501	15962.2	14991.6	12150.0	11682.1	12877.3	11096.2
AY131213.1	59999	2427.5	2727.9	7591.1	6597.3	2988.1	3659.8
EU528222.1	282571	8626.2	7524.8	11372.5	13306.3	8240.8	10086.6
AB487629.1	562108	4153.2	4856.8	1870.6	2635.9	1385.1	1793.9
EF097368.1	177104	15155.2	11908.3	12451.4	16037.8	10080.6	9864.7
GQ422442.1	586902	5824.2	5791.4	7173.0	10752.0	6142.0	8965.6
DQ451484.1	156890	14784.5	15649.7	14458.8	8474.2	12973.6	11578.4
FJ768950.1	537405	8693.0	7271.8	9849.3	11361.4	7413.4	9554.0
EF999384.1	250119	13636.2	12660.4	13710.6	11268.4	11886.9	11812.5
AJ867907.1	144374	5187.3	4179.0	4793.2	7109.5	2358.0	3081.4
EF471697.1	277235	4189.9	4069.1	9133.7	10171.7	3569.2	5598.1
GQ254283.1	574340	12398.2	11504.7	18148.7	17679.8	11947.3	11851.8
FJ477650.1	584565	7269.7	6012.7	8297.7	10169.1	5320.6	8236.2
FJ152724.1	317726	4058.7	3334.7	3967.1	3631.4	430.3	1216.9
EF520469.1	228829	9946.0	7015.9	7359.4	14053.4	6018.0	7090.2
FM873876.1	368602	4093.6	3871.6	3389.9	2120.1	538.5	1165.2
EF471233.1	220259	10044.9	5836.4	5962.7	11984.9	4016.7	6092.9
X92415.1	6857	1964.8	2251.3	6985.3	7151.2	351.5	1333.7
DQ802483.1	196880	1672.2	1779.7	2787.2	2220.9	2050.7	4793.0
DQ799440.1	184082	10907.7	9993.6	11366.3	11609.4	10280.6	11598.9
AJ277742.1	22985	1071.2	980.9	320.4	471.2	307.0	358.5
AF232922.1	22530	792.8	930.2	402.9	656.7	422.4	961.0
EU133883.1	237924	1242.5	1894.1	2715.0	1125.9	1926.6	728.6
EF602797.1	228235	13293.8	9800.3	7005.3	6488.0	10525.1	10870.7
GU138383.1	585406	7703.3	5695.5	8394.8	8477.6	7035.5	7000.5
DQ346507.1	153290	7836.7	8098.4	6369.4	9510.4	7098.8	7903.8
AY921769.1	114410	14092.1	14461.7	10369.4	12522.1	5123.3	5550.4
AY792262.1	123064	8589.3	6704.9	4660.8	11115.0	8445.3	9339.1
EU800906.1	330902	3304.6	2713.7	7567.0	8258.6	2408.3	4138.2

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EF516407.1 gg_id:220795 grassland soil clone FCPT738
EF516629.1 gg_id:226599 grassland soil clone FCPS510
GQ098789.1 gg_id:375227 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw702e
GQ086625.1 gg_id:401935 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw29
GQ104328.1 gg_id:458722 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
EU137573.1 gg_id:261673 Bartonella-positive fleas: and assembly patterns Oropsylla hirsuta (prairie dog flea) C
GQ111475.1 gg_id:407055 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw668c08
GQ114415.1 gg_id:415925 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw(
GQ102105.1 gg_id:377684 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw561b0
GQ105274.1 gg_id:381091 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
GQ098132.1 gg_id:387454 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw40
GQ096711.1 gg_id:373702 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw4
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GQ097005.1 gg_id:418496 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw392e0
GQ096952.1 gg_id:409006 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw391g0
GQ097159.1 gg_id:465891 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
GQ104229.1 gg_id:467048 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
GQ038800.1 gg_id:434417 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu523c08
GQ096237.1 gg_id:406963 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw4
GQ099305.1 gg_id:410238 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
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GQ093416.1 gg_id:448008 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw4
GQ091471.1 gg_id:448774 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw346e0
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GQ087060.1 gg_id:404429 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw3
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GQ075148.1 gg_id:396242 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
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GQ096781.1 gg_id:382698 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
GQ114649.1 gg_id:435510 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw(

EF516407.1	220795	4441.4	5544.3	14126.4	9807.9	3615.3	5750.1
EF516629.1	226599	2758.0	4265.8	7879.0	6499.1	2620.6	4149.6
GQ098789.1	375227	22791.6	22331.1	14182.8	20970.2	26618.0	20668.0
GQ086625.1	401935	13353.0	12339.2	13129.4	13675.7	13637.7	12425.0
GQ104328.1	458722	19465.1	17059.4	12897.9	18749.2	12867.5	16446.1
EU137573.1	261673	12139.1	10829.0	20782.9	17851.5	13207.3	12043.1
GQ111475.1	407055	11454.4	6916.8	11653.8	12306.3	5329.7	10003.2
GQ114415.1	415925	13428.1	15945.1	13338.0	13190.6	16589.2	12454.4
GQ102105.1	377684	6990.2	8463.8	13833.2	7643.8	8499.6	5951.8
GQ105274.1	381091	26987.8	26014.6	26882.8	22684.8	26972.8	24902.0
GQ098132.1	387454	7921.0	4402.8	12403.2	13193.0	10712.9	14734.2
GQ096711.1	373702	6763.3	7537.8	13644.5	12074.1	10181.4	8081.8
GQ075529.1	437399	16014.2	15864.0	11562.8	12995.6	13461.8	12931.8
GQ097005.1	418496	3331.8	5643.9	7054.2	6747.5	10735.5	16713.5
GQ096952.1	409006	16823.2	18124.9	16188.4	17486.4	12428.5	19153.1
GQ097159.1	465891	6407.7	3830.5	972.5	5392.3	1203.7	2719.1
GQ104229.1	467048	24841.9	24559.1	21511.4	18951.0	23142.6	21606.2
GQ038800.1	434417	3791.4	4002.9	9926.6	7068.1	2056.4	4638.0
GQ096237.1	406963	16700.8	30526.1	20768.3	18113.9	1855.3	14775.8
GQ099305.1	410238	14643.9	7480.5	23660.2	15895.9	9299.3	9615.7
GQ096462.1	432824	7252.0	4853.8	16234.4	9040.1	6194.4	5890.5
GQ093416.1	448008	1659.1	1923.9	7085.4	1492.5	9972.4	4796.7
GQ091471.1	448774	13135.7	13034.7	12730.0	13732.5	19175.9	14526.4
GQ089297.1	397619	24841.9	24559.1	21511.4	18951.0	23142.6	21606.2
GQ087060.1	404429	12118.8	8005.3	12252.8	10528.2	7351.6	6846.7
GQ115312.1	435486	9337.4	4310.7	12785.4	7453.8	7305.1	4543.7
GQ075148.1	396242	19691.7	20921.2	13643.2	16058.7	14680.0	12996.8
GQ107032.1	387797	16168.0	12628.3	12691.6	13229.4	11993.7	11828.5
GQ068074.1	464557	16425.2	14554.9	7895.8	15292.5	9113.6	9871.2
GQ102779.1	376326	9848.6	9285.8	6928.2	13085.8	16658.9	17036.8
GQ102895.1	459159	12046.3	9629.4	19182.8	12590.1	13209.1	10088.4
GQ092747.1	373459	12963.2	9047.9	22000.2	14783.2	11735.7	12782.7
GQ099529.1	372407	17269.9	18312.9	16409.5	14533.9	12384.1	12764.8
GQ103643.1	412810	7997.3	7838.6	18163.3	26817.3	10278.9	9244.1
GQ102596.1	410127	14372.0	14180.3	18900.3	17070.7	16657.4	13696.8
GQ099429.1	464632	16347.3	10643.0	20669.2	16285.6	15258.7	14796.1
GQ109094.1	439620	17666.7	11853.5	14300.0	18426.1	14755.3	14186.3
GQ104528.1	410696	14331.7	11779.2	12937.3	15508.7	16060.1	15188.4
GQ114603.1	380261	6854.0	8749.8	11864.2	8007.1	5473.8	5700.0
GQ096781.1	382698	18651.9	18106.6	17296.5	17829.8	21346.0	18195.8
GQ114649.1	435510	4083.5	4937.4	6425.1	5045.8	5592.5	4442.4

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GQ098233.1 gg_id:433269 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw40
GQ114619.1 gg_id:388405 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw(
GQ094212.1 gg_id:464102 Topographical and Temporal Human Skin Microbiome skin alar crease clone nbw371
GQ111468.1 gg_id:422707 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw668b0
GQ085609.1 gg_id:460481 Topographical and Temporal Human Skin Microbiome skin palm clone nbw278b08c1
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GQ104461.1 gg_id:412259 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ102988.1 gg_id:436079 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
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GQ107173.1 gg_id:428160 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw
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GQ114227.1 gg_id:414764 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw59
GQ094029.1 gg_id:463167 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
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GQ097232.1 gg_id:388505 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
GQ115914.1 gg_id:410711 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw603a01c
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GQ099021.1 gg_id:432326 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ102941.1 gg_id:415230 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
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GQ107279.1 gg_id:429315 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw
DQ256345.1 gg_id:143304 subsurface water clone EV818BHEB5102702SAS26
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GQ102742.1 gg_id:438634 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw(

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GQ098233.1	433269	24760.0	26316.8	15948.4	20290.3	26377.0	21918.9
GQ114619.1	388405	16378.6	17654.8	11787.3	18129.0	19888.1	17257.5
GQ094212.1	464102	11344.0	10094.9	3273.3	14607.4	18001.5	16397.2
GQ111468.1	422707	9810.0	9553.8	10520.6	10527.0	11018.3	10683.3
GQ085609.1	460481	3470.5	3455.3	3640.7	8443.9	757.3	6710.8
GQ104589.1	455587	11156.8	10237.7	18548.7	12383.2	7891.4	8869.3
GQ104461.1	412259	15075.5	15570.5	11502.0	16389.5	20171.5	17317.9
GQ102988.1	436079	10610.0	12229.3	6308.6	13723.7	14813.6	14623.9
GQ096425.1	398936	18651.9	18106.6	17296.5	17829.8	21346.0	18195.8
GQ102784.1	415636	7373.5	9317.5	13743.4	8177.0	11385.6	8965.9
GQ085393.1	410572	19071.5	17425.1	23801.3	18969.7	16939.1	16085.6
GQ106545.1	406252	23028.7	20758.0	17549.6	21676.1	23791.5	19857.5
GQ107173.1	428160	12332.7	10678.2	11466.1	17748.6	3113.9	8879.6
EU071523.1	235958	26025.4	18197.5	38254.9	26336.7	19974.9	20445.4
GQ114227.1	414764	7997.3	7838.6	18163.3	26817.3	10278.9	9244.1
GQ094029.1	463167	23395.6	23013.1	13923.6	19771.8	22858.9	20904.8
GQ101675.1	396667	27137.3	26957.2	18519.0	19595.4	26117.8	23842.2
GQ085304.1	413610	9874.4	10775.3	11107.4	16317.5	13932.4	9919.5
GQ023870.1	485799	22831.3	22430.8	16730.1	16727.7	21259.3	27108.9
GQ114575.1	388872	10606.1	9885.7	10837.1	13619.5	12400.9	10614.1
GQ113741.1	466695	2381.1	6145.4	16982.6	5623.0	6302.1	9903.9
GQ073935.1	445834	8584.7	6924.1	7973.3	11288.8	5405.9	11834.2
GQ097232.1	388505	25281.7	26194.0	18492.7	18633.7	27606.9	23271.4
GQ115914.1	410711	14643.9	7480.5	23660.2	15895.9	9299.3	9615.7
GQ095299.1	410482	18996.5	16930.8	15826.4	18140.0	17029.2	15631.2
GQ106678.1	391522	24841.9	24559.1	21511.4	18951.0	23142.6	21606.2
GQ086345.1	465785	16335.4	17449.1	19833.7	15231.1	16872.6	14977.0
GQ101804.1	376575	13977.6	13052.7	9078.4	12994.2	8097.8	8702.7
GQ105672.1	418524	12907.0	15069.0	16419.2	15002.8	8754.8	10230.1
GQ096165.1	432866	16880.6	17084.5	18364.5	17938.7	22719.9	17394.5
GQ096363.1	379014	17466.9	16046.3	23155.3	16226.2	16000.2	13315.5
GQ086435.1	393269	11454.4	6916.8	11653.8	12306.3	5329.7	10003.2
GQ105982.1	415729	23738.7	25741.0	14622.0	16930.5	17988.1	16417.4
GQ099021.1	432326	10492.6	11155.3	5051.6	14498.1	19750.2	16503.6
GQ102941.1	415230	9926.0	7480.7	7809.2	12310.3	4347.9	4782.1
GQ114946.1	373715	28076.6	27436.8	16595.1	22041.1	26580.1	22866.6
GQ107279.1	429315	12656.6	12659.0	14769.2	12189.8	13295.1	12096.8
DQ256345.1	143304	14578.0	13180.2	25041.1	17255.9	16950.9	14089.1
GQ094491.1	468438	2781.4	3152.4	9620.6	7158.5	2175.4	3048.6
GQ102742.1	438634	1618.8	3273.9	8053.4	2791.1	4739.9	4085.7

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GQ107115.1 gg_id:424920 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw544h0
GQ096843.1 gg_id:425705 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
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GQ103833.1 gg_id:418376 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ100801.1 gg_id:375156 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor
GQ105647.1 gg_id:377103 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ096342.1 gg_id:408165 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ098368.1 gg_id:422228 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw558g
GQ106137.1 gg_id:416403 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ104812.1 gg_id:425760 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
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GQ114064.1 gg_id:373968 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ070810.1 gg_id:402690 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw
GQ091408.1 gg_id:458708 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw345f11
GQ096343.1 gg_id:407471 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ023241.1 gg_id:486427 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu2
GQ114581.1 gg_id:399812 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ097138.1 gg_id:414728 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
GQ102794.1 gg_id:441538 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ111868.1 gg_id:406510 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw
GQ086665.1 gg_id:412720 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw29
GQ087718.1 gg_id:447540 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
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GQ097149.1 gg_id:466069 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
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GQ102055.1 gg_id:467865 Topographical and Temporal Human Skin Microbiome skin palm clone nbw503a01c1
GQ087624.1 gg_id:434122 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ099644.1 gg_id:400966 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
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GQ091960.1 gg_id:410165 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ106810.1 gg_id:421982 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw541b1
GQ094349.1 gg_id:453897 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw

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GQ107115.1	424920	11928.6	11542.6	18394.6	11376.4	14853.7	10554.5
GQ096843.1	425705	18406.3	15756.1	12396.5	17735.9	18478.2	18234.3
GQ083263.1	437063	9046.5	3669.0	9977.9	11532.1	2064.0	4750.2
GQ103833.1	418376	15206.3	12987.2	18409.8	11990.5	11679.4	10474.5
GQ100801.1	375156	7540.0	6661.7	13230.4	9416.4	8140.1	6919.4
GQ105647.1	377103	13621.6	11805.8	2258.3	13760.0	7239.5	9489.9
GQ096342.1	408165	24281.9	24647.2	18949.5	18427.5	23083.2	22045.2
GQ098368.1	422228	12841.7	10271.9	15342.9	12426.3	8141.2	9266.3
GQ106137.1	416403	5647.7	5956.4	3093.2	6551.6	173.9	893.5
GQ104812.1	425760	6708.1	5966.4	10632.8	7607.5	6606.0	6017.4
GQ111143.1	455964	12466.6	7205.8	17232.9	13346.6	7136.5	8590.6
GQ086616.1	373667	6990.4	9001.8	13642.9	9730.8	11113.4	10078.5
GQ102962.1	397801	29744.7	30256.2	22818.0	23433.6	29209.9	24617.4
GQ093925.1	467995	6708.1	5966.4	10632.8	7607.5	6606.0	6017.4
GQ115782.1	431337	22799.8	22629.2	14453.3	18060.2	21129.7	20534.9
GQ114064.1	373968	5624.9	6733.7	13333.8	7579.3	5452.2	5054.7
GQ070810.1	402690	23738.7	25741.0	14622.0	16930.5	17988.1	16417.4
GQ091408.1	458708	13237.5	15233.2	7960.7	9777.3	17384.2	12309.9
GQ096343.1	407471	19367.8	17628.7	16606.3	18671.8	18386.8	13817.4
GQ023241.1	486427	10208.6	11082.3	13052.5	13899.6	13130.5	9818.6
GQ114581.1	399812	12323.4	13793.2	11305.5	11379.2	10006.4	11778.4
GQ097138.1	414728	8792.2	9563.4	11740.9	11033.0	5595.6	7139.3
GQ102794.1	441538	23738.7	25741.0	14622.0	16930.5	17988.1	16417.4
GQ111868.1	406510	4121.7	4009.6	3958.8	6280.2	5414.1	5208.0
GQ086665.1	412720	10475.5	11328.4	13431.8	10524.4	10505.8	9040.1
GQ087718.1	447540	175.7	401.3	232.0	509.2	179.9	140.6
GQ093128.1	391001	21190.6	21925.3	10376.8	15765.0	14178.1	11880.8
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GQ099644.1	400966	9765.3	6096.4	6589.9	10639.2	4756.0	9188.0
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GQ091960.1	410165	15749.0	16190.0	17688.2	16380.6	12680.0	13993.8
GQ106810.1	421982	13699.3	13471.8	17947.0	13471.2	12489.7	11318.6
GQ094349.1	453897	7535.9	8140.3	11982.2	13362.9	8300.8	7229.8

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o__Burkholderiales	f__Aquabacteriaceae
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GQ075566.1 gg_id:441817 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ071282.1 gg_id:445977 Topographical and Temporal Human Skin Microbiome skin back clone nbw238c02c1
GQ104720.1 gg_id:390907 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ020717.1 gg_id:488951 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ103075.1 gg_id:406036 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
GQ102888.1 gg_id:444602 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
GQ098424.1 gg_id:389209 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw559e
GQ098749.1 gg_id:445768 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw702a
GQ106248.1 gg_id:432146 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw.
GQ113310.1 gg_id:448286 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor
GQ093358.1 gg_id:395089 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw408g05c
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GQ114752.1 gg_id:441711 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
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GQ096365.1 gg_id:376418 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw4
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GQ072580.1 gg_id:454941 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw19
GQ096335.1 gg_id:467012 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw4
GQ037846.1 gg_id:411572 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ105245.1 gg_id:440822 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
GQ086558.1 gg_id:378396 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw29

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GQ071282.1	445977	23738.7	25741.0	14622.0	16930.5	17988.1	16417.4
GQ104720.1	390907	8607.7	8635.1	10357.7	10441.4	12919.9	10654.8
GQ020717.1	488951	4915.9	5941.0	13189.0	7589.9	3552.5	4683.4
GQ103075.1	406036	10838.5	12016.6	16221.4	14861.2	14516.1	10997.5
GQ102888.1	444602	9351.2	8075.8	8255.4	10916.6	8702.9	7271.6
GQ098424.1	389209	9412.9	7911.2	9985.0	11920.1	10741.3	10464.9
GQ098749.1	445768	15991.9	12499.2	15892.8	13889.6	12525.0	12841.9
GQ106248.1	432146	18590.8	17361.9	10524.6	19128.3	21660.5	17714.8
GQ113310.1	448286	9920.9	11472.6	10917.5	7658.1	5384.8	8685.8
GQ093358.1	395089	12634.6	14240.9	15860.9	11933.2	15293.5	11234.5
GQ022738.1	486932	5419.8	4962.8	11470.5	7436.6	4551.2	5005.8
GQ090489.1	449083	21544.1	20402.0	23330.0	19097.6	19364.3	17700.7
GQ090675.1	396029	12062.1	8987.3	18250.4	13527.6	10107.7	11769.4
GQ099524.1	441781	7827.4	3261.0	8757.3	10355.3	6104.7	4475.0
GQ093798.1	374432	8125.5	4651.6	6032.1	9683.4	4151.3	6527.4
GQ096327.1	456145	15423.6	13244.4	7522.7	17772.2	16212.8	17566.7
GQ085476.1	443536	23028.7	20758.0	17549.6	21676.1	23791.5	19857.5
GQ098725.1	374794	23028.7	20758.0	17549.6	21676.1	23791.5	19857.5
GQ092166.1	466491	10039.9	8283.3	21189.1	11944.0	9652.1	10187.0
GQ101059.1	447210	20729.1	19423.9	23627.3	19673.7	18957.8	17239.3
GQ105006.1	371118	18276.8	13832.6	21090.3	17573.7	15009.4	17254.6
GQ087190.1	394708	22040.2	20408.4	13043.6	21300.8	24996.9	18463.5
GQ106310.1	422914	11671.3	5939.6	6557.0	5486.6	5916.0	5342.7
GQ086795.1	409636	12452.0	10281.3	12014.9	12844.9	12208.1	12157.1
GQ070729.1	414392	10889.2	11122.7	14601.0	11156.2	13329.7	11198.3
GQ103755.1	424136	4121.7	4009.6	3958.8	6280.2	5414.1	5208.0
GQ090419.1	390059	16823.2	18124.9	16188.4	17486.4	12428.5	19153.1
GQ097553.1	436344	12332.7	10678.2	11466.1	17748.6	3113.9	8879.6
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GQ099652.1	404163	15747.5	15755.7	12482.6	17213.0	14228.3	16430.0
GQ114752.1	441711	8858.8	5542.5	23048.7	11487.9	5976.4	5982.0
GQ104307.1	448583	16192.3	12726.7	25139.3	20099.1	13291.2	15421.2
GQ096365.1	376418	8233.3	8263.8	7888.9	5976.8	7610.4	7208.6
GQ097278.1	443277	26987.8	26014.6	26882.8	22684.8	26972.8	24902.0
GQ072580.1	454941	1055.7	746.1	4113.6	6521.2	837.4	1082.4
GQ096335.1	467012	6763.3	7537.8	13644.5	12074.1	10181.4	8081.8
GQ037846.1	411572	1870.4	3361.7	9296.5	4676.8	8719.1	8417.0
GQ105245.1	440822	22505.5	21822.4	9602.6	19811.0	23012.1	20410.2
GQ086558.1	378396	13859.8	22330.0	15918.3	21204.9	16740.5	12258.7

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GQ070575.1	407600	15035.8	10970.6	13177.9	14851.8	10789.2	11511.1
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GQ099409.1	399762	14169.1	9114.9	12344.5	14280.4	11473.4	8398.4
GQ097028.1	439945	12312.0	6656.3	13645.4	13964.1	10236.0	13765.0
GQ096768.1	449866	18449.9	19405.4	16866.4	18135.4	26695.3	22146.6
GQ106343.1	426039	22040.2	20408.4	13043.6	21300.8	24996.9	18463.5
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GQ098483.1	418500	8404.0	8754.2	12162.2	15114.8	6773.9	6498.2
GQ115612.1	417680	19663.5	18524.2	21618.5	19414.8	21790.6	18575.2
GQ086408.1	439739	16777.2	16658.0	17353.1	14353.7	15620.7	14265.3
GQ098806.1	449936	17666.7	11853.5	14300.0	18426.1	14755.3	14186.3
GQ075944.1	442457	9581.8	9536.7	12423.6	6470.1	9513.2	6538.3
GQ095311.1	388150	9212.9	5377.9	4931.4	10245.9	1854.5	3457.7
GQ106986.1	431655	27892.1	28556.3	18037.2	22552.3	28249.6	24640.6
GQ103017.1	447533	227.1	217.5	917.4	2941.9	656.5	329.2
GQ102717.1	419400	18590.8	17361.9	10524.6	19128.3	21660.5	17714.8
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GQ072961.1	454208	3470.5	3455.3	3640.7	8443.9	757.3	6710.8
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GQ039021.1	398153	11176.6	11626.6	15517.6	10773.6	9530.0	8547.4
GQ107385.1	455603	15412.3	15641.7	22620.2	15160.3	14538.3	13399.5
GQ106615.1	461794	12816.2	14290.9	18663.1	14232.6	20845.2	16629.7
GQ090606.1	452225	26633.3	29329.8	15060.5	22013.5	27071.1	22938.2

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o__Burkholderiales	f__Aquabacteriaceae
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GQ102829.1 gg_id:423651 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
GQ072993.1 gg_id:426187 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw203g09c
GQ114081.1 gg_id:392633 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ106535.1 gg_id:449504 Topographical and Temporal Human Skin Microbiome skin back clone nbw537a07c1
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GQ102682.1 gg_id:440618 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ107251.1 gg_id:393521 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw
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GQ088961.1 gg_id:445450 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ097483.1 gg_id:427644 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw
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GQ106088.1 gg_id:438958 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ105098.1 gg_id:452870 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ103828.1 gg_id:382229 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n

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GQ096497.1	468254	17572.8	18804.4	15900.6	14254.6	19540.5	15461.3
GQ113322.1	415807	6545.2	6080.8	10104.6	8484.2	4346.0	5452.5
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GQ103015.1	382940	26421.7	27466.0	16762.0	21570.5	28581.2	23918.3
GQ104663.1	429008	9976.5	8307.3	6097.9	14587.1	5546.6	9806.4
GQ104027.1	447438	12374.9	7765.7	13446.0	13804.0	6191.8	9034.0
GQ095831.1	385721	15382.8	7774.2	11451.1	16367.4	5577.5	8112.5
GQ094929.1	386454	13388.2	12553.3	18120.6	14295.3	11595.9	11087.2
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GQ104852.1	385110	12518.0	5881.3	19183.3	14509.6	8463.3	9800.3
GQ101627.1	413474	16880.6	17084.5	18364.5	17938.7	22719.9	17394.5
GQ086582.1	416082	12181.5	9690.8	15508.7	12643.6	9988.5	8798.3
GQ085413.1	450756	20479.1	17491.8	20397.2	18620.7	18799.1	16127.9
GQ115299.1	448629	10357.3	5760.5	7324.0	15830.0	3813.8	5054.1
GQ085274.1	463119	16623.3	18109.6	11970.8	14023.9	16682.6	14108.5
GQ070452.1	417223	15497.2	16129.4	16409.9	17025.6	14852.4	14673.4
GQ106119.1	379763	8400.8	9136.9	7680.0	11029.7	14210.0	11439.5
GQ102829.1	423651	6246.1	1787.3	3563.6	10300.2	3741.5	8031.6
GQ072993.1	426187	16613.9	14460.1	13496.9	14160.3	14732.8	12705.5
GQ114081.1	392633	15251.7	15261.4	16756.4	16273.3	20693.7	16251.4
GQ106535.1	449504	21194.9	21114.3	18536.9	18768.3	22290.0	18557.2
GQ092993.1	441713	15747.5	15755.7	12482.6	17213.0	14228.3	16430.0
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GQ107251.1	393521	6407.7	3830.5	972.5	5392.3	1203.7	2719.1
GQ086428.1	460789	13229.1	13214.8	9987.3	10968.9	12605.3	11024.8
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GQ102668.1	413397	4121.7	4009.6	3958.8	6280.2	5414.1	5208.0
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GQ106088.1	438958	9337.4	4310.7	12785.4	7453.8	7305.1	4543.7
GQ105098.1	452870	5762.6	6217.8	6070.5	8289.8	10445.2	8535.8
GQ103828.1	382229	15154.5	13217.7	14771.6	14703.0	16155.3	12983.5

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GQ106249.1 gg_id:406431 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
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EF492894.1 gg_id:249177 Iron-manganese Nodule and Its Surrounding Soil soil around iron-manganese nodule
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GQ114769.1 gg_id:411005 Topographical and Temporal Human Skin Microbiome skin interdigital web space cl
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GQ092121.1 gg_id:463269 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw406c11
GQ093028.1 gg_id:378738 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw408c03
GQ103041.1 gg_id:402571 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
GQ068136.1 gg_id:376335 Topographical and Temporal Human Skin Microbiome skin alar crease clone nbw147
GQ076306.1 gg_id:398630 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw36
GQ102579.1 gg_id:421831 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ096829.1 gg_id:449828 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
GQ072505.1 gg_id:453594 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw19
GQ111423.1 gg_id:457930 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw667b0
GQ110995.1 gg_id:426366 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
GQ108014.1 gg_id:377198 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ115805.1 gg_id:436149 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw601f08c
GQ087965.1 gg_id:404054 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ022031.1 gg_id:487637 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu3
GQ074900.1 gg_id:402912 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n

GQ085536.1	411390	10502.7	11852.8	6301.4	14923.9	5561.2	6453.5
GQ098565.1	416737	10981.5	12355.6	17517.7	11095.5	9205.6	9218.0
GQ115256.1	386568	20479.1	17491.8	20397.2	18620.7	18799.1	16127.9
GQ106249.1	406431	6708.1	5966.4	10632.8	7607.5	6606.0	6017.4
GQ114933.1	415757	13101.1	13558.2	16134.0	12801.1	10629.3	10304.9
GQ096966.1	441345	15747.5	15755.7	12482.6	17213.0	14228.3	16430.0
EF492894.1	249177	10198.3	9100.1	8153.8	9527.1	6855.0	7991.7
GQ085471.1	465859	9560.5	9475.1	6431.5	12536.2	15551.0	13302.1
GQ091415.1	425662	10493.5	9969.7	11634.9	11016.2	12343.1	10766.3
GQ114769.1	411005	16880.6	17084.5	18364.5	17938.7	22719.9	17394.5
GQ098492.1	396632	20555.4	23725.4	27565.7	24147.0	28416.9	21071.3
GQ092694.1	451150	9140.9	3575.3	10192.6	11007.0	2751.4	5271.1
GQ102720.1	382094	10004.4	14418.9	12501.9	9292.8	14613.0	13647.9
DQ234213.2	142213	11694.8	12394.7	14786.1	9834.5	7816.6	5479.7
GQ097188.1	457141	13954.4	10736.6	15824.0	13421.7	11371.8	11773.2
GQ101915.1	374941	13998.3	10200.5	14696.7	15536.5	6174.8	7055.9
GQ103764.1	467644	25012.4	25583.4	16876.9	22597.5	24990.7	23299.5
GQ097141.1	456141	13463.4	13962.1	14814.6	12498.1	10684.1	11089.2
GQ105091.1	425034	10641.6	12068.9	14505.6	8249.9	15661.9	12699.6
GQ091838.1	391547	9765.3	6096.4	6589.9	10639.2	4756.0	9188.0
GQ097198.1	433566	19417.2	20314.6	10868.9	15726.9	20740.5	17007.7
GQ095694.1	393563	13388.2	12553.3	18120.6	14295.3	11595.9	11087.2
GQ114612.1	463474	14899.2	12806.6	16263.5	15729.6	13781.0	14524.6
GQ086319.1	467374	16911.3	14068.1	16723.0	15570.5	13198.6	13177.8
GQ107377.1	406988	10582.9	10420.3	14415.1	11961.6	11137.9	9436.2
GQ086602.1	451694	14765.1	14169.3	11474.8	12714.3	15196.8	12864.5
GQ092121.1	463269	17072.7	18760.5	13561.1	14835.2	18431.6	14550.0
GQ093028.1	378738	11608.0	7927.2	9525.2	13775.8	4798.0	5986.6
GQ103041.1	402571	10395.0	10621.3	16827.4	11808.9	9788.0	9661.4
GQ068136.1	376335	12518.0	5881.3	19183.3	14509.6	8463.3	9800.3
GQ076306.1	398630	22040.2	20408.4	13043.6	21300.8	24996.9	18463.5
GQ102579.1	421831	14635.0	15334.4	9634.8	16300.5	16174.3	17158.9
GQ096829.1	449828	15857.4	15559.6	16385.4	14922.5	12738.0	12652.4
GQ072505.1	453594	528.4	1638.7	2617.2	1066.8	3575.2	6752.9
GQ111423.1	457930	15584.8	11582.0	16897.6	16107.3	14326.6	18112.2
GQ110995.1	426366	8151.0	7014.3	13101.8	9860.8	6089.8	5721.4
GQ108014.1	377198	5704.2	6455.9	1342.5	9630.3	14336.9	12052.6
GQ115805.1	436149	0.7	0.7	1.1	0.6	0.6	0.6
GQ087965.1	404054	14840.4	16121.6	15923.0	12105.4	14837.5	13330.8
GQ022031.1	487637	10221.5	6235.4	6011.9	10614.5	5668.9	8150.7
GQ074900.1	402912	5666.9	4103.3	10549.5	7902.5	2707.2	3629.9

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GQ111186.1 gg_id:446133 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ091204.1 gg_id:436685 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw343d05
GQ083235.1 gg_id:449798 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ098458.1 gg_id:383428 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw559h
GQ098493.1 gg_id:410233 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw560c
GQ087845.1 gg_id:398067 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw359e0
GQ086548.1 gg_id:450402 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw29
GQ099817.1 gg_id:381560 Topographical and Temporal Human Skin Microbiome skin alar crease clone nbw474
GQ103964.1 gg_id:445028 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ103315.1 gg_id:372786 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw698h02
GQ106114.1 gg_id:444942 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw5
GQ097123.1 gg_id:399543 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
GQ096187.1 gg_id:428299 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw4
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GQ103991.1 gg_id:386013 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
AY662011.1 gg_id:137411 uranium-contaminated groundwater clone 005C-A03
GQ098197.1 gg_id:424331 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw40
GQ105503.1 gg_id:452787 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw5
GQ071248.1 gg_id:389319 Topographical and Temporal Human Skin Microbiome skin back clone nbw237h02c1
GQ098849.1 gg_id:438771 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw557c
GQ103090.1 gg_id:377696 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
GQ037260.1 gg_id:387456 Topographical and Temporal Human Skin Microbiome skin palm clone nbu391a12c1
GQ104220.1 gg_id:437030 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
GQ096372.1 gg_id:409307 Topographical and Temporal Human Skin Microbiome skin back clone nbw387d07c1
GQ101923.1 gg_id:383792 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw500h07c
GQ095730.1 gg_id:386125 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw4
GQ094983.1 gg_id:415251 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ092769.1 gg_id:389569 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ115257.1 gg_id:407710 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw6
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GQ099405.1 gg_id:403120 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw51
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GQ089214.1 gg_id:452186 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw3
GQ076253.1 gg_id:426520 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw36
GQ099039.1 gg_id:410329 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ097787.1 gg_id:428364 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw456g02
GQ105964.1 gg_id:393173 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw

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GQ111186.1	446133	15920.3	11152.4	20083.8	17056.3	15200.2	11803.8
GQ091204.1	436685	7378.2	7202.1	12248.7	8602.5	7553.3	6849.2
GQ083235.1	449798	17429.3	10622.9	9297.2	16784.1	5972.3	10457.2
GQ098458.1	383428	27175.4	26365.2	15376.4	22036.1	25048.4	24167.0
GQ098493.1	410233	9765.3	6096.4	6589.9	10639.2	4756.0	9188.0
GQ087845.1	398067	33814.6	19664.7	14452.1	17849.5	22902.2	19138.3
GQ086548.1	450402	11975.0	6772.2	13973.1	14508.9	7454.6	11525.6
GQ099817.1	381560	24841.9	24559.1	21511.4	18951.0	23142.6	21606.2
GQ103964.1	445028	8600.1	10289.5	13625.1	10734.7	7383.0	7858.7
GQ103315.1	372786	11276.3	7652.6	13558.2	12100.3	8099.0	10353.3
GQ106114.1	444942	175.7	401.3	232.0	509.2	179.9	140.6
GQ097123.1	399543	175.7	401.3	232.0	509.2	179.9	140.6
GQ096187.1	428299	9933.7	10331.7	9991.2	12438.0	18102.0	14701.2
GQ106286.1	454497	8036.4	8943.2	10974.1	5737.8	4422.5	6495.4
GQ103991.1	386013	4740.4	3801.0	13137.3	5947.9	2471.5	1891.2
AY662011.1	137411	13084.0	11793.5	17409.9	14144.5	12754.4	11974.1
GQ098197.1	424331	8737.4	8214.8	11223.9	10664.9	10286.0	8944.9
GQ105503.1	452787	15423.6	13244.4	7522.7	17772.2	16212.8	17566.7
GQ071248.1	389319	15199.7	12997.7	24021.2	13137.8	11161.2	10406.5
GQ098849.1	438771	9814.5	8188.3	4611.9	9868.7	6915.8	8609.6
GQ103090.1	377696	23592.2	25701.4	22860.3	19588.2	24148.6	19824.1
GQ037260.1	387456	14634.8	16226.3	17198.6	11367.3	15253.1	13107.0
GQ104220.1	437030	6741.2	3465.0	10358.9	9504.5	4427.1	4288.0
GQ096372.1	409307	28799.4	26846.8	27260.5	23337.2	24970.9	24378.9
GQ101923.1	383792	12825.0	8576.3	33486.0	12479.7	14495.3	6838.9
GQ095730.1	386125	20923.8	20872.2	10952.8	16384.4	20151.1	19838.4
GQ094983.1	415251	23569.6	21936.6	14782.3	26334.8	21798.9	20220.1
GQ092769.1	389569	6246.1	1787.3	3563.6	10300.2	3741.5	8031.6
GQ115257.1	407710	15956.5	17103.5	18262.5	12693.1	17016.4	14425.4
GQ095889.1	419027	3470.5	3455.3	3640.7	8443.9	757.3	6710.8
GQ096712.1	442178	6407.7	3830.5	972.5	5392.3	1203.7	2719.1
GQ087481.1	393707	18402.6	16136.8	19567.4	18565.3	14750.1	15866.9
GQ106815.1	452505	15816.2	6051.7	13021.3	14661.9	3455.5	7300.4
GQ099405.1	403120	6708.1	5966.4	10632.8	7607.5	6606.0	6017.4
GQ091527.1	378786	20892.1	18635.7	11838.6	20309.6	23634.6	18908.2
GQ089214.1	452186	15862.8	13410.0	13404.0	15642.6	8769.8	11153.7
GQ076253.1	426520	11367.5	8881.7	7885.8	11868.8	5672.3	5840.6
GQ099039.1	410329	19465.1	17059.4	12897.9	18749.2	12867.5	16446.1
GQ097787.1	428364	1055.7	746.1	4113.6	6521.2	837.4	1082.4
GQ105964.1	393173	18033.6	13976.1	17991.3	18350.6	15172.2	15538.6

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GQ072845.1 gg_id:392268 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw201h06c
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GQ096061.1 gg_id:458680 Topographical and Temporal Human Skin Microbiome skin back clone nbw386b01c1
FJ193807.1 gg_id:312871 Genetic inventory 'KSC-Astrotek' spacecraft assembly clean room during DAWN missi
CU466880.1 gg_id:305233 Evry wastewater treatment plant anoxic basin clone
DQ658766.1 gg_id:167126 -Defined Acid Drainage Shen-bu Copper Mine China acid mine drainage clone JYC-2N
EU137533.1 gg_id:274869 Bartonella-positive fleas: and assembly patterns Oropsylla hirsuta (prairie dog flea) C
GQ103460.1 gg_id:424126 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
GQ104459.1 gg_id:385502 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ088092.1 gg_id:423439 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ114318.1 gg_id:395924 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw59
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GQ098412.1 gg_id:402761 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw559c
GQ099345.1 gg_id:408167 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw5C
GQ088457.1 gg_id:429581 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw3
GQ098548.1 gg_id:460195 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw703e
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GQ097165.1 gg_id:383370 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
GQ105915.1 gg_id:458158 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw

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GQ096369.1	397786	11199.8	10987.1	11659.4	12768.9	14818.6	12181.2
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GQ072845.1	392268	8862.9	11053.5	13860.1	18410.3	13410.5	9845.6
GQ108016.1	372209	19465.1	17059.4	12897.9	18749.2	12867.5	16446.1
GQ096061.1	458680	6407.7	3830.5	972.5	5392.3	1203.7	2719.1
FJ193807.1	312871	9832.0	9576.5	21547.7	12446.3	12152.9	11057.5
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DQ658766.1	167126	12617.9	10974.2	11946.7	12184.3	9758.8	9432.9
EU137533.1	274869	12062.9	10108.2	17538.5	13482.8	10916.3	10840.1
GQ103460.1	424126	24151.7	24428.8	12428.8	17064.8	25790.7	22331.8
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GQ088092.1	423439	15747.5	15755.7	12482.6	17213.0	14228.3	16430.0
GQ114318.1	395924	9549.8	10696.8	10313.4	11333.9	13423.7	11203.4
GQ106176.1	423510	12581.9	8440.4	19086.0	17619.1	8341.7	9412.4
GQ045560.1	381974	327.3	201.2	608.9	3021.3	234.7	220.3
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GQ098412.1	402761	10553.2	8066.9	14654.0	12134.6	7503.1	8181.0
GQ099345.1	408167	6693.6	6504.8	8592.3	10123.9	6601.4	5008.1
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GQ098548.1	460195	18649.0	18711.2	7592.7	14196.7	18666.9	15038.3
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GQ091924.1	402126	12651.7	12790.4	7252.5	11431.1	12132.6	10292.2
GQ111811.1	445564	10004.4	14418.9	12501.9	9292.8	14613.0	13647.9
GQ097221.1	455427	0.7	0.7	1.1	0.6	0.6	0.6
GQ023723.1	485949	16823.2	18124.9	16188.4	17486.4	12428.5	19153.1
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GQ090370.1	463885	16661.2	18174.1	16656.6	18160.6	23852.8	20051.6
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GQ103535.1 gg_id:376511 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
GQ114021.1 gg_id:455741 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor
GQ115853.1 gg_id:461450 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw602c03c
DQ532149.1 gg_id:163947 Geographical Variation Microbial Burden and Spacecraft Assembly Jet Propulsion Lal
GQ086082.1 gg_id:419032 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ098511.1 gg_id:411500 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw560f
GQ093779.1 gg_id:459883 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw42
GQ097167.1 gg_id:461634 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
GQ102840.1 gg_id:449730 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
GQ107793.1 gg_id:442957 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw554d07
GQ102104.1 gg_id:405771 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw561b0
GQ087622.1 gg_id:449932 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ096402.1 gg_id:409531 Topographical and Temporal Human Skin Microbiome skin back clone nbw387g06c1
GQ101805.1 gg_id:380974 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw499e07c
GQ105619.1 gg_id:443672 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ093133.1 gg_id:423325 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw42
GQ115795.1 gg_id:424008 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw601e10c
GQ097181.1 gg_id:383298 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
GQ075588.1 gg_id:423398 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ092209.1 gg_id:441618 Topographical and Temporal Human Skin Microbiome skin palm clone nbw411a10c1
GQ069897.1 gg_id:410757 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw243b0
GQ115797.1 gg_id:377470 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw601e12c
EU887796.1 gg_id:354443 and RFLP anaerobes Nisargruna biogas plant anaerobic digester clone 56IVSN
GQ102278.1 gg_id:465545 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
GQ112468.1 gg_id:397090 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw
GQ093921.1 gg_id:375326 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
GQ111943.1 gg_id:390620 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw
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GQ083395.1 gg_id:382383 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ111823.1 gg_id:422183 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw
GQ101656.1 gg_id:468045 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw497f11c
GQ103464.1 gg_id:459681 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
GQ102629.1 gg_id:396678 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
FJ999599.1 gg_id:394369 sponge Haliclona simulans South China Sea clone B27
GQ114372.1 gg_id:450085 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw59
GQ104473.1 gg_id:423244 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ103973.1 gg_id:373168 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ104691.1 gg_id:370959 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
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GQ020675.1 gg_id:488994 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n

GQ099020.1	460169	16827.7	14003.7	7506.4	18852.7	17944.5	16406.1
GQ103535.1	376511	16880.6	17084.5	18364.5	17938.7	22719.9	17394.5
GQ114021.1	455741	10129.8	10434.4	17446.8	11015.9	9676.0	8474.8
GQ115853.1	461450	14723.5	14113.0	14932.7	20834.8	17923.5	15477.3
DQ532149.1	163947	12538.7	10499.5	20521.4	13249.2	11056.1	10076.4
GQ086082.1	419032	26972.3	26610.2	23369.9	23015.7	26708.0	24497.2
GQ098511.1	411500	8729.3	10182.4	12387.4	12184.8	17885.0	13887.6
GQ093779.1	459883	18595.4	18201.3	18830.8	22354.1	17753.7	16922.1
GQ097167.1	461634	11190.2	11314.8	17320.5	11432.2	11206.6	9501.5
GQ102840.1	449730	9033.2	10511.9	13012.2	10586.8	13767.9	9966.5
GQ107793.1	442957	13233.6	14631.6	18246.2	14400.6	16254.2	13098.3
GQ102104.1	405771	21379.4	17217.6	14244.0	19141.0	16352.5	16922.7
GQ087622.1	449932	10999.7	9577.7	11364.4	13086.0	11858.2	11417.8
GQ096402.1	409531	11442.6	10313.5	8667.7	13205.8	8960.2	13071.2
GQ101805.1	380974	12332.7	10678.2	11466.1	17748.6	3113.9	8879.6
GQ105619.1	443672	21190.6	21925.3	10376.8	15765.0	14178.1	11880.8
GQ093133.1	423325	4885.3	5555.5	6142.4	5958.4	5106.9	3993.7
GQ115795.1	424008	19367.8	17628.7	16606.3	18671.8	18386.8	13817.4
GQ097181.1	383298	13762.9	11669.7	14327.9	16267.6	10801.6	9630.3
GQ075588.1	423398	16680.7	16152.9	10878.4	14481.9	15139.0	14517.8
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GQ069897.1	410757	6696.1	6481.5	5336.4	9065.6	12231.9	10282.7
GQ115797.1	377470	33814.6	19664.7	14452.1	17849.5	22902.2	19138.3
EU887796.1	354443	23418.7	16619.7	33147.2	25362.6	18463.4	19160.9
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GQ112468.1	397090	15920.3	11152.4	20083.8	17056.3	15200.2	11803.8
GQ093921.1	375326	1095.5	896.9	2000.9	946.9	266.8	595.9
GQ111943.1	390620	13308.4	12515.5	5527.1	15489.5	23438.0	17693.5
GQ086641.1	404860	24233.2	22330.0	18336.4	20892.4	20695.3	19784.6
GQ083395.1	382383	9337.4	4310.7	12785.4	7453.8	7305.1	4543.7
GQ111823.1	422183	1895.9	3123.3	2390.3	9140.3	1925.3	4841.7
GQ101656.1	468045	8265.6	8685.1	17355.6	10130.1	10254.5	6808.9
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GQ114372.1	450085	5334.1	6758.2	12605.4	8991.0	6496.2	5695.1
GQ104473.1	423244	4551.9	2410.5	5859.6	4269.7	3225.1	6004.3
GQ103973.1	373168	7997.3	7838.6	18163.3	26817.3	10278.9	9244.1
GQ104691.1	370959	23028.7	20758.0	17549.6	21676.1	23791.5	19857.5
GQ098323.1	457430	15276.5	18293.2	5883.6	4849.3	2917.7	5780.8
GQ020675.1	488994	13542.4	12293.1	8419.3	13885.4	10552.3	11185.9

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GQ106277.1 gg_id:379099 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw.
GQ106012.1 gg_id:450769 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw!
FJ193271.1 gg_id:350492 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior
GQ104499.1 gg_id:464471 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ097162.1 gg_id:379714 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
GQ099720.1 gg_id:406130 Topographical and Temporal Human Skin Microbiome skin alar crease clone nbw473
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AF035052.1 gg_id:7151 Aquabacterium parvum str. B6
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GQ102389.1 gg_id:430322 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw7
GQ104071.1 gg_id:415413 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw562f08
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GQ087560.1 gg_id:467415 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ105736.1 gg_id:373767 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw5
EF653582.1 gg_id:240768 water s Dong Tinghu clone DTH12

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FJ193271.1	350492	23418.7	16619.7	33147.2	25362.6	18463.4	19160.9
GQ104499.1	464471	10344.8	11123.1	10481.0	12374.4	16224.3	13173.2
GQ097162.1	379714	30841.2	29648.7	21659.3	23016.3	29765.3	26158.2
GQ099720.1	406130	17429.3	10622.9	9297.2	16784.1	5972.3	10457.2
GQ086390.1	387564	6407.7	3830.5	972.5	5392.3	1203.7	2719.1
GQ076171.1	436607	13935.5	10966.4	14507.3	13759.3	9256.0	11436.2
GQ095377.1	412682	16313.8	15807.8	6809.5	17828.3	24050.1	18585.0
AF035052.1	7151	5474.2	2871.2	6415.3	4070.8	2474.5	3591.2
GQ099663.1	409195	15920.3	11152.4	20083.8	17056.3	15200.2	11803.8
GQ107351.1	428208	15747.5	15755.7	12482.6	17213.0	14228.3	16430.0
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GQ107907.1	428819	9015.9	8803.9	13483.8	11018.7	9795.9	9387.5
GQ075543.1	468213	23147.9	22455.8	22676.7	16437.2	15901.2	16234.2
GQ109023.1	402543	12478.4	12587.1	15273.8	13740.7	13075.5	13652.4
GQ096705.1	406483	23418.7	16619.7	33147.2	25362.6	18463.4	19160.9
GQ099375.1	380856	29744.7	30256.2	22818.0	23433.6	29209.9	24617.4
GQ113914.1	402266	5975.9	6916.2	9118.9	8865.3	7653.7	11086.0
GQ114490.1	454947	11717.2	7438.8	5763.2	11728.7	5342.9	8452.4
GQ097446.1	453601	23592.2	25701.4	22860.3	19588.2	24148.6	19824.1
GQ102818.1	450030	15920.3	11152.4	20083.8	17056.3	15200.2	11803.8
GQ101898.1	420221	17831.0	11486.5	25550.8	18597.5	13132.7	14838.2
GQ096089.1	405457	16192.3	12726.7	25139.3	20099.1	13291.2	15421.2
GQ107068.1	392520	12332.7	10678.2	11466.1	17748.6	3113.9	8879.6
GQ114424.1	378339	14607.2	8930.4	22762.0	17456.1	9501.1	13063.2
GQ098431.1	380015	22092.6	19611.7	24526.1	20430.4	19521.5	18768.8
GQ094362.1	463580	6708.1	5966.4	10632.8	7607.5	6606.0	6017.4
GQ082970.1	464942	0.7	0.7	1.1	0.6	0.6	0.6
GQ095871.1	430856	11901.8	9649.2	13458.4	13035.8	12032.9	11329.3
GQ105564.1	403080	23569.6	21936.6	14782.3	26334.8	21798.9	20220.1
GQ096357.1	395332	11363.7	8579.4	11831.8	12004.2	11071.3	11909.4
GQ102389.1	430322	16939.2	11722.1	26266.3	18568.0	10813.3	16526.3
GQ104071.1	415413	26090.6	26804.5	19594.0	19295.5	25852.2	22938.8
GQ094524.1	450796	6411.0	5354.4	9760.3	10773.4	5202.5	6206.4
GQ102957.1	438094	12853.9	10240.2	18110.9	13025.8	10859.3	11295.7
GQ115361.1	443941	14991.3	11105.8	15448.2	15491.8	15114.4	12962.1
GQ087560.1	467415	16240.9	16275.2	12604.8	15043.6	16245.4	15155.9
GQ105736.1	373767	29744.7	30256.2	22818.0	23433.6	29209.9	24617.4
EF653582.1	240768	6906.5	6304.3	14902.2	10024.2	3692.6	7692.2

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GQ085424.1 gg_id:422806 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw275e05c
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GQ092624.1 gg_id:428678 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ103587.1 gg_id:398392 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
GQ088174.1 gg_id:396962 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw3
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GQ097213.1 gg_id:380705 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
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GQ096856.1	379106	8893.6	9436.0	15457.4	10185.3	13557.4	9884.9
GQ112317.1	371104	15920.3	11152.4	20083.8	17056.3	15200.2	11803.8
GQ085424.1	422806	9337.4	4310.7	12785.4	7453.8	7305.1	4543.7
GQ104571.1	392064	3156.9	2891.4	12006.6	3770.6	5666.4	3666.0
GQ092624.1	428678	12020.6	10860.2	15954.4	13851.1	9124.0	9830.4
GQ103587.1	398392	12354.8	13279.2	15635.8	14345.9	13055.6	11890.1
GQ088174.1	396962	28799.4	26846.8	27260.5	23337.2	24970.9	24378.9
GQ070834.1	451508	19875.6	17279.7	14502.5	18500.8	22523.8	19796.5
GQ107060.1	395148	20229.2	17852.7	25548.0	19502.8	19827.9	19685.1
GQ087599.1	409034	20892.1	18635.7	11838.6	20309.6	23634.6	18908.2
GQ096619.1	454209	9765.3	6096.4	6589.9	10639.2	4756.0	9188.0
GQ086991.1	404400	9542.6	9917.4	11953.2	11943.9	15685.5	12362.7
GQ114386.1	373411	13983.8	14400.0	16597.1	12670.3	17488.7	12074.1
GQ075507.1	417427	13388.2	12553.3	18120.6	14295.3	11595.9	11087.2
GQ107346.1	385095	27175.4	26365.2	15376.4	22036.1	25048.4	24167.0
GQ105085.1	457972	5139.1	7964.3	8838.7	10830.3	12988.8	19802.9
GQ106759.1	390955	25012.4	25583.4	16876.9	22597.5	24990.7	23299.5
GQ099654.1	427288	17666.7	11853.5	14300.0	18426.1	14755.3	14186.3
GQ085374.1	392948	17811.7	14945.4	21515.7	20121.7	12745.2	15761.3
GQ114527.1	414059	14933.5	12803.9	11833.4	14238.0	11544.2	11126.6
GQ097790.1	417520	10843.3	8762.4	24119.1	10585.1	13175.2	7562.5
GQ096322.1	384357	264.1	971.7	5644.2	1157.0	621.3	1591.9
GQ101764.1	405535	29744.7	30256.2	22818.0	23433.6	29209.9	24617.4
GQ095901.1	378474	15769.9	13305.0	14489.8	14373.9	15964.6	11555.2
GQ015397.1	494269	12182.6	12523.4	19839.6	13260.4	8151.3	10900.1
GQ102546.1	388041	13401.8	5547.8	16948.5	14533.1	7715.9	9231.7
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GQ102778.1	408054	5359.6	2239.7	4902.1	7010.3	2785.6	5432.5
GQ093044.1	410558	21315.8	21273.7	11898.5	20264.4	26983.5	21478.4
GQ102203.1	389506	22040.2	20408.4	13043.6	21300.8	24996.9	18463.5
GQ113274.1	460822	15185.5	15334.4	11716.3	16300.5	17865.4	15944.1
GQ097213.1	380705	8558.5	7498.8	15604.1	12894.1	8684.1	7747.4
GQ097174.1	445004	11297.1	11410.4	11624.2	8303.0	10942.4	9688.7
GQ092987.1	398381	11821.9	3152.6	7822.1	8313.8	3286.7	5569.6
GQ105325.1	390204	14662.0	5314.1	10402.8	16721.5	3212.4	6750.9
GQ097056.1	418918	20793.1	19558.7	21706.3	17836.7	18155.4	16413.9
GQ090536.1	427225	23503.6	23629.4	17009.5	18957.8	22326.6	21418.3
GQ105129.1	454577	14050.2	12579.8	15539.1	13134.4	12189.1	11923.5
GQ085331.1	444595	6791.7	6891.6	15710.7	8077.0	6796.3	5712.7

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GQ107416.1 gg_id:401745 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw
GQ059794.1 gg_id:453077 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
AY662015.1 gg_id:136395 uranium-contaminated groundwater clone 005C-F01
GQ102754.1 gg_id:426821 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ105492.1 gg_id:417538 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ096406.1 gg_id:405265 Topographical and Temporal Human Skin Microbiome skin back clone nbw387g10c1
GQ096250.1 gg_id:459256 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ114550.1 gg_id:435522 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ106292.1 gg_id:427867 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
GQ099601.1 gg_id:456380 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw51
GQ107036.1 gg_id:450401 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw543h1
GQ087512.1 gg_id:374827 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw358d0
GQ101479.1 gg_id:391097 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw495f
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GQ340181.1 gg_id:532736 Prokaryotic Marathonas Reservoir Greece water column clone K07-63-BAC
GQ106498.1 gg_id:456829 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ065880.1 gg_id:445218 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw94a10
GQ058982.1 gg_id:386277 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbu58
GQ114479.1 gg_id:388259 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ105570.1 gg_id:432947 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ092040.1 gg_id:441616 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw405d01
GQ104228.1 gg_id:443965 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
GQ108232.1 gg_id:430008 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw604b08
GQ096499.1 gg_id:442513 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw389a0
GQ103568.1 gg_id:397691 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
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GQ106359.1 gg_id:449858 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
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GQ102121.1 gg_id:458248 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw561d0
GQ083421.1 gg_id:448823 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ105661.1 gg_id:405154 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
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GQ104420.1 gg_id:452618 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n

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GQ112251.1	405699	29744.7	30256.2	22818.0	23433.6	29209.9	24617.4
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GQ059794.1	453077	9328.4	8277.4	10417.8	10247.3	9914.1	9886.8
AY662015.1	136395	14148.2	7678.7	17260.6	14157.9	2845.4	5940.5
GQ102754.1	426821	20643.6	21604.8	22250.9	17289.2	22730.4	18474.1
GQ105492.1	417538	9926.0	7480.7	7809.2	12310.3	4347.9	4782.1
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GQ107036.1	450401	14411.4	15149.4	18125.5	12184.4	13963.6	12328.8
GQ087512.1	374827	14474.8	11348.9	9794.5	15465.7	12059.4	11305.1
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GQ099164.1	437620	14395.9	14242.2	17997.3	12026.9	21354.5	16431.2
GQ340181.1	532736	6903.4	6573.9	10923.0	7876.5	6809.2	6714.0
GQ106498.1	456829	11605.6	11135.4	15619.9	13113.4	12286.5	10314.3
GQ065880.1	445218	15276.5	18293.2	5883.6	4849.3	2917.7	5780.8
GQ058982.1	386277	9708.3	4536.6	12228.2	8926.0	3560.4	5158.6
GQ114479.1	388259	17518.8	17887.3	18654.3	16582.8	20266.5	18945.8
GQ105570.1	432947	24151.7	24428.8	12428.8	17064.8	25790.7	22331.8
GQ092040.1	441616	9423.0	8179.0	13539.7	10344.8	7175.6	7682.7
GQ104228.1	443965	13163.2	9890.8	10827.6	13699.4	7773.7	9854.0
GQ108232.1	430008	19367.8	17628.7	16606.3	18671.8	18386.8	13817.4
GQ096499.1	442513	26633.3	29329.8	15060.5	22013.5	27071.1	22938.2
GQ103568.1	397691	15747.5	15755.7	12482.6	17213.0	14228.3	16430.0
GQ112221.1	427924	18590.8	17361.9	10524.6	19128.3	21660.5	17714.8
GQ106359.1	449858	12975.1	7842.4	3724.8	12082.5	4867.5	8590.5
GQ098868.1	451237	14710.7	13878.4	17981.1	14373.2	10647.7	11944.6
GQ092748.1	439130	3791.4	4002.9	9926.6	7068.1	2056.4	4638.0
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GQ114707.1	388921	23592.2	25701.4	22860.3	19588.2	24148.6	19824.1
GQ106194.1	415892	14534.1	10341.5	8176.2	16018.9	8973.7	11229.0
GQ091452.1	400806	8570.8	7156.0	10481.6	11033.6	6474.7	7619.5
GQ085258.1	384045	12332.7	10678.2	11466.1	17748.6	3113.9	8879.6
GQ085262.1	417230	27188.5	26832.2	22248.9	21420.6	27038.1	22990.6
GQ104420.1	452618	18633.7	18198.8	14381.4	17742.7	18583.4	16426.5

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GQ106120.1 gg_id:406577 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw!
GQ099273.1 gg_id:376632 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ115539.1 gg_id:406820 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw687b1:
AM412127.1 gg_id:250172 Aquabacterium sp. str. P-136
GQ104024.1 gg_id:399685 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw562a0!
GQ098817.1 gg_id:391878 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw703a
GQ074868.1 gg_id:411231 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
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GQ093004.1 gg_id:400509 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw407h04c
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GQ114541.1 gg_id:459807 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw(
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AY622246.1 gg_id:107588 subsurface soil clone B-N19
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GQ111400.1 gg_id:447309 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw666f11

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GQ106120.1	406577	12512.8	13068.9	13458.5	14651.2	13147.6	13059.6
GQ099273.1	376632	20783.0	18835.4	22661.8	18253.9	18348.0	17583.6
GQ115539.1	406820	4447.0	5366.9	13065.0	6857.1	3068.5	5029.4
AM412127.1	250172	18159.2	11003.8	17653.9	16178.4	10277.4	12069.6
GQ104024.1	399685	8904.4	9767.3	10923.1	15821.2	11417.2	9706.7
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GQ074868.1	411231	25726.5	34485.8	34254.0	30089.7	34113.1	30788.1
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GQ098252.1	372902	14568.7	10837.1	21709.4	16050.3	10551.1	13390.0
GQ088823.1	435620	15747.5	15755.7	12482.6	17213.0	14228.3	16430.0
GQ087600.1	434175	18590.8	17361.9	10524.6	19128.3	21660.5	17714.8
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GQ105039.1	432907	22292.2	20939.6	20951.6	17182.7	20264.9	18896.6
GQ094575.1	397115	10537.8	9782.6	3281.2	12447.0	13409.4	12157.1
GQ092357.1	428249	6226.1	4954.9	9865.6	9457.9	11648.7	6084.2
GQ092767.1	426637	9753.0	11390.2	12718.9	10337.8	10971.0	9233.7
GQ107242.1	408722	12676.6	8820.9	15538.9	11851.0	9546.3	10089.8
GQ083299.1	407867	9839.9	8391.1	11394.5	10582.6	10136.3	11271.4
GQ102174.1	433310	26207.6	25387.3	24814.4	18447.0	25211.7	21858.9
GQ104639.1	441724	28799.4	26846.8	27260.5	23337.2	24970.9	24378.9
GQ098540.1	408917	8929.0	3088.8	4041.7	12879.8	1325.7	3305.3
GQ102227.1	400853	10679.4	6917.5	16591.6	11234.4	10093.2	7780.6
GQ070488.1	384166	13367.9	17232.5	11811.3	13930.6	16463.3	14076.3
GQ107609.1	413866	23592.2	25701.4	22860.3	19588.2	24148.6	19824.1
GQ092841.1	395021	17007.2	13393.7	13577.1	18484.0	11058.8	12324.6
GQ104512.1	429039	21190.6	21925.3	10376.8	15765.0	14178.1	11880.8
GQ085287.1	412408	21190.6	21925.3	10376.8	15765.0	14178.1	11880.8
GQ094432.1	414093	8862.9	11053.5	13860.1	18410.3	13410.5	9845.6
GQ088836.1	393142	17324.0	18637.4	16559.6	15964.3	15772.2	15787.6
GQ093004.1	400509	11368.0	12339.0	16190.8	10351.6	12373.5	9767.2
GQ115826.1	374192	22167.7	22552.7	21185.5	18455.8	22277.6	19658.7
GQ114541.1	459807	7436.0	8375.0	18149.1	9007.4	9432.2	7287.8
GQ111819.1	397776	12544.0	12117.9	8444.3	14388.0	15385.9	11528.2
AY622246.1	107588	10117.1	8634.3	11012.5	11719.0	12638.7	12179.8
GQ091448.1	401521	12374.9	7765.7	13446.0	13804.0	6191.8	9034.0
GQ102587.1	439788	327.3	201.2	608.9	3021.3	234.7	220.3
GQ075015.1	390653	24457.1	25443.2	17617.2	20481.3	25008.1	22039.4
GQ095788.1	404137	27175.4	26365.2	15376.4	22036.1	25048.4	24167.0
GQ111400.1	447309	17752.2	17856.5	18902.1	16227.7	19324.5	16632.2

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GQ069024.1	389648	7595.0	6557.9	6880.9	17932.4	6715.8	7403.2
GQ084804.1	396211	6890.0	6764.8	6701.0	7860.6	4028.2	4653.4
GQ106568.1	462068	5996.0	8181.5	11121.6	15405.1	9426.7	7302.9
GQ092838.1	388454	8212.8	7903.6	5555.5	9663.7	10275.4	9596.3
GQ095752.1	452249	15747.5	15755.7	12482.6	17213.0	14228.3	16430.0
GQ091982.1	389015	0.7	0.7	1.1	0.6	0.6	0.6
GQ098595.1	465965	8783.9	7608.4	6689.7	9528.5	7905.5	8120.2
GQ107701.1	412268	28811.8	28615.8	19175.4	22885.4	30814.5	24184.7
GQ094196.1	453201	8928.5	4363.7	13260.6	9823.7	5302.7	6415.7
GQ115240.1	429515	11602.3	8580.6	22019.5	13042.9	9595.7	9610.9
GQ074972.1	395082	14407.7	14521.6	19086.1	13833.2	14911.8	12409.6
GQ075570.1	406791	28811.8	28615.8	19175.4	22885.4	30814.5	24184.7
GQ100873.1	376799	8403.8	7862.9	12852.1	11395.2	8754.7	7792.9
GQ099041.1	446938	22525.2	20809.9	17135.3	17178.8	19368.5	19834.7
GQ095705.1	389032	21683.8	19127.5	17417.4	17707.2	20309.4	16353.8
GQ085392.1	429102	16378.6	17654.8	11787.3	18129.0	19888.1	17257.5
GQ104568.1	407991	10113.6	9582.4	9373.4	12386.5	11076.9	11113.0
GQ101139.1	430619	28811.8	28615.8	19175.4	22885.4	30814.5	24184.7
GQ083398.1	419438	18188.7	14748.7	16703.1	20236.9	19284.0	27133.1
GQ069100.1	444806	13388.2	12553.3	18120.6	14295.3	11595.9	11087.2
GQ113298.1	383564	10140.3	9249.5	17182.8	11311.0	8509.6	11036.1
GQ094593.1	415340	6243.5	6008.0	11611.6	8007.8	7042.8	5941.1
GQ083343.1	463101	17429.3	10622.9	9297.2	16784.1	5972.3	10457.2
GQ115546.1	446699	5647.7	5956.4	3093.2	6551.6	173.9	893.5
GQ106130.1	383666	7508.5	8783.9	15281.9	9453.9	12695.9	8254.6
GQ075013.1	402546	17146.9	18827.6	16078.8	14548.1	19074.0	15645.4
GQ103988.1	379085	25071.2	23053.6	25691.0	22699.7	22338.9	20503.6
GQ099270.1	387050	16459.8	16168.9	12250.4	16697.1	18422.1	18428.3
GQ099427.1	400652	9698.8	11213.1	8478.1	10573.4	11945.3	9461.8
GQ101670.1	461931	20479.1	17491.8	20397.2	18620.7	18799.1	16127.9
GQ113344.1	433398	13502.4	12930.4	18097.1	11540.0	13098.1	10957.2
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GQ087551.1	389397	6763.3	7537.8	13644.5	12074.1	10181.4	8081.8
GQ103846.1	440327	15450.2	8377.0	19169.0	16053.4	5709.9	8392.4
GQ106503.1	401153	21315.8	21273.7	11898.5	20264.4	26983.5	21478.4
GQ099779.1	437721	12518.0	5881.3	19183.3	14509.6	8463.3	9800.3
GQ089327.1	457907	11718.6	14909.9	14547.6	10920.3	7741.3	7364.2