AB042501.2 gg_id:17793 Halomonas sp. str. TAG C4
AF140007.1 gg_id:8134 Halomonas sp. str. ML-185
GU212635.1 gg_id:559842 Halomonas sp. str. H57B76
FJ978741.1 gg_id:436100 feces clone CL_F_444
GU001906.1 gg_id:550587 Halomonas pacifica str. PL51
FJ152554.1 gg_id:331625 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX1A_
AY505526.1 gg_id:101462 Halomonas variabilis str. GSP28
EU880513.1 gg_id:303578 Halomonas sp. str. P56
X92151.1 gg_id:51042 Lake Bogoria isolate 24B1
DQ001682.1 gg_id:157952 Microbial seeps asphalt seep clone B101-20
FJ978758.1 gg_id:373671 feces clone CL_F_464
FJ153012.1 gg_id:328530 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX4CI
U85873.1 gg_id:8145 Halomonas variabilis str. SW48
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DQ128258.1 gg_id:200527 Unique Microbial Fluids Chinese Continental Scientific Drilling drilling fluid clone CCS
GU001901.1 gg_id:593434 Halomonas halophila str. PLD
EF143431.1 gg_id:188268 Halomonas aquamarina WP02-1-81
FJ444974.1 gg_id:573554 Halomonas sp. str. whb28
EU722713.1 gg_id:352742 Halomonas salina str. SBC8
AJ306893.1 gg_id:33823 Halomonas variabilis str. DSM 3051
EU432575.1 gg_id:259254 Halomonas sp. str. 10043
FJ418176.1 gg_id:358381 Modicisalibacter sp. str. YIM 90637
FJ607360.1 gg_id:542842 Halomonas sp. str. SeaH-As8w
FJ152704.1 gg_id:321200 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX1A_
AB305300.1 gg_id:231115 Chromohalobacter sp. str. Sa11-3XX
FN257741.1 gg_id:553188 Halomonas maura str. S-31
AY952453.1 gg_id:114486 Halomonas sp. str. B12
GU397433.1 gg_id:523209 Halomonas sp. str. AAD2
GU166164.1 gg_id:579641 intestinal tract larvae (Musca domestica) direct cloning and sequencing genes whea
FJ172099.1 gg_id:312851 Halomonas sp. str. SBC13
EU594554.1 gg_id:271380 Pseudomonas fluorescens str. 2-4
FJ978736.1 gg_id:417685 feces clone CL_F_438
DQ280368.1 gg_id:143508 Halomonas sp. str. BH843
GU397429.1 gg_id:516866 Halomonas sp. str. AAD12
AY647309.1 gg_id:104617 Halomonas desiderata str. MSU3810
AF170753.1 gg_id:8146 Halomonas sp. str. QSSC9-11
EU159469.4 gg_id:240141 Halomonas taiwanensis str. Halo30-01
EF627999.1 gg_id:231117 Halomonas sp. str. P15
FJ172096.1 gg_id:317854 Halomonas sp. str. SBC16

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| GU001906.1 | 550587 | 143.9 | 282.1 | 928.5 | 732.1 | 1103.3 | 2086.9 |
| FJ152554.1 | 331625 | 4626.1 | 7853.8 | 5754.3 | 5517.0 | 13763.5 | 9019.3 |
| AY505526.1 | 101462 | 775.6 | 109.2 | 109.2 | 541.3 | 1839.1 | 1743.0 |
| EU880513.1 | 303578 | 5145.1 | 3593.3 | 3535.4 | 6124.4 | 5656.9 | 5361.8 |
| X92151.1 | 51042 | 6127.7 | 5285.3 | 5057.7 | 6542.9 | 4713.1 | 4536.9 |
| DQ001682.1 | 157952 | 54.7 | 119.4 | 202.7 | 161.4 | 440.0 | 981.2 |
| FJ978758.1 | 373671 | 9379.2 | 9659.5 | 8216.1 | 8364.0 | 13296.9 | 9446.4 |
| FJ153012.1 | 328530 | 2028.9 | 1791.1 | 5240.3 | 2632.0 | 1803.3 | 2042.4 |
| U85873.1 | 8145 | 9557.3 | 8326.2 | 5452.7 | 7840.5 | 8568.7 | 6809.7 |
| GU397430.1 | 531203 | 9642.7 | 10169.6 | 8372.4 | 9979.6 | 12367.9 | 10857.0 |
| FJ978750.1 | 375726 | 9688.9 | 6637.6 | 7908.9 | 7821.8 | 7977.8 | 6794.1 |
| AB305246.1 | 229538 | 1559.2 | 1413.1 | 2722.8 | 1891.2 | 2256.8 | 2971.8 |
| DQ128258.1 | 200527 | 3378.9 | 3651.6 | 2126.7 | 2984.1 | 1097.9 | 3865.5 |
| GU001901.1 | 593434 | 2964.2 | 2552.0 | 4296.8 | 4804.9 | 8007.7 | 4014.9 |
| EF143431.1 | 188268 | 504.8 | 939.2 | 781.9 | 531.7 | 1464.0 | 1318.5 |
| FJ444974.1 | 573554 | 3366.3 | 3923.9 | 5497.7 | 3993.4 | 5807.7 | 6179.2 |
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| FJ418176.1 | 358381 | 1229.3 | 1463.1 | 3010.3 | 3066.4 | 4416.0 | 4243.9 |
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| FJ152704.1 | 321200 | 2969.7 | 4170.3 | 5218.7 | 1910.9 | 7161.0 | 4774.9 |
| AB305300.1 | 231115 | 993.3 | 979.3 | 2392.8 | 873.6 | 4561.9 | 1991.1 |
| FN257741.1 | 553188 | 1192.4 | 1516.7 | 1793.8 | 1563.9 | 2491.0 | 3302.4 |
| AY952453.1 | 114486 | 4634.0 | 5665.3 | 7424.2 | 6126.8 | 11828.9 | 12660.7 |
| GU397433.1 | 523209 | 16362.7 | 17791.0 | 12030.4 | 12561.2 | 16201.9 | 13335.6 |
| GU166164.1 | 579641 | 3306.3 | 3052.1 | 3437.1 | 4589.4 | 1935.7 | 2849.5 |
| FJ172099.1 | 312851 | 6627.0 | 5281.6 | 7173.5 | 6583.0 | 7140.9 | 8198.7 |
| EU594554.1 | 271380 | 1080.2 | 1800.8 | 3305.0 | 2457.1 | 1944.1 | 1200.3 |
| FJ978736.1 | 417685 | 2288.7 | 2510.3 | 2415.1 | 3099.9 | 4824.5 | 5015.9 |
| DQ280368.1 | 143508 | 3646.0 | 3974.0 | 3379.2 | 2567.2 | 4770.8 | 1519.4 |
| GU397429.1 | 516866 | 10090.7 | 10061.7 | 8786.8 | 10248.7 | 13760.7 | 11284.5 |
| AY647309.1 | 104617 | 2380.3 | 2982.7 | 3861.8 | 2321.7 | 2335.1 | 3682.1 |
| AF170753.1 | 8146 | 6618.5 | 5067.5 | 3774.0 | 3797.7 | 5804.1 | 3249.8 |
| EU159469.4 | 240141 | 3370.7 | 4566.5 | 8852.2 | 3428.7 | 9251.0 | 9788.3 |
| EF627999.1 | 231117 | 1664.5 | 1302.0 | 916.3 | 265.3 | 234.3 | 180.9 |
| FJ172096.1 | 317854 | 1634.8 | 1322.9 | 1503.2 | 785.5 | 1338.3 | 1375.2 |

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EU909458.3 gg_id:347570 Halomonas sp. str. Hwa
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AF054286.1 gg_id:8133 Halomonas campisalis str. ATCC 700597 4A
GU001898.1 gg_id:589958 Halomonas shengliensis str. PL16
DQ289060.1 gg_id:144478 Halomonas cf. campisalis 'campaniae' HKS 3
AM110945.1 gg_id:139641 Bacillus subtilis B-3064
AF173968.1 gg_id:71016 Halomonas variabilis str. KT1111
FJ796247.1 gg_id:555230 Halomonas sp. str. JS46
EU822512.1 gg_id:317124 Halomonas xinjiangensis str. TRM 0175
EU447166.1 gg_id:272400 Halomonas sp. str. AGD 3
FJ152923.1 gg_id:351851 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX4CI
GU252151.1 gg_id:591123 Halomonas sp. str. CC-SPL15-4
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GU001886.1 gg_id:548230 Halomonas shengliensis str. PL207
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AY922995.1 gg_id:153241 Halomonas phoceae str. CCUG 5096
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AB354933.1 gg_id:237271 Halomonas taeheungii str. NM5
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AM110962.1 gg_id:140938 Halomonas sp. str. 2006
GU001905.1 gg_id:544868 Halomonas salifodinae str. PL43
AJ876735.1 gg_id:157900 Halomonas sp. PH1226
EU308357.1 gg_id:363386 Halomonas sp. str. TB1612
AF211860.1 gg_id:28015 Halomonas alimentaria str. YKJ-16
U85871.1 gg_id:8143 Halomonas variabilis str. SW04
EF157249.1 gg_id:255098 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon
EU684463.1 gg_id:289972 Halomonas venusta str. Kh-10-91
AM110954.1 gg_id:140937 Halomonas sp. str. 1013
DQ768627.1 gg_id:244318 Halomonas meridiana MARC4B
AJ306892.1 gg_id:38116 Halomonas subglaciescola str. DSM 4683
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DQ129871.2 gg_id:137560 Halomonas sp. LCKW-Isolate10A
FJ764764.1 gg_id:552836 Halomonas sp. str. E-090
EU382220.1 gg_id:261457 Bacillus subtilis str. 15-2
AB069958.1 gg_id:67708 Halomonas sp. SK1

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| GU397428.1 | 514707 | 5014.8 | 5504.2 | 8700.6 | 7301.1 | 10979.9 | 7042.3 |
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| FJ444954.1 | 513000 | 724.3 | 1051.8 | 2165.3 | 2045.9 | 2068.3 | 2341.8 |
| EU909458.3 | 347570 | 11767.0 | 8983.0 | 11816.1 | 12194.2 | 11744.5 | 11523.9 |
| AM111020.1 | 140975 | 10688.8 | 6249.1 | 6333.1 | 6931.0 | 11552.2 | 7158.7 |
| AF054286.1 | 8133 | 219.0 | 317.0 | 208.1 | 170.7 | 1812.0 | 1238.4 |
| GU001898.1 | 589958 | 11288.1 | 11303.8 | 5395.2 | 8954.8 | 14688.9 | 12357.7 |
| DQ289060.1 | 144478 | 839.9 | 508.0 | 1367.6 | 1986.8 | 925.3 | 548.4 |
| AM110945.1 | 139641 | 4727.9 | 2387.1 | 3369.8 | 3681.1 | 2914.3 | 4251.5 |
| AF173968.1 | 71016 | 2429.5 | 2797.6 | 786.1 | 1858.1 | 214.6 | 474.0 |
| FJ796247.1 | 555230 | 6748.0 | 6595.3 | 6497.4 | 4008.9 | 4300.8 | 1567.3 |
| EU822512.1 | 317124 | 252.7 | 434.3 | 724.9 | 163.4 | 1950.3 | 1352.2 |
| EU447166.1 | 272400 | 289.3 | 390.5 | 800.7 | 945.2 | 1018.6 | 1766.5 |
| FJ152923.1 | 351851 | 696.4 | 705.9 | 486.9 | 648.2 | 60.6 | 1498.3 |
| GU252151.1 | 591123 | 823.9 | 882.3 | 1955.4 | 1662.7 | 5452.2 | 1862.2 |
| NR_027219.1 | 571751 | 907.6 | 1490.4 | 1207.2 | 849.1 | 547.4 | 697.8 |
| GU001886.1 | 548230 | 1862.2 | 1551.7 | 2583.4 | 2553.9 | 4977.2 | 2973.0 |
| FJ978688.1 | 571906 | 462.7 | 733.5 | 1415.9 | 700.3 | 1703.9 | 2020.3 |
| AM110934.1 | 139678 | 3625.7 | 4723.9 | 5321.7 | 4053.7 | 8409.9 | 8186.0 |
| AY922995.1 | 153241 | 368.8 | 484.2 | 865.8 | 563.2 | 382.6 | 387.2 |
| GU217705.1 | 583245 | 866.9 | 740.8 | 1716.6 | 957.6 | 1486.5 | 461.3 |
| AJ294348.1 | 75905 | 4208.0 | 3021.8 | 2332.3 | 2185.6 | 498.1 | 931.9 |
| AB354933.1 | 237271 | 4631.3 | 3629.4 | 3403.9 | 2874.6 | 1580.2 | 2029.3 |
| FJ152888.1 | 347546 | 3130.9 | 3582.8 | 2804.9 | 3808.1 | 3005.7 | 3280.5 |
| AM111019.1 | 140888 | 3893.0 | 3265.7 | 6746.2 | 2965.3 | 2205.4 | 3601.7 |
| AM110962.1 | 140938 | 18.1 | 19.4 | 20.9 | 57.8 | 69.7 | 24.4 |
| GU001905.1 | 544868 | 3594.6 | 2352.9 | 3963.4 | 4224.9 | 1870.2 | 3214.4 |
| AJ876735.1 | 157900 | 2465.1 | 1691.5 | 3148.4 | 2492.6 | 1626.3 | 3283.0 |
| EU308357.1 | 363386 | 5456.7 | 3504.8 | 4929.8 | 5795.9 | 4322.8 | 4721.3 |
| AF211860.1 | 28015 | 5651.0 | 6096.5 | 9819.8 | 6601.4 | 8904.4 | 8791.8 |
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| EU684463.1 | 289972 | 9503.8 | 7026.7 | 5516.4 | 8647.0 | 7285.4 | 8248.1 |
| AM110954.1 | 140937 | 3466.9 | 4343.6 | 3376.7 | 4607.8 | 4541.3 | 4560.8 |
| DQ768627.1 | 244318 | 5459.7 | 4359.3 | 3738.6 | 4463.6 | 7748.5 | 5621.4 |
| AJ306892.1 | 38116 | 43.2 | 40.1 | 37.5 | 68.4 | 2426.4 | 64.5 |
| DQ458819.1 | 156772 | 1023.2 | 1174.7 | 842.1 | 1232.7 | 3071.9 | 1856.0 |
| DQ129871.2 | 137560 | 5892.1 | 8937.2 | 3788.2 | 6805.3 | 11167.6 | 9324.6 |
| FJ764764.1 | 552836 | 2572.4 | 1135.5 | 1163.3 | 2477.2 | 1907.8 | 2233.5 |
| EU382220.1 | 261457 | 2143.8 | 2320.1 | 3522.4 | 2458.2 | 5733.2 | 4159.9 |
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X93493.1 gg_id:8136 Halomonas pantelleriensis str. AAP
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EU075119.1 gg_id:246266 Halomonas sp. str. CSQ5
AY669165.1 gg_id:102493 Halomonas venusta OC-4
EU308351.1 gg_id:367476 Halomonas sp. str. FIB163_2
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AY382579.2 gg_id:95058 Halomonas koreensis str. SS20
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DQ358666.1 gg_id:269110 Halomonas sp. str. YIM DKMY60
AM490136.1 gg_id:203382 Halomonas sp. str. IB-O18
FJ984862.3 gg_id:577434 Halomonas sp. str. YCSA28
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EF442769.1 gg_id:206143 Halomonas salaria str. 5-3
AF212202.2 gg_id:40996 Halomonas neptunia str. Eplume1; ATCC BAA-805; CECT 5815; DSM 15720; CCM 7107
AF139993.1 gg_id:24119 Halomonas sp. str. ML-027
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AY035894.1 gg_id:36784 Halomonas cupida str. An1
FJ429198.1 gg_id:357869 Halomonas sp. str. JSM 078169
EU735712.1 gg_id:347232 Biological Arsenic Remediation Project Groundwater Aquifer soil clone 2As2
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AM111093.1 gg_id:140764 Halomonas sp. str. 8059
EF628007.1 gg_id:231641 Halomonas sp. str. P24
EU624431.1 gg_id:284938 Halomonas aquamarina str. S6-07
EF121853.1 gg_id:177035 Halomonas shenglis str. SL014B-85T
AM110951.1 gg_id:140755 Halomonas sp. str. 1005
AY167282.1 gg_id:82157 Halomonas variabilis str. ANT9112
AJ616910.1 gg_id:99504 Halomonas organivorans str. G-16.1
GU397427.1 gg_id:522529 Halomonas sp. str. AAD1
EU447162.1 gg_id:262835 Halomonas sp. str. CH3
EF674852.1 gg_id:255434 Halomonas xinjiangensis str. YIM 91125
FJ973521.1 gg_id:396322 Halomonas venusta str. NBSL13
X92148.1 gg_id:113719 Crater Lake isolate 29C1
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| GU001893.1 | 571136 | 2860.6 | 2988.2 | 4929.3 | 3722.3 | 4441.7 | 3454.3 |
| FN397896.1 | 462928 | 4052.7 | 5611.4 | 2859.1 | 3038.3 | 2352.0 | 2693.6 |
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| AY505528.1 | 101792 | 330.5 | 369.5 | 324.1 | 150.7 | 1946.2 | 851.3 |
| EU075119.1 | 246266 | 2207.4 | 1443.7 | 2359.2 | 1907.7 | 1664.2 | 2835.1 |
| AY669165.1 | 102493 | 1898.7 | 1207.5 | 868.9 | 551.4 | 1469.9 | 498.9 |
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| AY849802.1 | 110100 | 155.8 | 202.6 | 110.5 | 93.3 | 193.0 | 170.2 |
| AY382579.2 | 95058 | 2096.9 | 2761.8 | 5293.1 | 4464.0 | 4718.1 | 4179.4 |
| DQ270727.1 | 144159 | 425.8 | 379.4 | 305.5 | 604.5 | 954.3 | 759.2 |
| DQ358666.1 | 269110 | 947.7 | 1921.8 | 4587.0 | 3531.6 | 2351.0 | 2216.1 |
| AM490136.1 | 203382 | 1329.0 | 626.3 | 2109.9 | 1725.8 | 696.7 | 1582.5 |
| FJ984862.3 | 577434 | 1445.4 | 1792.9 | 4245.4 | 2509.7 | 2945.3 | 4896.7 |
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| EF442769.1 | 206143 | 246.0 | 232.5 | 209.9 | 272.5 | 566.5 | 159.2 |
| AF212202.2 | 40996 | 4627.6 | 3633.1 | 3568.8 | 2884.9 | 1598.0 | 2037.2 |
| AF139993.1 | 24119 | 244.0 | 358.1 | 383.9 | 280.9 | 2343.1 | 1128.9 |
| DQ015832.1 | 139755 | 52.3 | 62.7 | 134.1 | 94.0 | 153.8 | 125.1 |
| AY035894.1 | 36784 | 2097.4 | 2109.1 | 1949.0 | 2514.3 | 3163.4 | 2089.1 |
| FJ429198.1 | 357869 | 5152.5 | 5624.0 | 4946.9 | 5880.0 | 5318.4 | 4105.3 |
| EU735712.1 | 347232 | 894.5 | 1054.7 | 1231.8 | 581.2 | 4086.7 | 2350.9 |
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| AM111093.1 | 140764 | 771.1 | 768.5 | 1143.3 | 596.6 | 278.7 | 585.7 |
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| EU624431.1 | 284938 | 526.9 | 812.9 | 1158.2 | 1137.0 | 684.8 | 1478.2 |
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| AM110951.1 | 140755 | 84.6 | 134.1 | 282.7 | 145.4 | 582.8 | 497.8 |
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| GU397427.1 | 522529 | 9365.0 | 7104.1 | 4226.4 | 9932.0 | 10680.8 | 8893.6 |
| EU447162.1 | 262835 | 11651.4 | 12974.7 | 8263.0 | 8759.2 | 14395.2 | 12296.2 |
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GQ375779.1 gg_id:581670 Halomonas sp. str. D02
AM941746.1 gg_id:277216 Kushneria aurantia str. A10
DQ087259.1 gg_id:132883 Salicola marensis 7Sa10
GU397403.1 gg_id:515060 Salicola marasensis str. W4B
DQ129689.1 gg_id:137579 Pseudomonas salina str. B2
GU397402.1 gg_id:522270 Salicola salis str. W7B
AF211871.1 gg_id:55625 Zymobacter palmae str. ATCC 51623
EU735693.1 gg_id:354231 archaeal structures oil contaminated and soils China pristine soil Jidong Oilfield clone
DQ072719.1 gg_id:134569 Halospina denitrificans str. HGD 1-3
D14555.1 gg_id:8114 Zymobacter palmae str. T109
AB021383.1 gg_id:8811 Pseudomonas halophila str. DSM 3050T
EU305727.1 gg_id:340031 Pseudomonas sp. str. TBZ33
AY987840.1 gg_id:128215 Microbial Salterns Maras salterns clone 2B4
GQ375775.1 gg_id:564683 Chromohalobacter sp. str. B02
EU308410.1 gg_id:368617 Halomonas sp. str. TB21_12
DQ641495.1 gg_id:215031 Chromohalobacter tunisiensis str. Lit 2
GQ246216.1 gg_id:578822 Kushneria sp. str. YCWA18
FJ463811.1 gg_id:580770 Chromohalobacter sp. str. ST307
FJ444986.1 gg_id:554249 Halomonas taeanensis str. whb40
EU735657.1 gg_id:309472 archaeal structures oil contaminated and soils China pristine soil Jidong Oilfield clone
DQ421388.1 gg_id:156429 Halotalea alkalilenta str. AW-7
EU487856.1 gg_id:568866 lucinid bivalve- symbiotic system: significance geochemical habitat on and gill symbi
EU487858.1 gg_id:570303 lucinid bivalve- symbiotic system: significance geochemical habitat on and gill symbi
EF508132.1 gg_id:241778 evidence unusual symbiont gills Acesta excavata bivalve gill specimen Ae1 320 m dep
AB054156.1 gg_id:48284 marine sponge clone HOC22
AB054159.1 gg_id:35099 marine sponge clone HOC25
FJ999614.1 gg_id:420931 sponge Haliclona simulans South China Sea clone B96
EF379881.1 gg_id:216695 sea water Victoria Harbor (Hong Kong) area clone PC-FL10-68
EU799754.1 gg_id:306969 It's all ranking aquatic Newport Harbour RI clone 1C227399
AM259847.1 gg_id:210420 Spatial sponge- Mediterranean Tethya aurantium sponge cortex clone TAA-10-33
AY907757.1 gg_id:137084 identification picoplankton contrasting waters Arabian Sea water clone A314008
AY907755.1 gg_id:137083 identification picoplankton contrasting waters Arabian Sea water clone A314005
DQ513029.1 gg_id:161219 Microbial life fluids ridge flank crustal fluid clone FS142-29B-02
EU287155.1 gg_id:243868 Pacific arctic surface sediment clone P13-62
EF572288.1 gg_id:228537 Coco's Island site 23 marine clone S23_387
DQ289914.1 gg_id:167947 Microbial Carbon and Nitrogen Cycling Sediments South Atlantic Bight Permeable Sh
EU979089.1 gg_id:329740 Effects intercropping Rhizobium inoculation on microbial biomass and rhizosphere be
EF574537.1 gg_id:239885 site S25 near Coco's Island marine clone S25_881
AM259920.1 gg_id:237509 Chondrilla nucula-specific sponge mesohyl clone CN46
AY386332.1 gg_id:98593 marine str. HTCC2089
EF061958.1 gg_id:181469 Xiamen China mangrove sediment clone XME25

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| GQ375779.1 | 581670 | 54.6 | 180.7 | 189.6 | 93.7 | 89.5 | 87.0 |
| AM941746.1 | 277216 | 511.2 | 841.6 | 1484.7 | 418.1 | 1367.5 | 4101.4 |
| DQ087259.1 | 132883 | 1920.5 | 1749.0 | 1676.7 | 1835.8 | 2551.2 | 2052.4 |
| GU397403.1 | 515060 | 1482.4 | 3416.3 | 945.5 | 640.4 | 1308.8 | 2726.5 |
| DQ129689.1 | 137579 | 2427.1 | 2454.6 | 3566.4 | 3372.2 | 4062.2 | 3312.3 |
| GU397402.1 | 522270 | 2252.0 | 1749.7 | 1947.8 | 1957.1 | 2334.6 | 1990.9 |
| AF211871.1 | 55625 | 224.7 | 265.2 | 810.8 | 230.2 | 515.0 | 796.1 |
| EU735693.1 | 354231 | 1082.0 | 1943.8 | 2457.4 | 1265.1 | 2567.7 | 2402.9 |
| DQ072719.1 | 134569 | 1905.5 | 2813.0 | 3737.3 | 2119.9 | 10337.3 | 6104.4 |
| D14555.1 | 8114 | 4696.9 | 3485.5 | 5070.9 | 6201.8 | 6752.6 | 6108.8 |
| AB021383.1 | 8811 | 1850.6 | 2780.6 | 3406.2 | 1798.9 | 4997.1 | 3514.5 |
| EU305727.1 | 340031 | 2478.7 | 3756.5 | 4311.9 | 3433.7 | 9043.9 | 5392.6 |
| AY987840.1 | 128215 | 45.2 | 65.2 | 115.9 | 67.0 | 121.3 | 32.9 |
| GQ375775.1 | 564683 | 6306.2 | 6207.7 | 3985.5 | 5490.5 | 9875.7 | 7690.6 |
| EU308410.1 | 368617 | 272.8 | 919.6 | 547.5 | 447.5 | 1060.5 | 669.9 |
| DQ641495.1 | 215031 | 727.7 | 732.0 | 2520.8 | 726.0 | 1406.3 | 1441.6 |
| GQ246216.1 | 578822 | 5904.4 | 5215.4 | 4218.3 | 4147.3 | 5914.4 | 6124.4 |
| FJ463811.1 | 580770 | 3322.8 | 2273.9 | 1856.2 | 3322.2 | 3526.5 | 1372.7 |
| FJ444986.1 | 554249 | 411.9 | 1278.4 | 1544.2 | 755.2 | 3032.6 | 3413.7 |
| EU735657.1 | 309472 | 1270.5 | 1591.1 | 1658.4 | 1141.2 | 3325.4 | 3003.3 |
| DQ421388.1 | 156429 | 915.3 | 1092.2 | 1891.8 | 580.4 | 1249.2 | 1646.8 |
| EU487856.1 | 568866 | 728.8 | 642.1 | 793.5 | 3672.8 | 1566.5 | 3030.0 |
| EU487858.1 | 570303 | 539.6 | 543.5 | 1030.1 | 919.3 | 2576.0 | 1573.6 |
| EF508132.1 | 241778 | 1675.6 | 2442.4 | 3353.4 | 1708.5 | 4315.8 | 2511.5 |
| AB054156.1 | 48284 | 3987.8 | 5000.1 | 4005.0 | 2494.1 | 5160.3 | 4208.7 |
| AB054159.1 | 35099 | 4451.2 | 5008.6 | 4700.2 | 4792.8 | 6268.2 | 6804.4 |
| FJ999614.1 | 420931 | 6158.7 | 5453.8 | 6120.1 | 4935.7 | 9126.3 | 7147.7 |
| EF379881.1 | 216695 | 2410.9 | 2818.5 | 4559.2 | 1818.1 | 1989.8 | 4495.5 |
| EU799754.1 | 306969 | 773.3 | 930.1 | 1363.0 | 1872.6 | 4586.0 | 3038.4 |
| AM259847.1 | 210420 | 2079.7 | 1443.6 | 1929.0 | 2645.4 | 1884.6 | 4124.5 |
| AY907757.1 | 137084 | 1408.3 | 846.9 | 1809.4 | 1954.4 | 2455.6 | 2892.6 |
| AY907755.1 | 137083 | 6148.4 | 4707.8 | 6062.3 | 7141.4 | 7725.3 | 8827.7 |
| DQ513029.1 | 161219 | 1010.6 | 1327.4 | 411.4 | 2025.6 | 864.4 | 1979.8 |
| EU287155.1 | 243868 | 395.0 | 497.8 | 745.5 | 498.9 | 1399.7 | 1394.7 |
| EF572288.1 | 228537 | 3299.4 | 1392.7 | 1908.5 | 1051.3 | 455.7 | 1010.3 |
| DQ289914.1 | 167947 | 2242.6 | 1937.6 | 1985.5 | 497.9 | 1405.2 | 121.7 |
| EU979089.1 | 329740 | 7123.5 | 8191.9 | 5288.3 | 4281.0 | 6830.5 | 5579.0 |
| EF574537.1 | 239885 | 3473.3 | 2611.7 | 3197.8 | 2962.8 | 3746.0 | 2639.9 |
| AM259920.1 | 237509 | 96.5 | 180.4 | 178.4 | 211.5 | 299.3 | 268.8 |
| AY386332.1 | 98593 | 108.6 | 140.5 | 164.7 | 78.3 | 361.5 | 342.2 |
| EF061958.1 | 181469 | 61.5 | 90.7 | 50.7 | 100.5 | 107.0 | 76.2 |

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| o__Oceanospirillales | f__HTCC2188 |
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| s__unclassified | 1848 |
| s__unclassified | 186 |
| s__unclassified | 1863 |
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| s__unclassified | 2138 |
| s__unclassified | 2154 |
| s__unclassified | 2233 |
| s__unclassified | 376 |
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| s__unclassified | 587 |
| s__unclassified | 111 |
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| s__unclassified | 816 |
| s__Marinomonas aquimarina | 1715 |
| s__Marinomonas mediterranea | 1151 |

FM242299.1 gg_id:336560 sequences sediment clone 29 T9d-oil
EU887784.1 gg_id:317155 and RFLP anaerobes Nisargruna biogas plant anaerobic digester clone 21IISN
AY212672.1 gg_id:104571 water 20 m downstream manure clone 224ds20
DQ354722.1 gg_id:152853 subsurface water clone DR550SWSAEE23
EU373830.1 gg_id:262549 southern Cretan margin (eastern Mediterranean Sea) canyon and slope sediment clc
DQ351750.1 gg_id:146687 Microbial Adherent Sediment Particles Heavy Metal Contaminated North Sea Surfac
EF157250.1 gg_id:235311 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon
AY344367.2 gg_id:91272 Lake Kauhako 30 m clone K2-30-25
GU061024.1 gg_id:543804 Evaluation culturing methods cultivate previously Yel Sea intertidal beach clone SF2S
GQ337269.1 gg_id:532913 Hydrography shapes biogeography deep Arctic Ocean water depth 428m clone CB18
GQ349203.1 gg_id:544164 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
FM242421.1 gg_id:315848 sequences sediment clone 18 T12d-oil
EU265950.1 gg_id:536666 transition and zone within near-shore anoxic basin: Nitinat Lake depth 20 m clone Ni
EU801454.1 gg_id:316013 It's all ranking aquatic Chesapeake Bay MD clone 3C002749
AB262385.1 gg_id:160146 Microbial Ishigaki-jima Island Japan sea water Ishigaki Port clone IG-1-25
GQ259231.1 gg_id:514087 Microbial activities coastal marine sediments and column Svalbard deep water clone
EU592358.1 gg_id:583231 Seasonal changes Salton Sea hypersaline water clone SSW83Ap
EU050827.1 gg_id:246352 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_06_91
EU491768.1 gg_id:263897 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39
EU799676.1 gg_id:306629 It's all ranking aquatic Newport Harbour RI clone 1C227304
GQ349449.1 gg_id:588121 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
AY907800.1 gg_id:137086 identification picoplankton contrasting waters Arabian Sea water clone A714013
EU803061.1 gg_id:332281 It's all ranking aquatic Northeast Colon Panama clone 4C230470
AY942761.1 gg_id:145162 but species richness marine sponge Cymbastela concentrica clone Cc044
EU544859.1 gg_id:264271 free-living particle- aggregate- archaeal and Laptev Sea >60 um size fraction (aggrega
EU799735.1 gg_id:324875 It's all ranking aquatic Newport Harbour RI clone 1C227378
AB526337.1 gg_id:546239 Spongiibacter sp. str. JAM-GA14
AM990674.1 gg_id:278054 culturable oligotrophic ocean (South Pacific Gyre) sea water
FJ889619.1 gg_id:559242 Melitea sp. str. ZS5-23
EF176580.1 gg_id:181920 Litincola lipolitica str. IMCC1097
FJ745130.1 gg_id:565326 Transporter genes expressed coastal response dissolved organic carbon surface wate
EU652550.1 gg_id:278194 Seasonal variation microbial Yel Sea sediment clone A8S-109
AM930471.1 gg_id:275885 involved Tripneustes gratilla (Echinoidea) cloning and FISH host body wall lesions clc
AB006765.1 gg_id:8206 Marinobacterium jannaschii str. IFO15466
FN556570.1 gg_id:514502 Marinobacterium sp. str. JW3.2b
FJ202983.1 gg_id:326600 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k
DQ219356.1 gg_id:142532 Marinobacterium sp. str. 2085(b)
EF190070.1 gg_id:193559 s Qinghai oilfield clone GSX3
AY563030.1 gg_id:100162 Marinobacterium halophilum str. Mano11
AJ843079.1 gg_id:114569 Marinomonas aquimarina str. 11OM3 = CECT 5078
EU188448.1 gg_id:366487 Marinomonas sp. str. IVIA-Po-101

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|---|---|---|---|---|---|---|---|
| FM242299.1 | 336560 | 511.8 | 1144.6 | 1700.4 | 1267.7 | 3589.0 | 2799.3 |
| EU887784.1 | 317155 | 734.8 | 1216.3 | 2957.6 | 783.5 | 4693.0 | 5459.9 |
| AY212672.1 | 104571 | 672.7 | 933.5 | 1783.7 | 4713.1 | 1394.0 | 3974.6 |
| DQ354722.1 | 152853 | 2359.2 | 2999.0 | 3946.2 | 4273.7 | 6841.5 | 7254.9 |
| EU373830.1 | 262549 | 9041.3 | 10331.7 | 6081.4 | 9322.2 | 10176.0 | 10730.9 |
| DQ351750.1 | 146687 | 455.8 | 495.9 | 407.4 | 249.0 | 173.4 | 449.0 |
| EF157250.1 | 235311 | 3408.7 | 4051.0 | 2511.2 | 2376.6 | 5498.8 | 4578.8 |
| AY344367.2 | 91272 | 3089.4 | 1830.0 | 460.8 | 3843.0 | 4434.0 | 1436.6 |
| GU061024.1 | 543804 | 5848.4 | 7062.6 | 7112.6 | 6397.0 | 11287.4 | 12680.8 |
| GQ337269.1 | 532913 | 781.4 | 460.5 | 699.2 | 561.1 | 483.0 | 343.7 |
| GQ349203.1 | 544164 | 578.1 | 1092.2 | 2293.4 | 1180.1 | 2010.8 | 2715.3 |
| FM242421.1 | 315848 | 2308.2 | 2097.0 | 1970.2 | 2684.0 | 1361.4 | 2235.9 |
| EU265950.1 | 536666 | 1045.3 | 1265.9 | 6316.3 | 2381.0 | 5098.3 | 2447.9 |
| EU801454.1 | 316013 | 7063.3 | 8129.6 | 10810.4 | 6283.0 | 13263.5 | 9947.6 |
| AB262385.1 | 160146 | 6428.7 | 2068.3 | 10748.5 | 9050.2 | 7310.5 | 7787.7 |
| GQ259231.1 | 514087 | 1789.1 | 1634.6 | 1221.3 | 3458.7 | 2558.2 | 2571.0 |
| EU592358.1 | 583231 | 3724.5 | 3761.0 | 3418.2 | 4782.2 | 7120.1 | 6903.4 |
| EU050827.1 | 246352 | 3939.9 | 4114.1 | 2817.3 | 5598.9 | 6769.5 | 5528.8 |
| EU491768.1 | 263897 | 2173.2 | 2507.4 | 6284.9 | 4548.1 | 4739.4 | 3488.4 |
| EU799676.1 | 306629 | 4826.0 | 6926.5 | 9141.4 | 6704.6 | 10008.8 | 10616.1 |
| GQ349449.1 | 588121 | 7486.3 | 8659.1 | 9768.1 | 8210.3 | 12211.2 | 12041.8 |
| AY907800.1 | 137086 | 3509.6 | 3456.5 | 3931.1 | 4497.5 | 5022.1 | 4759.4 |
| EU803061.1 | 332281 | 44.8 | 58.6 | 139.1 | 86.7 | 136.6 | 60.0 |
| AY942761.1 | 145162 | 120.2 | 125.3 | 136.0 | 109.6 | 89.0 | 221.7 |
| EU544859.1 | 264271 | 10881.1 | 6559.6 | 11774.1 | 11055.0 | 8025.5 | 7993.7 |
| EU799735.1 | 324875 | 1207.2 | 2126.4 | 2522.0 | 1871.2 | 2837.3 | 3696.1 |
| AB526337.1 | 546239 | 1744.6 | 1891.2 | 3227.4 | 2014.8 | 6563.6 | 6333.9 |
| AM990674.1 | 278054 | 558.1 | 845.7 | 1389.5 | 354.9 | 1319.1 | 1544.9 |
| FJ889619.1 | 559242 | 2524.5 | 3130.3 | 5329.1 | 4526.6 | 7514.3 | 6766.8 |
| EF176580.1 | 181920 | 2195.4 | 3464.5 | 442.2 | 1955.4 | 2453.0 | 1049.4 |
| FJ745130.1 | 565326 | 1408.8 | 1771.3 | 936.1 | 492.4 | 753.7 | 838.5 |
| EU652550.1 | 278194 | 801.7 | 826.5 | 863.2 | 650.0 | 1530.7 | 1546.0 |
| AM930471.1 | 275885 | 23.2 | 30.1 | 46.9 | 62.4 | 237.3 | 98.3 |
| AB006765.1 | 8206 | 6587.4 | 6943.0 | 4514.2 | 5714.6 | 6350.6 | 5068.5 |
| FN556570.1 | 514502 | 42.8 | 106.3 | 244.6 | 100.2 | 891.9 | 127.9 |
| FJ202983.1 | 326600 | 4865.7 | 3532.1 | 5258.5 | 4595.5 | 5668.2 | 3712.9 |
| DQ219356.1 | 142532 | 1384.4 | 2589.8 | 4004.7 | 2123.2 | 6446.6 | 4400.7 |
| EF190070.1 | 193559 | 88.1 | 130.4 | 49.1 | 104.9 | 111.6 | 326.7 |
| AY563030.1 | 100162 | 3351.5 | 4215.9 | 9319.5 | 5775.5 | 12630.1 | 7818.2 |
| AJ843079.1 | 114569 | 990.3 | 781.5 | 1602.1 | 1242.0 | 2259.9 | 2005.9 |
| EU188448.1 | 366487 | 416.4 | 415.0 | 939.8 | 432.5 | 5357.2 | 2994.8 |

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| s__Marinomonas sp. MED121 | 1121 |
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| s__Marinospirillum insulare | 1598 |
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| s__Neptunomonas japonica | 399 |
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| s__Oceanospirillum maris | 915 |
| s__unclassified | 1252 |
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NR_028636.1 gg_id:582426 Marinomonas primoryensis str. KMM 3633
DQ403809.1 gg_id:150764 Marinomonas blandensis str. MED 121
EU195937.1 gg_id:248961 Marinomonas sp. str. P111
AJ238597.1 gg_id:8210 Marinomonas protea
EU722311.1 gg_id:354249 Marinomonas sp. str. S3-34
EF382680.1 gg_id:209816 Marinomonas sp. BSi20579 str. Bsi20579
DQ311094.1 gg_id:144989 Marinomonas sp. str. NJ548
DQ517862.1 gg_id:160848 Marinomonas sp. str. BSi20385
AB074194.1 gg_id:52278 Marinomonas primoryensis str. KMM 3634
DQ421580.2 gg_id:208776 Salt Marsh Prokaryotes salt marsh clone SIMO-4215
AJ627909.1 gg_id:103719 Marinomonas ushuaiensis str. U1
AY539835.1 gg_id:101289 Marinomonas pontica str. 46-16
DQ011528.1 gg_id:120729 Marinomonas communis str. LMG 2864
DQ923437.1 gg_id:174575 Marinomonas sp. W-3
AB242868.1 gg_id:142302 Marinomonas sanya str. F128
AY730245.1 gg_id:101261 Marinomonas sp. M6-20A
AF321017.2 gg_id:30213 Marinomonas sp. GOBB3-320
EU188447.1 gg_id:362695 Marinomonas sp. str. IVIA-Po-159
AJ717294.1 gg_id:105555 Marinomonas sp. str. BJK13
NR_029228.1 gg_id:554750 Marinomonas vaga str. 40; ATCC 27119
DQ676859.1 gg_id:172752 Marinomonas sp. str. ASs2032
DQ007439.1 gg_id:124798 Marinomonas sp. str. BSi20101
EU427306.1 gg_id:274342 Marinomonas sp. MSI03
EU188443.1 gg_id:359821 Marinomonas sp. str. IVIA-Po-145
EU188441.1 gg_id:362238 Marinomonas sp. str. IVIA-Po-185
DQ520888.1 gg_id:161293 Marinomonas sp. str. BSi20461
DQ517876.1 gg_id:160773 Marinomonas sp. str. BSi20548
DQ537501.1 gg_id:160057 Marinomonas sp. str. BSi20388
AB098513.1 gg_id:75039 Marinospirillum insulare str. NB11
AB006769.1 gg_id:8111 Marinospirillum minutulum str. ATCC19193
AB006770.1 gg_id:8112 Marinospirillum megaterium
AB291228.1 gg_id:246798 Neptunomonas japonica str. JAMM 1610
FJ889618.1 gg_id:544882 Neptunomonas sp. str. NF4-29
AB288092.1 gg_id:239047 Neptunomonas japonica str. JAMM 0745
AF053734.1 gg_id:8190 Neptunomonas naphthovorans str. NAG-2N-126
FJ764762.1 gg_id:570916 Nitrincola sp. str. E-048
FJ973520.1 gg_id:440184 Nitrincola lacisaponensis str. NBSL11
AB006763.1 gg_id:8178 Oceanospirillum maris subsp. williamsae str. IFO15468
AB006764.1 gg_id:8176 Oceanospirillum multiglobuliferum str. IFO13614
AB006761.1 gg_id:8184 Oceanospirillum beijerinckii subsp. pelagicum str. IFO13612
FJ403091.1 gg_id:367944 Disease- changes healthy and diseased colonies Caribbean coral Montastrea faveolat

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|---|---|---|---|---|---|---|---|
| NR_028636.1 | 582426 | 1367.5 | 1479.1 | 1926.4 | 2172.6 | 2942.9 | 1946.2 |
| DQ403809.1 | 150764 | 67.8 | 130.6 | 117.6 | 86.6 | 154.7 | 268.6 |
| EU195937.1 | 248961 | 234.7 | 277.5 | 907.8 | 335.2 | 1413.9 | 637.5 |
| AJ238597.1 | 8210 | 988.2 | 1358.2 | 2317.7 | 3305.9 | 544.9 | 1434.6 |
| EU722311.1 | 354249 | 231.3 | 366.6 | 777.4 | 445.7 | 580.9 | 573.0 |
| EF382680.1 | 209816 | 1072.3 | 2554.5 | 7620.0 | 3189.6 | 9880.9 | 9050.1 |
| DQ311094.1 | 144989 | 191.0 | 286.8 | 1008.0 | 391.9 | 1421.5 | 1039.7 |
| DQ517862.1 | 160848 | 817.7 | 1441.9 | 2105.3 | 1811.5 | 4180.7 | 3754.1 |
| AB074194.1 | 52278 | 611.4 | 568.4 | 1658.4 | 1496.5 | 966.7 | 1188.3 |
| DQ421580.2 | 208776 | 239.6 | 327.2 | 387.5 | 132.8 | 333.9 | 1088.0 |
| AJ627909.1 | 103719 | 120.3 | 245.0 | 475.3 | 437.4 | 796.5 | 1030.4 |
| AY539835.1 | 101289 | 2622.5 | 2866.2 | 3242.2 | 2979.1 | 3522.5 | 2504.7 |
| DQ011528.1 | 120729 | 1219.6 | 1693.5 | 3006.0 | 1137.1 | 2348.9 | 3159.2 |
| DQ923437.1 | 174575 | 225.3 | 406.2 | 595.5 | 1102.3 | 218.6 | 585.9 |
| AB242868.1 | 142302 | 441.9 | 481.0 | 655.8 | 891.7 | 1240.9 | 314.9 |
| AY730245.1 | 101261 | 2449.7 | 1680.8 | 1819.3 | 1864.5 | 527.3 | 917.4 |
| AF321017.2 | 30213 | 9830.3 | 10456.6 | 5812.2 | 8672.1 | 14052.9 | 11883.7 |
| EU188447.1 | 362695 | 2089.7 | 1697.1 | 2542.0 | 878.6 | 1708.7 | 1920.3 |
| AJ717294.1 | 105555 | 813.5 | 625.1 | 2315.7 | 888.2 | 104.8 | 1334.2 |
| NR_029228.1 | 554750 | 22.7 | 45.8 | 63.1 | 62.5 | 286.7 | 177.5 |
| DQ676859.1 | 172752 | 412.5 | 639.3 | 768.7 | 1023.9 | 1008.7 | 790.2 |
| DQ007439.1 | 124798 | 62.9 | 70.4 | 218.2 | 89.5 | 1020.3 | 934.3 |
| EU427306.1 | 274342 | 154.0 | 229.4 | 1186.4 | 675.8 | 797.3 | 848.6 |
| EU188443.1 | 359821 | 177.2 | 148.6 | 1284.6 | 306.6 | 108.2 | 269.4 |
| EU188441.1 | 362238 | 5092.7 | 3172.8 | 3499.7 | 3073.8 | 7505.5 | 3222.2 |
| DQ520888.1 | 161293 | 572.2 | 893.5 | 1465.5 | 1378.5 | 3847.8 | 2999.0 |
| DQ517876.1 | 160773 | 2136.2 | 2032.8 | 4113.9 | 2079.6 | 6264.6 | 3873.3 |
| DQ537501.1 | 160057 | 4611.3 | 6246.4 | 3280.3 | 4642.4 | 6068.9 | 6092.3 |
| AB098513.1 | 75039 | 1727.1 | 1698.4 | 4058.6 | 2354.8 | 2418.8 | 3259.0 |
| AB006769.1 | 8111 | 3836.6 | 2174.0 | 3750.3 | 4021.9 | 6050.3 | 7207.7 |
| AB006770.1 | 8112 | 93.0 | 389.6 | 1220.1 | 593.4 | 243.2 | 567.1 |
| AB291228.1 | 246798 | 523.7 | 851.9 | 1858.3 | 447.1 | 447.0 | 806.9 |
| FJ889618.1 | 544882 | 788.0 | 791.5 | 4230.7 | 519.3 | 1596.3 | 2560.6 |
| AB288092.1 | 239047 | 1818.6 | 1283.1 | 1447.1 | 1074.3 | 2773.5 | 1732.2 |
| AF053734.1 | 8190 | 725.9 | 791.0 | 946.0 | 888.3 | 2367.1 | 1390.4 |
| FJ764762.1 | 570916 | 2633.4 | 1377.8 | 2062.7 | 1982.6 | 4661.8 | 3609.2 |
| FJ973520.1 | 440184 | 6443.7 | 6336.7 | 4765.8 | 5693.6 | 8951.6 | 8757.8 |
| AB006763.1 | 8178 | 518.9 | 475.8 | 1481.5 | 730.2 | 2584.7 | 1742.6 |
| AB006764.1 | 8176 | 3584.0 | 3320.4 | 3905.8 | 4181.4 | 7255.6 | 5439.7 |
| AB006761.1 | 8184 | 667.9 | 1569.7 | 2328.8 | 869.4 | 1797.9 | 2550.9 |
| FJ403091.1 | 367944 | 786.5 | 830.3 | 1946.7 | 1070.3 | 4649.0 | 1659.0 |

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| s__Oleibacter marinus | 1266 |
| s__unclassified | 1236 |
| s__unclassified | 1526 |
| s__unclassified | 1780 |
| s__unclassified | 1792 |
| s__unclassified | 576 |
| s__unclassified | 802 |
| s__unclassified | 94 |
| s__unclassified | 991 |
| s__unclassified | 1412 |
| s__unclassified | 1586 |
| s__unclassified | 1706 |
| s__unclassified | 52 |
| s__proteobacterium symbiont of Osedax frankpressi | 45 |
| s__proteobacterium symbiont of Osedax sp. MB3 | 732 |
| s__proteobacterium symbiont of Osedax sp. MB4 | 2182 |
| s__unclassified | 1046 |
| s__unclassified | 120 |
| s__unclassified | 1286 |
| s__unclassified | 1336 |
| s__unclassified | 1457 |
| s__unclassified | 1548 |
| s__unclassified | 1558 |
| s__unclassified | 1637 |
| s__unclassified | 1671 |
| s__unclassified | 1735 |
| s__unclassified | 1754 |
| s__unclassified | 1871 |
| s__unclassified | 2008 |
| s__unclassified | 2048 |
| s__unclassified | 2054 |
| s__unclassified | 2082 |
| s__unclassified | 2094 |
| s__unclassified | 2129 |
| s__unclassified | 2198 |
| s__unclassified | 319 |
| s__unclassified | 461 |
| s__unclassified | 464 |
| s__unclassified | 472 |
| s__unclassified | 56504 |
| s__unclassified | 57220 |

AB435650.1 gg_id:461486 Oceanobacter sp. str. 1O14
AB006767.1 gg_id:8201 Oceanobacter kriegii str. IFO15467
AM930467.1 gg_id:272107 involved Tripneustes gratilla (Echinoidea) cloning and FISH host body wall lesions clc
EF648125.1 gg_id:238098 dynamics during produced water treatment aerobic activated sludge clone XJ46
DQ071156.1 gg_id:134464 marine surface water clone Surf1.32
FJ403082.1 gg_id:364829 Disease- changes healthy and diseased colonies Caribbean coral Montastrea faveolat
EF648167.1 gg_id:254655 dynamics during produced water treatment aerobic activated sludge clone XJ137
GQ426888.1 gg_id:592739 Thalassolituus sp. IMCC1826 str. IMCC 1826
AJ302699.1 gg_id:20487 Oceanospirillum sp. ME101
EU980447.1 gg_id:326525 Oleispira sp. str. DFH11
EU236351.1 gg_id:298239 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg91A7
EU050832.1 gg_id:244721 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_09_46
AJ426421.1 gg_id:47332 Oleispira antarctica str. RB-9
AY577900.1 gg_id:105462 roots new deep sea polychaete (Osedax frankpressi gen n. sp. novum) clone BoneC3
DQ906761.1 gg_id:161773 and marine microorganisms Antarctic sea ice lower 10 cm clone AntCL3E3
EU050834.1 gg_id:236381 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_02_57
GQ349742.1 gg_id:587033 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
AY697896.1 gg_id:101312 Antarctica clone F3C18
AY922202.1 gg_id:114064 whalefall clone 131636
GU391221.1 gg_id:516971 Thalassolituus sp. str. JYr12
EF468717.1 gg_id:221209 Marinobacterium marisflavum str. IMCC4074
DQ206422.1 gg_id:140325 microbial mediates arsenate reduction soda lake water clone ML-S-4
DQ279852.1 gg_id:142469 Marinomonas sp. str. Y5
AY967730.1 gg_id:115234 Influence starvation ozone and selected isolates on survival southern Jasus edwardsi
FN377729.1 gg_id:593776 Marinobacterium sp. RS-21
AY549003.2 gg_id:101658 marine bone clone sacC13A1
EF379568.1 gg_id:206232 sea water Victoria Harbor (Hong Kong) area clone VH-PA5-10
EF422409.1 gg_id:213472 Marinospirillum sp. str. ANL-isoa
GU291323.1 gg_id:589506 Anaerobic sulfide-oxidizing couple acidification and nitrogen cycling heavy metal we
EU544727.1 gg_id:262299 free-living particle- aggregate- archaeal and Laptev Sea 0.22-1.0 um size fraction (fre
NR_024654.1 gg_id:541001 Pseudospirillum japonicum str. ATCC 19191
FJ628206.1 gg_id:555032 transition and zone within near-shore basin: brackish water anoxic fjord Nitinat Lake
FJ403057.1 gg_id:364908 Disease- changes healthy and diseased colonies Caribbean coral Montastrea faveolat
AM747817.1 gg_id:311032 Oceaniserpentilla haliotidis
AY136131.2 gg_id:155199 Oceanobacter sp. str. RED65
FJ202960.1 gg_id:353341 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k
GQ131677.1 gg_id:376032 Neptuniibacter sp. str. antisso-13
AY549004.2 gg_id:101822 marine bone clone Osedax_sym1
AY549002.2 gg_id:101490 marine bone clone sacC13A2
AF140000.1 gg_id:8195 Oceanospirillum sp. str. ML-158
AF140002.1 gg_id:27457 Oceanospirillum sp. str. ML-165

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| AB435650.1 | 461486 | 1600.8 | 991.4 | 2201.3 | 1494.9 | 2267.9 | 1940.0 |
| AB006767.1 | 8201 | 1019.3 | 1156.5 | 2759.5 | 1656.7 | 6207.9 | 2579.8 |
| AM930467.1 | 272107 | 1470.4 | 1101.2 | 1998.8 | 1288.0 | 2104.2 | 1888.9 |
| EF648125.1 | 238098 | 3722.9 | 4669.4 | 2258.1 | 2367.2 | 5208.2 | 5004.0 |
| DQ071156.1 | 134464 | 1795.8 | 1546.8 | 2070.7 | 1735.4 | 2944.2 | 2407.8 |
| FJ403082.1 | 364829 | 5385.0 | 4593.6 | 3741.0 | 6800.4 | 8005.9 | 4089.4 |
| EF648167.1 | 254655 | 642.6 | 334.8 | 785.8 | 643.9 | 327.0 | 219.2 |
| GQ426888.1 | 592739 | 399.6 | 652.8 | 1678.8 | 321.4 | 4817.5 | 1729.5 |
| AJ302699.1 | 20487 | 5909.8 | 5709.9 | 7132.0 | 6003.4 | 9565.8 | 7055.6 |
| EU980447.1 | 326525 | 168.9 | 433.4 | 998.8 | 768.3 | 764.8 | 2013.9 |
| EU236351.1 | 298239 | 936.0 | 1394.5 | 1824.4 | 1664.1 | 4817.4 | 3553.4 |
| EU050832.1 | 244721 | 6059.1 | 2602.2 | 4424.0 | 6832.5 | 9208.2 | 3999.7 |
| AJ426421.1 | 47332 | 1636.9 | 1701.2 | 1656.5 | 2139.5 | 3829.0 | 3062.7 |
| AY577900.1 | 105462 | 3283.3 | 1703.9 | 3057.6 | 2529.5 | 2800.6 | 3218.0 |
| DQ906761.1 | 161773 | 2624.9 | 4141.8 | 2529.4 | 2567.1 | 4264.8 | 4199.0 |
| EU050834.1 | 236381 | 2347.7 | 3042.1 | 1315.0 | 1648.8 | 1871.1 | 3171.3 |
| GQ349742.1 | 587033 | 1675.4 | 1435.4 | 2884.5 | 1556.6 | 1815.8 | 3394.4 |
| AY697896.1 | 101312 | 1207.3 | 2540.7 | 2331.7 | 2717.4 | 5597.3 | 4425.1 |
| AY922202.1 | 114064 | 881.6 | 475.8 | 492.0 | 1110.4 | 2098.9 | 1756.5 |
| GU391221.1 | 516971 | 1766.9 | 2939.1 | 4242.6 | 3439.5 | 5342.4 | 3784.5 |
| EF468717.1 | 221209 | 23.6 | 42.6 | 68.4 | 88.7 | 78.6 | 47.8 |
| DQ206422.1 | 140325 | 370.7 | 324.9 | 833.9 | 424.0 | 497.3 | 667.8 |
| DQ279852.1 | 142469 | 460.1 | 984.1 | 1120.7 | 863.7 | 1397.7 | 1302.7 |
| AY967730.1 | 115234 | 426.2 | 519.8 | 870.2 | 484.7 | 2235.8 | 1683.1 |
| FN377729.1 | 593776 | 1564.1 | 2730.0 | 3472.2 | 2309.3 | 12317.9 | 4321.9 |
| AY549003.2 | 101658 | 6942.2 | 7809.5 | 6011.3 | 8610.5 | 9789.0 | 7506.6 |
| EF379568.1 | 206232 | 39.3 | 49.8 | 106.6 | 76.0 | 100.6 | 86.1 |
| EF422409.1 | 213472 | 3857.1 | 5349.1 | 1991.4 | 3066.3 | 4811.6 | 5857.4 |
| GU291323.1 | 589506 | 176.6 | 478.6 | 602.1 | 246.4 | 202.7 | 657.4 |
| EU544727.1 | 262299 | 2518.9 | 2193.1 | 1343.0 | 2419.5 | 3212.3 | 3419.1 |
| NR_024654.1 | 541001 | 155.8 | 299.5 | 217.7 | 188.6 | 271.3 | 311.5 |
| FJ628206.1 | 555032 | 352.5 | 791.2 | 1455.0 | 639.9 | 947.1 | 1000.7 |
| FJ403057.1 | 364908 | 16911.9 | 16757.3 | 13825.7 | 12118.7 | 14433.4 | 13444.2 |
| AM747817.1 | 311032 | 114.2 | 401.8 | 363.0 | 208.5 | 1690.4 | 1717.7 |
| AY136131.2 | 155199 | 30.0 | 87.0 | 56.7 | 62.9 | 63.7 | 32.2 |
| FJ202960.1 | 353341 | 96.0 | 139.1 | 260.9 | 229.0 | 191.5 | 281.4 |
| GQ131677.1 | 376032 | 337.5 | 612.1 | 1348.5 | 685.4 | 2661.3 | 3941.3 |
| AY549004.2 | 101822 | 163.0 | 224.6 | 558.1 | 319.1 | 396.9 | 545.8 |
| AY549002.2 | 101490 | 6125.7 | 5330.1 | 5466.2 | 6028.1 | 6654.0 | 6815.9 |
| AF140000.1 | 8195 | 2837.6 | 3895.5 | 4065.1 | 4718.9 | 7581.3 | 6189.1 |
| AF140002.1 | 27457 | 210.6 | 141.6 | 481.9 | 307.4 | 950.4 | 3966.3 |

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|---|---|---|---|
| k__Bacteria | k__Bacteria | p__Proteobacteria | c__Gammaproteobacteria |
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| o__Oceanospirillales | f__Oceanospirillaceae |
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| o__Oceanospirillales | f__Oceanospirillaceae |
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| o__Oceanospirillales | f__Oceanrickettsiaceae |
| o__Oceanospirillales | f__Oleiphilaceae |
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| s__unclassified | 654 |
| s__unclassified | 737 |
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| s__unclassified | 1249 |
| s__unclassified | 1595 |
| s__unclassified | 1820 |
| s__unclassified | 2021 |
| s__unclassified | 209 |
| s__unclassified | 953 |
| s__Congregibacter litoralis | 1235 |
| s__unclassified | 1352 |
| s__unclassified | 1730 |
| s__unclassified | 1877 |
| s__unclassified | 1986 |
| s__unclassified | 2090 |
| s__unclassified | 231 |
| s__unclassified | 234 |
| s__unclassified | 243 |
| s__unclassified | 305 |
| s__unclassified | 81 |
| s__marine gamma proteobacterium HTCC2080 | 1047 |
| s__marine gamma proteobacterium HTCC2080 | 1786 |
| s__marine gamma proteobacterium HTCC2143 | 724 |
| s__unclassified | 1034 |
| s__unclassified | 1056 |
| s__unclassified | 1078 |
| s__unclassified | 1105 |
| s__unclassified | 113 |
| s__unclassified | 1149 |
| s__unclassified | 1195 |
| s__unclassified | 1314 |
| s__unclassified | 1346 |
| s__unclassified | 1349 |
| s__unclassified | 1357 |
| s__unclassified | 1394 |
| s__unclassified | 1402 |
| s__unclassified | 143 |
| s__unclassified | 144 |

NR_028788.1 gg_id:579521 Marinospirillum alkaliphilum str. Z4; JCM 11312
EF067915.1 gg_id:245142 endolithic microbes marine basalts aerobic enrichment s innoculated basalt Brown B
AM930473.1 gg_id:274407 involved Tripneustes gratilla (Echinoidea) cloning and FISH host body wall lesions cl
GQ349823.1 gg_id:569636 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
GQ349756.1 gg_id:561025 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
DQ123914.1 gg_id:154336 Oceanrickettsia ariakensis
DQ015830.1 gg_id:139543 Antarctic lake water clone ELB19-203
GU061314.1 gg_id:578191 Evaluation culturing methods cultivate previously Yel Sea intertidal beach seawater
FM242233.1 gg_id:333373 sequences sediment clone 26 T0h-oil
FJ717225.1 gg_id:554141 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United King
NR_025432.1 gg_id:537713 Oleiphilus messinensis str. ME102; DSM 13489
EF067910.1 gg_id:251507 endolithic microbes marine basalts aerobic enrichment s innoculated basalt Brown B
AY007676.1 gg_id:26630 marine isolate NOR5
GU118892.1 gg_id:542707 Threatened Corals Provide Microbial Habitats clone Past_M04
EU707294.1 gg_id:336455 sulfur oxidizing Wadden Sea sediments Janssand intertidal sandy sediment 0 2 cm d
DQ330945.1 gg_id:159205 Guerrero Negro hypersaline microbial mat clone 05D2Z66
AM882556.1 gg_id:337698 Structure along hydrocarbon contamination coastal sediment oil polluted water pet
DQ330798.1 gg_id:159069 Guerrero Negro hypersaline microbial mat clone 02D2Z51
EU707308.1 gg_id:354827 sulfur oxidizing Wadden Sea sediments Janssand intertidal sandy sediment 0 3 cm d
EF632657.1 gg_id:235343 Unique microbial contrasting aquatic altitude Andean Altiplano (northern Chile) sedi
EU707317.1 gg_id:350845 sulfur oxidizing Wadden Sea sediments Janssand intertidal sandy sediment middle f
EU161717.1 gg_id:255918 Haliea rubra str. CM41_15a
EF632658.1 gg_id:236929 Unique microbial contrasting aquatic altitude Andean Altiplano (northern Chile) sedi
AY386339.1 gg_id:96871 marine str. HTCC2080
AAVV01000015.1 gg_id:190442 marine str. HTCC2080
NZ_AAVT01000006.1 gg_id:189314 marine str. HTCC2143
GU230327.1 gg_id:589757 Multilevel approach along Rio de la Plata-South Atlantic Ocean coastal water clone
EU544810.1 gg_id:275233 free-living particle- aggregate- archaeal and Laptev Sea 1.0-60 um size fraction ( sus
DQ009134.1 gg_id:126508 bacterioplankton clone SPOTSAPR01_5m162
EU700144.1 gg_id:295036 Study on Shantou Bay Marine Sediments Microorganisms sediment clone STU2
AB015519.1 gg_id:8181 deep-sea sediment clone BD1-7
EU394576.1 gg_id:335051 Coccolithophore bloom dynamics shape (NE-Atl) northern Bay Biscay pelagic particle
EU491036.1 gg_id:262064 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount South Rift X
EU491078.1 gg_id:273214 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount South Rift X
EU491056.1 gg_id:262397 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount South Rift X
EF379800.1 gg_id:206237 sea water Victoria Harbor (Hong Kong) area clone PC-PA11-51
FN396694.1 gg_id:549550 constant flux thermophilic cold seabed Arctic marine surface sediment clone s5_0_V
AM882531.1 gg_id:338117 Structure along hydrocarbon contamination coastal sediment oil polluted water pet
FJ203132.1 gg_id:351157 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c
GU061619.1 gg_id:578346 and function microbial mesoscale eddy perturbations South China Sea clone CE2-DC
FJ717243.1 gg_id:536934 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United King

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|---|---|---|---|---|---|---|---|
| NR_028788.1 | 579521 | 1431.5 | 1801.9 | 2519.7 | 831.7 | 1992.9 | 736.1 |
| EF067915.1 | 245142 | 338.2 | 431.7 | 1741.1 | 748.9 | 4981.8 | 1383.2 |
| AM930473.1 | 274407 | 1739.2 | 2098.5 | 2580.0 | 1187.0 | 1538.7 | 2187.8 |
| GQ349823.1 | 569636 | 6568.6 | 6446.3 | 10268.3 | 9685.8 | 9704.9 | 5639.7 |
| GQ349756.1 | 561025 | 1908.3 | 1739.4 | 2036.9 | 5027.3 | 2717.7 | 3376.2 |
| DQ123914.1 | 154336 | 52.8 | 52.7 | 314.9 | 106.8 | 140.4 | 67.0 |
| DQ015830.1 | 139543 | 477.6 | 467.7 | 1631.0 | 2199.8 | 955.9 | 874.7 |
| GU061314.1 | 578191 | 9234.7 | 6751.7 | 7707.4 | 8086.2 | 9377.0 | 8561.4 |
| FM242233.1 | 333373 | 1670.1 | 1986.9 | 4287.4 | 2633.7 | 5705.7 | 3345.6 |
| FJ717225.1 | 554141 | 863.3 | 1296.6 | 3926.5 | 2284.6 | 1749.2 | 2270.5 |
| NR_025432.1 | 537713 | 158.2 | 301.6 | 484.1 | 199.2 | 1172.5 | 535.2 |
| EF067910.1 | 251507 | 4459.5 | 4097.4 | 6234.7 | 6757.9 | 6042.7 | 5037.8 |
| AY007676.1 | 26630 | 251.9 | 548.2 | 810.5 | 321.6 | 795.8 | 1294.7 |
| GU118892.1 | 542707 | 5724.4 | 4916.0 | 9308.1 | 10200.5 | 5500.8 | 6404.0 |
| EU707294.1 | 336455 | 249.3 | 328.0 | 442.8 | 163.3 | 123.6 | 919.4 |
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| DQ009134.1 | 126508 | 2246.0 | 2045.6 | 4870.4 | 3803.4 | 4960.0 | 2791.7 |
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EU244006.1 gg_id:357193 16SrRNA probes river Leine sediment clone sls1121
AM997955.1 gg_id:570446 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A
EU491047.1 gg_id:265525 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount South Rift X
EU592383.1 gg_id:553196 Seasonal changes Salton Sea hypersaline water clone SSW145N
FN398053.1 gg_id:592957 Haliea sp. str. 7SM29 = CECT 7447
DQ513020.1 gg_id:159939 Microbial life fluids ridge flank crustal fluid clone FS142-64B-02
EU544827.1 gg_id:277594 free-living particle- aggregate- archaeal and Laptev Sea 1.0-60 um size fraction ( susp
GQ348262.1 gg_id:563632 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
GU118865.1 gg_id:579784 Threatened Corals Provide Microbial Habitats clone Mfra_M11
EU652555.1 gg_id:279539 Seasonal variation microbial Yel Sea sediment clone D8S-18
EU236417.1 gg_id:302021 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg92F9
EF123465.1 gg_id:241462 Microbial disease microbial mats on Siderastrea siderea three regions wider Caribbea
GQ347825.1 gg_id:563082 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
EF471467.1 gg_id:258367 Fast Screening and Estuarine Operon Libraries whole surface water Chesapeake Bay
AM990941.1 gg_id:540228 along Egyptian Mediterranean coast mediterranean coastal waters 500 offshore 0.5
EF123461.1 gg_id:245864 Microbial disease microbial mats on Siderastrea siderea three regions wider Caribbea
EU287241.1 gg_id:246295 Pacific arctic surface sediment clone S11-58
EU544811.1 gg_id:265700 free-living particle- aggregate- archaeal and Laptev Sea 1.0-60 um size fraction ( susp
GU061614.1 gg_id:552256 and function microbial mesoscale eddy perturbations South China Sea clone CE2-DC
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AY693815.1 gg_id:102960 anaerobic sludge clone EUB3
DQ396099.1 gg_id:150972 deep-sea octacoral clone ctg_NISAA05
AF468388.1 gg_id:80239 Arctic sea ice ARK10038
FJ905759.1 gg_id:510210 s Tonga-Kermadec iron oxide sediments Volcano 1 Tonga Arc clone V1F161b
DQ351747.1 gg_id:150492 Microbial Adherent Sediment Particles Heavy Metal Contaminated North Sea Surfac
EU491750.1 gg_id:272039 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39
EU050825.1 gg_id:251646 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_07_55
AY386336.1 gg_id:96552 marine str. HTCC2223
EU010139.1 gg_id:235473 Biogeography Singapore seawaters seawater clone B24
DQ070803.1 gg_id:149537 Prokaryotic Structures Seafloor Basalts Varying Age and Juan de Fuca Ridge basalt gl
AB294961.1 gg_id:219188 -dependent & analyses hydrothermal system off Taketomi Island Japan microbial ma
EU707310.1 gg_id:320148 sulfur oxidizing Wadden Sea sediments Janssand sediment -490cm clone JS9_43
AB476262.1 gg_id:561798 Compositional and functional transition epibiotic microbial hydrothermal vent galath
GQ347899.1 gg_id:555942 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
AM259790.1 gg_id:216671 Spatial sponge- Mediterranean Tethya aurantium sponge endosome clone TAI-8-20
EU491031.1 gg_id:271029 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount South Rift X
GQ249557.1 gg_id:555216 Microbial anaerobic sediments Bay Cadiz (Spain) marine sediment: 12-14 cm layer cl
EU544829.1 gg_id:273948 free-living particle- aggregate- archaeal and Laptev Sea 1.0-60 um size fraction ( susp
FJ203170.1 gg_id:333574 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c
DQ009135.1 gg_id:121881 bacterioplankton clone SPOTSAPR01_5m185
FJ205329.1 gg_id:544776 Prokaryotic deep-sea hydrothermal region East Lau Spreading Centre deep marine se

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| EU244006.1 | 357193 | 800.4 | 888.7 | 1080.0 | 1140.8 | 1363.8 | 1141.0 |
| AM997955.1 | 570446 | 380.3 | 701.8 | 685.2 | 305.2 | 227.7 | 622.0 |
| EU491047.1 | 265525 | 2609.3 | 3022.5 | 1770.9 | 1917.7 | 5997.9 | 3637.9 |
| EU592383.1 | 553196 | 45.4 | 115.5 | 123.3 | 72.5 | 171.3 | 59.0 |
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| AM990941.1 | 540228 | 2666.6 | 2047.9 | 5848.7 | 3825.4 | 4350.8 | 4588.1 |
| EF123461.1 | 245864 | 2089.1 | 2166.8 | 1362.7 | 2527.4 | 3560.9 | 3302.7 |
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| DQ351747.1 | 150492 | 753.7 | 1085.1 | 1034.6 | 967.7 | 1649.3 | 1518.1 |
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| EU050825.1 | 251646 | 465.6 | 837.4 | 1436.9 | 1618.1 | 5917.2 | 3836.4 |
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AY386334.1 gg_id:97734 marine str. HTCC2148
EU491062.1 gg_id:271257 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount South Rift X
EU652559.1 gg_id:278975 Seasonal variation microbial Yel Sea sediment clone D8S-33
GU061452.1 gg_id:593389 and function microbial mesoscale eddy perturbations South China Sea clone CE1-DC
FJ203235.1 gg_id:320209 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c
AY771747.2 gg_id:141002 Arctic Pseudomonas fluorescens clone SE12
AM997950.1 gg_id:575798 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A
EU491383.1 gg_id:261733 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X3 clone
GQ347513.1 gg_id:542803 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
FJ202535.1 gg_id:320618 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k
EU652558.1 gg_id:278702 Seasonal variation microbial Yel Sea sediment clone B8S-55
AM997517.1 gg_id:563606 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A
EU491037.1 gg_id:272117 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount South Rift X
EU544821.1 gg_id:259019 free-living particle- aggregate- archaeal and Laptev Sea 1.0-60 um size fraction ( susp
AY498633.1 gg_id:103771 Piscirickettsia salmonis IRE-91A
AF452607.1 gg_id:55809 hypersaline Mono Lake clone ML310M-42
AF507823.1 gg_id:62733 Mono Lake at depth 17.5 m station 6 July 2000 clone ML617.5J-3 proteobacterium
DQ403810.1 gg_id:154488 Reinekia blandensis str. MED 297
AJ561121.1 gg_id:87543 Reinekea marinisedimentorum str. DSM 15388
GQ456131.1 gg_id:578010 Reinekea sp. IMCC4489 str. IMCC 4489
GQ348323.1 gg_id:570256 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
GQ441232.1 gg_id:578562 and dynamic mat present vs. active nitrogen-fixing microorganisms marine microbia
GQ441197.1 gg_id:532996 and dynamic mat present vs. active nitrogen-fixing microorganisms marine microbia
EF177670.1 gg_id:175318 Saccharospirillum sp. str. Y25
GQ250189.1 gg_id:545665 Saccharospirillum sp. IMCC4453 str. IMCC 4453
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AB193953.1 gg_id:108916 deep-sea vent clone Sd-EB02
AB499797.1 gg_id:573269 microbial hydrothermal vent and seep sponges-- thioautotrophic Japan:Sumisu Cald
GQ345482.1 gg_id:590055 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
AB278146.1 gg_id:185252 hydrothermal vent prokaryotes trapped 0.2- and 0.1-micro-m-filtrates obtained Mar
GQ346343.1 gg_id:550034 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
AB479080.1 gg_id:454474 Calyptogena nautilei symbiont
EU403436.1 gg_id:275217 Calyptogena ponderosa endosymbiont 6
AB112462.1 gg_id:90596 Suiyo Seamount hydrothermal plume clone SUP05-30
GQ345480.1 gg_id:553479 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
DQ009465.1 gg_id:126024 bacterioplankton clone SPOTSMAY03_890m6
AB176400.1 gg_id:193967 Microbial Hydrothermal System Suiyo Seamount on Izu-Ogasawara Arc vent area wa
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GQ346517.1 gg_id:558448 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
GQ346038.1 gg_id:536500 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich

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| EU491062.1 | 271257 | 301.4 | 539.5 | 1379.2 | 883.4 | 1915.0 | 1261.0 |
| EU652559.1 | 278975 | 12614.0 | 10737.1 | 7114.6 | 9776.3 | 9496.4 | 7673.3 |
| GU061452.1 | 593389 | 2972.1 | 2685.0 | 3313.7 | 2137.3 | 6417.0 | 5681.5 |
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| AY498633.1 | 103771 | 92.9 | 278.1 | 271.2 | 86.8 | 198.8 | 190.7 |
| AF452607.1 | 55809 | 1819.3 | 2275.1 | 720.4 | 816.1 | 733.7 | 1695.8 |
| AF507823.1 | 62733 | 105.0 | 238.8 | 655.2 | 404.9 | 1151.5 | 188.3 |
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| GQ441197.1 | 532996 | 8948.5 | 7648.8 | 4793.0 | 6204.8 | 7338.9 | 6922.4 |
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| GQ250189.1 | 545665 | 2854.2 | 6255.6 | 1938.7 | 673.2 | 4484.7 | 2546.6 |
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| AB193953.1 | 108916 | 323.1 | 598.0 | 1011.2 | 224.5 | 1699.3 | 970.2 |
| AB499797.1 | 573269 | 6569.0 | 6640.1 | 4363.3 | 9525.7 | 6694.9 | 5872.9 |
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| GQ346038.1 | 536500 | 11959.1 | 14064.2 | 2937.7 | 6390.0 | 4907.8 | 3260.4 |

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GQ345799.1 gg_id:582850 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
GQ345795.1 gg_id:589578 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
GQ346697.1 gg_id:582711 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
AB453761.1 gg_id:571917 Sulfur-Oxidizing Deep-sea Sponges deep-sea sponge Characella sp. (Pachastrelliidae)
GQ345709.1 gg_id:582923 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
GQ348271.1 gg_id:559212 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
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GQ345820.1 gg_id:562953 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
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EU403437.1 gg_id:265068 Vesicomya sp. mt-III symbiont 7
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GQ345849.1 gg_id:591808 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
DQ009424.1 gg_id:117723 bacterioplankton clone SPOTSFEB02_70m2
GQ346196.1 gg_id:580086 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
GQ345926.1 gg_id:581473 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
AB193948.1 gg_id:108910 deep-sea vent clone Sc-EB08
AB244977.1 gg_id:560000 lineage scale-worm genus Branchipolynoe deep-sea hydrothermal vent symbiont fre
GQ350803.1 gg_id:550092 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
AM911378.2 gg_id:369008 Phenotype-specific (Scleractinia) their implications coral's nutrition health and cold-
AY951931.1 gg_id:114761 Bathymodiolus azoricus thioautotrophic gill symbiont

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| GQ345991.1 | 590578 | 10239.5 | 10293.3 | 9963.2 | 9721.5 | 10237.9 | 9981.6 |
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| GQ346697.1 | 582711 | 6573.1 | 7877.2 | 12397.7 | 9379.1 | 10649.9 | 9100.8 |
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| GQ346103.1 | 549420 | 9148.0 | 10666.5 | 6340.0 | 9736.1 | 12389.6 | 10308.4 |
| GQ346252.1 | 553712 | 1284.6 | 1356.7 | 2066.9 | 991.0 | 2131.3 | 1010.4 |
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GQ346536.1 gg_id:568526 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
GU108540.1 gg_id:555184 active chemolithoautotrophic prokaryotes sulfidic zone Black pelagic redoxcline dete
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GQ346688.1 gg_id:569285 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
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GQ346418.1 gg_id:578694 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
GQ346535.1 gg_id:585267 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
GQ337088.1 gg_id:580119 Hydrography shapes biogeography deep Arctic Ocean water depth 1000m clone BB(
DQ513047.1 gg_id:160840 Microbial life fluids ridge flank crustal fluid clone CTD005-15B-02
GQ346389.1 gg_id:589239 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
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FJ745105.1 gg_id:553872 Transporter genes expressed coastal response dissolved organic carbon surface wate
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EU638746.1 gg_id:306754 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n
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GU117979.1 gg_id:581250 Threatened Corals Provide Microbial Habitats clone Acer_F12
EU491869.1 gg_id:267568 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39
AY386342.1 gg_id:97969 marine str. HTCC2151

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| GQ345879.1 | 534636 | 6811.6 | 6396.8 | 4395.0 | 5144.5 | 5194.0 | 4693.4 |
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| GU108540.1 | 555184 | 2788.8 | 3003.0 | 1822.7 | 2058.5 | 2624.2 | 2038.3 |
| GQ345506.1 | 533664 | 12314.6 | 13684.2 | 14855.6 | 11231.9 | 15986.3 | 12792.2 |
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| GQ346264.1 | 579957 | 4713.1 | 2875.9 | 5719.5 | 6111.1 | 4100.9 | 5166.7 |
| GQ345700.1 | 594218 | 10033.0 | 12109.7 | 8079.2 | 7792.2 | 7777.2 | 6868.7 |
| GQ347135.1 | 566058 | 3453.7 | 3067.1 | 1459.2 | 4424.4 | 5393.3 | 4045.8 |
| GQ345612.1 | 591185 | 11109.6 | 8977.7 | 10512.5 | 12213.3 | 9823.9 | 8082.4 |
| GQ346510.1 | 559357 | 6185.0 | 4831.4 | 7076.9 | 4528.1 | 8346.2 | 3695.1 |
| DQ009467.1 | 125536 | 3565.2 | 2425.0 | 4670.4 | 4292.3 | 5555.9 | 3581.3 |
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| GQ345630.1 | 589590 | 5792.8 | 3638.8 | 3874.3 | 6009.4 | 8008.9 | 6578.0 |
| GQ347589.1 | 578816 | 3659.2 | 6162.8 | 4759.1 | 5415.3 | 5644.1 | 4541.9 |
| AB193931.1 | 108891 | 9653.1 | 8666.1 | 3287.5 | 8137.7 | 9223.3 | 9038.2 |
| FJ825949.1 | 568805 | 2304.9 | 2351.8 | 1210.3 | 2610.6 | 3073.7 | 4697.9 |
| GQ345617.1 | 555029 | 9892.7 | 9366.6 | 2216.9 | 9097.4 | 12738.2 | 10151.8 |
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| GQ346535.1 | 585267 | 8147.8 | 6894.5 | 7007.0 | 7809.8 | 10415.5 | 8223.8 |
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GU061277.1 gg_id:588515 Evaluation culturing methods cultivate previously Yel Sea intertidal beach seawater
GQ349185.1 gg_id:588789 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
AF468261.1 gg_id:80175 Arctic pack ice; northern Fram Strait; 80 31.1 N; 01 deg 59.7 min E clone ARKDMS-58
EU050830.1 gg_id:255358 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_08_75
AJ581349.1 gg_id:92209 Mediterranean sponge clone E01-9C-12
GQ337223.1 gg_id:591094 Hydrography shapes biogeography deep Arctic Ocean water depth 900m clone CB1
EU800017.1 gg_id:313341 It's all ranking aquatic Newport Harbour RI clone 1C227703
FJ403058.1 gg_id:361395 Disease- changes healthy and diseased colonies Caribbean coral Montastrea faveolat
EU005712.1 gg_id:264274 Major activity inside and outside natural iron-fertilized phytoplankton bloom 3 micro
GU061256.1 gg_id:540813 Evaluation culturing methods cultivate previously Yel Sea intertidal beach seawater
GQ349050.1 gg_id:557301 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
DQ015809.1 gg_id:140174 Antarctic lake water clone ELB16-104
FM242300.1 gg_id:337520 sequences sediment clone 3 T9d-oil
EU050829.1 gg_id:255625 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_07_49
AY701467.1 gg_id:108544 dinoflagellate symbiont clone GCDE08_AE
DQ666550.1 gg_id:167594 Actinobacillus capsulatus str. 266/7370
DQ666548.1 gg_id:170688 Actinobacillus capsulatus str. 266/5603
DQ229009.1 gg_id:160043 Haemophilus parasuis str. ME4
AY362891.1 gg_id:101090 Actinobacillus indolicus str. 46KC2
AF268965.1 gg_id:22523 Actinobacillus indolicus str. H1422
AF268962.1 gg_id:31672 Actinobacillus indolicus str. H1269
EF396307.1 gg_id:246454 Actinobacillus indolicus WB52/06-1
DQ229002.1 gg_id:160636 Actinobacillus pleuropneumoniae 262/04
FJ437063.1 gg_id:368836 Actinobacillus porcinus str. 35NTS
EF173411.1 gg_id:207951 Actinobacillus porcitonsillarum str. WT6N
EF173406.1 gg_id:207735 Actinobacillus porcitonsillarum str. WT5A
EF173407.1 gg_id:212933 Actinobacillus porcitonsillarum str. WT1B
EF173404.1 gg_id:213833 Actinobacillus porcitonsillarum str. WT2A
AF025839.1 gg_id:9515 Actinobacillus rossii str. JF1390
EU074771.1 gg_id:244021 Actinobacillus succinogenes str. S.JST
AY362898.1 gg_id:102230 Actinobacillus succinogenes str. CCUG 43843
AF015299.1 gg_id:9589 Actinobacillus suis str. CCM5586
AY362900.1 gg_id:106038 Actinobacillus ureae str. CCUG 2139
AJ295746.3 gg_id:52835 Haemophilus parahaemolyticus str. NCTC 8479T
AY029174.1 gg_id:69899 Actinobacillus arthritidis str. 13/225/95
AF268949.1 gg_id:73428 Actinobacillus minor str. H1473
FJ939592.1 gg_id:569406 Haemophilus parahaemolyticus str. PN129
AY465359.1 gg_id:109412 Actinobacillus equuli str. B96/12; JF2421
GQ074659.1 gg_id:420587 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw164g
AF268947.1 gg_id:31668 Actinobacillus minor str. H1468
EF396305.1 gg_id:244335 Haemophilus parasuis WB25/06-1

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| GU061277.1 | 588515 | 322.6 | 1819.0 | 1656.1 | 1765.5 | 3357.1 | 2984.0 |
| GQ349185.1 | 588789 | 5483.0 | 4822.0 | 3773.9 | 7126.7 | 3724.9 | 4899.9 |
| AF468261.1 | 80175 | 4296.0 | 5503.2 | 10682.4 | 8247.8 | 9868.7 | 6511.7 |
| EU050830.1 | 255358 | 839.1 | 1544.8 | 3673.6 | 3414.2 | 6296.9 | 3676.5 |
| AJ581349.1 | 92209 | 818.7 | 1078.4 | 733.7 | 890.6 | 1682.1 | 2652.8 |
| GQ337223.1 | 591094 | 2679.4 | 3122.4 | 3000.1 | 4179.4 | 6142.5 | 6888.2 |
| EU800017.1 | 313341 | 1163.5 | 2397.3 | 2630.9 | 872.5 | 2437.9 | 4034.4 |
| FJ403058.1 | 361395 | 6757.6 | 4848.3 | 6228.3 | 6539.2 | 7620.4 | 6347.2 |
| EU005712.1 | 264274 | 2742.9 | 2585.0 | 3859.4 | 4128.7 | 4586.2 | 4499.1 |
| GU061256.1 | 540813 | 9871.1 | 8844.7 | 7637.6 | 11046.5 | 12717.7 | 12296.2 |
| GQ349050.1 | 557301 | 4933.7 | 6743.1 | 3326.0 | 3706.8 | 6686.5 | 7556.4 |
| DQ015809.1 | 140174 | 2823.2 | 4635.6 | 4250.9 | 3212.6 | 6011.5 | 4678.5 |
| FM242300.1 | 337520 | 1098.3 | 757.7 | 552.0 | 773.8 | 2233.2 | 882.6 |
| EU050829.1 | 255625 | 3878.5 | 3468.5 | 1327.6 | 2657.6 | 2717.9 | 3613.8 |
| AY701467.1 | 108544 | 1478.3 | 1669.3 | 679.9 | 2758.2 | 4173.1 | 2124.5 |
| DQ666550.1 | 167594 | 4349.8 | 5424.2 | 7499.6 | 5056.3 | 4563.0 | 7279.8 |
| DQ666548.1 | 170688 | 1984.9 | 2592.0 | 2045.0 | 1823.3 | 2384.5 | 2473.5 |
| DQ229009.1 | 160043 | 1063.3 | 980.8 | 2256.4 | 3465.1 | 2407.5 | 3101.5 |
| AY362891.1 | 101090 | 5324.6 | 5483.6 | 6785.3 | 8167.3 | 8475.2 | 7020.7 |
| AF268965.1 | 22523 | 4547.3 | 2324.3 | 3805.8 | 3919.3 | 2735.5 | 3617.0 |
| AF268962.1 | 31672 | 2638.9 | 1321.1 | 2831.9 | 2659.0 | 2058.9 | 4741.7 |
| EF396307.1 | 246454 | 1947.2 | 1436.7 | 3138.9 | 3652.9 | 2287.5 | 4824.4 |
| DQ229002.1 | 160636 | 836.1 | 335.8 | 726.7 | 590.0 | 274.8 | 340.3 |
| FJ437063.1 | 368836 | 2009.6 | 1734.1 | 1730.5 | 2904.9 | 2572.2 | 2961.8 |
| EF173411.1 | 207951 | 1445.6 | 1149.0 | 3438.6 | 2077.1 | 1113.7 | 3595.6 |
| EF173406.1 | 207735 | 1463.2 | 941.8 | 1974.9 | 2044.4 | 1071.4 | 3507.8 |
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| EF173404.1 | 213833 | 1446.2 | 1151.4 | 3438.5 | 2083.2 | 1109.6 | 3872.2 |
| AF025839.1 | 9515 | 212.9 | 333.6 | 203.4 | 527.6 | 324.1 | 309.7 |
| EU074771.1 | 244021 | 10319.3 | 12120.7 | 4703.0 | 8587.7 | 11963.0 | 7708.8 |
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| AF015299.1 | 9589 | 1408.3 | 1593.2 | 2048.6 | 1992.0 | 1921.5 | 1860.9 |
| AY362900.1 | 106038 | 519.4 | 442.4 | 1939.2 | 476.1 | 254.5 | 343.3 |
| AJ295746.3 | 52835 | 205.3 | 100.3 | 1073.7 | 229.3 | 1614.0 | 575.8 |
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| EF396305.1 | 244335 | 2358.7 | 1752.4 | 3272.9 | 3599.2 | 1708.2 | 4368.7 |

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| s__Avibacterium paragallinarum | 7305 |
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| s__Bibersteinia trehalosi | 6660 |
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| s__unclassified | 6373 |
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| s__unclassified | 7282 |
| s__Gallibacterium anatis | 6431 |
| s__Gallibacterium anatis | 6432 |

AY172727.1 gg_id:91684 Bisgaard taxon 26 biovar 1 str. F66
AF145255.1 gg_id:9586 Actinobacillus capsulatus str. 63595
EU746660.2 gg_id:347029 Actinobacillus minor str. 202
AF359941.1 gg_id:21084 Acidithiobacillus thiooxidans str. KCTC 8928P
ACQL01000137.1 gg_id:384731 Actinobacillus minor str. NM305
AF224295.1 gg_id:73432 Actinobacillus capsulatus str. P796
DQ926691.1 gg_id:180536 Actinobacillus porcitonsillarum str. 71123
EF173412.1 gg_id:212302 Actinobacillus porcitonsillarum str. WT7N
DQ229007.1 gg_id:160015 Actinobacillus minor 2134
AF381187.1 gg_id:70103 Actinobacillus cf. equuli str. CCUG 19799
DQ926692.1 gg_id:191170 Actinobacillus porcitonsillarum str. 73706
AF268948.1 gg_id:74197 Actinobacillus minor str. H1470
AF247720.1 gg_id:58548 Actinobacillus equuli str. I5445/4
GQ074426.1 gg_id:385551 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw162g
FJ435959.1 gg_id:367622 Actinobacillus minor str. 33PN
AF247723.1 gg_id:70395 Actinobacillus lignieresii str. F 264
AF247717.1 gg_id:58549 Actinobacillus arthritidis str. F 141
AF224285.1 gg_id:72378 Actinobacillus capsulatus str. CCUG 37035
AF268945.1 gg_id:27164 Actinobacillus minor str. H1284
AF247722.1 gg_id:73342 Actinobacillus lignieresii str. F 127
AB512009.1 gg_id:562676 Aggregatibacter actinomycetemcomitans str. OMZ534
AB548673.1 gg_id:531143 Aggregatibacter actinomycetemcomitans str. JCM 12985
CP001607.1 gg_id:518655 Aggregatibacter aphrophilus str. NJ8700
AF227858.1 gg_id:49556 str. 86355
AF224299.1 gg_id:17538 Haemophilus segnis str. MCCM 00337
EU826042.1 gg_id:551715 Avibacterium sp. str. HP95
AY498868.1 gg_id:104700 Haemophilus paragallinarum str. NCTC 11296T
AY498871.1 gg_id:99711 Haemophilus paragallinarum str. SA7177
AY498870.1 gg_id:99555 Haemophilus paragallinarum str. Modesto
NC_006300.1 gg_id:471413 Mannheimia succiniciproducens str. MBEL55E
AY029193.1 gg_id:22261 Mannheimia succiniciproducens str. MBEL55E
DQ841185.1 gg_id:186374 Pasteurella trehalosi str. 06-106810
AY757729.1 gg_id:111227 Pasteurellaceae I6
AF227862.1 gg_id:31902 Pasteurella sp. str. 37234
AY172730.1 gg_id:91205 Bisgaard taxon 32 str. 5108/S2/90
AY172729.1 gg_id:91016 Bisgaard taxon 32 str. HPA106
EU331064.1 gg_id:578335 Chelonobacter oris str. 1662
EU331067.1 gg_id:590073 Chelonobacter oris str. 17123
AY362926.1 gg_id:99165 Pasteurella testudinis str. CCUG 19802
GQ423354.1 gg_id:563660 Gallibacterium anatis str. Yu-ZMD-XP-3-QG
GQ423350.1 gg_id:551687 Gallibacterium anatis str. Yu-ZMD-XP-1-QG-3

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| AY172727.1 | 91684 | 1140.9 | 431.9 | 762.3 | 784.7 | 1065.2 | 1105.7 |
| AF145255.1 | 9586 | 688.2 | 727.8 | 1995.7 | 1251.5 | 1679.3 | 1316.3 |
| EU746660.2 | 347029 | 2122.8 | 1624.9 | 2551.9 | 1990.3 | 1206.2 | 3469.8 |
| AF359941.1 | 21084 | 736.8 | 916.9 | 2907.4 | 1999.5 | 4507.9 | 3023.4 |
| ACQL01000137.1 | 384731 | 1843.6 | 1105.7 | 1898.0 | 3107.1 | 1512.8 | 2142.6 |
| AF224295.1 | 73432 | 60.5 | 124.3 | 329.9 | 157.1 | 113.3 | 140.7 |
| DQ926691.1 | 180536 | 561.4 | 779.7 | 4674.2 | 1612.3 | 1415.4 | 1732.3 |
| EF173412.1 | 212302 | 520.7 | 598.4 | 2489.0 | 1253.3 | 512.7 | 814.9 |
| DQ229007.1 | 160015 | 626.1 | 523.7 | 1478.2 | 1272.9 | 857.0 | 2940.2 |
| AF381187.1 | 70103 | 519.1 | 837.5 | 2728.4 | 968.4 | 991.4 | 797.7 |
| DQ926692.1 | 191170 | 280.7 | 541.3 | 2234.5 | 498.5 | 406.1 | 1113.2 |
| AF268948.1 | 74197 | 401.1 | 501.4 | 1170.1 | 1037.8 | 724.5 | 1707.6 |
| AF247720.1 | 58548 | 3331.2 | 3559.4 | 5796.5 | 3209.8 | 4495.2 | 3690.9 |
| GQ074426.1 | 385551 | 4347.5 | 2890.5 | 5862.4 | 4309.5 | 4264.8 | 4211.3 |
| FJ435959.1 | 367622 | 406.6 | 561.6 | 1377.8 | 696.9 | 1196.3 | 2154.3 |
| AF247723.1 | 70395 | 857.3 | 1462.4 | 5438.3 | 1666.5 | 3225.2 | 2139.2 |
| AF247717.1 | 58549 | 390.2 | 828.4 | 3532.1 | 402.8 | 1049.9 | 724.4 |
| AF224285.1 | 72378 | 821.6 | 865.0 | 3422.2 | 2203.1 | 2325.5 | 4903.5 |
| AF268945.1 | 27164 | 1482.3 | 1037.7 | 1952.8 | 2059.2 | 1099.7 | 3532.8 |
| AF247722.1 | 73342 | 170.1 | 237.4 | 775.9 | 174.5 | 1163.4 | 415.7 |
| AB512009.1 | 562676 | 3482.2 | 3320.2 | 3552.3 | 4548.3 | 4724.0 | 4144.3 |
| AB548673.1 | 531143 | 43.9 | 36.0 | 60.4 | 59.2 | 85.4 | 63.5 |
| CP001607.1 | 518655 | 581.2 | 1164.4 | 1817.8 | 859.5 | 905.6 | 864.3 |
| AF227858.1 | 49556 | 5236.4 | 4930.0 | 5089.8 | 5947.7 | 6583.2 | 7271.2 |
| AF224299.1 | 17538 | 149.2 | 569.7 | 541.5 | 410.4 | 1790.7 | 691.8 |
| EU826042.1 | 551715 | 2266.5 | 2252.9 | 5136.3 | 3316.4 | 3481.3 | 1964.1 |
| AY498868.1 | 104700 | 388.8 | 478.8 | 678.5 | 712.9 | 386.4 | 766.8 |
| AY498871.1 | 99711 | 276.9 | 337.5 | 1497.5 | 608.9 | 1919.9 | 773.2 |
| AY498870.1 | 99555 | 1998.9 | 1715.7 | 3844.9 | 4666.1 | 4352.4 | 2627.2 |
| NC_006300.1 | 471413 | 290.9 | 225.5 | 1329.8 | 270.5 | 1159.1 | 781.4 |
| AY029193.1 | 22261 | 1461.1 | 1252.5 | 734.5 | 653.2 | 1168.8 | 1153.1 |
| DQ841185.1 | 186374 | 1083.6 | 1220.1 | 3880.4 | 2099.2 | 4121.2 | 2270.1 |
| AY757729.1 | 111227 | 6876.8 | 9187.3 | 5667.8 | 8141.4 | 11692.0 | 8262.2 |
| AF227862.1 | 31902 | 1349.5 | 1432.0 | 1769.5 | 665.4 | 1925.8 | 1551.6 |
| AY172730.1 | 91205 | 1694.4 | 1999.4 | 6108.1 | 3340.2 | 486.1 | 1469.3 |
| AY172729.1 | 91016 | 15972.3 | 17245.8 | 14938.1 | 12500.1 | 17949.8 | 13715.4 |
| EU331064.1 | 578335 | 422.9 | 733.6 | 1923.5 | 896.7 | 828.9 | 574.7 |
| EU331067.1 | 590073 | 109.2 | 137.6 | 1655.8 | 358.2 | 1710.1 | 921.0 |
| AY362926.1 | 99165 | 19.8 | 54.1 | 236.9 | 44.7 | 76.4 | 35.9 |
| GQ423354.1 | 563660 | 3094.4 | 2286.6 | 2690.8 | 1998.7 | 2828.9 | 522.2 |
| GQ423350.1 | 551687 | 62.6 | 68.7 | 126.2 | 87.7 | 116.8 | 52.4 |

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| k__Bacteria | k__Bacteria | p__Proteobacteria | c__Gammaproteobacteria |
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| o__Pasteurellales | f__Pasteurellaceae |
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| s__Gallibacterium anatis | 6672 |
| s__Gallibacterium anatis | 7322 |
| s__Gallibacterium anatis | 7442 |
| s__Gallibacterium anatis | 7443 |
| s__Gallibacterium anatis | 7545 |
| s__Gallibacterium genomosp. 1 | 7384 |
| s__Gallibacterium genomosp. 3 | 7023 |
| s__Gallibacterium melopsittaci | 6871 |
| s__unclassified | 6419 |
| s__unclassified | 6563 |
| s__Haemophilus ducreyi | 7354 |
| s__Haemophilus haemolyticus | 6279 |
| s__Haemophilus haemolyticus | 6300 |
| s__Haemophilus haemolyticus | 6327 |
| s__Haemophilus haemolyticus | 6382 |
| s__Haemophilus haemolyticus | 6537 |
| s__Haemophilus haemolyticus | 6608 |
| s__Haemophilus haemolyticus | 6682 |
| s__Haemophilus haemolyticus | 6781 |
| s__Haemophilus haemolyticus | 6805 |
| s__Haemophilus haemolyticus | 7075 |
| s__Haemophilus haemolyticus | 7213 |
| s__Haemophilus haemolyticus | 7293 |
| s__Haemophilus haemolyticus | 7364 |
| s__Haemophilus haemolyticus | 7606 |
| s__Haemophilus influenzae | 6978 |
| s__Haemophilus influenzae | 7198 |
| s__Haemophilus influenzae | 7531 |
| s__Haemophilus parainfluenzae | 6385 |
| s__Haemophilus parainfluenzae | 6558 |
| s__Haemophilus parainfluenzae | 6624 |
| s__Haemophilus parainfluenzae | 6666 |
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| s__Haemophilus parainfluenzae | 7182 |
| s__Haemophilus parainfluenzae | 7505 |
| s__Haemophilus parainfluenzae | 7549 |
| s__Haemophilus parasuis | 6341 |
| s__Haemophilus parasuis | 6887 |

GQ423347.1 gg_id:543050 Gallibacterium anatis str. Yu-HL-huang-1-SLG
AF228009.1 gg_id:70476 Gallibacterium anatis str. 12158
AF228007.1 gg_id:73745 Gallibacterium anatis str. IPDH 697/78
AY038594.1 gg_id:73007 Gallibacterium anatis str. Hom.3
AF224310.1 gg_id:74034 Actinobacillus cf. salpingitidis CCUG 28018 salpingitidis
AY038591.1 gg_id:64296 Gallibacterium genomosp. 1 str. Gerl.3191
EU339201.1 gg_id:571594 Gallibacterium genomosp. 3 str. F448
EU339196.1 gg_id:534387 Gallibacterium melopsittaci str. F450
EU423995.1 gg_id:569567 Gallibacterium trehalosifermentans str. B7/99/1
FJ841971.3 gg_id:542079 Gallibacterium anatis str. Yu-JZ-YQ-5-SLG
NC_002940.2 gg_id:129218 Haemophilus ducreyi str. 35000HP
EU185475.1 gg_id:239174 Haemophilus haemolyticus str. D62.2
EU185365.1 gg_id:248286 Haemophilus haemolyticus str. 24P12H3
EU185437.1 gg_id:253598 Haemophilus haemolyticus str. 61224
EU185346.1 gg_id:243151 Haemophilus haemolyticus str. 14P38
EU185429.1 gg_id:237127 Haemophilus haemolyticus str. 54P15H1
EU185362.1 gg_id:237256 Haemophilus haemolyticus str. 1P2H1
EU185484.1 gg_id:236050 Haemophilus haemolyticus str. K22.1
EU185482.1 gg_id:254806 Haemophilus haemolyticus str. K142.1
EU185421.1 gg_id:236390 Haemophilus haemolyticus str. 3P5H
EU185485.1 gg_id:240164 Haemophilus haemolyticus str. L52.2
EU185444.1 gg_id:245827 Haemophilus haemolyticus str. 68P29H
EU185436.1 gg_id:243777 Haemophilus haemolyticus str. 60P12H2
EU185338.1 gg_id:251582 Haemophilus haemolyticus str. 11P8H5
EU185407.1 gg_id:236863 Haemophilus haemolyticus str. 32P3H1
EU185473.1 gg_id:252539 Haemophilus influenzae str. D152.1
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AY613497.1 gg_id:110972 Haemophilus influenzae str. M8467
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EF509248.1 gg_id:220552 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aerug
GQ106447.1 gg_id:375695 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw!
GQ010997.1 gg_id:498669 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
EF509106.1 gg_id:219857 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aerug
EF511111.1 gg_id:222083 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aerug
EF511117.1 gg_id:226358 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aerug
EF511150.1 gg_id:218497 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aerug
EF509136.1 gg_id:220176 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aerug
GQ011135.1 gg_id:498531 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
EF511057.1 gg_id:224454 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aerug
DQ229028.1 gg_id:161434 Haemophilus parasuis 393/03-4
DQ228991.1 gg_id:160451 Haemophilus parasuis VS7-1

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|---|---|---|---|---|---|---|---|
| GQ423347.1 | 543050 | 6015.5 | 5125.6 | 6117.4 | 4255.8 | 8467.5 | 7281.9 |
| AF228009.1 | 70476 | 176.8 | 179.9 | 702.9 | 242.2 | 1099.0 | 654.5 |
| AF228007.1 | 73745 | 852.7 | 627.5 | 865.4 | 579.0 | 1129.2 | 373.1 |
| AY038594.1 | 73007 | 281.8 | 295.5 | 597.7 | 379.4 | 414.3 | 314.1 |
| AF224310.1 | 74034 | 281.5 | 274.0 | 582.8 | 351.8 | 426.1 | 274.0 |
| AY038591.1 | 64296 | 609.7 | 467.8 | 3211.3 | 1120.7 | 399.5 | 518.3 |
| EU339201.1 | 571594 | 1506.2 | 1386.6 | 3679.5 | 2333.5 | 5514.3 | 3044.0 |
| EU339196.1 | 534387 | 3041.5 | 3460.7 | 4656.5 | 4516.9 | 8362.2 | 5087.8 |
| EU423995.1 | 569567 | 110.3 | 394.9 | 567.2 | 322.3 | 2210.7 | 573.3 |
| FJ841971.3 | 542079 | 1096.3 | 1095.6 | 1467.8 | 1090.6 | 1342.7 | 543.9 |
| NC_002940.2 | 129218 | 617.9 | 986.1 | 5003.9 | 1803.9 | 3669.5 | 2453.0 |
| EU185475.1 | 239174 | 1043.0 | 1147.3 | 3498.0 | 2338.4 | 2460.9 | 1623.1 |
| EU185365.1 | 248286 | 653.2 | 385.4 | 1279.8 | 1814.3 | 1557.9 | 1110.6 |
| EU185437.1 | 253598 | 545.8 | 588.2 | 1474.5 | 1255.0 | 1059.8 | 810.9 |
| EU185346.1 | 243151 | 1191.2 | 756.4 | 3281.7 | 3130.9 | 1832.6 | 2894.4 |
| EU185429.1 | 237127 | 634.0 | 852.7 | 2532.8 | 1449.7 | 1779.4 | 1193.8 |
| EU185362.1 | 237256 | 1450.0 | 968.0 | 3315.0 | 3444.9 | 3061.8 | 1856.0 |
| EU185484.1 | 236050 | 1630.6 | 1103.3 | 3288.8 | 3746.3 | 3312.3 | 1982.7 |
| EU185482.1 | 254806 | 3871.1 | 3803.4 | 4408.0 | 3443.9 | 3433.7 | 3262.6 |
| EU185421.1 | 236390 | 1470.8 | 1062.2 | 3701.5 | 3385.8 | 2884.2 | 1773.3 |
| EU185485.1 | 240164 | 1638.9 | 1112.8 | 3459.0 | 3739.8 | 3286.0 | 1856.5 |
| EU185444.1 | 245827 | 289.6 | 285.7 | 3381.5 | 1293.8 | 546.6 | 429.3 |
| EU185436.1 | 243777 | 713.7 | 1203.4 | 3797.1 | 1419.7 | 2466.8 | 1543.9 |
| EU185338.1 | 251582 | 1455.0 | 990.8 | 3184.5 | 3486.8 | 3054.6 | 1985.5 |
| EU185407.1 | 236863 | 601.0 | 974.9 | 4119.0 | 1939.0 | 2022.7 | 2100.6 |
| EU185473.1 | 252539 | 958.7 | 989.8 | 3046.6 | 3349.4 | 2324.3 | 1459.6 |
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| EF511979.1 | 218564 | 3928.3 | 3304.4 | 7051.1 | 5373.9 | 5260.8 | 4669.4 |
| EF509248.1 | 220552 | 8286.7 | 7583.3 | 2408.3 | 6736.0 | 7196.7 | 8467.4 |
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| EF509106.1 | 219857 | 744.3 | 386.1 | 1522.6 | 776.5 | 619.3 | 585.7 |
| EF511111.1 | 222083 | 7774.0 | 7203.0 | 3262.5 | 4150.8 | 3535.3 | 2816.0 |
| EF511117.1 | 226358 | 42.9 | 224.7 | 373.1 | 157.4 | 239.7 | 159.9 |
| EF511150.1 | 218497 | 2334.8 | 1928.2 | 2311.7 | 2639.9 | 1722.7 | 1487.2 |
| EF509136.1 | 220176 | 5331.2 | 4724.6 | 4614.7 | 3630.2 | 4652.9 | 3288.2 |
| GQ011135.1 | 498531 | 7429.3 | 8023.6 | 5681.9 | 3444.7 | 7539.7 | 5267.1 |
| EF511057.1 | 224454 | 8920.4 | 7073.9 | 4466.5 | 3902.7 | 5182.9 | 3732.9 |
| DQ229028.1 | 161434 | 2600.6 | 2185.2 | 384.9 | 1373.9 | 2216.2 | 1531.6 |
| DQ228991.1 | 160451 | 1273.5 | 744.0 | 1501.5 | 1736.4 | 1035.0 | 1393.4 |

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| s__Mannheimia granulomatis | 7039 |
| s__Mannheimia granulomatis | 7457 |
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AB370297.1 gg_id:271851 Haemophilus parasuis str. 332
FJ667952.1 gg_id:540531 Haemophilus parasuis str. Nagasaki
DQ229016.1 gg_id:161508 Haemophilus parasuis RW
FJ667979.1 gg_id:513849 Haemophilus parasuis str. NO145
EU909653.1 gg_id:354221 Haemophilus sp. str. CCUG 17210
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FJ983093.1 gg_id:414943 Aspects Oral Microbiome subgingival plaque clone
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GQ091843.1 gg_id:409269 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
EU341202.1 gg_id:255127 Evaluation Rapid Technologies Estimate Microbial Burden and Commercial Airline Ca
GQ087761.1 gg_id:421332 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
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X87978.1 gg_id:9509 Haemophilus influenzae str. 16N
AY362910.1 gg_id:102232 Haemophilus parasuis str. Bakos B26
AY005033.1 gg_id:72532 subgingival dental plaque clone BJ095
GQ083015.1 gg_id:429541 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
DQ228998.1 gg_id:160846 Haemophilus parasuis P015/96
EU909656.1 gg_id:340606 Haemophilus sp. str. CCUG 18082
AJ290754.2 gg_id:44396 Haemophilus parainfluenzae str. P1525
EU137565.1 gg_id:261499 Bartonella-positive fleas: and assembly patterns Oropsylla hirsuta (prairie dog flea) C
GQ113941.1 gg_id:391680 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor
FJ558391.1 gg_id:531822 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat
GQ116286.1 gg_id:429653 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw690g02
EU909680.1 gg_id:307019 Haemophilus sp. str. PN24
AB176910.1 gg_id:114966 Histophilus somni str. 129Pt
AF053901.1 gg_id:9609 Mannheimia granulomatis str. Ph13; CCUG 26828
DQ301924.2 gg_id:146654 Mannheimia granulomatis str. W4672/1
AF053896.1 gg_id:9605 Mannheimia ruminalis str. HPA98; CCUG38466
AY425286.1 gg_id:107110 Mannheimia ruminalis str. HPA109
AY425283.1 gg_id:106648 Mannheimia ruminalis str. HPA113

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| FJ463836.1 | 363177 | 1154.1 | 1079.2 | 3469.0 | 2857.2 | 3112.5 | 2015.7 |
| AB370297.1 | 271851 | 587.0 | 691.6 | 2622.8 | 1149.9 | 1782.6 | 1146.6 |
| FJ667952.1 | 540531 | 361.4 | 441.7 | 1514.4 | 1118.9 | 684.9 | 516.5 |
| DQ229016.1 | 161508 | 184.4 | 543.3 | 1161.3 | 808.9 | 390.2 | 798.3 |
| FJ667979.1 | 513849 | 3603.4 | 3584.4 | 8499.6 | 3947.5 | 5220.6 | 5530.2 |
| EU909653.1 | 354221 | 1394.5 | 719.0 | 1803.0 | 2937.1 | 1736.5 | 2477.9 |
| FJ558112.1 | 526872 | 2242.5 | 1244.6 | 4518.8 | 4553.8 | 2926.0 | 3123.7 |
| FJ667959.1 | 560868 | 358.0 | 654.2 | 1122.1 | 1363.1 | 1534.6 | 1128.9 |
| EU185432.1 | 245942 | 378.4 | 917.1 | 2000.9 | 1196.5 | 1247.8 | 949.4 |
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| GQ087742.1 | 420505 | 1548.5 | 902.8 | 2984.8 | 3588.9 | 2503.8 | 2683.3 |
| AB078972.1 | 30824 | 408.1 | 496.5 | 994.5 | 1734.5 | 1434.3 | 996.4 |
| EU185439.1 | 239937 | 1763.5 | 926.6 | 2759.2 | 3679.9 | 2928.5 | 1709.6 |
| FJ558093.1 | 517548 | 3558.0 | 2314.3 | 6537.1 | 6078.2 | 3639.3 | 4293.3 |
| FJ983093.1 | 414943 | 9594.5 | 10996.2 | 6030.4 | 9638.8 | 9953.1 | 10333.5 |
| GQ083506.1 | 440265 | 5828.0 | 3242.1 | 3313.4 | 6014.3 | 3268.5 | 3083.3 |
| GQ114305.1 | 423130 | 1776.4 | 1213.8 | 4035.2 | 3425.2 | 1988.3 | 2891.9 |
| GQ074383.1 | 392625 | 1247.4 | 1044.8 | 3834.3 | 3510.8 | 1378.6 | 2351.4 |
| GQ116263.1 | 457345 | 2190.4 | 994.2 | 3687.0 | 4015.4 | 2237.5 | 2895.4 |
| GQ091843.1 | 409269 | 1475.7 | 746.7 | 3451.1 | 3276.9 | 2307.3 | 2007.5 |
| EU341202.1 | 255127 | 2184.5 | 2212.5 | 4073.1 | 3900.9 | 3276.2 | 3406.8 |
| GQ087761.1 | 421332 | 2346.2 | 1164.9 | 3851.8 | 3998.0 | 2980.3 | 3028.7 |
| EU185461.1 | 235553 | 187.1 | 264.7 | 1662.8 | 407.8 | 450.2 | 274.7 |
| X87978.1 | 9509 | 1191.8 | 642.0 | 2955.9 | 3004.1 | 1112.5 | 2120.6 |
| AY362910.1 | 102232 | 1748.6 | 1853.3 | 3876.2 | 3055.4 | 2612.8 | 2511.4 |
| AY005033.1 | 72532 | 37.0 | 133.6 | 369.4 | 211.8 | 168.7 | 87.3 |
| GQ083015.1 | 429541 | 1132.4 | 721.1 | 2581.8 | 2722.5 | 1714.2 | 2107.3 |
| DQ228998.1 | 160846 | 1843.3 | 1487.8 | 3450.0 | 4295.0 | 3433.0 | 3056.6 |
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| AJ290754.2 | 44396 | 1430.5 | 2344.8 | 2659.7 | 2462.7 | 1798.7 | 2295.7 |
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| GQ113941.1 | 391680 | 212.7 | 356.1 | 1490.2 | 1551.5 | 579.0 | 432.4 |
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| GQ116286.1 | 429653 | 13543.4 | 13174.6 | 13498.0 | 13313.6 | 15496.9 | 13059.5 |
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| AB176910.1 | 114966 | 40.7 | 64.1 | 73.0 | 180.5 | 63.1 | 39.5 |
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| DQ301924.2 | 146654 | 2257.2 | 620.5 | 2502.0 | 3472.4 | 1323.1 | 1054.8 |
| AF053896.1 | 9605 | 1726.9 | 509.3 | 1809.7 | 2848.2 | 1091.1 | 1090.0 |
| AY425286.1 | 107110 | 3368.6 | 1486.2 | 3533.2 | 4488.4 | 2226.6 | 5142.0 |
| AY425283.1 | 106648 | 2290.1 | 604.8 | 1891.5 | 2588.8 | 959.7 | 1228.4 |

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| s__Mannheimia ruminalis | 7525 |
| s__Mannheimia varigena | 6349 |
| s__Mannheimia varigena | 6734 |
| s__Mannheimia varigena | 7166 |
| s__unclassified | 6369 |
| s__unclassified | 6387 |
| s__unclassified | 6452 |
| s__unclassified | 6845 |
| s__unclassified | 7065 |
| s__unclassified | 7259 |
| s__unclassified | 7430 |
| s__unclassified | 7459 |
| s__unclassified | 7572 |
| s__Nicoletella semolina | 6415 |
| s__Pasteurella aerogenes | 7105 |
| s__Pasteurella canis | 7255 |
| s__Pasteurella mairii | 7231 |
| s__Pasteurella multocida | 6840 |
| s__Pasteurella multocida | 6982 |
| s__Pasteurella multocida | 7225 |
| s__Pasteurella pneumotropica | 7454 |
| s__unclassified | 6290 |
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| s__unclassified | 6878 |
| s__unclassified | 6888 |

AY425290.1 gg_id:102351 Mannheimia ruminalis str. HPA114
NR_024897.1 gg_id:575542 Mannheimia varigena str. 177; CCUG 38462
DQ301926.2 gg_id:149765 Mannheimia varigena str. 3997/82
DQ301927.2 gg_id:148422 Mannheimia varigena str. H39
U57069.1 gg_id:9606 Mannheimia haemolytica str. PH192
AY362913.1 gg_id:102691 Mannheimia granulomatis str. ATCC 49244
AF224287.1 gg_id:38515 Pasteurella haemolytica str. CCUG 28148
AF053891.1 gg_id:9614 Mannheimia glucosida str. P737; CCUG 38459
U57072.1 gg_id:9590 Mannheimia haemolytica str. PH704
DQ301923.1 gg_id:145499 Mannheimia glucosida str. P933
AF224286.1 gg_id:72830 Mannheimia sp. MCCM 00145
U57070.1 gg_id:9601 Mannheimia haemolytica str. PH40
AY425282.1 gg_id:106492 Mannheimia varigena str. V1835
AY508828.1 gg_id:105688 Nicoletella semolina str. CCUG 43643
U66492.1 gg_id:9498 Pasteurella aerogenes str. P
EF579842.1 gg_id:278925 Pasteurella canis str. Group868/2
DQ211736.1 gg_id:171809 Pasteurella mairii str. JF3176
EU652767.1 gg_id:286210 Pasteurella subsp. multocida str. Pmww07824
AY299318.1 gg_id:103885 Pasteurella multocida str. PM80
AY507110.1 gg_id:104353 Pasteurella multocida str. X225
AB279579.1 gg_id:187444 Pasteurella sp. str. V6
AY299315.1 gg_id:103457 Pasteurella multocida str. PM64
AY362925.1 gg_id:99002 Pasteurella stomatis str. CCUG 17979
AY299319.1 gg_id:104032 Pasteurella multocida str. PM82
AF224296.1 gg_id:69985 Pasteurella pneumotropica str. NCTC 10827
AY362920.1 gg_id:107231 Pasteurella dagmatis str. CCUG 12397
AY299316.1 gg_id:103590 Pasteurella multocida str. PM106
FJ832327.1 gg_id:579924 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P1Q301_30F04
FJ976392.1 gg_id:552339 Interindividual healthy human oral microbiota mouth clone 24B192
AY362918.1 gg_id:103434 Pasteurella caballi str. ATCC 49197
AJ251339.1 gg_id:32352 Bisgaardia hudsonenesis str. 98-D-690B
AY362917.1 gg_id:103283 Pasteurella bettyae str. CCUG 2042
EU681975.1 gg_id:289990 microflora imbalances intestine dogs inflammatory bowel disease duodenum dog IBI
EU681998.1 gg_id:293231 microflora imbalances intestine dogs inflammatory bowel disease duodenum health
GQ111280.1 gg_id:419174 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
AY172732.1 gg_id:91315 Bisgaard taxon 40 str. B301529/00/1
AY465363.1 gg_id:109416 Actinobacillus rossii str. B96/45; JF2425
AY362894.1 gg_id:101590 Actinobacillus muris str. NCTC 12432
GQ111657.1 gg_id:453130 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
M75052.1 gg_id:9466 Pasteurella species
AF224311.1 gg_id:36769 Haemophilus sp. str. MCCM 01557

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|---|---|---|---|---|---|---|---|
| AY425290.1 | 102351 | 2477.5 | 841.4 | 3024.5 | 4186.8 | 1901.4 | 1723.0 |
| NR_024897.1 | 575542 | 939.2 | 976.2 | 936.3 | 1063.8 | 897.4 | 1352.7 |
| DQ301926.2 | 149765 | 1978.0 | 1766.8 | 3182.4 | 1943.2 | 2330.2 | 2935.5 |
| DQ301927.2 | 148422 | 3347.6 | 2646.6 | 2859.2 | 2546.5 | 2376.2 | 7174.4 |
| U57069.1 | 9606 | 2386.5 | 842.3 | 3185.0 | 4149.3 | 2062.9 | 1447.7 |
| AY362913.1 | 102691 | 821.1 | 847.0 | 1912.5 | 538.0 | 304.2 | 380.3 |
| AF224287.1 | 38515 | 1719.5 | 1339.4 | 2155.6 | 1423.9 | 1407.8 | 2096.6 |
| AF053891.1 | 9614 | 1913.0 | 742.7 | 2701.7 | 3647.8 | 2309.5 | 1268.7 |
| U57072.1 | 9590 | 1750.2 | 2004.8 | 3212.8 | 5100.3 | 546.7 | 3266.0 |
| DQ301923.1 | 145499 | 2209.7 | 1436.0 | 3066.1 | 3032.5 | 950.5 | 1521.4 |
| AF224286.1 | 72830 | 546.1 | 163.0 | 2405.4 | 1830.2 | 74.1 | 933.8 |
| U57070.1 | 9601 | 3583.9 | 2617.1 | 3331.4 | 2033.5 | 3000.9 | 5375.6 |
| AY425282.1 | 106492 | 1815.2 | 1781.7 | 1210.5 | 1738.3 | 1717.2 | 2425.0 |
| AY508828.1 | 105688 | 453.9 | 272.4 | 1788.6 | 700.1 | 108.4 | 487.9 |
| U66492.1 | 9498 | 772.3 | 170.7 | 2849.2 | 4632.5 | 346.4 | 2059.7 |
| EF579842.1 | 278925 | 1930.7 | 1980.3 | 2059.5 | 2034.5 | 897.1 | 1534.1 |
| DQ211736.1 | 171809 | 659.3 | 840.3 | 1009.8 | 2806.2 | 836.0 | 1592.6 |
| EU652767.1 | 286210 | 1623.1 | 2082.6 | 712.1 | 1492.2 | 467.2 | 312.7 |
| AY299318.1 | 103885 | 1931.7 | 2305.0 | 3958.1 | 2062.4 | 649.3 | 764.2 |
| AY507110.1 | 104353 | 1337.4 | 1479.9 | 2924.8 | 1722.6 | 765.1 | 986.8 |
| AB279579.1 | 187444 | 27.7 | 26.3 | 23.0 | 53.8 | 71.0 | 17.6 |
| AY299315.1 | 103457 | 1553.8 | 1388.4 | 2461.9 | 2443.3 | 1427.9 | 1755.4 |
| AY362925.1 | 99002 | 3432.4 | 4290.0 | 6321.4 | 6325.5 | 3521.8 | 4342.3 |
| AY299319.1 | 104032 | 768.8 | 943.1 | 2480.1 | 1980.8 | 1168.8 | 1285.7 |
| AF224296.1 | 69985 | 2075.3 | 3149.9 | 4468.1 | 3534.0 | 4197.7 | 3969.2 |
| AY362920.1 | 107231 | 4757.6 | 4697.0 | 4617.2 | 4849.6 | 2286.9 | 4594.8 |
| AY299316.1 | 103590 | 1643.5 | 1369.8 | 2594.5 | 2495.9 | 1385.9 | 1622.5 |
| FJ832327.1 | 579924 | 135.2 | 370.7 | 723.5 | 319.5 | 453.5 | 142.2 |
| FJ976392.1 | 552339 | 509.5 | 800.8 | 1408.4 | 1330.3 | 1397.1 | 946.4 |
| AY362918.1 | 103434 | 3933.7 | 3203.0 | 4700.8 | 7973.1 | 6388.3 | 5975.9 |
| AJ251339.1 | 32352 | 44.6 | 74.0 | 200.5 | 76.8 | 1033.1 | 91.8 |
| AY362917.1 | 103283 | 20.2 | 30.5 | 51.8 | 72.4 | 73.1 | 26.9 |
| EU681975.1 | 289990 | 308.2 | 279.0 | 486.5 | 396.9 | 856.4 | 506.3 |
| EU681998.1 | 293231 | 3981.9 | 4157.5 | 5373.3 | 5336.8 | 4227.1 | 3888.4 |
| GQ111280.1 | 419174 | 3343.2 | 4183.9 | 7091.7 | 5416.8 | 6050.1 | 4770.8 |
| AY172732.1 | 91315 | 66.5 | 45.5 | 93.5 | 110.4 | 115.2 | 120.8 |
| AY465363.1 | 109416 | 353.3 | 574.9 | 649.8 | 721.7 | 292.8 | 483.3 |
| AY362894.1 | 101590 | 57.3 | 126.7 | 386.0 | 268.5 | 435.4 | 144.2 |
| GQ111657.1 | 453130 | 5930.7 | 5493.5 | 5031.4 | 5362.7 | 6599.7 | 5253.2 |
| M75052.1 | 9466 | 321.8 | 366.8 | 1287.5 | 226.5 | 887.5 | 570.9 |
| AF224311.1 | 36769 | 48.8 | 90.0 | 51.2 | 75.6 | 72.7 | 31.9 |

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|---|---|---|---|
| k__Bacteria | k__Bacteria | p__Proteobacteria | c__Gammaproteobacteria |
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| s__unclassified | 7398 |
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| s__unclassified | 7627 |
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| s__Volucribacter psittacicida | 6600 |
| s__Acinetobacter baylyi | 3403 |
| s__Acinetobacter baylyi | 3520 |
| s__Acinetobacter baylyi | 3725 |
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| s__Acinetobacter baylyi | 3957 |
| s__Acinetobacter guillouiae | 3379 |
| s__Acinetobacter guillouiae | 3388 |
| s__Acinetobacter guillouiae | 3441 |
| s__Acinetobacter guillouiae | 3443 |
| s__Acinetobacter guillouiae | 3472 |
| s__Acinetobacter guillouiae | 3489 |
| s__Acinetobacter guillouiae | 3602 |
| s__Acinetobacter guillouiae | 3616 |
| s__Acinetobacter guillouiae | 3844 |
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| s__Acinetobacter guillouiae | 4027 |
| s__Acinetobacter gyllenbergii | 3432 |
| s__Acinetobacter gyllenbergii | 3455 |
| s__Acinetobacter gyllenbergii | 3742 |
| s__Acinetobacter haemolyticus | 3359 |
| s__Acinetobacter haemolyticus | 3394 |
| s__Acinetobacter haemolyticus | 3605 |
| s__Acinetobacter haemolyticus | 3830 |
| s__Acinetobacter haemolyticus | 4064 |

Y17190.1 gg_id:9547 Lonepinella koalarum str. ACM 3896
X89379.1 gg_id:9511 Phocoenobacter uteri str. M1063U = NCTC 12872
AY362907.1 gg_id:107128 Haemophilus haemoglobinophilus str. CCUG 3714
FJ960217.1 gg_id:571320 bottlenose dolphin upper respiratory tract blowhole clone D9A4_107
AF487728.1 gg_id:82586 Pasteurella gallinarum str. NCTC 11051
GQ111114.1 gg_id:453851 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
DQ113707.1 gg_id:134081 Assssmnt alng cnn intstnl trct dg ilm cln I2-02
AF224293.1 gg_id:35735 Pasteurella sp. str. MCCM 02539
GQ072607.1 gg_id:457136 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw19
EU826048.1 gg_id:579141 Avibacterium sp. str. MCCM 01291
AF487729.1 gg_id:82728 Pasteurella gallinarum str. R44sv
AF224304.1 gg_id:71067 Pasteurella sp. str. MCCM 02120
AY362922.1 gg_id:107519 Pasteurella langaaensis str. CCUG 15566
DQ851143.1 gg_id:164515 Haemophilus simiae str. ROG53
AY216870.1 gg_id:85860 Volucribacter amazonae str. B96/5
NR_025724.1 gg_id:535122 Volucribacter psittacicida str. Gerl. 236/81; CCUG 47536
AF509820.1 gg_id:60271 Acinetobacter baylyi str. B2
FJ009376.1 gg_id:331932 Acinetobacter baylyi str. H2
AM410708.1 gg_id:194118 Acinetobacter baylyi str. A7 LUH9557 = ACI846
FJ976560.1 gg_id:584494 Acinetobacter soli str. LCR52
AF509821.1 gg_id:60274 Acinetobacter baylyi str. C5
AF509822.1 gg_id:60277 Acinetobacter baylyi str. A7
AM412162.1 gg_id:242026 Acinetobacter sp. str. P-110
FJ009371.1 gg_id:333962 Acinetobacter johnsonii str. H10
AY536009.1 gg_id:129982 sp. str. BCaL1
FM177774.1 gg_id:518457 Acinetobacter berezinae str. LUH 9667
Z93444.1 gg_id:43948 Acinetobacter sp. str. ATCC 11171 Group eleven
AF509832.1 gg_id:60258 Acinetobacter genomosp. 11 str. A23
FM177776.1 gg_id:522874 Acinetobacter guillouiae str. A23 = DSM 14960
AF143841.1 gg_id:69970 hydrocarbon-degrading consortium clone AF2-1D
FM177775.1 gg_id:531947 Acinetobacter guillouiae str. LUH 7013
Z93443.1 gg_id:8344 Acinetobacter sp. str. ATCC 17924 Group ten
FN395270.1 gg_id:384502 Acinetobacter sp. str. FR-W3CA
EU705457.1 gg_id:323060 Microbial Burden and Analyses Phoenix Spacecraft Assembly Kennedy Space Centre
FJ192308.1 gg_id:326859 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior
FJ263916.1 gg_id:314055 Acinetobacter johnsonii str. BA2
AF509830.1 gg_id:56661 Acinetobacter tandoii str. 4N13
FJ607355.1 gg_id:534204 Acinetobacter junii str. SeaH-As6s
GQ488001.1 gg_id:535015 Microbial metal soil polluted heavy metals clone V8-111
AY586400.2 gg_id:109340 Acinetobacter haemolyticus str. AR-46
GQ409505.1 gg_id:545881 Acinetobacter sp. str. Du6

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|---|---|---|---|---|---|---|---|
| Y17190.1 | 9547 | 3119.6 | 2461.2 | 5795.9 | 6715.2 | 5479.7 | 4741.5 |
| X89379.1 | 9511 | 63.8 | 100.9 | 50.8 | 88.0 | 75.2 | 41.1 |
| AY362907.1 | 107128 | 1232.9 | 562.1 | 946.5 | 1892.3 | 745.2 | 1560.5 |
| FJ960217.1 | 571320 | 497.5 | 1130.4 | 2766.0 | 2757.6 | 7466.0 | 2770.0 |
| AF487728.1 | 82586 | 437.3 | 457.3 | 371.8 | 1698.7 | 1481.4 | 1421.2 |
| GQ111114.1 | 453851 | 1793.3 | 2006.6 | 1679.0 | 1786.9 | 992.7 | 1310.8 |
| DQ113707.1 | 134081 | 219.2 | 436.2 | 1556.4 | 1525.6 | 4019.5 | 1444.4 |
| AF224293.1 | 35735 | 4566.4 | 2910.7 | 5257.3 | 6202.4 | 6314.4 | 4311.7 |
| GQ072607.1 | 457136 | 1147.8 | 837.9 | 1033.4 | 2192.7 | 1450.5 | 1905.9 |
| EU826048.1 | 579141 | 1322.5 | 978.8 | 1718.5 | 2844.6 | 1542.9 | 1825.2 |
| AF487729.1 | 82728 | 959.4 | 1094.6 | 2563.4 | 5988.5 | 4111.0 | 4049.5 |
| AF224304.1 | 71067 | 628.4 | 476.9 | 2097.5 | 3293.3 | 781.7 | 1594.7 |
| AY362922.1 | 107519 | 1305.6 | 747.3 | 2016.1 | 2267.5 | 3410.6 | 2226.0 |
| DQ851143.1 | 164515 | 43.9 | 104.1 | 62.9 | 67.6 | 286.4 | 91.9 |
| AY216870.1 | 85860 | 2001.9 | 1981.7 | 2403.2 | 2256.7 | 4667.6 | 3293.6 |
| NR_025724.1 | 535122 | 1623.3 | 1584.3 | 2257.5 | 1667.1 | 3661.5 | 2765.9 |
| AF509820.1 | 60271 | 4068.8 | 5091.5 | 1960.6 | 3901.6 | 5293.5 | 5431.4 |
| FJ009376.1 | 331932 | 165.7 | 181.1 | 207.3 | 158.1 | 412.7 | 1338.6 |
| AM410708.1 | 194118 | 961.0 | 628.7 | 391.3 | 440.9 | 680.5 | 2666.1 |
| FJ976560.1 | 584494 | 972.2 | 896.2 | 593.2 | 600.9 | 1361.9 | 2300.5 |
| AF509821.1 | 60274 | 215.2 | 235.1 | 60.4 | 92.3 | 92.7 | 1135.6 |
| AF509822.1 | 60277 | 8500.8 | 9892.8 | 6537.6 | 4884.8 | 10687.4 | 10191.4 |
| AM412162.1 | 242026 | 2774.8 | 1642.1 | 1195.6 | 1545.9 | 1467.1 | 5452.9 |
| FJ009371.1 | 333962 | 2322.1 | 1844.7 | 1349.5 | 1613.8 | 1485.1 | 3300.8 |
| AY536009.1 | 129982 | 2159.2 | 2718.5 | 2572.0 | 359.2 | 1305.9 | 3787.6 |
| FM177774.1 | 518457 | 1229.8 | 1203.2 | 1938.0 | 761.4 | 968.0 | 3127.9 |
| Z93444.1 | 43948 | 4575.6 | 3828.8 | 7414.4 | 4846.7 | 5626.3 | 9732.7 |
| AF509832.1 | 60258 | 5521.5 | 8376.5 | 4213.8 | 5580.8 | 9183.5 | 7921.9 |
| FM177776.1 | 522874 | 2470.6 | 1972.5 | 1556.5 | 1703.7 | 1569.6 | 4129.2 |
| AF143841.1 | 69970 | 6688.6 | 6632.3 | 6712.1 | 6869.0 | 12207.0 | 9471.2 |
| FM177775.1 | 531947 | 1029.3 | 692.5 | 636.1 | 107.6 | 351.8 | 1932.5 |
| Z93443.1 | 8344 | 632.4 | 519.9 | 371.2 | 527.3 | 128.7 | 2490.4 |
| FN395270.1 | 384502 | 1905.0 | 1258.1 | 1060.2 | 920.1 | 363.0 | 2904.0 |
| EU705457.1 | 323060 | 3960.7 | 3635.8 | 3980.5 | 3500.8 | 5468.6 | 8398.4 |
| FJ192308.1 | 326859 | 3259.7 | 2893.0 | 5488.4 | 3695.3 | 3605.0 | 9256.4 |
| FJ263916.1 | 314055 | 1879.7 | 1745.7 | 3090.2 | 916.4 | 2665.7 | 6699.9 |
| AF509830.1 | 56661 | 6353.7 | 5663.8 | 4636.0 | 5156.5 | 5747.8 | 7408.6 |
| FJ607355.1 | 534204 | 7833.1 | 8102.7 | 8745.1 | 9421.7 | 10687.1 | 10588.7 |
| GQ488001.1 | 535015 | 4809.9 | 3186.8 | 3318.5 | 3009.3 | 4329.9 | 7914.6 |
| AY586400.2 | 109340 | 1885.6 | 1336.0 | 636.0 | 911.5 | 565.3 | 6900.6 |
| GQ409505.1 | 545881 | 2049.8 | 744.0 | 622.6 | 425.8 | 438.7 | 3654.8 |

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DQ675067.1 gg_id:173204 microbial production water -temperature petroleum reservoir clone QHO-B17
FJ193164.1 gg_id:343114 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior
AY689035.1 gg_id:100228 Acinetobacter sp. str. 3C_8
GQ070596.1 gg_id:418636 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw:
DQ257427.1 gg_id:142775 Acinetobacter johnsonii str. CAI-14
FJ191887.1 gg_id:343089 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior
EU536549.1 gg_id:286873 profile human microbiota antecubital fossa (inner elbow) skin clone nbt215g07
EU275352.1 gg_id:253188 Acinetobacter johnsonii str. CONC8
FJ192142.1 gg_id:347156 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior
DQ675069.1 gg_id:168062 microbial production water -temperature petroleum reservoir clone QHO-B26
CU466803.1 gg_id:336593 Evry wastewater treatment plant anoxic basin clone
FJ192398.1 gg_id:334639 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior
EU705366.1 gg_id:309203 Microbial Burden and Analyses Phoenix Spacecraft Assembly Kennedy Space Centre
GU124494.1 gg_id:535160 endosymbiotic (Stal) (rice brown planthopper) Acinetobacter endosymbiont Nilapar
FJ191727.1 gg_id:334971 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior
AB196244.1 gg_id:115340 Acinetobacter johnsonii str. IC001
FJ900940.1 gg_id:563501 Polymorphism microbial reservoirs water cut stage oil field clone L-36
FJ192385.1 gg_id:316225 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior
AY167841.1 gg_id:77294 Acinetobacter johnsonii str. SAFR-006
FJ192696.1 gg_id:338444 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior
DQ675057.1 gg_id:165070 microbial production water -temperature petroleum reservoir clone QHO-B9
FJ192370.1 gg_id:310406 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior
FJ192156.1 gg_id:320031 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior
X86591.1 gg_id:8390 Acinetobacter sp str. 1F-19
AB369040.1 gg_id:537750 and microbial oils produced Asia petroleum crude oil (Qatar Land Light) clone PT-QTl
AB369043.1 gg_id:573441 and microbial oils produced Asia petroleum crude oil (Qatar Land Light) clone PT-QTl
GQ102953.1 gg_id:436668 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
DQ675078.1 gg_id:165523 microbial production water -temperature petroleum reservoir clone QHO-B28
FJ948288.1 gg_id:578231 Isolation and identification endophytic three medicinal plants leaf clone HQ
FJ192211.1 gg_id:352732 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior
FJ192879.1 gg_id:328708 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior
GQ111297.1 gg_id:467170 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
EU169147.1 gg_id:241109 Acinetobacter johnsonii str. B33
GQ102212.1 gg_id:371878 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
EU240429.1 gg_id:235992 Acinetobacter johnsonii str. B178
EU504845.1 gg_id:268774 cecal contents Mus musculus strain C57BL/6J; myd2 clone myd2_aaa03b10
GQ102805.1 gg_id:450958 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
GQ106991.1 gg_id:445417 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw543d0
FJ192003.1 gg_id:322306 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior
EU705479.1 gg_id:345817 Microbial Burden and Analyses Phoenix Spacecraft Assembly Kennedy Space Centre
FJ192503.1 gg_id:308433 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior

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| DQ675067.1 | 173204 | 4667.0 | 4896.4 | 3598.0 | 4978.6 | 4151.6 | 6408.9 |
| FJ193164.1 | 343114 | 11040.7 | 10180.0 | 7178.6 | 6325.9 | 10511.8 | 9680.1 |
| AY689035.1 | 100228 | 687.1 | 703.1 | 1228.8 | 1363.9 | 2966.5 | 2633.9 |
| GQ070596.1 | 418636 | 7953.4 | 5866.0 | 5739.1 | 4859.0 | 7459.5 | 7940.5 |
| DQ257427.1 | 142775 | 6551.3 | 5820.1 | 3538.7 | 5891.9 | 7392.6 | 9161.2 |
| FJ191887.1 | 343089 | 1039.3 | 1502.7 | 1262.3 | 177.6 | 248.9 | 3324.8 |
| EU536549.1 | 286873 | 4379.4 | 3040.5 | 2022.2 | 2895.4 | 6616.8 | 8180.9 |
| EU275352.1 | 253188 | 4657.6 | 5498.6 | 3476.0 | 3033.2 | 3672.0 | 7243.5 |
| FJ192142.1 | 347156 | 2408.5 | 1993.3 | 801.0 | 1381.0 | 1146.2 | 7323.0 |
| DQ675069.1 | 168062 | 901.9 | 742.0 | 443.5 | 410.2 | 1260.0 | 3170.6 |
| CU466803.1 | 336593 | 5340.5 | 4794.9 | 4233.6 | 4738.9 | 4853.8 | 7351.7 |
| FJ192398.1 | 334639 | 2438.0 | 2497.1 | 1847.1 | 2069.6 | 2794.0 | 7063.0 |
| EU705366.1 | 309203 | 4844.4 | 3261.8 | 2321.2 | 3516.1 | 3994.1 | 5781.2 |
| GU124494.1 | 535160 | 299.2 | 364.6 | 226.7 | 181.8 | 115.8 | 2725.1 |
| FJ191727.1 | 334971 | 2342.9 | 2409.7 | 1326.8 | 1484.3 | 1272.8 | 5094.6 |
| AB196244.1 | 115340 | 5324.3 | 4836.6 | 4816.3 | 4640.9 | 8695.5 | 7978.0 |
| FJ900940.1 | 563501 | 2641.4 | 2315.3 | 1064.1 | 1389.2 | 3867.0 | 6028.8 |
| FJ192385.1 | 316225 | 6543.3 | 4197.3 | 6375.7 | 6332.7 | 1621.0 | 5638.9 |
| AY167841.1 | 77294 | 7451.1 | 5515.2 | 9354.7 | 6463.7 | 6667.0 | 9287.3 |
| FJ192696.1 | 338444 | 12234.8 | 11160.5 | 9667.9 | 9586.2 | 11442.5 | 11335.8 |
| DQ675057.1 | 165070 | 965.1 | 1666.0 | 733.8 | 99.7 | 192.5 | 2903.1 |
| FJ192370.1 | 310406 | 11365.4 | 12841.5 | 4224.7 | 8469.4 | 9248.6 | 8729.3 |
| FJ192156.1 | 320031 | 2182.1 | 2339.3 | 894.7 | 1406.1 | 1317.4 | 5261.0 |
| X86591.1 | 8390 | 1002.2 | 1133.2 | 438.5 | 330.5 | 1073.7 | 2965.7 |
| AB369040.1 | 537750 | 3895.5 | 3839.7 | 3098.0 | 4564.7 | 4212.1 | 5930.7 |
| AB369043.1 | 573441 | 4275.9 | 4044.0 | 1135.1 | 3654.2 | 6997.4 | 6968.7 |
| GQ102953.1 | 436668 | 16093.2 | 13858.3 | 10565.5 | 13376.5 | 15659.8 | 13684.4 |
| DQ675078.1 | 165523 | 8815.9 | 8850.2 | 6388.8 | 11877.1 | 11469.9 | 12141.1 |
| FJ948288.1 | 578231 | 1625.5 | 1719.9 | 829.1 | 412.5 | 517.3 | 3161.0 |
| FJ192211.1 | 352732 | 4008.1 | 3977.9 | 2573.5 | 3492.3 | 3714.4 | 5848.6 |
| FJ192879.1 | 328708 | 10305.4 | 11125.7 | 4263.6 | 7190.9 | 7533.2 | 7871.0 |
| GQ111297.1 | 467170 | 680.2 | 874.9 | 812.3 | 816.3 | 1742.2 | 2522.2 |
| EU169147.1 | 241109 | 7702.4 | 7345.1 | 1743.5 | 1716.7 | 1909.0 | 5594.2 |
| GQ102212.1 | 371878 | 8361.0 | 8049.4 | 11747.6 | 7271.0 | 15004.7 | 13906.0 |
| EU240429.1 | 235992 | 5526.2 | 4933.4 | 4549.9 | 4204.0 | 5512.2 | 8653.1 |
| EU504845.1 | 268774 | 6330.7 | 4516.0 | 4019.1 | 4366.3 | 5948.8 | 6095.9 |
| GQ102805.1 | 450958 | 8760.5 | 6822.4 | 3019.5 | 5242.4 | 11068.4 | 11514.0 |
| GQ106991.1 | 445417 | 8068.4 | 4667.9 | 4303.6 | 4566.2 | 3766.8 | 5237.4 |
| FJ192003.1 | 322306 | 1224.5 | 2331.1 | 2152.7 | 813.3 | 1440.8 | 3408.7 |
| EU705479.1 | 345817 | 3128.3 | 3976.1 | 3713.3 | 2929.4 | 5381.5 | 7904.5 |
| FJ192503.1 | 308433 | 11691.1 | 12699.0 | 4963.5 | 11946.4 | 15457.8 | 15503.4 |

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| s__Acinetobacter johnsonii | 3996 |
| s__Acinetobacter johnsonii | 3999 |
| s__Acinetobacter johnsonii | 4005 |
| s__Acinetobacter johnsonii | 4032 |
| s__Acinetobacter johnsonii | 4039 |
| s__Acinetobacter johnsonii | 4042 |
| s__Acinetobacter johnsonii | 4053 |
| s__Acinetobacter johnsonii | 4055 |
| s__Acinetobacter johnsonii | 4066 |
| s__Acinetobacter johnsonii | 4078 |
| s__Acinetobacter johnsonii | 4093 |
| s__Acinetobacter johnsonii | 4094 |
| s__Acinetobacter johnsonii | 4102 |
| s__Acinetobacter johnsonii | 4110 |
| s__Acinetobacter lwoffii | 3369 |
| s__Acinetobacter lwoffii | 3373 |
| s__Acinetobacter lwoffii | 3494 |
| s__Acinetobacter lwoffii | 3497 |
| s__Acinetobacter lwoffii | 3500 |
| s__Acinetobacter lwoffii | 3580 |
| s__Acinetobacter lwoffii | 3591 |
| s__Acinetobacter lwoffii | 3715 |
| s__Acinetobacter lwoffii | 3765 |
| s__Acinetobacter lwoffii | 3870 |
| s__Acinetobacter lwoffii | 4074 |
| s__Acinetobacter lwoffii | 4099 |
| s__Acinetobacter radioresistens | 3893 |
| s__Acinetobacter radioresistens | 3954 |
| s__Acinetobacter rhizosphaerae | 3343 |
| s__Acinetobacter rhizosphaerae | 3395 |
| s__Acinetobacter rhizosphaerae | 3397 |
| s__Acinetobacter rhizosphaerae | 3405 |
| s__Acinetobacter rhizosphaerae | 3434 |
| s__Acinetobacter rhizosphaerae | 3534 |
| s__Acinetobacter rhizosphaerae | 3576 |
| s__Acinetobacter rhizosphaerae | 3613 |
| s__Acinetobacter rhizosphaerae | 3699 |
| s__Acinetobacter rhizosphaerae | 3709 |
| s__Acinetobacter rhizosphaerae | 3810 |
| s__Acinetobacter rhizosphaerae | 3848 |
| s__Acinetobacter rhizosphaerae | 3863 |

GQ075991.1 gg_id:423128 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw:
AF188300.1 gg_id:8391 Acinetobacter johnsonii str. P152
FJ192666.1 gg_id:347685 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior
FJ192917.1 gg_id:322094 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior
GQ104230.1 gg_id:460452 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
EF429006.1 gg_id:216324 Acinetobacter sp. str. GIST-OutAn1
DQ675059.1 gg_id:170409 microbial production water -temperature petroleum reservoir clone QHO-B11
FJ191867.1 gg_id:341096 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior
FJ192302.1 gg_id:329438 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior
GQ080422.1 gg_id:372278 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw:
GQ072927.1 gg_id:452753 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw202h03c
DQ675049.1 gg_id:169400 microbial production water -temperature petroleum reservoir clone QHO-B8
FJ191856.1 gg_id:329425 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior
AB369019.1 gg_id:576274 and microbial oils produced Asia petroleum crude oil (Arabian Medium) clone PT-ARI
AY277551.1 gg_id:89870 Acinetobacter lwoffii str. 1E
FJ672802.1 gg_id:521318 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
DQ834359.1 gg_id:165112 Acinetobacter sp. str. FLL8
FJ373029.1 gg_id:311265 Acinetobacter lwoffii str. S3-2
DQ223660.1 gg_id:160030 Acinetobacter sp. zf-IRht15
X86572.1 gg_id:8361 Acinetobacter sp str. AC-40
DQ371237.1 gg_id:155206 Acinetobacter lwoffii str. FORb
AF188302.1 gg_id:8363 Acinetobacter lwoffii str. A382
AY176770.1 gg_id:78649 Acinetobacter lwoffii str. HJ7
EU240445.1 gg_id:237709 Acinetobacter lwoffii str. B190
AM412164.1 gg_id:249976 Acinetobacter sp. str. P-126
DQ144736.1 gg_id:139182 Acinetobacter lwoffii str. LS2
FJ191915.1 gg_id:310933 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior
AM495259.1 gg_id:250455 Acinetobacter radioresistens str. INBS1
FJ816058.1 gg_id:569388 Acinetobacter calcoaceticus str. PUCM1011
AM157426.1 gg_id:141393 Acinetobacter calcoaceticus mother C3
EU921462.1 gg_id:328793 Acinetobacter calcoaceticus str. HIRFA26
EU118781.1 gg_id:245216 Acinetobacter calcoaceticus str. AGL 17
GQ469890.1 gg_id:587465 Acinetobacter calcoaceticus str. PUCM1031
FJ816055.1 gg_id:510012 Acinetobacter calcoaceticus str. PUCM1008
FJ009370.1 gg_id:334071 Acinetobacter calcoaceticus str. H11
AM410707.1 gg_id:177547 Acinetobacter calcoaceticus str. ACI34 = RUH 0583
FJ816049.1 gg_id:567940 Acinetobacter calcoaceticus str. PUCM1002
FJ816073.1 gg_id:543130 Acinetobacter calcoaceticus str. PUCM1026
EF601824.1 gg_id:228947 Acinetobacter sp. str. NX2
EU921468.1 gg_id:321731 Acinetobacter calcoaceticus str. HIRGA36
DQ536511.1 gg_id:161691 Acinetobacter rhizosphaerae str. BIHB 723

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|---|---|---|---|---|---|---|---|
| GQ075991.1 | 423128 | 1349.8 | 1702.3 | 1450.8 | 1802.4 | 832.5 | 2741.0 |
| AF188300.1 | 8391 | 6361.0 | 7045.5 | 5350.9 | 5783.8 | 9361.6 | 8840.6 |
| FJ192666.1 | 347685 | 2135.1 | 1660.4 | 2466.5 | 2584.8 | 656.1 | 3228.3 |
| FJ192917.1 | 322094 | 8304.4 | 8774.4 | 8826.5 | 10150.1 | 11699.6 | 11185.4 |
| GQ104230.1 | 460452 | 3910.1 | 3769.0 | 3276.2 | 3285.8 | 4819.7 | 7282.3 |
| EF429006.1 | 216324 | 211.1 | 204.2 | 88.3 | 144.0 | 318.6 | 664.1 |
| DQ675059.1 | 170409 | 3560.6 | 4006.1 | 1601.5 | 2689.8 | 7227.5 | 6133.0 |
| FJ191867.1 | 341096 | 2438.9 | 2762.1 | 1276.2 | 1822.0 | 2061.3 | 5331.0 |
| FJ192302.1 | 329438 | 3587.2 | 3283.5 | 1951.6 | 4664.7 | 3643.8 | 4794.1 |
| GQ080422.1 | 372278 | 5017.4 | 4007.4 | 3643.8 | 4745.9 | 4485.4 | 6614.3 |
| GQ072927.1 | 452753 | 9893.1 | 10126.5 | 10617.4 | 9707.5 | 10256.7 | 11368.6 |
| DQ675049.1 | 169400 | 3019.3 | 2427.5 | 3493.7 | 4355.6 | 3083.6 | 4184.8 |
| FJ191856.1 | 329425 | 2928.2 | 3271.2 | 2848.2 | 2248.0 | 2265.0 | 5202.8 |
| AB369019.1 | 576274 | 13420.1 | 13331.4 | 8559.5 | 10619.1 | 13819.8 | 13749.0 |
| AY277551.1 | 89870 | 16460.3 | 14515.8 | 14302.7 | 11099.0 | 17129.2 | 16845.9 |
| FJ672802.1 | 521318 | 8589.2 | 7711.8 | 5212.0 | 4710.3 | 10291.6 | 7501.6 |
| DQ834359.1 | 165112 | 12240.4 | 9859.6 | 7313.9 | 6961.5 | 10128.2 | 12310.1 |
| FJ373029.1 | 311265 | 1471.8 | 1372.5 | 618.2 | 836.5 | 1740.6 | 4829.4 |
| DQ223660.1 | 160030 | 7724.9 | 7532.5 | 3267.4 | 4482.6 | 3425.0 | 4802.8 |
| X86572.1 | 8361 | 179.4 | 431.3 | 589.5 | 296.4 | 1323.2 | 355.1 |
| DQ371237.1 | 155206 | 11431.5 | 11409.8 | 5654.2 | 7662.2 | 11460.4 | 10117.8 |
| AF188302.1 | 8363 | 8959.0 | 8781.8 | 6156.2 | 6578.7 | 8702.0 | 9633.4 |
| AY176770.1 | 78649 | 8771.0 | 6201.4 | 2676.3 | 8498.9 | 11733.5 | 11252.4 |
| EU240445.1 | 237709 | 1300.8 | 1329.6 | 647.5 | 754.2 | 1874.5 | 4103.0 |
| AM412164.1 | 249976 | 2451.6 | 1968.6 | 3635.4 | 1107.9 | 4819.5 | 7174.6 |
| DQ144736.1 | 139182 | 3132.6 | 4003.6 | 3146.8 | 3615.6 | 6924.0 | 8289.6 |
| FJ191915.1 | 310933 | 1189.6 | 906.7 | 1596.1 | 1817.3 | 1270.3 | 2882.8 |
| AM495259.1 | 250455 | 2007.0 | 1687.5 | 2551.2 | 3412.7 | 6272.7 | 3496.6 |
| FJ816058.1 | 569388 | 2018.8 | 1664.5 | 2185.3 | 1667.9 | 1267.1 | 3909.3 |
| AM157426.1 | 141393 | 9961.4 | 10603.3 | 7174.0 | 9059.1 | 12735.3 | 13548.3 |
| EU921462.1 | 328793 | 2522.9 | 2153.9 | 2301.3 | 1913.0 | 2091.8 | 4593.4 |
| EU118781.1 | 245216 | 3106.2 | 2924.6 | 3044.0 | 2624.2 | 2766.7 | 5078.7 |
| GQ469890.1 | 587465 | 1887.0 | 1563.6 | 2149.8 | 1663.1 | 1270.0 | 3809.4 |
| FJ816055.1 | 510012 | 2955.2 | 2961.3 | 3909.3 | 3802.6 | 2994.7 | 3758.2 |
| FJ009370.1 | 334071 | 2125.1 | 1725.5 | 2185.3 | 1832.3 | 1411.8 | 4093.1 |
| AM410707.1 | 177547 | 1798.8 | 1704.5 | 1645.7 | 1219.3 | 1510.0 | 2420.9 |
| FJ816049.1 | 567940 | 5521.3 | 5853.3 | 1958.2 | 7525.6 | 7884.0 | 7269.2 |
| FJ816073.1 | 543130 | 1369.2 | 753.3 | 511.1 | 758.5 | 361.6 | 3612.2 |
| EF601824.1 | 228947 | 2470.0 | 2224.3 | 2646.8 | 2337.2 | 2183.6 | 4423.3 |
| EU921468.1 | 321731 | 2898.1 | 3020.3 | 3241.3 | 2200.7 | 1865.2 | 5185.4 |
| DQ536511.1 | 161691 | 4715.8 | 3965.0 | 6416.2 | 1547.8 | 4255.0 | 6332.7 |

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| k__Bacteria | k__Bacteria | p__Proteobacteria | c__Gammaproteobacteria |
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| s__Acinetobacter rhizosphaerae | 3901 |
| s__Acinetobacter rhizosphaerae | 3990 |
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| s__Acinetobacter rhizosphaerae | 4104 |
| s__Acinetobacter schindleri | 3575 |
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| s__Acinetobacter schindleri | 3866 |
| s__Acinetobacter tjernbergiae | 4103 |
| s__Acinetobacter towneri | 3573 |
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| s__Acinetobacter ursingii | 3319 |
| s__Acinetobacter venetianus | 3560 |
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AM921638.1 gg_id:257154 Acinetobacter rhizosphaerae PhyCEm-460
AY277552.1 gg_id:90549 Acinetobacter calcoaceticus str. AVP2-2
AY364536.1 gg_id:94206 Acinetobacter rhizosphaerae str. IH9
FJ976570.1 gg_id:578667 Acinetobacter calcoaceticus str. LCR61
DQ129724.2 gg_id:248172 Acinetobacter calcoaceticus str. HPC399
FJ373024.1 gg_id:327004 Acinetobacter schindleri str. W1-2
GQ080249.1 gg_id:459017 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw:
GU339299.1 gg_id:542053 Acinetobacter schindleri str. EH74
GU004025.1 gg_id:581771 heterotrophic nitrifying biofilm clone 16SN42
GQ082321.1 gg_id:426536 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw11
GU004026.1 gg_id:554705 heterotrophic nitrifying biofilm clone 16SN43
AF509826.1 gg_id:60264 Acinetobacter tjernbergiae str. 7B02
NR_028849.1 gg_id:537702 Acinetobacter towneri str. AB1110; DSM 14962
AF509824.1 gg_id:60268 Acinetobacter towneri str. 2N01
AJ275039.1 gg_id:54545 Acinetobacter ursingii str. LUH 4763
EU258609.1 gg_id:277749 Acinetobacter venetianus str. ACI574
GQ007238.1 gg_id:502426 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
AB286521.1 gg_id:210171 Reducing production and domination comamonadaceae reducing oxygen supply was
AF357182.1 gg_id:48029 Alvinella pompejana symbiont APG130A
FJ674507.1 gg_id:518521 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
GQ451319.1 gg_id:569668 Fecal Yunnan snub-nosed monkey feces clone J341
EF468657.1 gg_id:218490 Acinetobacter sp. str. TD5
AY047216.1 gg_id:39106 Acinetobacter haemolyticus
EU467937.1 gg_id:293369 cheetah feces clone CE2_e09
EU779466.1 gg_id:321405 Hartmann's Mountain Zebra feces clone AFZEB_aaj72f01
EU467673.1 gg_id:302118 naked mole-rat feces clone molerat_2g12_1
FJ976593.1 gg_id:550870 Acinetobacter sp. str. LCR84
FJ672033.1 gg_id:520896 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
EU779403.1 gg_id:311420 Hartmann's Mountain Zebra feces clone AFZEB_aaj70a08
AY633608.1 gg_id:101304 Acinetobacter seohaensis str. SW-100
EU463254.1 gg_id:294712 naked mole-rat feces clone molerat_aai72d06
FJ672865.1 gg_id:517631 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
EU777000.1 gg_id:344560 Naked mole-rat feces clone molerat_2g01
GQ077574.1 gg_id:415516 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1210e(
AM412161.1 gg_id:250903 Acinetobacter sp. str. P-134
FJ672928.1 gg_id:523993 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
AB207814.1 gg_id:167038 Acinetobacter psychrotolerans str. Ths
EU160535.1 gg_id:347520 diagnosis central-venous infections cultivation-dependent and techniques biofilm sc
EU604244.1 gg_id:274092 Acinetobacter baylyi str. 1477
FJ193878.1 gg_id:338023 Genetic inventory 'KSC-Astrotek' spacecraft assembly clean room during DAWN missi
EU463244.1 gg_id:290621 naked mole-rat feces clone molerat_aai72c02

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| FJ976570.1 | 578667 | 1660.9 | 1072.8 | 1655.7 | 1270.5 | 644.5 | 4106.9 |
| DQ129724.2 | 248172 | 3084.4 | 3151.4 | 3868.5 | 3381.1 | 2862.3 | 4916.0 |
| FJ373024.1 | 327004 | 3076.3 | 2578.5 | 2291.1 | 5296.9 | 4102.8 | 7186.1 |
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| GU339299.1 | 542053 | 1349.1 | 1129.6 | 1571.9 | 1578.4 | 2510.9 | 3202.4 |
| GU004025.1 | 581771 | 1055.7 | 1558.6 | 1353.3 | 884.4 | 6085.1 | 3453.7 |
| GQ082321.1 | 426536 | 4037.8 | 4560.1 | 4724.8 | 5442.2 | 6624.8 | 7019.9 |
| GU004026.1 | 554705 | 16224.5 | 14314.5 | 12038.8 | 11954.1 | 14199.7 | 15067.0 |
| AF509826.1 | 60264 | 658.2 | 860.3 | 1897.3 | 734.5 | 224.5 | 1076.2 |
| NR_028849.1 | 537702 | 2545.5 | 2866.5 | 684.7 | 1584.8 | 3104.6 | 2875.4 |
| AF509824.1 | 60268 | 2719.8 | 2768.8 | 835.0 | 1066.8 | 2950.9 | 3417.5 |
| AJ275039.1 | 54545 | 744.8 | 751.5 | 437.3 | 427.9 | 931.2 | 2185.5 |
| EU258609.1 | 277749 | 3753.8 | 3558.0 | 5614.4 | 5351.6 | 6175.4 | 6707.6 |
| GQ007238.1 | 502426 | 2775.0 | 2287.0 | 1064.8 | 3274.1 | 5088.6 | 3976.3 |
| AB286521.1 | 210171 | 4086.5 | 3104.2 | 4177.7 | 5104.1 | 3374.9 | 4912.6 |
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| FJ674507.1 | 518521 | 14282.5 | 13029.2 | 9530.2 | 9379.9 | 12579.6 | 12761.2 |
| GQ451319.1 | 569668 | 913.5 | 680.3 | 771.0 | 189.9 | 212.9 | 1610.7 |
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| EU463254.1 | 294712 | 1046.3 | 1295.6 | 290.9 | 893.8 | 1951.1 | 4172.0 |
| FJ672865.1 | 517631 | 1214.1 | 755.1 | 2301.0 | 1289.8 | 4142.9 | 4389.9 |
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| EU604244.1 | 274092 | 341.4 | 185.6 | 202.5 | 167.2 | 415.8 | 1218.6 |
| FJ193878.1 | 338023 | 964.4 | 1800.9 | 1849.8 | 934.9 | 1718.0 | 2800.3 |
| EU463244.1 | 290621 | 5775.6 | 5850.0 | 2883.9 | 5259.5 | 12315.7 | 5564.8 |

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FJ851148.1 gg_id:569494 Acinetobacter sp. str. P4
U10875.1 gg_id:8400 Acinetobacter lwoffii str. ATCC 17925
FJ193928.1 gg_id:317023 Genetic inventory 'KSC-Astrotek' spacecraft assembly clean room during DAWN missi
FJ193896.1 gg_id:356161 Genetic inventory 'KSC-Astrotek' spacecraft assembly clean room during DAWN missi
EU124829.1 gg_id:245300 Gut microbes gut Helicoverpa armigera living on cotton plant clone 10
EU465090.1 gg_id:288912 African elephant feces clone AFYEL_aaj67h10
EF525671.1 gg_id:218350 Acinetobacter baumannii str. Serdang1
DQ834354.1 gg_id:170113 Acinetobacter sp. str. FLL7
FJ816048.1 gg_id:564236 Acinetobacter calcoaceticus str. PUCM1001
GQ088876.1 gg_id:380649 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
EU705448.1 gg_id:340228 Microbial Burden and Analyses Phoenix Spacecraft Assembly Kennedy Space Centre
FJ193982.1 gg_id:333983 Genetic inventory 'KSC-Astrotek' spacecraft assembly clean room during DAWN missi
GQ069608.1 gg_id:407828 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
FJ193755.1 gg_id:325011 Genetic inventory 'KSC-Astrotek' spacecraft assembly clean room during DAWN missi
GQ080268.1 gg_id:431095 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
FJ477061.1 gg_id:533635 Acinetobacter xiamenensis str. KSL 4-102
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DQ824717.1 gg_id:186196 human fecal clone RL185_aaj72b10
DQ860032.1 gg_id:247964 anchovy intestinal microflora clone F1T
AF509827.1 gg_id:60263 Acinetobacter bouvetii str. 4B02
FJ674492.1 gg_id:519299 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface
GQ097172.1 gg_id:411031 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
DQ187381.1 gg_id:139909 Acinetobacter calcoaceticus
EU560851.1 gg_id:563369 Assessment genetic Apriona germari (Hope) larvae normalization techniques intestir
AF526908.2 gg_id:62949 Acinetobacter radioresistens str. 50v1
EF436374.1 gg_id:215173 library-based ruminal water buffalo (Bubalus bubalis) rumen fluid clone BRC88
EU352764.1 gg_id:276866 Acinetobacter haemolyticus str. NK 2.BH-7
Z93982.1 gg_id:8320 activated sludge clone T58
FJ675544.1 gg_id:523482 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface
AF509828.1 gg_id:60261 Acinetobacter grimontii str. 17A04
AF336348.1 gg_id:40632 Acinetobacter sp. str. Wuba16
FJ672724.1 gg_id:528677 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface
EU921471.1 gg_id:351367 Acinetobacter baumannii str. HIRGP40
FJ193816.1 gg_id:354830 Genetic inventory 'KSC-Astrotek' spacecraft assembly clean room during DAWN missi
EU337120.1 gg_id:513402 Acinetobacter sp. str. 1B3
AF189695.1 gg_id:48977 Acinetobacter sp. str. BC187
AF159045.1 gg_id:8371 Acinetobacter calcoaceticus str. A2
FJ671697.1 gg_id:522240 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface
FJ816080.1 gg_id:536705 Acinetobacter calcoaceticus str. PUCM1503

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| EF103560.1 | 191684 | 1501.4 | 907.2 | 1033.7 | 367.8 | 243.5 | 2039.9 |
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| FJ193896.1 | 356161 | 4138.4 | 3206.3 | 5202.8 | 4838.2 | 5151.0 | 6089.9 |
| EU124829.1 | 245300 | 782.2 | 596.8 | 1036.9 | 554.1 | 619.6 | 4303.3 |
| EU465090.1 | 288912 | 7253.1 | 6942.2 | 6135.9 | 6953.8 | 8801.9 | 8461.0 |
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| GQ088876.1 | 380649 | 2420.4 | 2905.0 | 4226.4 | 4079.2 | 3790.7 | 4328.0 |
| EU705448.1 | 340228 | 3437.7 | 2477.0 | 768.6 | 3245.6 | 3962.6 | 6566.5 |
| FJ193982.1 | 333983 | 3003.7 | 2771.3 | 5248.5 | 661.6 | 1449.1 | 3957.6 |
| GQ069608.1 | 407828 | 2866.7 | 3220.8 | 3950.5 | 1369.4 | 3828.3 | 4329.6 |
| FJ193755.1 | 325011 | 15558.8 | 18836.6 | 7152.3 | 10007.3 | 9233.2 | 10626.5 |
| GQ080268.1 | 431095 | 900.2 | 730.4 | 1010.9 | 1021.4 | 304.7 | 2328.5 |
| FJ477061.1 | 533635 | 131.9 | 224.9 | 216.6 | 120.7 | 126.6 | 386.8 |
| Z93988.1 | 8321 | 2979.4 | 2866.9 | 233.1 | 1189.1 | 2976.0 | 4214.6 |
| DQ116000.1 | 131304 | 237.4 | 120.8 | 45.9 | 82.2 | 189.6 | 294.0 |
| DQ824717.1 | 186196 | 289.3 | 273.2 | 165.4 | 98.8 | 1576.0 | 1525.9 |
| DQ860032.1 | 247964 | 2361.4 | 1289.4 | 508.7 | 1981.3 | 1501.7 | 5170.4 |
| AF509827.1 | 60263 | 7483.4 | 8827.8 | 5975.5 | 6732.4 | 7372.7 | 7499.3 |
| FJ674492.1 | 519299 | 2756.2 | 2458.4 | 3351.9 | 2859.6 | 5831.1 | 6488.8 |
| GQ097172.1 | 411031 | 4726.9 | 4062.9 | 3806.8 | 5522.7 | 7651.7 | 5899.0 |
| DQ187381.1 | 139909 | 1716.0 | 994.6 | 1634.6 | 1523.7 | 782.4 | 3397.2 |
| EU560851.1 | 563369 | 7089.1 | 6255.4 | 3724.6 | 4662.0 | 5849.1 | 7478.0 |
| AF526908.2 | 62949 | 1241.9 | 912.6 | 381.4 | 1415.3 | 7133.6 | 3708.5 |
| EF436374.1 | 215173 | 2721.5 | 3400.2 | 5726.1 | 1666.4 | 4632.3 | 4089.3 |
| EU352764.1 | 276866 | 5545.9 | 2615.9 | 4014.5 | 6029.6 | 2450.6 | 5509.5 |
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| FJ675544.1 | 523482 | 4124.4 | 3725.8 | 4332.2 | 5421.0 | 7140.3 | 7889.8 |
| AF509828.1 | 60261 | 7037.3 | 6432.7 | 7901.5 | 10006.6 | 11232.5 | 9711.3 |
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| FJ672724.1 | 528677 | 2238.5 | 2254.7 | 3450.9 | 2573.3 | 4813.6 | 6259.0 |
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| FJ193816.1 | 354830 | 2171.0 | 2237.8 | 3213.3 | 2168.7 | 2578.3 | 4865.3 |
| EU337120.1 | 513402 | 11953.8 | 11494.5 | 7978.6 | 8842.2 | 9818.4 | 12048.6 |
| AF189695.1 | 48977 | 2968.1 | 3371.7 | 1368.3 | 2577.2 | 2690.3 | 4557.5 |
| AF159045.1 | 8371 | 1993.6 | 2870.9 | 2387.4 | 3301.2 | 3174.9 | 4826.8 |
| FJ671697.1 | 522240 | 5727.0 | 5037.5 | 1315.9 | 7432.9 | 8800.0 | 9335.9 |
| FJ816080.1 | 536705 | 2176.1 | 1912.6 | 1177.7 | 1198.8 | 1671.1 | 4808.3 |

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AJ633635.1 gg_id:107477 Acinetobacter sp. phenon 9 str. LUH 1738 = ACI647
GQ045794.1 gg_id:391261 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
AJ303014.1 gg_id:73559 Acinetobacter sp. str. LBV326 (97 10 4186)
EU360111.1 gg_id:582701 Acinetobacter calcoaceticus str. PB16
EF432578.2 gg_id:206376 Acinetobacter calcoaceticus str. HB1-1
Z93447.1 gg_id:8313 Acinetobacter sp. str. ATCC 17905 Group TU14
DQ834356.1 gg_id:171431 Acinetobacter sp. str. SLH4
EU513394.1 gg_id:277540 Acinetobacter calcoaceticus str. TMPSB-D12
EF205268.1 gg_id:199813 Arctic gold mine fracture water clone Lupin-1130m-1-MDA-aci1
GQ069882.1 gg_id:445385 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw242h0
FJ675523.1 gg_id:522826 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
EU467678.1 gg_id:301128 naked mole-rat feces clone molerat_2b06_1
FJ009590.1 gg_id:546906 Acinetobacter baumannii str. IP026
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AJ296556.1 gg_id:30013 uranium mining depository deponie B1 clone GR-B1-2-35 GR-B1-2-35
EF429004.1 gg_id:204497 Acinetobacter sp. str. GIST-Out1
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AY823621.1 gg_id:115347 Acinetobacter calcoaceticus str. SW1
EU594561.1 gg_id:277462 Acinetobacter sp. str. 4-2
FJ151628.1 gg_id:342972 Acinetobacter calcoaceticus str. HNR
EU774032.1 gg_id:314572 Cheetah feces clone CE2_e07
AB167206.1 gg_id:107919 Acinetobacter sp. str. c33
FJ675182.1 gg_id:524252 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
EU240404.1 gg_id:256200 Acinetobacter calcoaceticus str. B120
X80285.1 gg_id:8331 Acinetobacter calcoaceticus
EU705523.1 gg_id:354028 Microbial Burden and Analyses Phoenix Spacecraft Assembly Kennedy Space Centre
FJ820996.1 gg_id:511035 Acinetobacter sp. str. PT22
DQ856498.1 gg_id:250517 intestinal microflora Chinese mitten crab (Eriocheir sinensis) clone C1A
Z93434.1 gg_id:8311 Acinetobacter calcoaceticus str. ATCC 23055T group one
EU272861.1 gg_id:358174 Acinetobacter sp. str. MK28
GQ174293.1 gg_id:414197 Acinetobacter sp. str. PP-2
FJ263921.1 gg_id:318166 Acinetobacter septicus str. BA9
GQ092219.1 gg_id:403040 Topographical and Temporal Human Skin Microbiome skin palm clone nbw411b09c:
AM412160.1 gg_id:247994 Acinetobacter sp. str. P-133
DQ464150.1 gg_id:158313 acid mine drainage clone D1-48
EU073105.1 gg_id:350209 Acinetobacter sp. str. TS39
FJ193900.1 gg_id:317914 Genetic inventory 'KSC-Astrotek' spacecraft assembly clean room during DAWN missi
EF203410.1 gg_id:264736 Acinetobacter sp. str. URAM1
FJ671719.1 gg_id:525292 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I

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| AJ633635.1 | 107477 | 8929.0 | 9903.3 | 7687.6 | 8883.1 | 13788.8 | 14184.4 |
| GQ045794.1 | 391261 | 4263.0 | 5654.3 | 1700.7 | 1608.4 | 1668.6 | 4811.0 |
| AJ303014.1 | 73559 | 1424.8 | 1236.9 | 1414.7 | 615.1 | 692.7 | 3303.8 |
| EU360111.1 | 582701 | 2141.0 | 1778.9 | 1537.6 | 1213.9 | 980.4 | 3936.4 |
| EF432578.2 | 206376 | 1938.8 | 3818.3 | 4373.8 | 1219.8 | 3298.1 | 3411.3 |
| Z93447.1 | 8313 | 1251.1 | 1174.6 | 2650.8 | 1210.8 | 2050.7 | 4718.6 |
| DQ834356.1 | 171431 | 756.0 | 618.2 | 520.1 | 96.9 | 402.5 | 1631.5 |
| EU513394.1 | 277540 | 1699.1 | 1292.1 | 1219.4 | 868.3 | 572.4 | 3252.9 |
| EF205268.1 | 199813 | 1384.2 | 1651.2 | 1102.5 | 519.6 | 2404.6 | 4682.0 |
| GQ069882.1 | 445385 | 127.2 | 172.2 | 172.3 | 141.7 | 166.2 | 2769.1 |
| FJ675523.1 | 522826 | 1612.1 | 1422.6 | 1472.4 | 2061.3 | 2660.2 | 3194.3 |
| EU467678.1 | 301128 | 3930.7 | 4304.0 | 1531.8 | 2500.7 | 3964.9 | 3719.4 |
| FJ009590.1 | 546906 | 1424.8 | 1131.8 | 1929.9 | 685.3 | 892.3 | 3014.4 |
| FJ193144.1 | 352821 | 4213.3 | 5254.0 | 4848.3 | 4352.1 | 8018.5 | 9053.8 |
| AJ296556.1 | 30013 | 3521.8 | 2857.9 | 4856.4 | 3895.7 | 4433.0 | 5749.8 |
| EF429004.1 | 204497 | 6845.3 | 6574.1 | 4284.8 | 5735.0 | 8267.2 | 7444.7 |
| EU918130.1 | 332182 | 15984.9 | 14981.5 | 10286.7 | 12242.8 | 15256.0 | 14831.9 |
| FJ527818.1 | 540395 | 949.4 | 620.2 | 3019.5 | 961.8 | 600.4 | 1871.4 |
| GQ284482.1 | 590067 | 1037.9 | 698.0 | 418.6 | 455.0 | 240.7 | 3425.6 |
| AY823621.1 | 115347 | 3063.0 | 3034.5 | 5603.9 | 3001.7 | 2719.8 | 5434.0 |
| EU594561.1 | 277462 | 1713.3 | 1217.0 | 1281.7 | 2148.1 | 2664.3 | 3351.1 |
| FJ151628.1 | 342972 | 1228.9 | 756.4 | 454.7 | 188.6 | 846.9 | 2939.0 |
| EU774032.1 | 314572 | 914.7 | 1078.0 | 2293.9 | 764.9 | 734.6 | 2450.9 |
| AB167206.1 | 107919 | 3841.7 | 2574.8 | 3494.6 | 3798.5 | 2802.9 | 5230.5 |
| FJ675182.1 | 524252 | 2541.6 | 2136.2 | 5169.3 | 3328.8 | 2168.1 | 5647.0 |
| EU240404.1 | 256200 | 2523.4 | 2005.1 | 2355.5 | 1290.6 | 1633.2 | 5841.6 |
| X80285.1 | 8331 | 5333.0 | 4166.5 | 3531.7 | 5131.0 | 3556.8 | 5162.5 |
| EU705523.1 | 354028 | 4167.0 | 3101.3 | 2721.4 | 3343.8 | 3731.4 | 6784.7 |
| FJ820996.1 | 511035 | 2812.8 | 2786.4 | 2648.9 | 4099.4 | 8604.9 | 6680.8 |
| DQ856498.1 | 250517 | 988.6 | 1670.4 | 1359.2 | 794.9 | 1399.5 | 5248.8 |
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AM184255.1 gg_id:161481 Acinetobacter haemolyticus str. WAB1914
AY800383.1 gg_id:108973 Acinetobacter calcoaceticus
FJ193843.1 gg_id:324697 Genetic inventory 'KSC-Astrotek' spacecraft assembly clean room during DAWN missi
FJ791167.1 gg_id:543942 Hydrocarbon degraders -grade long term automative hydrocarbon contamination oil-
EU841481.1 gg_id:344669 Acinetobacter sp. str. 407
EU467641.1 gg_id:291175 naked mole-rat feces clone molerat_2d03
X89709.1 gg_id:8322 Acinetobacter sp str. DSM 587
GU370393.1 gg_id:518077 Acinetobacter sp. str. PD4
GQ383923.1 gg_id:582252 Acinetobacter sp. str. XJ127
FM874549.1 gg_id:360440 occupant source house mattress dust clone MD03C05
AB176230.1 gg_id:191845 Microbial Hydrothermal System Suiyo Seamount on Izu-Ogasawara Arc vent area wa
FJ544395.1 gg_id:453868 Acinetobacter junii str. tu13
DQ341260.1 gg_id:147489 Acinetobacter lwoffii str. F78
GQ045799.1 gg_id:415493 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
EU160530.1 gg_id:340699 diagnosis central-venous infections cultivation-dependent and techniques biofilm sc
FJ192953.1 gg_id:351059 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior
EU661697.1 gg_id:286733 Acinetobacter baumannii str. NBRAJG76
DQ441376.1 gg_id:190792 human intestinal biopsy clone CD125
DQ824733.1 gg_id:194641 human fecal clone RL185_aaj72d05
FJ672730.1 gg_id:516114 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
AY346313.2 gg_id:207698 Acinetobacter calcoaceticus str. HPC253
FM213385.2 gg_id:347588 Acinetobacter sp. str. MN33
AY847284.1 gg_id:110290 Acinetobacter baumannii str. Ab8
EF565936.1 gg_id:229145 Acinetobacter sp. str. NF4
AJ293691.1 gg_id:71951 Acinetobacter parvus str. LUH4616 (Aci602)
FN563424.1 gg_id:580752 Acinetobacter baumannii str. bpoe1353
AJ278311.2 gg_id:35076 Acinetobacter schindleri str. LUH5832T
EU467633.1 gg_id:287831 naked mole-rat feces clone molerat_2g07
GQ045189.1 gg_id:445146 Topographical and Temporal Human Skin Microbiome skin interdigital web space cl
EF059532.1 gg_id:219882 Acinetobacter sp. JN18_V5_C
FJ672809.1 gg_id:528886 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
EU463223.1 gg_id:302877 naked mole-rat feces clone molerat_aai71h09
FJ193977.1 gg_id:324684 Genetic inventory 'KSC-Astrotek' spacecraft assembly clean room during DAWN missi
EU560788.1 gg_id:562084 Assessment genetic intestinal flora Apriona germari (Hope) larvae -RFLP techniques
EU604241.1 gg_id:341709 Acinetobacter junii str. jfly-01
Z93987.1 gg_id:8330 activated sludge clone T27
FJ672176.1 gg_id:512623 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
EU221346.1 gg_id:235575 Acinetobacter calcoaceticus str. HM1C2
EU730929.1 gg_id:353461 Acinetobacter johnsonii str. 178
EU249988.1 gg_id:240369 Acinetobacter sp. str. PmeaMuc16
EU160536.1 gg_id:328674 diagnosis central-venous infections cultivation-dependent and techniques biofilm sc

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| AM184255.1 | 161481 | 1310.2 | 702.3 | 1257.5 | 577.0 | 808.8 | 2096.1 |
| AY800383.1 | 108973 | 2880.9 | 1161.9 | 1008.7 | 686.5 | 589.7 | 6474.5 |
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| FJ791167.1 | 543942 | 14240.3 | 13852.6 | 7848.8 | 11008.9 | 15393.1 | 13249.2 |
| EU841481.1 | 344669 | 2197.9 | 1262.0 | 1538.2 | 964.3 | 2167.6 | 3508.4 |
| EU467641.1 | 291175 | 1605.3 | 1043.4 | 808.1 | 957.1 | 1138.8 | 2991.0 |
| X89709.1 | 8322 | 6066.5 | 5865.0 | 2156.5 | 8470.2 | 10010.4 | 11057.3 |
| GU370393.1 | 518077 | 2574.1 | 2655.6 | 2954.4 | 2691.5 | 2797.2 | 5820.8 |
| GQ383923.1 | 582252 | 4146.3 | 3492.1 | 5033.9 | 3547.8 | 4292.7 | 6358.8 |
| FM874549.1 | 360440 | 188.1 | 180.0 | 149.7 | 72.0 | 465.3 | 2423.5 |
| AB176230.1 | 191845 | 3188.4 | 2914.1 | 3619.6 | 3137.3 | 3836.5 | 7479.3 |
| FJ544395.1 | 453868 | 2180.8 | 1438.7 | 1668.7 | 2041.2 | 471.0 | 3864.0 |
| DQ341260.1 | 147489 | 3794.2 | 3498.7 | 5177.4 | 4642.4 | 6993.8 | 7214.9 |
| GQ045799.1 | 415493 | 4798.9 | 4692.9 | 5005.9 | 4287.5 | 7845.0 | 8313.8 |
| EU160530.1 | 340699 | 10860.6 | 14308.0 | 15698.7 | 9418.9 | 17655.3 | 13464.3 |
| FJ192953.1 | 351059 | 8136.0 | 9397.3 | 9856.1 | 7687.6 | 9839.7 | 15318.7 |
| EU661697.1 | 286733 | 5890.5 | 5892.9 | 3478.1 | 5752.4 | 7164.4 | 8585.6 |
| DQ441376.1 | 190792 | 980.6 | 639.0 | 117.7 | 249.4 | 77.7 | 2235.8 |
| DQ824733.1 | 194641 | 123.7 | 167.8 | 237.9 | 152.3 | 197.3 | 342.1 |
| FJ672730.1 | 516114 | 9443.4 | 8119.6 | 5163.1 | 5407.1 | 12265.6 | 10700.0 |
| AY346313.2 | 207698 | 1901.2 | 1518.4 | 1537.9 | 898.4 | 618.0 | 4332.9 |
| FM213385.2 | 347588 | 3747.7 | 3241.8 | 3683.4 | 2263.2 | 2005.4 | 8305.9 |
| AY847284.1 | 110290 | 1894.5 | 1688.4 | 1759.3 | 1317.0 | 1009.2 | 4435.2 |
| EF565936.1 | 229145 | 28.9 | 18.1 | 30.8 | 53.9 | 53.6 | 27.7 |
| AJ293691.1 | 71951 | 1204.7 | 1329.2 | 945.4 | 120.9 | 153.8 | 4610.0 |
| FN563424.1 | 580752 | 868.0 | 425.3 | 733.8 | 341.8 | 902.6 | 1756.1 |
| AJ278311.2 | 35076 | 3135.8 | 2133.0 | 2609.7 | 3744.9 | 2974.0 | 5267.7 |
| EU467633.1 | 287831 | 1892.6 | 2400.2 | 2379.8 | 1498.0 | 7627.0 | 5261.0 |
| GQ045189.1 | 445146 | 6865.0 | 6818.0 | 5502.1 | 8833.9 | 12379.6 | 11432.7 |
| EF059532.1 | 219882 | 2181.2 | 1197.1 | 1671.3 | 1445.9 | 3555.7 | 4078.1 |
| FJ672809.1 | 528886 | 13073.2 | 11179.8 | 13208.1 | 12275.8 | 15104.8 | 11782.2 |
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| FJ672176.1 | 512623 | 2100.3 | 3257.5 | 4257.4 | 1100.5 | 3044.0 | 4439.6 |
| EU221346.1 | 235575 | 2516.9 | 1722.3 | 434.6 | 3147.7 | 1749.4 | 3791.9 |
| EU730929.1 | 353461 | 3069.9 | 2237.3 | 1676.5 | 2246.0 | 3551.7 | 5693.5 |
| EU249988.1 | 240369 | 1244.1 | 1066.6 | 1484.1 | 759.3 | 2765.9 | 5191.7 |
| EU160536.1 | 328674 | 5598.1 | 4591.6 | 1665.9 | 5814.6 | 6501.6 | 6538.1 |

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EU661696.1 gg_id:283320 Acinetobacter calcoaceticus str. NBRAJG75
EU921463.1 gg_id:345884 Acinetobacter calcoaceticus str. HIRFA27
FN433036.1 gg_id:565535 Acinetobacter beijerinckii CCM25B
AJ633639.1 gg_id:99113 Acinetobacter sp. str. LMG M71 = ACI788
EU467631.1 gg_id:302583 naked mole-rat feces clone molerat_2f06
FJ674356.1 gg_id:525396 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
DQ824645.1 gg_id:184299 human fecal clone RL185_aaj71a07
X81659.1 gg_id:8342 Acinetobacter species
AF336353.1 gg_id:37719 Acinetobacter sp. str. Wuba39
FJ263922.1 gg_id:304658 Acinetobacter septicus str. BA14
FJ816051.1 gg_id:564486 Acinetobacter calcoaceticus str. PUCM1004
X81668.1 gg_id:8375 Acinetobacter calcoaceticus
EF188656.1 gg_id:351236 Microbial Altamira Cave clone 400
EU090179.1 gg_id:250734 Acinetobacter calcoaceticus str. 11
FJ976566.1 gg_id:591323 Acinetobacter calcoaceticus str. LCR58
FJ194001.1 gg_id:310497 Genetic inventory 'KSC-Astrotek' spacecraft assembly clean room during DAWN missi
AY633607.1 gg_id:101152 Acinetobacter marinus str. SW-3
FJ672939.1 gg_id:515715 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
EU467653.1 gg_id:289405 naked mole-rat feces clone molerat_2b02_1
FJ671896.1 gg_id:521562 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
EU463121.1 gg_id:290186 naked mole-rat feces clone molerat_aai70b10
EU160533.1 gg_id:353347 diagnosis central-venous infections cultivation-dependent and techniques biofilm sc
NR_028852.1 gg_id:591121 Acinetobacter gerneri str. 9A01; DSM 14967
DQ856553.1 gg_id:244174 intestinal microflora Chinese mitten crab (Eriocheir sinensis) clone C3Q
FJ811875.1 gg_id:579258 Acinetobacter sp. str. MA3B-GFJ
EF127901.2 gg_id:255893 Acinetobacter sp. str. Y3A
AJ295007.1 gg_id:36199 Acinetobacter venetianus str. ATCC 31012
EU382216.1 gg_id:263259 Acinetobacter sp. str. DZ0503SBS4
AB167222.1 gg_id:107933 Acinetobacter sp. str. c61
FJ976597.1 gg_id:509344 Acinetobacter calcoaceticus
EU434432.1 gg_id:265496 Acinetobacter johnsonii str. a153
FJ672184.1 gg_id:510837 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
GQ281071.1 gg_id:577164 Acinetobacter sp. str. NBCS09
GQ258635.1 gg_id:542419 Acinetobacter soli str. SR2
GQ039005.1 gg_id:441923 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu4
FJ674942.1 gg_id:525865 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
FJ675650.1 gg_id:512333 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
FJ671967.1 gg_id:524433 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
EU934077.1 gg_id:333015 Acinetobacter sp. FR2_4 str. FR2_4con
AF390087.1 gg_id:49347 Acinetobacter sp. str. Sea-9
AJ633641.1 gg_id:103039 Acinetobacter sp. str. LMG V90 = ACI792

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| EU661696.1 | 283320 | 13006.0 | 13068.6 | 6815.5 | 10022.9 | 12212.7 | 10552.8 |
| EU921463.1 | 345884 | 1443.4 | 1235.2 | 995.1 | 922.4 | 762.9 | 2799.0 |
| FN433036.1 | 565535 | 3015.3 | 3001.6 | 4011.4 | 3638.6 | 2293.8 | 4344.8 |
| AJ633639.1 | 99113 | 1703.8 | 860.3 | 885.2 | 1959.8 | 767.6 | 4087.7 |
| EU467631.1 | 302583 | 1351.7 | 1103.3 | 717.9 | 922.3 | 1391.2 | 4180.6 |
| FJ674356.1 | 525396 | 2968.6 | 3637.9 | 4735.4 | 2798.0 | 6055.0 | 6688.1 |
| DQ824645.1 | 184299 | 1414.8 | 1234.4 | 2526.8 | 274.6 | 767.2 | 1134.7 |
| X81659.1 | 8342 | 2227.7 | 1619.3 | 1360.8 | 306.2 | 269.4 | 5176.3 |
| AF336353.1 | 37719 | 2832.8 | 2308.4 | 10654.1 | 3657.4 | 2507.3 | 2548.7 |
| FJ263922.1 | 304658 | 5327.0 | 5552.0 | 4372.8 | 4797.9 | 5907.7 | 5681.0 |
| FJ816051.1 | 564486 | 2073.9 | 1586.3 | 2164.3 | 1949.6 | 1405.1 | 3205.1 |
| X81668.1 | 8375 | 3336.2 | 1817.7 | 3517.7 | 3465.8 | 5720.5 | 6056.6 |
| EF188656.1 | 351236 | 4085.7 | 4317.2 | 5531.8 | 2406.1 | 4870.7 | 6233.2 |
| EU090179.1 | 250734 | 5568.1 | 7019.1 | 6113.6 | 5315.9 | 5975.9 | 6543.7 |
| FJ976566.1 | 591323 | 1838.6 | 1624.3 | 1281.4 | 1081.8 | 869.9 | 3713.7 |
| FJ194001.1 | 310497 | 3947.4 | 3196.2 | 2825.5 | 3652.1 | 4139.2 | 7405.9 |
| AY633607.1 | 101152 | 718.1 | 444.7 | 569.7 | 270.3 | 2019.9 | 2318.2 |
| FJ672939.1 | 515715 | 7370.7 | 7292.4 | 7526.9 | 7599.9 | 8344.8 | 9919.7 |
| EU467653.1 | 289405 | 9931.6 | 9665.6 | 7344.9 | 8360.1 | 14364.3 | 9125.1 |
| FJ671896.1 | 521562 | 3554.4 | 2756.5 | 2570.3 | 6037.1 | 8569.1 | 6080.1 |
| EU463121.1 | 290186 | 2166.9 | 3486.4 | 3079.0 | 4184.3 | 11334.6 | 6070.8 |
| EU160533.1 | 353347 | 1966.7 | 2879.0 | 1901.3 | 1939.9 | 3427.7 | 3479.3 |
| NR_028852.1 | 591121 | 4899.2 | 4721.5 | 3032.9 | 8385.3 | 6400.7 | 6828.8 |
| DQ856553.1 | 244174 | 1281.4 | 1750.3 | 706.3 | 163.8 | 157.0 | 2882.5 |
| FJ811875.1 | 579258 | 2868.0 | 2895.1 | 2303.6 | 1219.8 | 1705.0 | 5009.3 |
| EF127901.2 | 255893 | 846.3 | 475.5 | 534.3 | 102.5 | 88.1 | 1214.2 |
| AJ295007.1 | 36199 | 3785.5 | 3730.8 | 6167.0 | 4892.4 | 5430.4 | 6735.0 |
| EU382216.1 | 263259 | 1159.7 | 998.0 | 415.9 | 393.3 | 113.7 | 3609.5 |
| AB167222.1 | 107933 | 4432.8 | 3035.1 | 3655.1 | 4024.3 | 3686.6 | 5667.6 |
| FJ976597.1 | 509344 | 1445.7 | 1099.1 | 385.0 | 1243.0 | 1091.3 | 4809.3 |
| EU434432.1 | 265496 | 3258.0 | 2787.4 | 1749.9 | 2680.8 | 3256.5 | 7295.4 |
| FJ672184.1 | 510837 | 1866.8 | 1653.3 | 1461.6 | 2012.3 | 2307.6 | 4703.7 |
| GQ281071.1 | 577164 | 1417.9 | 988.9 | 856.6 | 750.6 | 438.4 | 3681.2 |
| GQ258635.1 | 542419 | 4865.3 | 4650.5 | 5185.1 | 5515.1 | 6340.3 | 5925.4 |
| GQ039005.1 | 441923 | 2448.5 | 1541.8 | 6300.2 | 5155.5 | 3261.2 | 3191.6 |
| FJ674942.1 | 525865 | 1574.1 | 1125.9 | 4777.2 | 2779.7 | 856.0 | 2285.3 |
| FJ675650.1 | 512333 | 5885.0 | 5459.1 | 6419.9 | 6160.7 | 8975.5 | 8083.5 |
| FJ671967.1 | 524433 | 10270.4 | 10858.4 | 9140.4 | 7921.2 | 11393.9 | 10575.8 |
| EU934077.1 | 333015 | 1578.3 | 1008.2 | 637.7 | 885.0 | 360.7 | 2641.5 |
| AF390087.1 | 49347 | 5575.2 | 6407.4 | 8291.5 | 6598.6 | 9209.2 | 9911.7 |
| AJ633641.1 | 103039 | 1260.4 | 719.0 | 349.6 | 284.0 | 1892.4 | 2488.7 |

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| s__unclassified | 3442 |
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| s__unclassified | 3652 |
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| s__unclassified | 3770 |
| s__unclassified | 3919 |
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| s__Enhydrobacter aerosaccus | 2443 |
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| s__Moraxella lacunata | 2477 |
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| s__Moraxella nonliquefaciens | 2512 |
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| s__unclassified | 2325 |
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AF543466.1 gg_id:58303 Alkanindiges hongkongensis str. HKU9
EU104153.1 gg_id:334424 Evidence Comamonadaceae determinants settling performance activated sludge clo
DQ640687.1 gg_id:228207 full-scale EBPR sludge clone Skagenf46
GQ076362.1 gg_id:455948 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw3E
EU636038.1 gg_id:278473 Antarctic str. 3C8
DQ847440.1 gg_id:171048 human forearm skin clone GL2-47
EU104133.1 gg_id:324983 Evidence Comamonadaceae determinants settling performance activated sludge clo
GQ464393.1 gg_id:548754 Detection during -ARDRA and sequencing frozen chicken storage container 90 days
DQ130041.1 gg_id:152336 microbial biota normal forearm human skin clone JEL30
GQ076390.1 gg_id:392111 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw3E
GQ080410.1 gg_id:388165 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
DQ336992.1 gg_id:147715 subsurface water clone EV818CFSSAHH42
DQ354732.1 gg_id:153465 subsurface water clone DR550SWSAEE45
DQ354720.1 gg_id:155859 subsurface water clone DR550SWSAEE20
EU104077.1 gg_id:307143 Evidence Comamonadaceae determinants settling performance activated sludge clo
AM905315.1 gg_id:238484 Microbial dynamics -arctic exposure hydrocarbons and bioremediation agent interti
FJ380170.1 gg_id:370141 ornithogenic Ross Sea region Antarctica AB1 soil clone 13/4/4G
DQ469231.1 gg_id:158223 Microbial and ecology water Zhong Tiaoshan mine Shanxi province China AMD clone
NR_029005.1 gg_id:591417 Enhydrobacter aerosaccus str. G; LMG 21877; ATCC 27094
GQ054317.1 gg_id:379908 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw1108
AY043376.1 gg_id:63603 Moraxella osloensis str. AU1220
DQ153085.1 gg_id:219896 Moraxella bovoculi str. 371
AF005167.1 gg_id:8243 Moraxella lacunata str. E3808
AF005169.1 gg_id:8245 Moraxella lacunata str. NCTC 7911
AF005161.1 gg_id:8237 Moraxella lacunata str. ATCC 17956
AF005162.1 gg_id:8238 Moraxella lacunata str. E7992
AF005178.1 gg_id:8274 Moraxella nonliquefaciens str. B6270/90
AF005176.1 gg_id:8272 Moraxella nonliquefaciens str. P2581/88
AF005186.1 gg_id:48597 Moraxella ovis str. ATCC 33078T
AF005185.1 gg_id:8278 Moraxella catarrhalis str. ATCC 25238T
FM873527.1 gg_id:360893 occupant source house mattress dust clone MA01E04
NR_028914.1 gg_id:585738 Moraxella canis str. N7; LMG 11194
DQ647927.1 gg_id:222016 Moraxella bovis str. Tifton I
AM420053.1 gg_id:246528 Noma subgingival plaque clone 202G06(oral)
AF005187.1 gg_id:8281 Moraxella caviae str. CCUG 355T
AF005188.1 gg_id:8261 Moraxella cuniculi str. CCUG 2154T
AF005189.1 gg_id:8249 Moraxella cuniculi str. CCUG 27179
EF396294.1 gg_id:255045 Moraxella sp. CD12CA4
GQ070485.1 gg_id:467388 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
AY212599.1 gg_id:100893 water 20 m downstream manure clone 148ds20
DQ823176.1 gg_id:170920 Techniques Microbial Studies Oregon Caves National Monument Quad 3 on trail clo

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| AF543466.1 | 58303 | 1117.5 | 889.2 | 2889.5 | 873.7 | 1119.7 | 710.5 |
| EU104153.1 | 334424 | 329.2 | 420.8 | 704.0 | 264.3 | 2038.1 | 2101.2 |
| DQ640687.1 | 228207 | 20.5 | 78.1 | 94.5 | 70.3 | 59.7 | 62.4 |
| GQ076362.1 | 455948 | 7657.4 | 9843.7 | 5744.1 | 6204.6 | 9142.0 | 7232.9 |
| EU636038.1 | 278473 | 374.0 | 787.3 | 1086.8 | 434.5 | 201.7 | 1018.5 |
| DQ847440.1 | 171048 | 1511.3 | 791.9 | 1115.2 | 2149.9 | 323.2 | 2553.2 |
| EU104133.1 | 324983 | 121.9 | 219.4 | 868.1 | 111.7 | 200.3 | 1020.4 |
| GQ464393.1 | 548754 | 3133.7 | 2539.9 | 3654.9 | 3210.8 | 2256.8 | 3623.7 |
| DQ130041.1 | 152336 | 2314.7 | 2426.5 | 2229.9 | 2980.0 | 4557.7 | 5513.3 |
| GQ076390.1 | 392111 | 471.7 | 525.6 | 425.6 | 313.0 | 994.0 | 2327.9 |
| GQ080410.1 | 388165 | 10662.6 | 12498.7 | 6265.3 | 8107.6 | 14798.6 | 12962.4 |
| DQ336992.1 | 147715 | 9685.0 | 9469.7 | 4184.3 | 5834.8 | 10644.5 | 11944.5 |
| DQ354732.1 | 153465 | 27.8 | 83.5 | 131.0 | 43.6 | 1305.2 | 787.0 |
| DQ354720.1 | 155859 | 2612.1 | 2193.6 | 968.7 | 3220.2 | 4487.8 | 3968.4 |
| EU104077.1 | 307143 | 769.8 | 1368.0 | 2376.5 | 1188.8 | 3990.7 | 4188.2 |
| AM905315.1 | 238484 | 558.5 | 702.8 | 1399.7 | 544.6 | 1739.4 | 2163.1 |
| FJ380170.1 | 370141 | 1942.8 | 1351.4 | 1321.5 | 971.3 | 2348.3 | 5576.7 |
| DQ469231.1 | 158223 | 604.1 | 485.0 | 1653.8 | 245.2 | 1669.0 | 4292.2 |
| NR_029005.1 | 591417 | 528.6 | 687.6 | 1482.8 | 316.6 | 368.6 | 1183.9 |
| GQ054317.1 | 379908 | 10266.3 | 12532.8 | 6435.6 | 7636.2 | 8427.2 | 7947.3 |
| AY043376.1 | 63603 | 1824.9 | 2532.7 | 2355.1 | 1292.4 | 1492.7 | 4187.2 |
| DQ153085.1 | 219896 | 3273.7 | 2595.8 | 1898.4 | 5729.6 | 5730.8 | 6271.9 |
| AF005167.1 | 8243 | 2035.4 | 1535.3 | 380.1 | 871.0 | 1643.7 | 1468.7 |
| AF005169.1 | 8245 | 1657.0 | 1505.0 | 894.6 | 1867.8 | 3014.5 | 2040.6 |
| AF005161.1 | 8237 | 1868.6 | 1583.7 | 1073.8 | 1266.3 | 2819.5 | 1562.2 |
| AF005162.1 | 8238 | 1658.7 | 1512.0 | 930.6 | 1775.7 | 3418.0 | 2564.1 |
| AF005178.1 | 8274 | 3415.9 | 3692.2 | 4683.8 | 3709.5 | 4496.8 | 4940.6 |
| AF005176.1 | 8272 | 7316.2 | 7885.5 | 6024.4 | 5544.6 | 6770.4 | 8702.5 |
| AF005186.1 | 48597 | 1901.5 | 3017.9 | 2629.4 | 4058.1 | 1923.1 | 2800.2 |
| AF005185.1 | 8278 | 3632.0 | 3698.5 | 4507.4 | 4038.9 | 6867.7 | 5017.9 |
| FM873527.1 | 360893 | 6651.4 | 6787.6 | 5081.6 | 3062.5 | 2918.1 | 5351.9 |
| NR_028914.1 | 585738 | 4379.9 | 3576.2 | 3924.0 | 4834.3 | 6835.7 | 6389.7 |
| DQ647927.1 | 222016 | 3417.3 | 2736.7 | 2030.3 | 5960.9 | 5523.1 | 6693.4 |
| AM420053.1 | 246528 | 883.9 | 1377.1 | 2330.0 | 411.4 | 1091.2 | 3257.8 |
| AF005187.1 | 8281 | 4617.6 | 4520.5 | 4131.5 | 6743.2 | 6511.2 | 5553.9 |
| AF005188.1 | 8261 | 671.0 | 554.7 | 1726.8 | 2106.2 | 3012.8 | 3781.3 |
| AF005189.1 | 8249 | 340.4 | 462.3 | 311.0 | 629.1 | 3598.5 | 1197.7 |
| EF396294.1 | 255045 | 2883.0 | 3228.8 | 3838.9 | 4733.1 | 5681.0 | 5944.9 |
| GQ070485.1 | 467388 | 862.9 | 1035.5 | 1461.0 | 1481.3 | 1393.7 | 1738.1 |
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| DQ823176.1 | 170920 | 29.7 | 103.3 | 47.6 | 58.7 | 75.8 | 179.0 |

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| s__unclassified | 179 |
| s__unclassified | 2220 |
| s__unclassified | 329 |
| s__unclassified | 479 |
| s__unclassified | 936 |
| s__unclassified | 954 |
| s__Psychrobacter aquaticus | 2888 |
| s__Psychrobacter celer | 3117 |
| s__Psychrobacter cryohalolentis | 3033 |
| s__Psychrobacter cryohalolentis | 3136 |
| s__Psychrobacter marincola | 3010 |
| s__Psychrobacter marincola | 3141 |
| s__Psychrobacter marincola | 3195 |
| s__Psychrobacter marincola | 3254 |
| s__Psychrobacter marincola | 3294 |
| s__Psychrobacter nivimaris | 2890 |
| s__Psychrobacter pacificensis | 2533 |
| s__Psychrobacter pacificensis | 2943 |
| s__Psychrobacter pacificensis | 3044 |
| s__Psychrobacter psychrophilus | 2909 |
| s__Psychrobacter pulmonis | 2301 |
| s__Psychrobacter pulmonis | 2523 |
| s__Psychrobacter pulmonis | 2581 |
| s__Psychrobacter pulmonis | 2595 |
| s__Psychrobacter pulmonis | 2640 |
| s__Psychrobacter pulmonis | 2786 |
| s__Psychrobacter pulmonis | 3268 |
| s__Psychrobacter sp. PRwf-1 | 3265 |
| s__unclassified | 2310 |
| s__unclassified | 2312 |
| s__unclassified | 2372 |
| s__unclassified | 2404 |
| s__unclassified | 2408 |
| s__unclassified | 2423 |
| s__unclassified | 2428 |
| s__unclassified | 2437 |
| s__unclassified | 2446 |
| s__unclassified | 2463 |
| s__unclassified | 2472 |
| s__unclassified | 2517 |
| s__unclassified | 2520 |

AY212663.1 gg_id:99626 water 20 m downstream manure clone 216ds20
AY622230.1 gg_id:101684 subsurface soil clone C-CL42
DQ660872.1 gg_id:237806 DongChuan copper pyrites PRC determined acid mine drainage (AMD) clone DC-II-2
DQ458033.1 gg_id:158925 acid mine drainage clone DX63
DQ354716.1 gg_id:153505 subsurface water clone DR550SWSAEE15b
DQ824588.1 gg_id:176013 human fecal clone RL185_aaj70b01
AJ830006.1 gg_id:104541 Psychrobacter aquaticus str. CMS 58
AY842259.1 gg_id:110467 Psychrobacter celer str. SW-238
AY771717.1 gg_id:108691 Psychrobacter fozii str. S2-83
NC_007969.1 gg_id:157086 Psychrobacter cryohalolentis str. K5
DQ270712.1 gg_id:141337 Psychrobacter sp. B-3151
EU652044.1 gg_id:275703 Psychrobacter marincola str. aa-20
AF441202.1 gg_id:44896 Psychrobacter jeotgali str. YKJ-105
NR_025458.1 gg_id:562316 Psychrobacter marincola str. KMM 277
AJ539104.1 gg_id:79510 Psychrobacter salsus str. DD48
AJ313425.1 gg_id:101537 Psychrobacter nivimaris str. 88/2-7
AB016054.1 gg_id:24089 Psychrobacter pacificensis str. NIBH P2J2
AY057116.1 gg_id:27938 Psychrobacter meningitidis str. SGHMS
AB016056.1 gg_id:18681 Psychrobacter pacificensis str. NIBH P2J13
AY167308.1 gg_id:82364 Psychrobacter glacincola str. ANT9253
AY372913.1 gg_id:144095 marine sponge Rhabdastrella globostellata symbiont
EU434452.1 gg_id:269448 Psychrobacter pulmonis str. a40
EU434447.1 gg_id:263373 Psychrobacter pulmonis str. a72
EU434352.1 gg_id:276381 Psychrobacter pulmonis str. a161
EU434446.1 gg_id:263158 Psychrobacter pulmonis str. a60
AJ437696.1 gg_id:85442 Psychrobacter pulmonis str. CECT 5989T
EU434362.1 gg_id:269048 Psychrobacter pulmonis str. a131
NC_009524.1 gg_id:229173 Psychrobacter sp. str. PRwf-1
FJ613297.1 gg_id:533763 Psychrobacter faecalis str. hyss7
EU000245.1 gg_id:324143 Psychrobacter maritimus str. KOPRI_22337
EU845548.1 gg_id:313200 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
EU880519.1 gg_id:311744 Psychrobacter nivimaris str. P24a
EF101551.1 gg_id:182841 Psychrobacter pulmonis str. KOPRI24933
AY167281.1 gg_id:82289 Psychrobacter glacincola str. ANT9104
EU433332.1 gg_id:271451 Psychrobacter sp. str. BSs20154
AJ312213.1 gg_id:32985 Psychrobacter glacincola str. DSM 12194T
DQ860047.1 gg_id:251317 anchovy intestinal microflora clone F2N
AM110989.1 gg_id:140965 Psychrobacter sp. str. 3035
EU434353.1 gg_id:264946 Psychrobacter pulmonis str. a163
DQ677868.1 gg_id:253685 Psychrobacter sp. BF02-S11
AY497354.1 gg_id:106855 Psychrobacter sp. str. 20

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| AY212663.1 | 99626 | 3790.9 | 3542.0 | 9829.9 | 5604.5 | 9778.3 | 10685.6 |
| AY622230.1 | 101684 | 3402.5 | 3138.9 | 1566.5 | 1314.1 | 1794.1 | 2885.6 |
| DQ660872.1 | 237806 | 321.0 | 194.3 | 318.6 | 482.3 | 1524.1 | 394.1 |
| DQ458033.1 | 158925 | 1248.4 | 2573.4 | 2694.5 | 1669.5 | 2590.2 | 4055.3 |
| DQ354716.1 | 153505 | 3336.6 | 4612.6 | 4862.3 | 1006.2 | 2751.5 | 6083.6 |
| DQ824588.1 | 176013 | 29.1 | 37.4 | 63.8 | 58.6 | 68.2 | 68.0 |
| AJ830006.1 | 104541 | 5709.7 | 5432.6 | 5710.2 | 4714.9 | 6475.7 | 6789.7 |
| AY842259.1 | 110467 | 4790.9 | 4591.0 | 4499.2 | 4262.2 | 5749.4 | 6772.0 |
| AY771717.1 | 108691 | 154.2 | 171.6 | 212.1 | 246.9 | 189.5 | 168.5 |
| NC_007969.1 | 157086 | 329.4 | 247.1 | 391.6 | 437.6 | 205.2 | 198.1 |
| DQ270712.1 | 141337 | 1286.3 | 1123.5 | 1718.9 | 1246.0 | 4624.7 | 4223.9 |
| EU652044.1 | 275703 | 251.9 | 309.9 | 167.8 | 224.0 | 872.5 | 513.6 |
| AF441202.1 | 44896 | 1216.1 | 1593.8 | 1290.9 | 656.1 | 3336.2 | 3892.0 |
| NR_025458.1 | 562316 | 1814.9 | 2775.4 | 1584.0 | 1026.3 | 4861.3 | 4241.7 |
| AJ539104.1 | 79510 | 164.4 | 277.9 | 340.4 | 178.1 | 252.1 | 700.5 |
| AJ313425.1 | 101537 | 1983.9 | 1715.3 | 1363.4 | 1507.3 | 2205.6 | 2871.7 |
| AB016054.1 | 24089 | 5012.8 | 5666.3 | 4420.1 | 5097.9 | 4858.6 | 5026.4 |
| AY057116.1 | 27938 | 596.9 | 826.5 | 1378.3 | 1064.2 | 2562.1 | 2973.6 |
| AB016056.1 | 18681 | 103.5 | 137.0 | 177.7 | 105.0 | 3067.5 | 1400.2 |
| AY167308.1 | 82364 | 4426.8 | 4668.2 | 3693.5 | 2938.5 | 3367.3 | 5128.3 |
| AY372913.1 | 144095 | 2172.2 | 3227.3 | 3557.3 | 1608.8 | 4446.2 | 5256.0 |
| EU434452.1 | 269448 | 4254.8 | 4610.9 | 3935.5 | 3482.1 | 4834.0 | 5237.4 |
| EU434447.1 | 263373 | 8116.9 | 6804.0 | 5931.0 | 5783.0 | 7332.1 | 8035.5 |
| EU434352.1 | 276381 | 9143.9 | 10116.3 | 7593.2 | 5692.2 | 6294.5 | 6445.2 |
| EU434446.1 | 263158 | 4530.3 | 5490.9 | 4913.6 | 3482.2 | 4326.5 | 4263.2 |
| AJ437696.1 | 85442 | 4251.4 | 4683.1 | 4777.2 | 3651.2 | 3879.2 | 5897.2 |
| EU434362.1 | 269048 | 3314.1 | 3719.2 | 4545.8 | 2668.0 | 4257.3 | 4790.3 |
| NC_009524.1 | 229173 | 1739.4 | 1983.6 | 1695.8 | 1263.6 | 2004.0 | 2130.1 |
| FJ613297.1 | 533763 | 3312.3 | 2726.7 | 3400.0 | 2048.9 | 1656.3 | 2088.4 |
| EU000245.1 | 324143 | 1524.9 | 1039.1 | 662.8 | 885.4 | 1514.0 | 1368.0 |
| EU845548.1 | 313200 | 5563.0 | 6090.4 | 3804.0 | 4973.6 | 6859.0 | 6924.6 |
| EU880519.1 | 311744 | 1715.2 | 1321.6 | 845.4 | 1493.0 | 3173.8 | 4056.7 |
| EF101551.1 | 182841 | 984.7 | 1077.5 | 864.5 | 732.7 | 784.3 | 1076.5 |
| AY167281.1 | 82289 | 6578.1 | 6129.8 | 5328.6 | 6512.1 | 7351.0 | 7123.1 |
| EU433332.1 | 271451 | 10550.2 | 9590.4 | 11477.9 | 7479.2 | 11569.3 | 9684.4 |
| AJ312213.1 | 32985 | 2459.8 | 1843.6 | 1056.6 | 1357.4 | 2178.8 | 2209.8 |
| DQ860047.1 | 251317 | 1025.0 | 854.9 | 317.0 | 774.3 | 1036.4 | 1466.4 |
| AM110989.1 | 140965 | 2466.0 | 2486.8 | 2217.7 | 4491.9 | 6010.3 | 6541.8 |
| EU434353.1 | 264946 | 260.8 | 471.2 | 1323.6 | 115.0 | 117.5 | 601.2 |
| DQ677868.1 | 253685 | 282.7 | 361.4 | 895.7 | 349.8 | 206.9 | 312.7 |
| AY497354.1 | 106855 | 192.7 | 244.2 | 233.9 | 233.7 | 348.0 | 184.1 |

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| k__Bacteria | k__Bacteria | p__Proteobacteria | c__Gammaproteobacteria |
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| s__unclassified | 2559 |
| s__unclassified | 2574 |
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| s__unclassified | 2604 |
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| s__unclassified | 2670 |
| s__unclassified | 2689 |
| s__unclassified | 2693 |
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| s__unclassified | 3103 |

NR_025531.1 gg_id:561741 Psychrobacter fozii str. NF23; LMG 21280
AF005192.1 gg_id:8298 Psychrobacter phenylpyruvicus str. 752/52
AM111050.1 gg_id:140908 Psychrobacter sp. str. 7195
NR_027204.1 gg_id:566452 Psychrobacter arenosus str. R7; KMM 3659
EU434405.1 gg_id:263288 Psychrobacter maritimus str. a336
GQ093417.1 gg_id:420929 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw4
EF101546.1 gg_id:181752 Psychrobacter aquimaris str. KOPRI24928
AM111057.1 gg_id:140806 Psychrobacter sp. str. 7319
AY722804.1 gg_id:103680 Psychrobacter aquimaris str. SW-210
AY864643.1 gg_id:110044 Psychrobacter sp. str. DVS7b
AY198113.1 gg_id:80503 Psychrobacter sp. HLA
AY513645.1 gg_id:103196 Psychrobacter alimentarius str. JG-100
NR_027225.1 gg_id:543076 Psychrobacter maritimus str. Pi2-20; KMM 3646
AY167286.1 gg_id:81385 Psychrobacter sp. str. ANT9153
AJ272303.1 gg_id:71508 Psychrobacter proteolyticus str. 116
AY771724.1 gg_id:143446 Psychrobacter glacincola S3-14
EU845549.1 gg_id:332859 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
AJ309942.1 gg_id:51114 Psychrobacter immobilis str. DSM 7229T
EU075123.1 gg_id:242630 Psychrobacter sp. str. En40
AM269904.1 gg_id:160677 Psychrobacter sp. str. ES-10
EU434395.1 gg_id:273089 Psychrobacter maritimus str. a325
AY444822.1 gg_id:137201 Psychrobacter arcticum str. 273-4
EU370412.1 gg_id:266113 Psychrobacter faecalis str. 88Z1
AY864649.1 gg_id:110450 Psychrobacter sp. str. DVS6c
EU434433.1 gg_id:275103 Psychrobacter pulmonis str. a195
FJ900925.1 gg_id:552614 Polymorphism microbial reservoirs water cut stage oil field clone L-48
EU845208.1 gg_id:323141 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
AM237354.1 gg_id:154195 Psychrobacter faecalis OS-38
EU434386.1 gg_id:271742 Psychrobacter maritimus str. a281
AJ609556.1 gg_id:100627 Psychrobacter frigidicola str. DSM 12411
EU834258.1 gg_id:312816 Psychrobacter frigidicola str. DS35
DQ337513.1 gg_id:147051 Psychrobacter psychrophilus BBDP29
U85878.1 gg_id:8302 Psychrobacter glacincola str. IC018
U39399.1 gg_id:8253 Psychrobacter immobilis str. ATCC 43116
U85876.1 gg_id:8300 Psychrobacter glacincola str. IC084
FJ979856.1 gg_id:376137 Psychrobacter sp. str. tsz26
EU845706.1 gg_id:335347 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
EF154276.1 gg_id:176716 Psychrobacter alimentarius str. 36
AM111006.1 gg_id:140871 Psychrobacter sp. str. 3055
AF170743.1 gg_id:8257 Psychrobacter sp. str. QSSC5-4
EU915471.1 gg_id:326012 Psychrobacter phenylpyruvicus str. 123

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| NR_025531.1 | 561741 | 44.2 | 52.9 | 219.4 | 74.5 | 69.4 | 31.3 |
| AF005192.1 | 8298 | 2076.2 | 2226.0 | 1964.5 | 1282.9 | 2182.8 | 2353.0 |
| AM111050.1 | 140908 | 2418.4 | 3069.7 | 3507.8 | 1922.4 | 1946.9 | 2387.7 |
| NR_027204.1 | 566452 | 6191.8 | 2605.7 | 3862.8 | 1562.6 | 1145.1 | 1849.1 |
| EU434405.1 | 263288 | 1556.4 | 2089.9 | 2499.8 | 1351.2 | 1805.7 | 3180.9 |
| GQ093417.1 | 420929 | 5118.2 | 4846.3 | 3813.6 | 3910.3 | 5147.5 | 4571.9 |
| EF101546.1 | 181752 | 67.9 | 62.9 | 55.1 | 100.3 | 69.6 | 79.7 |
| AM111057.1 | 140806 | 1492.9 | 1768.6 | 369.9 | 2448.2 | 3018.0 | 2728.7 |
| AY722804.1 | 103680 | 26.0 | 40.7 | 87.9 | 55.7 | 447.9 | 39.5 |
| AY864643.1 | 110044 | 177.4 | 219.0 | 331.6 | 293.6 | 374.2 | 344.3 |
| AY198113.1 | 80503 | 11335.7 | 10521.4 | 7721.1 | 8833.3 | 11315.0 | 9780.4 |
| AY513645.1 | 103196 | 2362.1 | 1575.3 | 524.6 | 1034.6 | 1874.7 | 1614.6 |
| NR_027225.1 | 543076 | 111.0 | 138.1 | 65.2 | 103.2 | 230.3 | 109.2 |
| AY167286.1 | 81385 | 1960.2 | 1927.1 | 3019.4 | 2157.4 | 1817.1 | 3545.2 |
| AJ272303.1 | 71508 | 13783.0 | 12407.6 | 12552.1 | 11639.6 | 16775.4 | 15569.4 |
| AY771724.1 | 143446 | 886.0 | 1131.5 | 1098.6 | 1023.3 | 1880.6 | 1107.1 |
| EU845549.1 | 332859 | 276.3 | 508.4 | 247.3 | 350.0 | 519.6 | 509.0 |
| AJ309942.1 | 51114 | 198.8 | 241.2 | 556.0 | 227.6 | 469.5 | 1229.7 |
| EU075123.1 | 242630 | 7229.9 | 6985.2 | 6110.6 | 7198.2 | 7600.0 | 7748.5 |
| AM269904.1 | 160677 | 6387.1 | 6056.9 | 3305.7 | 8352.5 | 7277.0 | 7791.7 |
| EU434395.1 | 273089 | 10863.3 | 10007.0 | 4016.3 | 2572.8 | 2203.4 | 5237.0 |
| AY444822.1 | 137201 | 118.5 | 114.4 | 196.2 | 151.5 | 93.3 | 60.1 |
| EU370412.1 | 266113 | 628.8 | 485.6 | 652.1 | 398.6 | 114.5 | 578.0 |
| AY864649.1 | 110450 | 8377.3 | 9661.4 | 4290.4 | 7945.1 | 12326.7 | 10275.2 |
| EU434433.1 | 275103 | 2201.8 | 2679.9 | 1838.5 | 1731.0 | 1809.6 | 1799.9 |
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| AM237354.1 | 154195 | 1088.1 | 1302.5 | 949.5 | 1064.3 | 880.1 | 1272.5 |
| EU434386.1 | 271742 | 2247.4 | 2243.8 | 1710.5 | 1618.1 | 2288.2 | 4084.9 |
| AJ609556.1 | 100627 | 154.4 | 139.6 | 84.8 | 146.7 | 460.8 | 103.2 |
| EU834258.1 | 312816 | 404.1 | 610.1 | 105.2 | 274.7 | 1019.5 | 978.7 |
| DQ337513.1 | 147051 | 4502.8 | 2343.2 | 2556.9 | 6332.3 | 1592.2 | 2394.2 |
| U85878.1 | 8302 | 213.9 | 195.8 | 482.3 | 418.0 | 629.8 | 173.3 |
| U39399.1 | 8253 | 60.0 | 312.5 | 261.8 | 115.7 | 55.5 | 156.2 |
| U85876.1 | 8300 | 91.4 | 75.2 | 235.3 | 153.1 | 646.1 | 103.9 |
| FJ979856.1 | 376137 | 1807.2 | 2338.9 | 5307.5 | 3996.5 | 3318.8 | 6714.5 |
| EU845706.1 | 335347 | 5621.2 | 5589.9 | 4855.8 | 4653.1 | 7057.1 | 6892.7 |
| EF154276.1 | 176716 | 9195.7 | 11298.7 | 5714.7 | 7332.3 | 12200.1 | 12035.6 |
| AM111006.1 | 140871 | 8744.8 | 6542.4 | 7301.2 | 4698.4 | 5711.1 | 6170.2 |
| AF170743.1 | 8257 | 546.0 | 1577.1 | 856.2 | 382.7 | 1511.3 | 1270.5 |
| EU915471.1 | 326012 | 2544.8 | 2554.6 | 2157.2 | 1481.2 | 2526.2 | 2776.2 |

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| s__Azomonas macrocytogenes | 175 |
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| s__Azotobacter beijerinckii | 1323 |

EU434444.1 gg_id:277032 Psychrobacter maritimus str. a226
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AY722805.1 gg_id:103825 Psychrobacter namhaensis str. SW-242
AJ871434.2 gg_id:109701 Sphingomonas asaccharolytica CP173-2
EU434577.1 gg_id:265418 Psychrobacter pulmonis str. b105
AJ430828.1 gg_id:75020 Psychrobacter luti str. NF11
AJ609555.1 gg_id:100472 Psychrobacter urativorans str. DSM 14009
EU844911.1 gg_id:309336 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
FN433003.1 gg_id:542035 Psychrobacter sp. str. a328
DQ173002.2 gg_id:155732 Psychrobacter sp. str. TSBY-37
U46144.1 gg_id:8297 Psychrobacter phenylpyruvicus str. ATCC 23333
AY771725.1 gg_id:142863 Psychrobacter alimentarius S3-15
DQ156147.1 gg_id:220416 Moraxella boevrei str. ATCC 700022
DQ337034.1 gg_id:146907 subsurface water clone EV818EB5CPSAJJ24
GQ063996.1 gg_id:379925 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw6
GQ008884.1 gg_id:500783 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
AM231087.1 gg_id:155496 Moraxella sp. Vas1N8
GQ093299.1 gg_id:437819 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw42
X95304.1 gg_id:8267 Moraxella osloensis str. Ben 58
DQ264418.1 gg_id:143131 universal microarray broader than typical library when sampling subsurface groundv
DQ026510.1 gg_id:136755 Photorhabdus luminescens str. PDBC HIP1
AY753196.2 gg_id:124309 Xenorhabdus nematophila str. PDBC SCX3 Indian
AB175658.1 gg_id:162524 Azomonas insignis str. ATCC 29361
AB175659.1 gg_id:173619 Azomonas insignis str. NCIB 9963
AB175654.1 gg_id:173614 Azomonas macrocytogenes str. IAM 15003
AJ278108.1 gg_id:66199 Pseudomonas sp. str. KY
FJ032011.1 gg_id:324228 Azotobacter vinelandii str. M
AY336565.1 gg_id:91237 Azotobacter vinelandii str. DSM576
EF100155.1 gg_id:217214 Azotobacter vinelandii str. ICMP 15215
EF100148.1 gg_id:205415 Azorhizophilus paspali str. ICMP 7470
AF302796.3 gg_id:38217 Pseudomonas indica
AAAU03000003.1 gg_id:133692 Azotobacter vinelandii str. AvOP
EF620449.1 gg_id:243090 Azotobacter vinelandii str. ISSDS-430
AB236162.1 gg_id:275455 Azotobacter tropicalis str. BKK.2
AB175655.1 gg_id:168352 Azotobacter armeniacus str. DSM 2284
EF620451.1 gg_id:257741 Azotobacter vinelandii str. ISSDS-435
AB175656.1 gg_id:173793 Azotobacter salinestris str. ATCC 49674
EF620446.1 gg_id:239704 Azotobacter vinelandii str. ISSDS-426
EF620447.1 gg_id:256056 Azotobacter vinelandii str. ISSDS-428
EF620443.1 gg_id:238882 Azotobacter vinelandii str. ISSDS-423
EF100152.1 gg_id:205128 Azotobacter beijerinckii str. ICMP 8673

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| EU434444.1 | 277032 | 1102.4 | 851.0 | 189.9 | 547.7 | 1206.0 | 671.3 |
| AM111062.1 | 140956 | 1820.7 | 1749.2 | 1128.1 | 2967.9 | 2545.1 | 2696.5 |
| AY722805.1 | 103825 | 613.2 | 542.1 | 592.4 | 380.1 | 68.9 | 573.6 |
| AJ871434.2 | 109701 | 3683.6 | 3464.4 | 2907.1 | 3135.1 | 3495.5 | 4759.9 |
| EU434577.1 | 265418 | 4295.8 | 4556.8 | 3402.6 | 3407.1 | 3213.3 | 4280.6 |
| AJ430828.1 | 75020 | 50.3 | 80.5 | 96.9 | 72.5 | 80.3 | 65.8 |
| AJ609555.1 | 100472 | 48.9 | 66.3 | 113.1 | 67.6 | 89.1 | 174.8 |
| EU844911.1 | 309336 | 246.0 | 305.5 | 334.0 | 402.9 | 644.4 | 576.0 |
| FN433003.1 | 542035 | 4095.6 | 4295.2 | 3196.4 | 5330.7 | 7722.6 | 9539.5 |
| DQ173002.2 | 155732 | 204.3 | 196.0 | 233.6 | 327.0 | 144.7 | 143.3 |
| U46144.1 | 8297 | 1267.7 | 1484.9 | 315.9 | 2068.3 | 2398.4 | 944.4 |
| AY771725.1 | 142863 | 195.3 | 259.3 | 402.1 | 402.9 | 755.5 | 323.7 |
| DQ156147.1 | 220416 | 1346.2 | 1180.0 | 666.2 | 1424.2 | 3599.9 | 1115.5 |
| DQ337034.1 | 146907 | 527.4 | 510.9 | 427.0 | 216.2 | 360.0 | 2080.5 |
| GQ063996.1 | 379925 | 1050.7 | 2152.1 | 806.8 | 1148.8 | 1272.6 | 1915.6 |
| GQ008884.1 | 500783 | 14864.5 | 18043.0 | 7399.7 | 10451.2 | 13517.8 | 11860.7 |
| AM231087.1 | 155496 | 188.0 | 178.4 | 630.6 | 303.9 | 427.8 | 808.8 |
| GQ093299.1 | 437819 | 20000.7 | 20605.6 | 19461.5 | 16776.5 | 21075.9 | 17886.6 |
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| DQ264418.1 | 143131 | 49.4 | 116.5 | 44.1 | 73.5 | 73.8 | 106.5 |
| DQ026510.1 | 136755 | 3608.5 | 3709.1 | 5926.1 | 2734.8 | 4664.9 | 3855.4 |
| AY753196.2 | 124309 | 2180.6 | 1397.7 | 1922.5 | 2305.9 | 671.4 | 3297.5 |
| AB175658.1 | 162524 | 1024.5 | 1814.7 | 1752.4 | 882.9 | 4804.3 | 5095.0 |
| AB175659.1 | 173619 | 7609.6 | 4973.2 | 2240.3 | 7489.6 | 9974.6 | 8941.8 |
| AB175654.1 | 173614 | 5528.5 | 6874.2 | 12349.2 | 5678.0 | 14552.7 | 11623.2 |
| AJ278108.1 | 66199 | 3469.6 | 4150.2 | 9395.3 | 4856.6 | 11439.5 | 5011.7 |
| FJ032011.1 | 324228 | 733.0 | 1054.8 | 1859.0 | 1758.8 | 9326.7 | 6963.8 |
| AY336565.1 | 91237 | 14273.0 | 11346.8 | 9987.2 | 11986.8 | 19117.1 | 15494.7 |
| EF100155.1 | 217214 | 228.9 | 691.5 | 2457.6 | 499.9 | 10926.5 | 7344.2 |
| EF100148.1 | 205415 | 1439.1 | 2243.1 | 1948.0 | 1514.3 | 6229.1 | 1851.3 |
| AF302796.3 | 38217 | 94.6 | 309.1 | 401.1 | 181.9 | 3035.2 | 277.3 |
| AAAU03000003.1 | 133692 | 366.4 | 740.7 | 1479.1 | 1093.3 | 9205.7 | 5914.5 |
| EF620449.1 | 243090 | 9634.9 | 6347.2 | 7632.9 | 12229.6 | 11422.3 | 9770.9 |
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| s__unclassified | 2164 |
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| s__Pseudomonas alcaligenes | 3426 |
| s__Pseudomonas alcaligenes | 3780 |
| s__Pseudomonas alcaligenes | 3792 |
| s__Pseudomonas alcaligenes | 3829 |
| s__Pseudomonas alcaligenes | 3855 |
| s__Pseudomonas alcaligenes | 3918 |
| s__Pseudomonas alcaligenes | 4059 |
| s__Pseudomonas alcaligenes | 4086 |
| s__Pseudomonas anguilliseptica | 1013 |
| s__Pseudomonas anguilliseptica | 1710 |
| s__Pseudomonas balearica | 534 |
| s__Pseudomonas balearica | 863 |
| s__Pseudomonas balearica | 965 |
| s__Pseudomonas borbori | 1179 |
| s__Pseudomonas borbori | 986 |
| s__Pseudomonas cedrina | 590 |
| s__Pseudomonas chlororaphis | 1017 |
| s__Pseudomonas chlororaphis | 1173 |
| s__Pseudomonas chlororaphis | 1268 |
| s__Pseudomonas chlororaphis | 1361 |
| s__Pseudomonas chlororaphis | 1529 |
| s__Pseudomonas chlororaphis | 162 |
| s__Pseudomonas chlororaphis | 1672 |
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| s__Pseudomonas chlororaphis | 987 |
| s__Pseudomonas citronellolis | 3320 |
| s__Pseudomonas citronellolis | 3389 |
| s__Pseudomonas citronellolis | 3514 |

EF620427.1 gg_id:246730 Azotobacter beijerinckii str. ISSDS-347
AB429526.1 gg_id:333725 Azotobacter beijerinckii str. C4
GQ388971.1 gg_id:543932 quality deterioration drinking system during serious red water outbreak clone J20
FJ544363.1 gg_id:434412 Pseudomonas alcaligenes str. st5-2
GQ389014.1 gg_id:510529 quality deterioration drinking system during serious red water outbreak clone J62
FJ793191.1 gg_id:520731 Archaea and Hot Spring Thailand Tao Dam hot spring clone TDB96
AY835998.1 gg_id:110273 Pseudomonas alcaligenes M4-7
EF199996.1 gg_id:175542 Pseudomonas alcaligenes str. DIP1
AY651923.1 gg_id:105788 Pseudomonas alcaligenes str. S3
FJ455454.1 gg_id:570727 Pseudomonas alcaligenes str. PNP-Y3
X99540.1 gg_id:8425 Pseudomonas anguilliseptica str. NCIMB 1949
AB021376.1 gg_id:8523 Pseudomonas anguilliseptica str. NCMB 1949T
EU741649.1 gg_id:311673 Pseudomonas sp. str. BQNR
GU339285.1 gg_id:536659 Pseudomonas balearica str. EH58
GQ480478.1 gg_id:577261 Pseudomonas stutzeri str. MR-5
AJ786789.1 gg_id:108066 Pseudomonas sp. R-20946
AJ786814.1 gg_id:108090 Pseudomonas sp. R-23040
NR_024912.1 gg_id:534702 Pseudomonas cedrina str. CFML 96-198; CIP 105541
AJ550465.1 gg_id:83510 Pseudomonas chlororaphis
AF094723.1 gg_id:53538 Pseudomonas chlororaphis str. ATCC 9446
AF094722.1 gg_id:69974 Pseudomonas chlororaphis str. ATCC 13985
AY839234.1 gg_id:110012 Pseudomonas aurantiaca str. YC4963
GU186113.1 gg_id:585304 Pseudomonas chlororaphis str. IHB B 1352
DQ813320.1 gg_id:170289 Pseudomonas sp. str. IBUN C16
DQ813327.1 gg_id:162642 Pseudomonas sp. str. IBUN S1804
DQ813321.1 gg_id:165579 Pseudomonas sp. str. IBUN S1407
FJ426278.1 gg_id:360625 Pseudomonas chlororaphis str. CB254
DQ525599.1 gg_id:160516 Pseudomonas chlororaphis str. S3f-36
EU158316.1 gg_id:239834 Pseudomonas sp. str. DK2
DQ682655.1 gg_id:164272 Pseudomonas aurantiaca str. NCIB 10068
AY216795.1 gg_id:81078 Pseudomonas chlororaphis 24_4
EF488969.1 gg_id:226426 Pseudomonas fluorescens str. PS7
FJ652607.1 gg_id:511076 Pseudomonas chlororaphis str. 30-84
FJ652609.1 gg_id:541680 Pseudomonas chlororaphis str. BS1393
DQ073039.1 gg_id:128103 Pseudomonas fluorescens str. PCL1606
EF528279.1 gg_id:222094 Pseudomonas fluorescens str. CICCHLJ Q59
AY509898.1 gg_id:103725 Pseudomonas chlororaphis str. DSM 6698
EF620458.1 gg_id:255132 Pseudomonas chlororaphis str. ISSDS-592
AF530070.1 gg_id:72643 Pseudomonas citronellolis str. TERIDB9
EU170480.1 gg_id:250888 Pseudomonas aeruginosa str. L-4
NR_026533.1 gg_id:560055 Pseudomonas citronellolis str. DSM 50332

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| EF620427.1 | 246730 | 80.3 | 244.7 | 746.0 | 79.8 | 12026.0 | 773.5 |
| AB429526.1 | 333725 | 5452.9 | 5792.2 | 4986.0 | 5017.9 | 9623.1 | 9347.6 |
| GQ388971.1 | 543932 | 5606.3 | 5262.5 | 2017.7 | 5937.7 | 15036.2 | 6952.4 |
| FJ544363.1 | 434412 | 1654.5 | 2180.4 | 6229.8 | 3505.0 | 8913.9 | 6883.9 |
| GQ389014.1 | 510529 | 43.4 | 78.5 | 100.4 | 79.2 | 4468.8 | 688.5 |
| FJ793191.1 | 520731 | 96.1 | 257.6 | 1149.9 | 626.9 | 8952.6 | 1226.2 |
| AY835998.1 | 110273 | 3337.7 | 3052.5 | 8725.2 | 5433.8 | 11773.7 | 7399.7 |
| EF199996.1 | 175542 | 5778.5 | 6075.3 | 3805.7 | 5092.9 | 12391.9 | 8170.9 |
| AY651923.1 | 105788 | 6318.0 | 5856.9 | 4641.5 | 5245.9 | 13515.1 | 9148.7 |
| FJ455454.1 | 570727 | 596.3 | 899.4 | 2441.3 | 686.1 | 10745.7 | 4870.4 |
| X99540.1 | 8425 | 2339.8 | 2006.2 | 7499.6 | 4064.5 | 10720.2 | 10791.2 |
| AB021376.1 | 8523 | 627.5 | 2036.7 | 2399.2 | 1492.4 | 6081.7 | 6140.5 |
| EU741649.1 | 311673 | 9575.2 | 9540.2 | 4514.3 | 7320.1 | 11724.6 | 10891.0 |
| GU339285.1 | 536659 | 292.6 | 205.7 | 422.3 | 239.5 | 3917.2 | 1101.1 |
| GQ480478.1 | 577261 | 5078.2 | 5355.5 | 2322.5 | 6565.1 | 8005.0 | 6943.9 |
| AJ786789.1 | 108066 | 1103.3 | 1269.0 | 3646.7 | 2400.3 | 10099.6 | 6526.7 |
| AJ786814.1 | 108090 | 287.1 | 844.1 | 1669.2 | 401.6 | 8312.5 | 12230.9 |
| NR_024912.1 | 534702 | 594.9 | 1048.0 | 1945.8 | 2062.9 | 1169.0 | 8128.2 |
| AJ550465.1 | 83510 | 2330.8 | 2379.4 | 5820.4 | 4852.1 | 2249.2 | 5084.2 |
| AF094723.1 | 53538 | 517.0 | 1083.6 | 1850.7 | 909.5 | 2606.2 | 5884.2 |
| AF094722.1 | 69974 | 722.8 | 1411.5 | 4051.6 | 1643.5 | 3812.3 | 5240.6 |
| AY839234.1 | 110012 | 340.9 | 616.5 | 1983.4 | 699.2 | 1287.0 | 4867.3 |
| GU186113.1 | 585304 | 345.1 | 745.3 | 2245.1 | 823.2 | 2435.2 | 7614.6 |
| DQ813320.1 | 170289 | 257.4 | 760.4 | 3114.6 | 973.0 | 3416.1 | 6119.3 |
| DQ813327.1 | 162642 | 8671.7 | 5937.3 | 8728.6 | 8478.4 | 9296.3 | 10831.5 |
| DQ813321.1 | 165579 | 364.5 | 781.6 | 2485.6 | 1031.0 | 1706.1 | 4883.0 |
| FJ426278.1 | 360625 | 297.2 | 587.3 | 1770.9 | 390.7 | 1662.8 | 3700.8 |
| DQ525599.1 | 160516 | 1872.0 | 2399.0 | 5296.9 | 3540.0 | 4706.8 | 5867.1 |
| EU158316.1 | 239834 | 1300.6 | 1307.9 | 3224.0 | 1345.8 | 3011.0 | 6382.9 |
| DQ682655.1 | 164272 | 343.6 | 690.7 | 1890.9 | 696.5 | 1331.3 | 5004.9 |
| AY216795.1 | 81078 | 245.0 | 433.0 | 387.5 | 208.6 | 598.3 | 1808.0 |
| EF488969.1 | 226426 | 743.8 | 1421.9 | 1481.2 | 1109.8 | 4969.9 | 7581.3 |
| FJ652607.1 | 511076 | 306.4 | 760.9 | 1476.5 | 423.5 | 1517.3 | 5278.4 |
| FJ652609.1 | 541680 | 1967.6 | 2389.0 | 5164.3 | 3509.6 | 5197.5 | 6784.9 |
| DQ073039.1 | 128103 | 773.5 | 1318.7 | 2887.9 | 1405.7 | 3134.5 | 6039.6 |
| EF528279.1 | 222094 | 2309.8 | 2947.0 | 4594.2 | 5497.0 | 6024.9 | 5697.0 |
| AY509898.1 | 103725 | 1898.9 | 2381.9 | 6095.9 | 3310.0 | 6464.6 | 9990.1 |
| EF620458.1 | 255132 | 661.0 | 1100.7 | 2816.6 | 1635.6 | 3108.9 | 5005.9 |
| AF530070.1 | 72643 | 2218.6 | 3187.7 | 6035.1 | 2380.9 | 8687.4 | 6572.4 |
| EU170480.1 | 250888 | 862.4 | 612.4 | 2967.8 | 1782.5 | 4510.9 | 2514.4 |
| NR_026533.1 | 560055 | 648.8 | 749.4 | 1109.5 | 659.8 | 5260.1 | 2521.0 |

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| s__Pseudomonas citronellolis | 3832 |
| s__Pseudomonas citronellolis | 4021 |
| s__Pseudomonas citronellolis | 4045 |
| s__Pseudomonas cuatrocienegasensis | 831 |
| s__Pseudomonas entomophila | 1256 |
| s__Pseudomonas entomophila | 170 |
| s__Pseudomonas entomophila | 2199 |
| s__Pseudomonas fragi | 1044 |
| s__Pseudomonas fragi | 1127 |
| s__Pseudomonas fragi | 1215 |
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| s__Pseudomonas fragi | 1461 |
| s__Pseudomonas fragi | 1513 |
| s__Pseudomonas fragi | 1688 |
| s__Pseudomonas fragi | 1883 |
| s__Pseudomonas fragi | 2061 |
| s__Pseudomonas fragi | 550 |
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| s__Pseudomonas fragi | 683 |
| s__Pseudomonas fragi | 798 |
| s__Pseudomonas fragi | 899 |
| s__Pseudomonas fragi | 972 |
| s__Pseudomonas fuscovaginae | 1816 |
| s__Pseudomonas koreensis | 105 |
| s__Pseudomonas koreensis | 136 |
| s__Pseudomonas koreensis | 1386 |
| s__Pseudomonas koreensis | 813 |
| s__Pseudomonas libanensis | 1129 |
| s__Pseudomonas libanensis | 1238 |
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| s__Pseudomonas libanensis | 2202 |
| s__Pseudomonas libanensis | 2214 |
| s__Pseudomonas libanensis | 37 |
| s__Pseudomonas libanensis | 618 |
| s__Pseudomonas libanensis | 641 |
| s__Pseudomonas libanensis | 649 |
| s__Pseudomonas libanensis | 692 |
| s__Pseudomonas libanensis | 807 |
| s__Pseudomonas lutea | 1989 |
| s__Pseudomonas mandelii | 1420 |

AY762360.1 gg_id:110795 Pseudomonas sp
AB021396.1 gg_id:8427 Pseudomonas citronellolis str. ATCC 13674T
EU834943.1 gg_id:327271 Pseudomonas aeruginosa str. ISTDF1
FJ976049.1 gg_id:462557 Pseudomonas cuatrocienegasensis str. 6jan04
AY907566.1 gg_id:112473 Pseudomonas entomophila str. L48
NC_008027.1 gg_id:160345 Pseudomonas entomophila str. L48
NC_008027.1 gg_id:160342 Pseudomonas entomophila str. L48
AY263480.1 gg_id:82986 Pseudomonas sp. WR7#2
FJ894412.1 gg_id:557030 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B2E; ear pu
AJ288146.1 gg_id:73856 Pseudomonas sp. SK-1-3-1
AY450555.1 gg_id:108448 Pseudomonas putida M
FJ950690.1 gg_id:463744 Pseudomonas psychrophila str. d390
AB041885.1 gg_id:41050 Pseudomonas psychrophila str. E-3
AY195842.1 gg_id:81514 Pseudomonas fragi str. SAPA2
AM421976.1 gg_id:354955 Pseudomonas sp. str. NJ-24
AY581134.1 gg_id:102069 Pseudomonas lundensis b85
AB204715.1 gg_id:138223 Pseudomonas fluorescens str. TM5-2
GU220068.1 gg_id:591142 Pseudomonas fragi str. CS11RH4
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AM409369.1 gg_id:183371 Pseudomonas sp. str. Nj-56
GQ375791.1 gg_id:580324 Pseudomonas putida str. DZQ8
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FJ151351.1 gg_id:338286 Pseudomonas fuscovaginae DAR 77797
EU730928.1 gg_id:354416 Pseudomonas fluorescens str. 166
AF468451.1 gg_id:79193 Pseudomonas koreensis str. Ps 1-2
FJ544330.1 gg_id:438282 Pseudomonas putida str. 813
FJ976084.1 gg_id:399673 Pseudomonas sp. str. 23jan04
EU434451.1 gg_id:274358 Pseudomonas libanensis str. a42
DQ377751.1 gg_id:156328 Pseudomonas grimontii PD 10
AY787208.1 gg_id:110848 Pseudomonas panacis str. CG20106
DQ073449.1 gg_id:131423 Pseudomonas libanensis str. R7
X86626.1 gg_id:8777 Pseudomonas sp str. GR-04
DQ071559.1 gg_id:134222 Pseudomonas libanensis str. R6
AY071916.1 gg_id:49007 Pseudomonas marginalis str. BJW1
DQ073450.1 gg_id:136233 Pseudomonas libanensis str. R8
GU198125.1 gg_id:585243 Pseudomonas fluorescens str. LMG 14675
GU213303.1 gg_id:535039 Pseudomonas sp. str. 4-13
AM396910.1 gg_id:165902 Pseudomonas sp. Nj-3 str. NJ-3
AB021401.1 gg_id:8733 Pseudomonas marginalis str. ATCC 10844T
EU184082.1 gg_id:255345 Pseudomonas lutea str. PSB2
EU048319.1 gg_id:253104 Pseudomonas fluorescens str. CMG3047

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|---|---|---|---|---|---|---|---|
| AY762360.1 | 110795 | 1075.2 | 1087.9 | 2596.0 | 1798.5 | 8719.5 | 2029.3 |
| AB021396.1 | 8427 | 1809.7 | 1361.2 | 5022.8 | 5759.7 | 3750.1 | 5986.8 |
| EU834943.1 | 327271 | 2554.1 | 3425.1 | 1649.8 | 3851.9 | 4323.6 | 3083.4 |
| FJ976049.1 | 462557 | 256.7 | 405.0 | 1291.2 | 747.4 | 2426.1 | 1946.1 |
| AY907566.1 | 112473 | 1223.6 | 1241.9 | 2647.0 | 2076.4 | 8721.2 | 3411.5 |
| NC_008027.1 | 160345 | 6570.9 | 6388.1 | 6427.4 | 6592.5 | 7319.0 | 3795.9 |
| NC_008027.1 | 160342 | 1762.9 | 2114.8 | 3452.6 | 1509.2 | 7145.4 | 5883.9 |
| AY263480.1 | 82986 | 3388.7 | 4303.2 | 3105.8 | 3201.1 | 9332.4 | 9081.6 |
| FJ894412.1 | 557030 | 512.2 | 601.9 | 1089.9 | 371.4 | 3080.3 | 6366.6 |
| AJ288146.1 | 73856 | 5507.5 | 5530.6 | 1684.4 | 1434.0 | 5387.8 | 6368.6 |
| AY450555.1 | 108448 | 241.9 | 446.9 | 751.5 | 189.3 | 3868.5 | 6110.5 |
| FJ950690.1 | 463744 | 7616.4 | 8343.2 | 2924.2 | 7274.9 | 5095.2 | 4729.2 |
| AB041885.1 | 41050 | 2599.5 | 3126.0 | 2305.0 | 1878.8 | 4981.8 | 5793.9 |
| AY195842.1 | 81514 | 390.8 | 719.9 | 989.7 | 217.4 | 4995.5 | 7393.2 |
| AM421976.1 | 354955 | 2653.7 | 3646.6 | 1629.7 | 1229.4 | 3706.0 | 6196.3 |
| AY581134.1 | 102069 | 3202.3 | 3060.6 | 2894.1 | 2847.1 | 8437.3 | 6775.2 |
| AB204715.1 | 138223 | 49.0 | 96.1 | 446.5 | 78.0 | 1602.3 | 3133.0 |
| GU220068.1 | 591142 | 107.0 | 245.5 | 739.1 | 143.8 | 2902.4 | 6087.2 |
| AY342004.1 | 92742 | 757.4 | 1400.6 | 1275.2 | 294.5 | 4326.3 | 9331.9 |
| AM409369.1 | 183371 | 377.2 | 679.5 | 991.7 | 213.5 | 4432.3 | 7233.3 |
| GQ375791.1 | 580324 | 222.8 | 426.6 | 685.1 | 153.1 | 3045.7 | 5494.0 |
| AY450556.1 | 108450 | 408.6 | 695.7 | 1049.3 | 248.2 | 4428.0 | 8729.3 |
| FJ151351.1 | 338286 | 148.3 | 481.2 | 1790.1 | 221.2 | 6853.5 | 5444.8 |
| EU730928.1 | 354416 | 1051.5 | 1536.0 | 2947.5 | 1975.8 | 5891.6 | 6467.8 |
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| EU434451.1 | 274358 | 905.9 | 2016.4 | 2769.6 | 759.6 | 8643.3 | 9077.8 |
| DQ377751.1 | 156328 | 963.0 | 1363.1 | 1496.7 | 1177.8 | 2317.3 | 3261.6 |
| AY787208.1 | 110848 | 4196.9 | 5503.5 | 4613.9 | 4094.0 | 7043.6 | 7658.9 |
| DQ073449.1 | 131423 | 2928.3 | 4235.7 | 5153.1 | 4844.3 | 7254.5 | 10976.6 |
| X86626.1 | 8777 | 292.2 | 618.1 | 905.5 | 281.1 | 995.4 | 4723.3 |
| DQ071559.1 | 134222 | 2660.6 | 4450.9 | 3498.8 | 3818.2 | 8628.6 | 11706.4 |
| AY071916.1 | 49007 | 1707.1 | 3506.4 | 1773.3 | 2722.7 | 5549.1 | 7355.5 |
| DQ073450.1 | 136233 | 2791.9 | 4482.0 | 4102.3 | 3792.8 | 8599.0 | 11320.4 |
| GU198125.1 | 585243 | 339.5 | 670.2 | 1440.5 | 1197.4 | 2978.5 | 5328.3 |
| GU213303.1 | 535039 | 448.2 | 950.9 | 2042.8 | 304.1 | 9606.4 | 10792.6 |
| AM396910.1 | 165902 | 495.7 | 907.2 | 858.6 | 481.9 | 4109.9 | 3570.0 |
| AB021401.1 | 8733 | 163.4 | 351.8 | 768.9 | 180.2 | 562.0 | 3061.1 |
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| EU048319.1 | 253104 | 978.5 | 1161.9 | 2258.5 | 3268.1 | 7129.2 | 9941.3 |

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DQ158873.1 gg_id:138914 Pseudomonas chlororphis str. GP72
EU434578.1 gg_id:264249 Pseudomonas fluorescens str. b101
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EU111733.2 gg_id:535392 Pseudomonas migulae str. CT22
DQ298151.1 gg_id:144530 -dependent and microbial assemblages silkworm midgut clone swm35
FJ665222.1 gg_id:561243 Study Prokarytic Selected Niches Western Ghats India ground swab mangrove forest
AF386081.1 gg_id:58546 Pseudomonas mediterranea str. CFBP 5488
AF386080.1 gg_id:58547 Pseudomonas mediterranea str. CFBP 5447
NC_009439.1 gg_id:223278 Pseudomonas mendocina str. ymp
FJ472860.1 gg_id:545756 Pseudomonas pseudoalcaligenes str. JM8
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GQ110671.1 gg_id:451048 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
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EU863612.1 gg_id:309046 Pseudomonas mendocina str. Lyso H
EU937753.1 gg_id:311713 Pseudomonas sp. str. JG 10 Iti 8
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EU927412.1 gg_id:319271 Pseudomonas mendocina str. 8-40B28
FJ544382.1 gg_id:395641 Pseudomonas pseudoalcaligenes str. sw04
EF175873.1 gg_id:181966 Pseudomonas sp. str. FSB
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AB231158.1 gg_id:145761 Pseudomonas pseudoalcaligenes HS-047
GQ008972.1 gg_id:500693 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
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EU841538.1 gg_id:303688 Pseudomonas mendocina str. 236
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AM184215.1 gg_id:159864 Pseudomonas mosselii str. WAB1873
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AB361588.1 gg_id:267059 Pseudomonas putida str. 152

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| AY303330.1 | 129363 | 272.7 | 892.9 | 2187.2 | 1963.2 | 7196.2 | 7779.5 |
| DQ158873.1 | 138914 | 6736.3 | 6132.5 | 7544.4 | 4971.1 | 7696.9 | 6267.6 |
| EU434578.1 | 264249 | 3749.6 | 4669.1 | 6041.6 | 5257.6 | 10502.5 | 14167.0 |
| AM933501.1 | 321988 | 2860.4 | 3898.8 | 5577.9 | 5006.4 | 9100.5 | 14214.6 |
| EU111739.2 | 547460 | 3699.5 | 4372.5 | 6153.6 | 4943.8 | 9600.0 | 15342.9 |
| GQ144359.1 | 467896 | 1021.7 | 2075.3 | 3087.6 | 2785.2 | 6031.3 | 13011.0 |
| EU111733.2 | 535392 | 588.5 | 1186.8 | 4268.2 | 2675.8 | 7204.2 | 14266.9 |
| DQ298151.1 | 144530 | 1856.1 | 1202.3 | 1157.0 | 1794.0 | 3555.3 | 5033.6 |
| FJ665222.1 | 561243 | 849.9 | 1008.8 | 3334.1 | 1987.9 | 3460.5 | 4143.8 |
| AF386081.1 | 58546 | 74.8 | 156.0 | 633.3 | 180.9 | 312.9 | 1150.3 |
| AF386080.1 | 58547 | 4999.6 | 5239.1 | 4408.7 | 4294.2 | 6349.7 | 7625.0 |
| NC_009439.1 | 223278 | 1888.0 | 1419.6 | 1724.4 | 1956.6 | 7029.0 | 4153.4 |
| FJ472860.1 | 545756 | 114.7 | 206.0 | 444.2 | 167.0 | 8372.1 | 491.3 |
| FJ594992.1 | 569922 | 14407.0 | 14491.2 | 12858.5 | 12956.0 | 19816.0 | 18501.5 |
| AF094734.1 | 99890 | 255.6 | 373.8 | 578.6 | 226.6 | 8733.2 | 2477.2 |
| GQ280045.1 | 510044 | 251.6 | 413.5 | 975.6 | 447.0 | 3070.5 | 2154.1 |
| EF151236.1 | 247968 | 955.0 | 914.3 | 8233.7 | 2452.1 | 5875.5 | 5879.6 |
| EF608169.1 | 540724 | 1271.3 | 447.4 | 558.3 | 694.9 | 6817.7 | 3034.9 |
| GQ094146.1 | 397132 | 582.3 | 786.7 | 795.8 | 905.9 | 1662.5 | 2513.0 |
| GQ110671.1 | 451048 | 5638.0 | 4770.6 | 3706.2 | 6751.4 | 10831.7 | 6447.7 |
| FJ544383.1 | 459179 | 4490.9 | 3788.9 | 6873.9 | 4774.2 | 12807.8 | 4646.6 |
| NC_009439.1 | 223275 | 123.4 | 275.7 | 218.3 | 156.3 | 8350.6 | 4246.3 |
| EU863612.1 | 309046 | 113.6 | 220.8 | 334.8 | 193.2 | 3347.8 | 2601.0 |
| EU937753.1 | 311713 | 307.6 | 614.3 | 1623.5 | 618.5 | 7328.5 | 1553.4 |
| AY880303.1 | 112002 | 57.4 | 103.3 | 340.1 | 91.1 | 4261.6 | 1279.2 |
| EU927412.1 | 319271 | 219.2 | 472.0 | 681.2 | 562.3 | 8841.4 | 4457.5 |
| FJ544382.1 | 395641 | 2825.6 | 5089.9 | 2833.7 | 3341.4 | 15797.4 | 6582.3 |
| EF175873.1 | 181966 | 63.0 | 104.2 | 131.5 | 63.3 | 309.0 | 154.6 |
| GQ015236.1 | 494428 | 6975.0 | 4146.1 | 3747.1 | 6732.5 | 8980.2 | 7541.9 |
| AB231158.1 | 145761 | 166.8 | 194.3 | 203.0 | 182.9 | 1284.3 | 1146.6 |
| GQ008972.1 | 500693 | 807.4 | 729.5 | 1574.7 | 468.8 | 12157.9 | 4559.6 |
| AJ007005.1 | 8544 | 100.6 | 291.0 | 2364.7 | 148.4 | 8236.3 | 5811.2 |
| FJ418771.1 | 367496 | 221.2 | 274.2 | 416.2 | 254.0 | 2609.1 | 970.2 |
| FJ426615.1 | 367244 | 1420.4 | 1109.5 | 2321.0 | 1315.2 | 8245.2 | 6151.2 |
| EU841538.1 | 303688 | 58.8 | 76.7 | 491.9 | 133.1 | 10056.9 | 2752.7 |
| AF326375.1 | 34621 | 135.3 | 484.7 | 764.0 | 450.3 | 3283.9 | 3251.4 |
| AJ006109.1 | 8516 | 8153.7 | 7129.0 | 14329.2 | 7370.1 | 13560.1 | 7612.6 |
| DQ837704.1 | 169290 | 341.0 | 665.7 | 1067.0 | 733.8 | 10973.5 | 4420.4 |
| AM184215.1 | 159864 | 1029.2 | 1643.1 | 3812.0 | 2562.8 | 8139.8 | 6237.0 |
| AF072688.2 | 8603 | 5768.1 | 4576.6 | 6467.1 | 5530.2 | 11714.9 | 6861.7 |
| AB361588.1 | 267059 | 1292.6 | 1692.7 | 3896.4 | 2101.7 | 6518.5 | 5044.0 |

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| s__Pseudomonas mosselii | 1339 |
| s__Pseudomonas mosselii | 1509 |
| s__Pseudomonas mosselii | 2060 |
| s__Pseudomonas mosselii | 2130 |
| s__Pseudomonas mosselii | 603 |
| s__Pseudomonas nitroreducens | 3340 |
| s__Pseudomonas nitroreducens | 3361 |
| s__Pseudomonas nitroreducens | 3437 |
| s__Pseudomonas nitroreducens | 3476 |
| s__Pseudomonas nitroreducens | 3511 |
| s__Pseudomonas nitroreducens | 3566 |
| s__Pseudomonas nitroreducens | 3639 |
| s__Pseudomonas nitroreducens | 3642 |
| s__Pseudomonas nitroreducens | 3671 |
| s__Pseudomonas nitroreducens | 3691 |
| s__Pseudomonas nitroreducens | 3705 |
| s__Pseudomonas nitroreducens | 3728 |
| s__Pseudomonas nitroreducens | 3793 |
| s__Pseudomonas nitroreducens | 3859 |
| s__Pseudomonas nitroreducens | 3911 |
| s__Pseudomonas nitroreducens | 3946 |
| s__Pseudomonas nitroreducens | 3980 |
| s__Pseudomonas nitroreducens | 4092 |
| s__Pseudomonas oleovorans | 1100 |
| s__Pseudomonas oleovorans | 1475 |
| s__Pseudomonas oleovorans | 180 |
| s__Pseudomonas oleovorans | 2243 |
| s__Pseudomonas oleovorans | 506 |
| s__Pseudomonas oryzihabitans | 1031 |
| s__Pseudomonas oryzihabitans | 1464 |
| s__Pseudomonas oryzihabitans | 1612 |
| s__Pseudomonas oryzihabitans | 235 |
| s__Pseudomonas oryzihabitans | 855 |
| s__Pseudomonas pachastrellae | 4081 |
| s__Pseudomonas rhizosphaerae | 2125 |
| s__Pseudomonas rhodesiae | 1139 |
| s__Pseudomonas rhodesiae | 485 |
| s__Pseudomonas rhodesiae | 86 |
| s__Pseudomonas savastanoi | 1222 |
| s__Pseudomonas savastanoi | 1563 |
| s__Pseudomonas savastanoi | 1699 |

AF181576.1 gg_id:29593 Pseudomonas cf. monteilii 9
AY395006.2 gg_id:97328 Pseudomonas sp. NAB2
GU377179.1 gg_id:514413 Pseudomonas putida str. LW
AM911660.1 gg_id:243912 Pseudomonas sp. str. RW5S2
EF178445.1 gg_id:199399 Pseudomonas mosselii str. 2R12
DQ803377.1 gg_id:180892 human fecal clone RL311_aam24h03
AM088473.1 gg_id:142760 Pseudomonas nitroreducens str. IAM 1439
FJ223883.1 gg_id:340099 Pseudomonas stutzeri 3
DQ803314.1 gg_id:188486 human fecal clone RL311_aam23h05
DQ803374.1 gg_id:195179 human fecal clone RL311_aam24g10
DQ803144.1 gg_id:189837 human fecal clone RL311_aam21b01
DQ834357.1 gg_id:165919 Pseudomonas sp. str. FLL9
DQ803243.1 gg_id:194461 human fecal clone RL311_aam22g07
DQ119331.1 gg_id:202772 Pseudomonas nitroreducens str. F16
DQ803331.1 gg_id:187182 human fecal clone RL311_aam24b05
DQ300314.1 gg_id:141244 Pseudomonas sp. str. L19
DQ286428.1 gg_id:144519 Pseudomonas sp. str. L51
DQ803292.1 gg_id:191096 human fecal clone RL311_aam23e10
EU814518.1 gg_id:309860 Pseudomonas sp. str. th16
EU869277.1 gg_id:340362 Pseudomonas sp. str. CR5
DQ803289.1 gg_id:199210 human fecal clone RL311_aam23e07
DQ803345.1 gg_id:182145 human fecal clone RL311_aam24c10
EU874610.1 gg_id:320306 Pseudomonas sp. str. PYD-2
AJ575816.1 gg_id:90761 Pseudomonas psychrotolerans str. C36
FJ217181.1 gg_id:575069 Pseudomonas oryzihabitans str. BBAL-03d
EU047553.1 gg_id:236258 Pseudomonas oleovorans str. TMPSB5
EF028693.1 gg_id:189438 Pseudomonas sp. str. BCL-53
AY623816.1 gg_id:159881 Pseudomonas oleovorans
EU977740.1 gg_id:544679 Pseudomonas oryzihabitans str. 1P03PC
EU977588.1 gg_id:569674 Pseudomonas plecoglossicida str. 1P03MC
AB248284.1 gg_id:150864 Pseudomonas fulva str. 10 (= KMM 3881)
EU977738.1 gg_id:569323 Pseudomonas oryzihabitans str. 1P03PA
EU977587.1 gg_id:553834 Pseudomonas oryzihabitans str. 1P03MB
AB125366.1 gg_id:100555 Pseudomonas pachastrellae str. KMM 330
AY152673.1 gg_id:78571 Pseudomonas rhizosphaerae str. IH5
DQ313384.1 gg_id:193809 Pseudomonas rhodesiae str. PCL1761
AJ830707.1 gg_id:101384 Pseudomonas rhodesiae KCM-R5
AY043360.1 gg_id:66023 Pseudomonas rhodesiae str. KK1
NZ_ACHU02000262.1 gg_id:549099 Pseudomonas syringae pv. tabaci str. ATCC 11528
AM265390.1 gg_id:178656 Pseudomonas savastanoi pv. fraxini str. PVFiF1
NR_024707.1 gg_id:546957 Pseudomonas savastanoi str. ATCC 13522

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|---|---|---|---|---|---|---|---|
| AF181576.1 | 29593 | 1429.7 | 1941.7 | 4707.5 | 3149.6 | 6179.6 | 6538.9 |
| AY395006.2 | 97328 | 14673.6 | 15170.0 | 12144.9 | 11558.6 | 23524.0 | 17589.9 |
| GU377179.1 | 514413 | 1332.2 | 1574.1 | 4120.2 | 2128.9 | 6363.7 | 4074.0 |
| AM911660.1 | 243912 | 658.0 | 592.0 | 894.3 | 610.9 | 1584.3 | 4942.9 |
| EF178445.1 | 199399 | 538.2 | 1186.1 | 778.8 | 301.1 | 3148.1 | 2625.6 |
| DQ803377.1 | 180892 | 5476.6 | 2866.1 | 9512.1 | 4809.7 | 5677.6 | 3472.0 |
| AM088473.1 | 142760 | 134.2 | 285.8 | 355.5 | 131.0 | 1542.9 | 871.2 |
| FJ223883.1 | 340099 | 12079.8 | 12112.5 | 12197.6 | 8988.8 | 13717.0 | 11128.1 |
| DQ803314.1 | 188486 | 1713.2 | 1675.1 | 1536.4 | 2526.7 | 7165.7 | 6068.3 |
| DQ803374.1 | 195179 | 2208.2 | 3300.3 | 1421.4 | 1340.2 | 9679.4 | 6522.4 |
| DQ803144.1 | 189837 | 337.4 | 485.0 | 2433.7 | 681.5 | 13110.8 | 4330.2 |
| DQ834357.1 | 165919 | 9349.1 | 7969.0 | 6056.1 | 6337.3 | 9281.4 | 5965.7 |
| DQ803243.1 | 194461 | 692.2 | 965.7 | 1198.0 | 843.8 | 5939.2 | 1312.9 |
| DQ119331.1 | 202772 | 4513.4 | 3498.8 | 8072.1 | 5692.4 | 15043.8 | 7608.0 |
| DQ803331.1 | 187182 | 1572.5 | 1135.0 | 2610.8 | 1518.3 | 11561.7 | 4067.9 |
| DQ300314.1 | 141244 | 6462.4 | 7480.2 | 7556.6 | 4118.3 | 10677.4 | 6937.8 |
| DQ286428.1 | 144519 | 8275.4 | 5395.5 | 9445.1 | 6411.3 | 9222.5 | 7094.4 |
| DQ803292.1 | 191096 | 4526.4 | 2841.4 | 2549.3 | 5601.3 | 4837.5 | 4590.4 |
| EU814518.1 | 309860 | 208.4 | 862.6 | 2031.6 | 281.6 | 6344.7 | 7399.6 |
| EU869277.1 | 340362 | 1772.5 | 1923.3 | 7211.4 | 2930.4 | 6369.1 | 6658.4 |
| DQ803289.1 | 199210 | 105.0 | 429.9 | 1639.3 | 266.4 | 6504.7 | 5201.0 |
| DQ803345.1 | 182145 | 2732.2 | 2349.2 | 1926.4 | 1045.6 | 11962.7 | 3227.9 |
| EU874610.1 | 320306 | 10263.7 | 5141.5 | 10246.9 | 7954.3 | 13717.2 | 7450.8 |
| AJ575816.1 | 90761 | 129.3 | 456.4 | 1141.3 | 368.9 | 4870.0 | 2958.8 |
| FJ217181.1 | 575069 | 397.8 | 545.7 | 1965.9 | 862.2 | 3686.5 | 2729.9 |
| EU047553.1 | 236258 | 5557.0 | 5722.0 | 1466.6 | 5701.1 | 5080.0 | 4474.3 |
| EF028693.1 | 189438 | 609.9 | 844.1 | 2860.1 | 1439.4 | 5965.7 | 3787.4 |
| AY623816.1 | 159881 | 79.7 | 181.9 | 580.4 | 181.0 | 405.4 | 1412.5 |
| EU977740.1 | 544679 | 1439.3 | 1996.4 | 2308.4 | 1595.9 | 11847.9 | 10011.6 |
| EU977588.1 | 569674 | 766.9 | 1686.6 | 1641.6 | 512.8 | 9821.9 | 7828.1 |
| AB248284.1 | 150864 | 367.3 | 819.2 | 1951.5 | 480.3 | 9040.5 | 6246.5 |
| EU977738.1 | 569323 | 1207.4 | 1813.4 | 1650.6 | 681.3 | 10375.8 | 8139.3 |
| EU977587.1 | 553834 | 1222.4 | 1856.2 | 1580.9 | 687.3 | 11665.2 | 8994.4 |
| AB125366.1 | 100555 | 2965.0 | 2395.1 | 1965.9 | 4422.2 | 4780.5 | 5274.9 |
| AY152673.1 | 78571 | 4024.4 | 5856.2 | 9630.0 | 5823.4 | 9851.5 | 8004.7 |
| DQ313384.1 | 193809 | 4519.4 | 6126.0 | 2478.9 | 5282.6 | 8827.4 | 8807.4 |
| AJ830707.1 | 101384 | 1111.8 | 1104.7 | 2151.6 | 2350.1 | 2226.5 | 7516.8 |
| AY043360.1 | 66023 | 1492.6 | 1738.3 | 3009.0 | 4450.2 | 6300.8 | 13452.6 |
| NZ_ACHU02000262.1 | 549099 | 874.0 | 1372.4 | 2701.2 | 2201.5 | 3683.7 | 6204.2 |
| AM265390.1 | 178656 | 1100.8 | 1569.6 | 3286.0 | 2801.5 | 6161.8 | 9984.5 |
| NR_024707.1 | 546957 | 1030.3 | 1496.9 | 3521.7 | 2803.4 | 6067.2 | 9004.0 |

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| s__Pseudomonas savastanoi | 1954 |
| s__Pseudomonas savastanoi | 2223 |
| s__Pseudomonas savastanoi | 2268 |
| s__Pseudomonas savastanoi | 757 |
| s__Pseudomonas stutzeri | 1010 |
| s__Pseudomonas stutzeri | 1090 |
| s__Pseudomonas stutzeri | 1162 |
| s__Pseudomonas stutzeri | 1311 |
| s__Pseudomonas stutzeri | 1350 |
| s__Pseudomonas stutzeri | 1368 |
| s__Pseudomonas stutzeri | 142 |
| s__Pseudomonas stutzeri | 1565 |
| s__Pseudomonas stutzeri | 1675 |
| s__Pseudomonas stutzeri | 1955 |
| s__Pseudomonas stutzeri | 2092 |
| s__Pseudomonas stutzeri | 2128 |
| s__Pseudomonas stutzeri | 2133 |
| s__Pseudomonas stutzeri | 2196 |
| s__Pseudomonas stutzeri | 2216 |
| s__Pseudomonas stutzeri | 2246 |
| s__Pseudomonas stutzeri | 2281 |
| s__Pseudomonas stutzeri | 301 |
| s__Pseudomonas stutzeri | 350 |
| s__Pseudomonas stutzeri | 389 |
| s__Pseudomonas stutzeri | 4029 |
| s__Pseudomonas stutzeri | 497 |
| s__Pseudomonas stutzeri | 57772 |
| s__Pseudomonas stutzeri | 670 |
| s__Pseudomonas stutzeri | 926 |
| s__Pseudomonas stutzeri | 939 |
| s__Pseudomonas stutzeri | 940 |
| s__Pseudomonas syringae group genomosp. 3 | 1246 |
| s__Pseudomonas syringae group genomosp. 3 | 1409 |
| s__Pseudomonas syringae group genomosp. 3 | 2187 |
| s__Pseudomonas syringae group genomosp. 3 | 322 |
| s__Pseudomonas syringae group genomosp. 3 | 849 |
| s__Pseudomonas syringae pv. coryli | 1274 |
| s__Pseudomonas syringae pv. coryli | 1570 |
| s__Pseudomonas syringae pv. coryli | 265 |
| s__Pseudomonas umsongensis | 12 |
| s__Pseudomonas umsongensis | 1384 |

AB021382.1 gg_id:8658 Pseudomonas meliae str. MAFF 301463T
NZ_ACXT01000186.1 gg_id:523171 Pseudomonas syringae pv. aesculi str. 2250
AM265391.1 gg_id:179161 Pseudomonas savastanoi pv. nerii str. ITM313
AY574914.1 gg_id:107034 Pseudomonas syringae str. RM29.1a
EF382724.1 gg_id:214723 Pseudomonas str. BSi20450
AJ288148.1 gg_id:53166 Pseudomonas stutzeri Makran
FJ671729.1 gg_id:526385 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
AY647159.1 gg_id:100165 Pseudomonas stutzeri str. ZWLR2-1; CCTCC (China Center Type Collection) M203096
DQ289072.1 gg_id:144984 Pseudomonas stutzeri Fe10
AM236243.1 gg_id:151390 Pseudomonas sp. AM10
FJ345693.1 gg_id:315478 Pseudomonas stutzeri str. LC2-8
AJ297767.1 gg_id:76785 Pseudomonas stutzeri HY-105
GQ260077.1 gg_id:510001 Pseudomonas stutzeri str. ICIRC103
AM111052.1 gg_id:140930 Pseudomonas sp. str. 7197
AF152596.1 gg_id:8485 Pseudomonas stutzeri str. 18
AJ312171.1 gg_id:60922 Pseudomonas stutzeri str. 24a50
AY486384.1 gg_id:105218 Pseudomonas stutzeri str. AU4823
FJ974059.1 gg_id:431541 Pseudomonas stutzeri str. JMC01
CU915125.1 gg_id:448893 and dynamics adapted microbiota during degradation Tunisian zarzatine enriched se
AM236237.1 gg_id:152595 Pseudomonas sp. AM4
AF284764.1 gg_id:41253 Pseudomonas stutzeri str. phen8
AB176955.1 gg_id:104939 Pseudomonas stutzeri str. KMM 235
GQ280051.1 gg_id:585761 Pseudomonas stutzeri str. BJ-41
AM236234.1 gg_id:151046 Methylobacterium extorquens AM1
EU327995.1 gg_id:243015 Pseudomonas stutzeri str. DA-1
EU771075.1 gg_id:338443 Pseudomonas stutzeri str. F22
AM236235.1 gg_id:154066 Pseudomonas sp. AM2
AF237677.1 gg_id:38888 Pseudomonas stutzeri str. M14C
U58661.1 gg_id:8460 Pseudomonas stutzeri str. JM300
AM110955.1 gg_id:140946 Pseudomonas sp. str. 1014
AJ270452.1 gg_id:18824 Pseudomonas stutzeri str. 11C2 marine sediment Schillig
AB001445.1 gg_id:50962 Pseudomonas syringae pv. morsprunorum str. MAFF 302280 pv.
AY574913.1 gg_id:106878 Pseudomonas syringae str. PNA29.1a
AB001441.1 gg_id:20629 Pseudomonas syringae pv. broussonetiae str. KOZ 8101 pv.
AB001449.1 gg_id:52123 Pseudomonas syringae pv. tagetis str. MAFF 302271 pv.
NC_004578.1 gg_id:82411 Pseudomonas syringae pv. tomato str. DC3000
AJ889841.1 gg_id:113295 Pseudomonas syringae pv. coryli str. NCPPB 4273
AM399035.1 gg_id:171964 Pseudomonas syringae pv. coryli str. ISPaVe 598
AM399036.1 gg_id:163475 Pseudomonas pv. syringae str. NCPPB 3869
AF506040.1 gg_id:66299 Pseudomonas fluorescens LCSAOTU1
AF068259.1 gg_id:8625 Pseudomonas jessenii str. CIP 105274

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|---|---|---|---|---|---|---|---|
| AB021382.1 | 8658 | 913.4 | 1230.7 | 2780.2 | 1571.2 | 4790.8 | 8848.6 |
| NZ_ACXT01000186.1 | 523171 | 5376.0 | 5398.9 | 5703.8 | 7730.7 | 7953.9 | 12797.9 |
| AM265391.1 | 179161 | 6497.2 | 6804.1 | 5666.5 | 8912.5 | 9736.2 | 11773.5 |
| AY574914.1 | 107034 | 396.2 | 1021.1 | 927.1 | 273.4 | 2947.9 | 3610.5 |
| EF382724.1 | 214723 | 6316.8 | 6871.7 | 2512.3 | 5779.9 | 7502.1 | 4340.9 |
| AJ288148.1 | 53166 | 6844.9 | 5962.6 | 4682.3 | 4544.5 | 10532.0 | 5838.3 |
| FJ671729.1 | 526385 | 3359.9 | 3161.9 | 2802.1 | 3433.1 | 8975.0 | 4829.9 |
| AY647159.1 | 100165 | 10538.7 | 6789.1 | 5382.7 | 11347.6 | 11435.8 | 10719.1 |
| DQ289072.1 | 144984 | 1952.9 | 1500.7 | 1378.3 | 2087.7 | 5697.1 | 3787.0 |
| AM236243.1 | 151390 | 60.1 | 82.4 | 70.1 | 163.4 | 220.3 | 168.4 |
| FJ345693.1 | 315478 | 6664.8 | 7256.7 | 7246.8 | 5795.5 | 14629.6 | 10970.2 |
| AJ297767.1 | 76785 | 3432.2 | 4206.1 | 4365.0 | 2667.1 | 4324.2 | 6072.4 |
| GQ260077.1 | 510001 | 1778.1 | 1523.4 | 1611.9 | 1064.1 | 8757.2 | 3396.9 |
| AM111052.1 | 140930 | 54.6 | 87.0 | 109.2 | 88.6 | 189.7 | 731.1 |
| AF152596.1 | 8485 | 15175.2 | 14895.5 | 13463.2 | 12407.7 | 18359.9 | 15284.8 |
| AJ312171.1 | 60922 | 2525.6 | 1813.2 | 3020.0 | 2171.1 | 8443.8 | 5066.0 |
| AY486384.1 | 105218 | 10722.4 | 10259.4 | 12924.2 | 9606.1 | 15189.2 | 13937.6 |
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| AM236237.1 | 152595 | 735.1 | 448.8 | 1196.8 | 309.3 | 2664.8 | 2348.9 |
| AF284764.1 | 41253 | 4641.6 | 4591.7 | 4734.2 | 3848.1 | 13115.7 | 9070.1 |
| AB176955.1 | 104939 | 1760.6 | 1655.5 | 1820.2 | 1075.5 | 7156.9 | 4812.4 |
| GQ280051.1 | 585761 | 241.1 | 521.1 | 1372.9 | 263.6 | 5382.3 | 2979.0 |
| AM236234.1 | 151046 | 656.4 | 1077.8 | 801.6 | 924.1 | 2851.1 | 5761.4 |
| EU327995.1 | 243015 | 2289.3 | 1707.9 | 575.6 | 508.7 | 6225.3 | 5805.0 |
| EU771075.1 | 338443 | 28.0 | 64.2 | 311.4 | 85.1 | 1915.0 | 398.0 |
| AM236235.1 | 154066 | 246.5 | 235.9 | 150.3 | 249.5 | 2698.7 | 1241.7 |
| AF237677.1 | 38888 | 2029.6 | 1876.5 | 1803.4 | 2941.4 | 4185.2 | 3655.5 |
| U58661.1 | 8460 | 4285.0 | 3741.6 | 1001.0 | 4777.1 | 8611.5 | 5796.4 |
| AM110955.1 | 140946 | 272.5 | 577.9 | 646.8 | 307.7 | 2702.4 | 1232.1 |
| AJ270452.1 | 18824 | 326.5 | 318.1 | 571.5 | 345.0 | 6025.6 | 2413.6 |
| AB001445.1 | 50962 | 219.1 | 490.6 | 1275.9 | 370.0 | 368.2 | 2146.7 |
| AY574913.1 | 106878 | 1089.9 | 1643.4 | 3046.5 | 2343.2 | 4394.5 | 8404.5 |
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| AB001449.1 | 52123 | 1173.7 | 1731.4 | 3267.9 | 2371.8 | 4312.1 | 8738.8 |
| NC_004578.1 | 82411 | 874.2 | 1294.2 | 1806.8 | 1736.9 | 4568.4 | 5389.0 |
| AJ889841.1 | 113295 | 922.2 | 1286.4 | 2656.7 | 1573.5 | 4767.3 | 8376.9 |
| AM399035.1 | 171964 | 1081.0 | 1521.8 | 3390.2 | 2831.5 | 6754.3 | 10136.0 |
| AM399036.1 | 163475 | 1048.6 | 1623.8 | 2757.6 | 1829.6 | 7262.9 | 10287.1 |
| AF506040.1 | 66299 | 2213.4 | 618.0 | 1031.7 | 1594.1 | 1683.6 | 3897.6 |
| AF068259.1 | 8625 | 4522.8 | 3570.0 | 5006.8 | 5314.3 | 7321.4 | 12526.8 |

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EU545412.1 gg_id:259831 Pseudomonas putida str. P13
EU627168.1 gg_id:279231 Pseudomonas putida str. NH.50
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AY081814.1 gg_id:68487 Pseudomonas veronii str. CA-4
AF268029.1 gg_id:22349 Pseudomonas grimontii str. CFML 97-514T
DQ178235.1 gg_id:139966 Pseudomonas fluorescens str. PC38
AY512620.1 gg_id:102881 Pseudomonas veronii str. A1YC2-5
AY512621.1 gg_id:103030 Pseudomonas veronii str. A1YdBTEX2-5
EU538127.1 gg_id:281863 profile human microbiota antecubital fossa (inner elbow) skin clone nbt82e01
AY512617.1 gg_id:107765 Pseudomonas veronii str. A1X/3A
FM213379.2 gg_id:306680 Pseudomonas meridiana str. KJPB15
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AB021398.1 gg_id:8638 Pseudomonas cichorii str. ATCC 10857T

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| GU185860.1 | 582087 | 203.0 | 506.0 | 1206.1 | 345.8 | 4267.0 | 3634.0 |
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| EU434532.1 | 269306 | 788.0 | 1352.7 | 3912.0 | 2206.6 | 6673.8 | 10514.3 |
| AY512614.1 | 107323 | 4009.5 | 4604.9 | 5678.3 | 2100.9 | 7015.2 | 9383.8 |
| EU545412.1 | 259831 | 1336.5 | 870.2 | 2377.0 | 1536.3 | 5531.3 | 5311.3 |
| EU627168.1 | 279231 | 2031.8 | 2561.6 | 1815.2 | 2081.8 | 8426.3 | 5312.8 |
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| DQ095891.1 | 128393 | 171.0 | 371.2 | 742.3 | 235.0 | 4648.8 | 3980.6 |
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| GU391518.1 | 539900 | 3104.7 | 2231.9 | 2731.6 | 2620.1 | 6681.0 | 13675.6 |
| FM955889.1 | 552742 | 1112.8 | 1577.7 | 2318.0 | 3911.4 | 12107.0 | 9096.7 |
| AB266613.1 | 165395 | 105.2 | 235.5 | 386.0 | 109.4 | 1855.7 | 1385.2 |
| GU191930.1 | 588031 | 585.5 | 857.0 | 1884.0 | 1166.5 | 6340.0 | 6370.3 |
| AF191224.1 | 72336 | 4456.0 | 4464.8 | 1594.3 | 5189.3 | 12471.5 | 9975.5 |
| AY050495.1 | 32635 | 257.4 | 605.6 | 1996.4 | 603.5 | 6353.0 | 4969.8 |
| DQ981460.1 | 205168 | 80.8 | 235.9 | 1016.2 | 89.8 | 3685.2 | 9208.8 |
| AB051693.1 | 52556 | 1536.3 | 1967.8 | 3386.7 | 3100.3 | 5069.4 | 11912.7 |
| AB330416.1 | 246575 | 2576.2 | 1453.2 | 2468.6 | 3540.0 | 5304.4 | 8284.1 |
| FJ426279.1 | 369265 | 1800.2 | 1756.2 | 3287.1 | 3900.0 | 3848.0 | 10918.4 |
| AB038136.1 | 47594 | 1370.6 | 1019.0 | 2173.1 | 1156.9 | 5553.5 | 5417.7 |
| DQ525597.1 | 159861 | 2719.5 | 3713.0 | 5093.0 | 4668.7 | 8252.1 | 11849.2 |
| DQ178231.1 | 140491 | 2345.1 | 3231.1 | 3893.7 | 3039.8 | 6981.2 | 10569.3 |
| AY512623.1 | 103318 | 4259.2 | 4233.1 | 3997.6 | 6937.2 | 10283.9 | 12955.5 |
| AY748440.1 | 99904 | 5940.7 | 2903.5 | 9311.6 | 8249.8 | 5118.2 | 8811.1 |
| AF539745.1 | 59301 | 2482.2 | 3494.3 | 5151.3 | 4964.7 | 8769.1 | 11347.4 |
| AM933507.1 | 334191 | 4362.5 | 4707.1 | 7419.4 | 5596.6 | 12090.0 | 17285.0 |
| DQ392980.1 | 153042 | 10382.7 | 8852.0 | 7333.8 | 9658.2 | 12601.3 | 10325.5 |
| AY081814.1 | 68487 | 1613.4 | 2271.3 | 3313.9 | 3074.8 | 6545.2 | 10545.1 |
| AF268029.1 | 22349 | 4506.7 | 4932.3 | 4429.4 | 5302.9 | 10272.2 | 11180.0 |
| DQ178235.1 | 139966 | 9519.0 | 9625.2 | 5407.7 | 9303.7 | 13627.0 | 15900.6 |
| AY512620.1 | 102881 | 1755.7 | 2710.7 | 4441.3 | 3000.2 | 8834.7 | 11270.8 |
| AY512621.1 | 103030 | 555.1 | 1331.1 | 2114.3 | 2499.8 | 7053.0 | 10844.8 |
| EU538127.1 | 281863 | 3341.7 | 2330.4 | 4476.3 | 3889.3 | 6518.1 | 9373.2 |
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| FM213379.2 | 306680 | 4264.0 | 5532.1 | 6848.6 | 5480.6 | 9541.7 | 12265.2 |
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| AB494444.1 | 543515 | 1330.4 | 2123.9 | 3178.9 | 2384.0 | 4868.1 | 8540.1 |
| AF364098.1 | 59382 | 1987.8 | 2892.7 | 4691.7 | 3884.9 | 8921.3 | 12376.5 |
| AB506066.1 | 576116 | 81.9 | 205.6 | 550.9 | 128.7 | 85.9 | 451.1 |
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| s__unclassified | 1086 |

EF101976.1 gg_id:190919 Pseudomonas cichorii str. IP1-05
AB512620.1 gg_id:550669 Pseudomonas sp. str. StFLB155
AY277555.1 gg_id:89393 Pseudomonas sp. str. AGP3-7
EU539385.1 gg_id:283924 profile human microbiota antecubital fossa (inner elbow) skin clone nbt238a10
EU536618.1 gg_id:285719 profile human microbiota antecubital fossa (inner elbow) skin clone nbt63h08
EU538392.1 gg_id:284751 profile human microbiota antecubital fossa (inner elbow) skin clone nbt88e05
AB088844.1 gg_id:79576 Pseudomonas sp. str. K23
EF672050.1 gg_id:253349 Burkholderia cepacia str. M45
EU536489.1 gg_id:280173 profile human microbiota antecubital fossa (inner elbow) skin clone nbt214f09
EU538918.1 gg_id:286009 profile human microbiota antecubital fossa (inner elbow) skin clone nbt95b08
EU535774.1 gg_id:286476 profile human microbiota antecubital fossa (inner elbow) skin clone nbt10f05
EU539846.1 gg_id:280184 profile human microbiota antecubital fossa (inner elbow) skin clone nbt106c10
EU538445.1 gg_id:282737 profile human microbiota antecubital fossa (inner elbow) skin clone nbt229g12
EF154273.1 gg_id:178880 Pseudomonas syringae str. 33
EU535280.1 gg_id:280196 profile human microbiota antecubital fossa (inner elbow) skin clone nbt01b07
AB547166.1 gg_id:515561 Pseudomonas sp. str. DSP-S3
FJ892984.1 gg_id:548837 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota HM2; ear p
EU877075.1 gg_id:341197 Pseudomonas putida str. EC3_2001
EU540274.1 gg_id:281449 profile human microbiota antecubital fossa (inner elbow) skin clone nbt113e10
AJ846274.1 gg_id:106541 Pseudomonas sp. HHS8
EF471903.1 gg_id:217410 Pseudomonas sp. str. GW28-5
AF320994.1 gg_id:33806 Pseudomonas tolaasii str. NZ027
Z76669.1 gg_id:8639 Pseudomonas syringae str. LMG 1247t1T (; pathovar reference strain)
EU540055.1 gg_id:281519 profile human microbiota antecubital fossa (inner elbow) skin clone nbt112e11
AY538263.1 gg_id:100141 Pseudomonas fluorescens str. PC17
AB108691.1 gg_id:83881 Pseudomonas putida str. AN2
EU538374.1 gg_id:280440 profile human microbiota antecubital fossa (inner elbow) skin clone nbt88b03
FJ893864.1 gg_id:554161 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B1E; ear pu
EF565945.1 gg_id:227761 Pseudomonas sp. str. 1043
AF094726.1 gg_id:71021 Pseudomonas fluorescens str. ATCC 17386
EU540294.1 gg_id:282548 profile human microbiota antecubital fossa (inner elbow) skin clone nbt114c12
FJ893943.1 gg_id:549107 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B1E; ear pu
AJ936933.1 gg_id:175024 Pseudomonas simiae
FJ894257.1 gg_id:543206 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B2E; ear pu
AY303316.1 gg_id:129966 Pseudomonas sp. str. ps6-35
EU930815.1 gg_id:307397 Pseudomonas putida str. PC
EU111704.2 gg_id:509199 Pseudomonas poae str. T23
AF313466.1 gg_id:35880 Pseudomonas veronii
EU538996.1 gg_id:284817 profile human microbiota antecubital fossa (inner elbow) skin clone nbt98h04
AJ295374.1 gg_id:19794 rape rhizosphere cse074
FJ788425.1 gg_id:537584 Pseudomonas putida str. Rs-198

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| EF101976.1 | 190919 | 293.6 | 707.8 | 2993.4 | 1268.0 | 743.6 | 2844.8 |
| AB512620.1 | 550669 | 152.1 | 365.7 | 803.0 | 215.4 | 7070.8 | 5305.9 |
| AY277555.1 | 89393 | 60.0 | 106.4 | 109.6 | 127.0 | 201.1 | 1317.3 |
| EU539385.1 | 283924 | 1481.4 | 1763.6 | 2365.3 | 1266.9 | 3843.9 | 8866.2 |
| EU536618.1 | 285719 | 451.8 | 860.3 | 1376.1 | 584.5 | 1235.1 | 6224.0 |
| EU538392.1 | 284751 | 10908.8 | 11745.4 | 13274.2 | 8696.9 | 13789.6 | 14716.5 |
| AB088844.1 | 79576 | 1524.5 | 2032.9 | 2007.5 | 1560.7 | 9449.0 | 8360.8 |
| EF672050.1 | 253349 | 1776.7 | 2399.7 | 3566.7 | 4004.7 | 12026.1 | 9329.2 |
| EU536489.1 | 280173 | 518.2 | 1350.7 | 1169.8 | 974.1 | 4071.2 | 10884.6 |
| EU538918.1 | 286009 | 1998.0 | 2163.5 | 3231.6 | 2407.4 | 5192.3 | 7214.5 |
| EU535774.1 | 286476 | 2412.9 | 3922.5 | 1504.8 | 1503.2 | 2421.9 | 4948.4 |
| EU539846.1 | 280184 | 6263.3 | 7543.1 | 6410.6 | 5688.8 | 9530.9 | 14046.8 |
| EU538445.1 | 282737 | 264.7 | 826.1 | 2225.5 | 368.6 | 1377.9 | 6669.0 |
| EF154273.1 | 178880 | 7287.3 | 7322.8 | 6456.8 | 7708.3 | 9415.6 | 9617.6 |
| EU535280.1 | 280196 | 876.4 | 1538.9 | 1995.6 | 525.7 | 6718.6 | 11591.3 |
| AB547166.1 | 515561 | 537.6 | 1202.0 | 2078.2 | 1274.2 | 4717.8 | 11333.1 |
| FJ892984.1 | 548837 | 7632.9 | 8869.8 | 8326.6 | 7368.0 | 10995.4 | 15877.6 |
| EU877075.1 | 341197 | 652.0 | 954.5 | 2647.6 | 1925.9 | 4138.7 | 4458.8 |
| EU540274.1 | 281449 | 5051.1 | 8609.6 | 4665.1 | 7401.7 | 13036.7 | 13291.7 |
| AJ846274.1 | 106541 | 4791.0 | 3656.9 | 4087.8 | 3820.4 | 5876.9 | 10039.2 |
| EF471903.1 | 217410 | 2513.7 | 2485.2 | 3348.3 | 3742.4 | 1702.7 | 2216.1 |
| AF320994.1 | 33806 | 1888.3 | 1495.4 | 1680.5 | 1240.6 | 1411.1 | 3258.5 |
| Z76669.1 | 8639 | 963.3 | 1547.5 | 2406.3 | 1855.8 | 5201.0 | 7948.8 |
| EU540055.1 | 281519 | 1066.9 | 3280.0 | 1187.4 | 803.2 | 7053.3 | 7063.4 |
| AY538263.1 | 100141 | 3350.5 | 4308.8 | 3837.7 | 4936.5 | 8129.9 | 10114.0 |
| AB108691.1 | 83881 | 455.1 | 808.0 | 3096.4 | 2405.9 | 3656.3 | 2960.9 |
| EU538374.1 | 280440 | 4594.1 | 5068.1 | 5178.3 | 5074.6 | 8433.8 | 12051.3 |
| FJ893864.1 | 554161 | 3568.9 | 4480.8 | 5152.5 | 3802.4 | 8026.9 | 10939.3 |
| EF565945.1 | 227761 | 3906.8 | 3457.7 | 2234.6 | 3548.7 | 3694.0 | 3514.0 |
| AF094726.1 | 71021 | 1022.5 | 1256.7 | 2543.4 | 3715.8 | 7868.8 | 8831.7 |
| EU540294.1 | 282548 | 296.2 | 776.7 | 1789.4 | 420.2 | 11374.9 | 9913.9 |
| FJ893943.1 | 549107 | 2564.9 | 3743.4 | 5550.2 | 2530.8 | 5973.0 | 11577.0 |
| AJ936933.1 | 175024 | 495.2 | 790.0 | 1289.6 | 425.1 | 2802.4 | 7303.0 |
| FJ894257.1 | 543206 | 9997.9 | 7376.8 | 9107.8 | 11989.9 | 10253.7 | 13641.6 |
| AY303316.1 | 129966 | 8906.9 | 9961.1 | 6306.8 | 9245.9 | 9732.8 | 8986.9 |
| EU930815.1 | 307397 | 1829.2 | 2833.6 | 4084.4 | 3810.2 | 7144.4 | 7212.6 |
| EU111704.2 | 509199 | 55.6 | 195.2 | 645.0 | 169.6 | 615.2 | 3491.0 |
| AF313466.1 | 35880 | 3687.6 | 4675.1 | 5694.0 | 4626.3 | 9401.5 | 12909.1 |
| EU538996.1 | 284817 | 1647.7 | 1684.4 | 3505.7 | 4926.4 | 2083.1 | 7329.7 |
| AJ295374.1 | 19794 | 58.3 | 142.7 | 655.6 | 524.3 | 416.8 | 4034.7 |
| FJ788425.1 | 537584 | 3195.7 | 4035.7 | 5672.9 | 4885.3 | 12092.2 | 10517.5 |

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| s__unclassified | 118 |

EU586045.1 gg_id:263481 Pseudomonas thivervalensis str. REG53
AF411855.1 gg_id:27138 Pseudomonas sp. str. 5B
FJ895023.1 gg_id:535208 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota BME; ear p
AM111013.1 gg_id:140933 Pseudomonas sp. str. 7001
FJ894165.1 gg_id:567845 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B1E; ear pı
FJ893919.1 gg_id:535538 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B1E; ear pı
EU536155.1 gg_id:282438 profile human microbiota antecubital fossa (inner elbow) skin clone nbt12d05
EU539504.1 gg_id:281649 profile human microbiota antecubital fossa (inner elbow) skin clone nbt104d03
FJ893323.1 gg_id:548944 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota WT1; ear p
EU537276.1 gg_id:280469 profile human microbiota antecubital fossa (inner elbow) skin clone nbt72c07
EU537576.1 gg_id:287001 profile human microbiota antecubital fossa (inner elbow) skin clone nbt74d05
AJ846283.1 gg_id:102559 Pseudomonas sp. HHS18
U70977.1 gg_id:8596 Pseudomonas putida str. MnB1
EU539409.1 gg_id:286623 profile human microbiota antecubital fossa (inner elbow) skin clone nbt238d04
FJ430676.1 gg_id:359401 Pseudomonas putida str. IMBG 294
FJ418773.1 gg_id:366528 Pseudomonas syringae pv. tomato str. 3
EU540208.1 gg_id:281422 profile human microbiota antecubital fossa (inner elbow) skin clone nbt247c03
DQ026520.1 gg_id:130002 Pseudomonas putida str. VH26042005
EU539855.1 gg_id:280330 profile human microbiota antecubital fossa (inner elbow) skin clone nbt106e11
EU540622.1 gg_id:281237 profile human microbiota antecubital fossa (inner elbow) skin clone nbt120h05
DQ256083.1 gg_id:143611 Pseudomonas fluorescens str. sp-f
AB294558.1 gg_id:204838 Pseudomonas putida str. NCB0308-456
FJ892909.1 gg_id:538158 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota HM1; ear p
DQ289076.1 gg_id:144195 Bacillus subtilis FM21
FJ893397.1 gg_id:563933 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota WT1; ear p
EU535682.1 gg_id:281049 profile human microbiota antecubital fossa (inner elbow) skin clone nbt09e10
EU539232.1 gg_id:286562 profile human microbiota antecubital fossa (inner elbow) skin clone nbt101f11
AJ271219.1 gg_id:72969 Pseudomonas putida str. P1
AY303321.1 gg_id:131310 Pseudomonas sp. str. ps6-49
EF016112.1 gg_id:195370 Pseudomonas sp. str. BSLY
AF374472.1 gg_id:67535 Pseudomonas costantinii str. CFBP 5705; HAMBI 2444
EU538183.1 gg_id:283248 profile human microbiota antecubital fossa (inner elbow) skin clone nbt81g06
Z76655.1 gg_id:8568 Pseudomonas asplenii str. LMG 2137T ()
FJ894960.1 gg_id:535843 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota BME; ear p
EU169189.1 gg_id:237380 Pseudomonas tolaasii str. B34
DQ318867.1 gg_id:152043 Pseudomonas syringae str. 6
FJ405884.1 gg_id:363503 Pseudomonas putida str. YJF1-21
EU538954.1 gg_id:283838 profile human microbiota antecubital fossa (inner elbow) skin clone nbt95h09
EU540146.1 gg_id:285849 profile human microbiota antecubital fossa (inner elbow) skin clone nbt246b03
EU537169.1 gg_id:285856 profile human microbiota antecubital fossa (inner elbow) skin clone nbt67g03
EU539367.1 gg_id:286796 profile human microbiota antecubital fossa (inner elbow) skin clone nbt237f01

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|---|---|---|---|---|---|---|---|
| EU586045.1 | 263481 | 70.2 | 159.6 | 911.9 | 564.5 | 339.0 | 1942.4 |
| AF411855.1 | 27138 | 5767.2 | 6521.3 | 8090.0 | 8211.2 | 11451.7 | 7797.0 |
| FJ895023.1 | 535208 | 4806.0 | 5668.8 | 5238.4 | 4289.7 | 8589.1 | 7348.3 |
| AM111013.1 | 140933 | 5234.3 | 6855.8 | 6144.5 | 6590.1 | 11390.1 | 7770.6 |
| FJ894165.1 | 567845 | 18834.0 | 18517.5 | 15034.2 | 15295.2 | 18513.8 | 18404.9 |
| FJ893919.1 | 535538 | 10027.5 | 8124.3 | 5561.1 | 10141.5 | 10308.7 | 14461.3 |
| EU536155.1 | 282438 | 767.0 | 1290.5 | 1893.6 | 324.7 | 6386.7 | 11460.1 |
| EU539504.1 | 281649 | 298.7 | 926.0 | 1204.3 | 435.8 | 3010.9 | 8521.6 |
| FJ893323.1 | 548944 | 15205.1 | 12119.8 | 5761.2 | 9209.9 | 13375.4 | 11818.7 |
| EU537276.1 | 280469 | 21993.3 | 16311.9 | 14316.0 | 13087.8 | 20351.8 | 19050.4 |
| EU537576.1 | 287001 | 1466.0 | 1569.4 | 1379.6 | 3418.5 | 1285.0 | 1739.1 |
| AJ846283.1 | 102559 | 4061.6 | 2773.8 | 2118.3 | 4517.5 | 10221.2 | 4058.7 |
| U70977.1 | 8596 | 2700.0 | 3368.6 | 4117.2 | 3668.1 | 8207.4 | 8199.1 |
| EU539409.1 | 286623 | 8865.3 | 8046.7 | 6217.3 | 6625.5 | 12288.2 | 16763.4 |
| FJ430676.1 | 359401 | 7192.6 | 7335.9 | 5720.9 | 9040.3 | 13997.3 | 14209.0 |
| FJ418773.1 | 366528 | 162.3 | 349.5 | 830.3 | 268.4 | 701.7 | 2053.5 |
| EU540208.1 | 281422 | 5019.9 | 6047.3 | 7654.9 | 5961.4 | 7991.3 | 13065.4 |
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| EU540622.1 | 281237 | 1557.9 | 1912.6 | 2750.6 | 988.1 | 5608.6 | 10264.2 |
| DQ256083.1 | 143611 | 4488.6 | 5188.6 | 12577.9 | 8616.9 | 8533.2 | 10020.5 |
| AB294558.1 | 204838 | 442.0 | 971.3 | 1737.0 | 752.5 | 9392.1 | 6254.2 |
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| DQ289076.1 | 144195 | 2216.9 | 1788.6 | 4110.4 | 3464.9 | 6435.1 | 6397.9 |
| FJ893397.1 | 563933 | 10488.9 | 8543.6 | 6937.1 | 11705.3 | 10711.1 | 13861.9 |
| EU535682.1 | 281049 | 8265.0 | 10216.2 | 8795.4 | 7795.6 | 9268.9 | 13243.2 |
| EU539232.1 | 286562 | 7216.7 | 3897.5 | 11324.2 | 8011.8 | 7918.7 | 11259.1 |
| AJ271219.1 | 72969 | 3058.7 | 3623.8 | 6157.2 | 4255.3 | 11156.2 | 7273.0 |
| AY303321.1 | 131310 | 7539.9 | 7650.2 | 5299.3 | 6146.8 | 9897.5 | 14030.0 |
| EF016112.1 | 195370 | 416.8 | 1010.2 | 1534.4 | 357.2 | 3696.3 | 9225.6 |
| AF374472.1 | 67535 | 2897.0 | 3667.8 | 7026.9 | 5132.9 | 7657.7 | 9905.9 |
| EU538183.1 | 283248 | 3876.4 | 5475.4 | 2700.9 | 2466.2 | 6145.2 | 8051.6 |
| Z76655.1 | 8568 | 838.1 | 1021.4 | 1931.7 | 736.4 | 5893.1 | 6848.7 |
| FJ894960.1 | 535843 | 2923.0 | 4157.2 | 4025.5 | 2998.4 | 7911.0 | 12318.7 |
| EU169189.1 | 237380 | 838.9 | 1815.7 | 1943.6 | 1056.7 | 8262.7 | 12762.3 |
| DQ318867.1 | 152043 | 1164.3 | 1634.6 | 3155.3 | 2195.6 | 4330.8 | 7711.9 |
| FJ405884.1 | 363503 | 680.6 | 625.7 | 762.6 | 2676.6 | 3952.1 | 4094.9 |
| EU538954.1 | 283838 | 5005.9 | 5908.6 | 3880.6 | 4674.7 | 8423.6 | 11861.2 |
| EU540146.1 | 285849 | 475.6 | 977.1 | 2358.0 | 319.2 | 2374.4 | 8558.7 |
| EU537169.1 | 285856 | 10055.6 | 11045.4 | 9503.2 | 8596.6 | 11779.2 | 14954.3 |
| EU539367.1 | 286796 | 1073.9 | 1349.9 | 4005.1 | 2577.2 | 1982.8 | 7081.6 |

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EU022590.1 gg_id:347835 Pseudomonas putida str. KBL1SM1
FJ894353.1 gg_id:561919 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B2E; ear pu
FJ893155.1 gg_id:557378 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota HM3; ear p
EU434400.1 gg_id:270408 Pseudomonas fluorescens str. a342
EF153018.1 gg_id:184271 Pseudomonas corrugata str. P94
AJ249825.2 gg_id:74089 Pseudomonas putida str. GPo1 (TF4-1L)
DQ402053.1 gg_id:155811 Pseudomonas fluorescens TC222
FJ894348.1 gg_id:548110 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B2E; ear pu
GU372931.1 gg_id:514461 Pseudomonas sp. str. CS3
EU537987.1 gg_id:280306 profile human microbiota antecubital fossa (inner elbow) skin clone nbt228e03
EU534747.1 gg_id:280344 profile human skin microbiota ear punch biopsy female C57BL/6J mouse clone nbt21
AF502594.1 gg_id:66559 Pseudomonas monteilii str. C11
AY900171.1 gg_id:142050 Pseudomonas fluorescens str. PCL1751
AF130950.1 gg_id:8581 Pseudomonas syringae str. A90
EU535916.1 gg_id:280150 profile human microbiota antecubital fossa (inner elbow) skin clone nbt06b10
EU538331.1 gg_id:284474 profile human microbiota antecubital fossa (inner elbow) skin clone nbt83f11
EU539948.1 gg_id:283585 profile human microbiota antecubital fossa (inner elbow) skin clone nbt108c07
DQ453708.1 gg_id:156738 Pseudomonas pv. savastanoi str. NCPPB-1344
FM955873.1 gg_id:540744 Pseudomonas sp. str. Asd M6-4
DQ257632.1 gg_id:147233 Pseudomonas putida str. MTCC 5110
EF062802.1 gg_id:183293 Pseudomonas sp. str. MY1402
AY690673.1 gg_id:99074 Sulfitobacter sp. str. GC07
AF100323.1 gg_id:8681 Pseudomonas thivervalensis str. SBK26; CFBP 11261T
DQ536518.1 gg_id:161371 Pseudomonas poae str. BIHB 752
EU434546.1 gg_id:258577 Pseudomonas fluorescens str. b59
EU539834.1 gg_id:287212 profile human microbiota antecubital fossa (inner elbow) skin clone nbt105h10
EU554430.1 gg_id:274557 Pseudomonas putida str. Ag04
GU186124.1 gg_id:548053 Pseudomonas fluorescens str. IHB B 1427
GQ174492.1 gg_id:446815 Pseudomonas sp. str. 32A
EU827496.1 gg_id:320652 Pseudomonas putida str. TFD49
FJ911604.1 gg_id:535159 Rhizobium sp. str. SPC RN2
GQ451221.1 gg_id:552947 Fecal Yunnan snub-nosed monkey feces clone J87
FJ894687.1 gg_id:574364 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota BME; ear p
EU538372.1 gg_id:286077 profile human microbiota antecubital fossa (inner elbow) skin clone nbt88a05
AF509330.1 gg_id:77086 Pseudomonas putida str. DSM 3601
FJ950670.1 gg_id:426126 Pseudomonas fluorescens str. d112
EF154274.1 gg_id:190873 Pseudomonas tolaasii str. 34
EU537208.1 gg_id:286436 profile human microbiota antecubital fossa (inner elbow) skin clone nbt68e07
GQ900609.1 gg_id:583278 Pseudomonas synxantha str. A1
EU536059.1 gg_id:284552 profile human microbiota antecubital fossa (inner elbow) skin clone nbt08a07
Z29622.1 gg_id:8723 Pseudomonas species

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| EU022590.1 | 347835 | 1964.9 | 2289.1 | 3392.3 | 4340.4 | 8106.9 | 5344.4 |
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| FJ893155.1 | 557378 | 4072.5 | 4860.0 | 4713.4 | 5849.3 | 5283.5 | 12786.0 |
| EU434400.1 | 270408 | 275.4 | 780.2 | 1227.2 | 185.0 | 9635.2 | 8786.3 |
| EF153018.1 | 184271 | 83.2 | 256.5 | 593.5 | 161.8 | 1009.9 | 5051.3 |
| AJ249825.2 | 74089 | 856.3 | 1426.0 | 3667.4 | 1563.7 | 3908.0 | 4046.8 |
| DQ402053.1 | 155811 | 849.3 | 1197.2 | 2671.9 | 2454.5 | 4400.2 | 5688.7 |
| FJ894348.1 | 548110 | 785.6 | 1471.0 | 1719.5 | 1587.8 | 4884.9 | 12158.7 |
| GU372931.1 | 514461 | 2279.2 | 2020.7 | 3509.7 | 3919.8 | 6682.4 | 6564.8 |
| EU537987.1 | 280306 | 4140.9 | 5445.1 | 6742.4 | 4269.2 | 9088.1 | 11292.5 |
| EU534747.1 | 280344 | 6126.3 | 6617.7 | 5298.3 | 5724.1 | 6462.3 | 12946.7 |
| AF502594.1 | 66559 | 5091.3 | 7936.4 | 2563.9 | 3566.9 | 4665.2 | 4398.5 |
| AY900171.1 | 142050 | 8810.9 | 6946.9 | 3970.8 | 12708.9 | 13401.6 | 14835.1 |
| AF130950.1 | 8581 | 1074.9 | 575.9 | 1122.4 | 368.4 | 674.0 | 1967.2 |
| EU535916.1 | 280150 | 4386.8 | 5907.5 | 5332.3 | 3817.9 | 8872.3 | 11357.4 |
| EU538331.1 | 284474 | 2400.3 | 3861.3 | 5175.7 | 3426.8 | 3530.5 | 8833.8 |
| EU539948.1 | 283585 | 505.2 | 1492.1 | 3326.8 | 992.0 | 1157.3 | 7337.5 |
| DQ453708.1 | 156738 | 867.1 | 1309.2 | 2876.8 | 2546.7 | 6063.7 | 8422.0 |
| FM955873.1 | 540744 | 182.4 | 388.1 | 1019.2 | 353.6 | 1276.2 | 2131.8 |
| DQ257632.1 | 147233 | 4053.3 | 5555.6 | 6430.9 | 3338.2 | 7683.3 | 8521.6 |
| EF062802.1 | 183293 | 7809.4 | 8612.8 | 11924.3 | 8787.4 | 16233.2 | 14763.7 |
| AY690673.1 | 99074 | 5565.8 | 3620.3 | 4797.2 | 3533.5 | 8085.4 | 4552.9 |
| AF100323.1 | 8681 | 225.5 | 527.7 | 1166.2 | 383.7 | 808.5 | 3044.2 |
| DQ536518.1 | 161371 | 2654.9 | 2365.8 | 2860.7 | 5517.1 | 4890.9 | 9125.9 |
| EU434546.1 | 258577 | 1592.2 | 2511.7 | 3699.1 | 1838.1 | 7057.1 | 11523.7 |
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| EU554430.1 | 274557 | 168.8 | 420.1 | 1217.2 | 369.5 | 3443.2 | 5217.9 |
| GU186124.1 | 548053 | 5839.7 | 4148.4 | 3509.7 | 5158.6 | 4543.2 | 6001.0 |
| GQ174492.1 | 446815 | 762.2 | 889.0 | 918.4 | 1467.9 | 3031.6 | 2009.5 |
| EU827496.1 | 320652 | 753.4 | 1153.2 | 2012.2 | 1603.9 | 11377.2 | 9601.8 |
| FJ911604.1 | 535159 | 14751.2 | 15232.1 | 5669.8 | 12246.3 | 20637.7 | 18447.8 |
| GQ451221.1 | 552947 | 881.7 | 698.8 | 994.7 | 560.4 | 5064.7 | 5056.4 |
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| AF509330.1 | 77086 | 316.0 | 409.3 | 1127.7 | 527.1 | 1280.7 | 2065.7 |
| FJ950670.1 | 426126 | 5967.7 | 8560.1 | 4223.9 | 4841.7 | 17412.4 | 13751.6 |
| EF154274.1 | 190873 | 847.3 | 1425.0 | 2875.3 | 914.6 | 3441.9 | 7881.8 |
| EU537208.1 | 286436 | 7170.8 | 8378.0 | 5060.3 | 6604.9 | 9329.2 | 11835.2 |
| GQ900609.1 | 583278 | 8600.3 | 8805.4 | 6372.0 | 8928.4 | 9232.8 | 9877.2 |
| EU536059.1 | 284552 | 13599.6 | 12982.3 | 14196.4 | 12332.9 | 16225.2 | 17916.4 |
| Z29622.1 | 8723 | 354.3 | 633.6 | 1093.1 | 254.3 | 1205.8 | 4826.6 |

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AF094727.1 gg_id:74186 Pseudomonas fluorescens str. ATCC 17397
EU540318.1 gg_id:280568 profile human microbiota antecubital fossa (inner elbow) skin clone nbt113b12
EF455752.1 gg_id:204831 Pseudomonas tolaasii ACCC 01267
DQ288949.1 gg_id:144539 Pseudomonas putida TG11
AJ889838.1 gg_id:113026 Pseudomonas avellanae str. BPIC 714
FJ894440.1 gg_id:542748 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B2E; ear pu
NC_010322.1 gg_id:263559 Pseudomonas putida str. GB-1
EU539417.1 gg_id:281214 profile human microbiota antecubital fossa (inner elbow) skin clone nbt238e04
AY030316.1 gg_id:21829 Pseudomonas graminis str. JPL-8
DQ095894.1 gg_id:130996 Pseudomonas plecoglossicida str. S5
EU538369.1 gg_id:281230 profile human microbiota antecubital fossa (inner elbow) skin clone nbt87h05
EU535337.1 gg_id:285434 profile human microbiota antecubital fossa (inner elbow) skin clone nbt01g05
EU538202.1 gg_id:285063 profile human microbiota antecubital fossa (inner elbow) skin clone nbt82h08
EU538980.1 gg_id:286677 profile human microbiota antecubital fossa (inner elbow) skin clone nbt97f09
GU012802.1 gg_id:577467 Pseudomonas putida str. 7
GQ404505.1 gg_id:566293 Pseudomonas putida str. cmmb
FJ894474.1 gg_id:561792 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B2E; ear pu
EU538172.1 gg_id:280144 profile human microbiota antecubital fossa (inner elbow) skin clone nbt81d04
CP000926.1 gg_id:269270 Pseudomonas putida str. GB-1
EF062807.1 gg_id:198623 Pseudomonas sp. str. MY1420
EU364534.1 gg_id:274628 Pseudomonas fluorescens str. CN078
Y11150.1 gg_id:8787 Pseudomonas graminis str. DSM 11363 ()
EU536058.1 gg_id:282327 profile human microbiota antecubital fossa (inner elbow) skin clone nbt08a03
AY623931.1 gg_id:105785 Pseudomonas rhodesiae str. CP-17
FJ981653.1 gg_id:535517 Flea Vectors Plague clone XC7
AY574282.1 gg_id:140321 Pseudomonas putida str. S16
AF134705.1 gg_id:46201 Pseudomonas fluorescens str. F113
AM111046.1 gg_id:140961 Pseudomonas sp. str. 7068
DQ371233.1 gg_id:153457 Pseudomonas sp. C1-2006 str. C1
FM208263.1 gg_id:326340 Pseudomonas sp. str. DSM 8628
EU534715.1 gg_id:281041 profile human skin microbiota ear punch biopsy female C57BL/6J mouse clone nbt18
EU535094.1 gg_id:284566 profile human skin microbiota ear punch biopsy female C57BL/6J mouse clone nbt18
DQ841246.1 gg_id:167487 Pseudomonas fluorescens str. WMQ_B
AB365797.1 gg_id:246399 Pseudomonas frederiksbergensis str. SS17
EU534871.1 gg_id:284343 profile human skin microbiota ear punch biopsy female C57BL/6J mouse clone nbt21
DQ318863.1 gg_id:151022 Pseudomonas syringae str. 8533
FJ893183.1 gg_id:565882 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota HM3; ear p
AM410088.1 gg_id:192714 Pseudomonas veronii str. C9-4zhy
AJ556801.1 gg_id:85062 Pseudomonas sp. MWH1
EF501777.1 gg_id:223959 microbiota and their potential application protective s sprouts clone DGGE gel band 8
AY456706.1 gg_id:105067 Pseudomonas putida str. P3

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| AF094727.1 | 74186 | 383.3 | 924.8 | 2339.8 | 718.6 | 1701.2 | 6690.8 |
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| EF455752.1 | 204831 | 13297.6 | 11658.5 | 9492.1 | 12877.7 | 10477.9 | 10910.5 |
| DQ288949.1 | 144539 | 240.8 | 471.5 | 1578.6 | 1131.1 | 2505.2 | 2103.2 |
| AJ889838.1 | 113026 | 3840.5 | 3772.3 | 4000.2 | 5980.1 | 7587.0 | 11267.4 |
| FJ894440.1 | 542748 | 10073.4 | 8219.5 | 8137.4 | 11431.1 | 13956.9 | 15456.1 |
| NC_010322.1 | 263559 | 4843.6 | 5721.2 | 6832.5 | 5411.5 | 14059.5 | 8835.3 |
| EU539417.1 | 281214 | 11869.5 | 10399.2 | 5953.0 | 12743.4 | 14483.3 | 14315.9 |
| AY030316.1 | 21829 | 7271.7 | 7541.3 | 8142.2 | 4151.7 | 8707.3 | 7600.8 |
| DQ095894.1 | 130996 | 2203.4 | 1768.5 | 3909.9 | 3471.4 | 6449.2 | 4699.3 |
| EU538369.1 | 281230 | 5248.7 | 6119.3 | 3449.9 | 2095.8 | 9893.7 | 10502.9 |
| EU535337.1 | 285434 | 3010.9 | 4817.4 | 8024.2 | 3640.3 | 5603.1 | 7616.4 |
| EU538202.1 | 285063 | 466.1 | 899.4 | 1725.1 | 1228.3 | 2484.4 | 10099.7 |
| EU538980.1 | 286677 | 4268.1 | 6811.7 | 6202.1 | 6237.2 | 9178.9 | 13815.3 |
| GU012802.1 | 577467 | 8072.1 | 4606.3 | 13882.3 | 9733.6 | 5923.8 | 12539.7 |
| GQ404505.1 | 566293 | 1562.0 | 1881.4 | 4769.0 | 2411.8 | 5820.3 | 4566.8 |
| FJ894474.1 | 561792 | 1107.6 | 1745.6 | 2075.0 | 1432.5 | 6384.4 | 12027.2 |
| EU538172.1 | 280144 | 6522.9 | 4932.9 | 13587.2 | 6415.7 | 7091.4 | 10850.0 |
| CP000926.1 | 269270 | 861.2 | 1140.8 | 2558.0 | 1932.2 | 8637.6 | 7814.0 |
| EF062807.1 | 198623 | 832.0 | 935.7 | 1366.0 | 362.7 | 3960.4 | 5606.5 |
| EU364534.1 | 274628 | 668.1 | 935.3 | 1863.8 | 1859.1 | 1196.8 | 7643.2 |
| Y11150.1 | 8787 | 388.7 | 2437.1 | 2838.0 | 1441.1 | 11255.3 | 10419.2 |
| EU536058.1 | 282327 | 13499.8 | 6530.0 | 10743.4 | 11943.2 | 11743.2 | 11845.7 |
| AY623931.1 | 105785 | 531.0 | 889.5 | 1787.2 | 455.3 | 4233.2 | 10008.2 |
| FJ981653.1 | 535517 | 17774.4 | 13070.1 | 11015.6 | 12770.1 | 23094.0 | 18713.0 |
| AY574282.1 | 140321 | 2247.5 | 1844.5 | 4114.0 | 3525.9 | 7767.6 | 5714.1 |
| AF134705.1 | 46201 | 1303.2 | 2025.5 | 3530.9 | 2747.6 | 7952.8 | 13929.3 |
| AM111046.1 | 140961 | 4427.2 | 2902.1 | 5065.9 | 8253.5 | 3600.8 | 3677.4 |
| DQ371233.1 | 153457 | 9291.4 | 9487.7 | 5892.5 | 8691.3 | 18521.6 | 11939.0 |
| FM208263.1 | 326340 | 580.2 | 624.6 | 1741.2 | 972.5 | 6065.4 | 3621.3 |
| EU534715.1 | 281041 | 5449.2 | 6389.6 | 6942.1 | 6092.9 | 10038.2 | 12074.7 |
| EU535094.1 | 284566 | 4334.7 | 4722.3 | 2530.1 | 3746.6 | 6152.2 | 8371.0 |
| DQ841246.1 | 167487 | 137.3 | 465.8 | 1547.5 | 760.7 | 1807.4 | 5991.3 |
| AB365797.1 | 246399 | 2624.2 | 2291.7 | 3289.5 | 6712.3 | 3077.9 | 9495.8 |
| EU534871.1 | 284343 | 3998.7 | 5700.6 | 2336.7 | 5324.2 | 8999.6 | 10957.3 |
| DQ318863.1 | 151022 | 1278.2 | 1628.6 | 2308.3 | 1827.5 | 5824.8 | 7679.8 |
| FJ893183.1 | 565882 | 4238.1 | 5705.6 | 6827.2 | 4375.3 | 8467.2 | 11947.6 |
| AM410088.1 | 192714 | 148.4 | 495.3 | 924.6 | 235.4 | 4684.4 | 5036.6 |
| AJ556801.1 | 85062 | 6604.7 | 6611.4 | 10049.7 | 6206.2 | 10765.7 | 11576.5 |
| EF501777.1 | 223959 | 3754.8 | 4056.0 | 7559.3 | 3519.9 | 11885.5 | 12465.1 |
| AY456706.1 | 105067 | 6566.1 | 6005.8 | 5729.3 | 6118.1 | 15023.7 | 12951.8 |

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AY900172.1 gg_id:142249 Pseudomonas fluorescens str. PCL1753
FJ894122.1 gg_id:558498 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B1E; ear pu
EU434349.1 gg_id:260230 Pseudomonas fluorescens str. a258
FJ894378.1 gg_id:556184 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B2E; ear pu
EU601175.1 gg_id:279245 Pseudomonas putida str. PBRs5
FJ892805.1 gg_id:572626 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota HM1; ear p
EF102852.1 gg_id:252507 Pseudomonas sp. str. G-229-23
FJ605372.1 gg_id:451091 Pseudomonas plecoglossicida str. Fn-2
EU373377.1 gg_id:276371 Pseudomonas fluorescens str. HNR16
EU652104.1 gg_id:274750 Pseudomonas sp. str. ybd-1
EU540251.1 gg_id:285021 profile human microbiota antecubital fossa (inner elbow) skin clone nbt248a11
EU536830.1 gg_id:286409 profile human microbiota antecubital fossa (inner elbow) skin clone nbt222d01
EU539844.1 gg_id:283892 profile human microbiota antecubital fossa (inner elbow) skin clone nbt106c05
FJ422406.1 gg_id:360669 Pseudomonas fluorescens str. CB32
EU537106.1 gg_id:279854 profile human microbiota antecubital fossa (inner elbow) skin clone nbt220g07
FJ894060.1 gg_id:561617 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B1E; ear pu
GU186116.1 gg_id:589957 Pseudomonas putida str. IHB B 1369
FN675869.1 gg_id:518676 Pseudomonas trivialis RE*1-1-14
EU538939.1 gg_id:285340 profile human microbiota antecubital fossa (inner elbow) skin clone nbt95f03
EU360314.1 gg_id:261260 Pseudomonas fluorescens str. 2313
FJ894338.1 gg_id:564449 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B2E; ear pu
GQ499333.1 gg_id:539966 Pseudomonas putida str. M1
DQ087528.1 gg_id:128047 Pseudomonas putida str. PBM11
FJ894369.1 gg_id:536140 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B2E; ear pu
AF320990.1 gg_id:37361 Pseudomonas tolaasii str. NCPPB 2325
FJ893610.1 gg_id:549815 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota WT3; ear p
NR_024909.1 gg_id:560291 Pseudomonas orientalis str. CFML 96-170; CIP 105540
EU539533.1 gg_id:285381 profile human microbiota antecubital fossa (inner elbow) skin clone nbt241d02
EU439425.1 gg_id:594417 Pseudomonas putida str. OK-St
FJ950631.1 gg_id:401370 Pseudomonas putida str. c255
EU434416.1 gg_id:264637 Pseudomonas fluorescens str. a1
EU535748.1 gg_id:286344 profile human microbiota antecubital fossa (inner elbow) skin clone nbt10c12
FM211694.1 gg_id:325970 Pseudomonas putida str. P9
FJ894346.1 gg_id:538400 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B2E; ear pu
EF102849.1 gg_id:241842 Pseudomonas putida str. G-4-14-1
AF482685.1 gg_id:66956 Pseudomonas sp. str. NMX
AY785748.1 gg_id:108233 Pseudomonas fluorescens OUCZ118
AB302402.1 gg_id:221292 Pseudomonas multiaromavorans str. C-18
AY738626.1 gg_id:102117 Pseudomonas putida
FJ893958.1 gg_id:571781 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B1E; ear pu
EU540301.1 gg_id:283128 profile human microbiota antecubital fossa (inner elbow) skin clone nbt114f12

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| AY900172.1 | 142249 | 182.5 | 419.8 | 1277.6 | 580.4 | 522.5 | 2328.2 |
| FJ894122.1 | 558498 | 6247.6 | 6599.4 | 5950.5 | 6100.0 | 6953.9 | 13600.4 |
| EU434349.1 | 260230 | 510.4 | 590.9 | 1170.7 | 413.8 | 4956.8 | 4684.3 |
| FJ894378.1 | 556184 | 7135.0 | 7038.8 | 4035.3 | 7808.1 | 16002.9 | 13165.0 |
| EU601175.1 | 279245 | 1482.6 | 1980.4 | 2017.4 | 1830.1 | 6592.3 | 3379.4 |
| FJ892805.1 | 572626 | 4055.6 | 3264.4 | 4920.6 | 4067.1 | 4194.8 | 9913.3 |
| EF102852.1 | 252507 | 831.7 | 1114.5 | 3002.4 | 1455.0 | 1900.6 | 4677.4 |
| FJ605372.1 | 451091 | 461.7 | 798.1 | 748.3 | 383.1 | 2965.6 | 1220.5 |
| EU373377.1 | 276371 | 852.2 | 850.4 | 1367.7 | 604.7 | 8370.2 | 5718.7 |
| EU652104.1 | 274750 | 1548.6 | 2016.7 | 2800.2 | 2564.4 | 7801.8 | 12991.4 |
| EU540251.1 | 285021 | 5088.8 | 6991.7 | 5246.1 | 5068.4 | 8363.5 | 10992.1 |
| EU536830.1 | 286409 | 4766.3 | 5048.9 | 3871.1 | 4709.1 | 6726.9 | 8831.4 |
| EU539844.1 | 283892 | 10116.5 | 9915.0 | 8473.8 | 8251.4 | 9407.5 | 13714.9 |
| FJ422406.1 | 360669 | 2192.9 | 1868.1 | 3359.7 | 6004.3 | 2870.9 | 7395.3 |
| EU537106.1 | 279854 | 1878.0 | 3211.7 | 3838.2 | 4011.5 | 4480.6 | 10901.2 |
| FJ894060.1 | 561617 | 9570.8 | 8530.1 | 9022.4 | 9221.9 | 13627.3 | 13651.9 |
| GU186116.1 | 589957 | 1111.4 | 1260.5 | 3107.4 | 2267.0 | 8899.0 | 8417.1 |
| FN675869.1 | 518676 | 5058.8 | 7505.4 | 9000.1 | 4540.0 | 11279.2 | 13321.9 |
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| EU360314.1 | 261260 | 1279.6 | 1816.9 | 2763.6 | 2495.1 | 5061.2 | 11525.2 |
| FJ894338.1 | 564449 | 524.7 | 1036.2 | 947.5 | 279.3 | 1714.3 | 7773.4 |
| GQ499333.1 | 539966 | 466.3 | 1433.0 | 2256.6 | 726.2 | 11736.8 | 10301.8 |
| DQ087528.1 | 128047 | 2018.1 | 2036.9 | 3838.2 | 3307.7 | 10293.4 | 7403.1 |
| FJ894369.1 | 536140 | 4032.0 | 5907.5 | 7854.5 | 5705.2 | 8875.6 | 14949.7 |
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| EU439425.1 | 594417 | 815.5 | 984.1 | 363.5 | 615.4 | 4570.4 | 3494.6 |
| FJ950631.1 | 401370 | 14216.6 | 10515.0 | 11480.2 | 14399.2 | 17120.1 | 14288.6 |
| EU434416.1 | 264637 | 4235.0 | 3991.0 | 3248.7 | 3441.9 | 8140.9 | 9014.2 |
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| FM211694.1 | 325970 | 3057.5 | 3893.1 | 5125.2 | 6352.4 | 9152.1 | 10743.5 |
| FJ894346.1 | 538400 | 8261.3 | 8351.9 | 9636.0 | 8236.9 | 13143.5 | 14487.7 |
| EF102849.1 | 241842 | 3073.9 | 2476.3 | 5102.0 | 4919.9 | 7426.0 | 8446.6 |
| AF482685.1 | 66956 | 462.2 | 363.0 | 1403.2 | 863.3 | 2459.3 | 2688.1 |
| AY785748.1 | 108233 | 1682.3 | 1542.4 | 1845.4 | 2380.0 | 1763.7 | 3620.1 |
| AB302402.1 | 221292 | 703.7 | 821.7 | 699.2 | 565.2 | 5396.1 | 3958.9 |
| AY738626.1 | 102117 | 432.9 | 1004.8 | 2144.7 | 1537.6 | 3812.9 | 4980.5 |
| FJ893958.1 | 571781 | 5777.3 | 5101.5 | 8014.9 | 5812.0 | 10041.2 | 12228.6 |
| EU540301.1 | 283128 | 7949.2 | 8103.1 | 5878.6 | 8088.3 | 11027.9 | 11149.1 |

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FJ950579.1 gg_id:402524 Pseudomonas putida str. c142
EU539837.1 gg_id:285008 profile human microbiota antecubital fossa (inner elbow) skin clone nbt106a06
EU540286.1 gg_id:279871 profile human microbiota antecubital fossa (inner elbow) skin clone nbt113h09
U81870.1 gg_id:8646 Pseudomonas sp. str. BI*7
AY303300.1 gg_id:129613 Pseudomonas sp. str. ps4-28
EU537958.1 gg_id:282775 profile human microbiota antecubital fossa (inner elbow) skin clone nbt228a05
FJ894406.1 gg_id:573458 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B2E; ear pu
AF100322.1 gg_id:8680 Pseudomonas brassicacearum str. NFM421; CFBP 11874
EU536400.1 gg_id:285545 profile human microbiota antecubital fossa (inner elbow) skin clone nbt213c12
DQ071557.1 gg_id:128217 Pseudomonas monteilii str. R1
AJ889839.1 gg_id:113774 Pseudomonas avellanae str. ISF 2059
EU538917.1 gg_id:281421 profile human microbiota antecubital fossa (inner elbow) skin clone nbt95b04
EU169164.1 gg_id:243916 Pseudomonas fluorescens str. B67
EU538578.1 gg_id:284694 profile human microbiota antecubital fossa (inner elbow) skin clone nbt232a06
EF645247.1 gg_id:238269 Pseudomonas plecoglossicida str. CGMCC 2093
EU540085.1 gg_id:284259 profile human microbiota antecubital fossa (inner elbow) skin clone nbt245c01
FJ894690.1 gg_id:551928 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota BME; ear p
EU536050.1 gg_id:285952 profile human microbiota antecubital fossa (inner elbow) skin clone nbt07g11
DQ318865.1 gg_id:156534 Pseudomonas syringae str. 8535
EF489479.1 gg_id:226767 Pseudomonas plecoglossicida
FJ894423.1 gg_id:538102 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B2E; ear pu
EU434397.1 gg_id:276367 Pseudomonas fluorescens str. a311
GU177878.1 gg_id:591085 Pseudomonas fluorescens str. FE1326
AF131104.1 gg_id:8590 Pseudomonas putida str. MTB5
EU539817.1 gg_id:285462 profile human microbiota antecubital fossa (inner elbow) skin clone nbt105d10
DQ377742.1 gg_id:151735 Pseudomonas migulae PD 1
EU538358.1 gg_id:280546 profile human microbiota antecubital fossa (inner elbow) skin clone nbt87a03
FJ895027.1 gg_id:573710 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota BME; ear p
FJ893564.1 gg_id:549060 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota WT2; ear p
EU535249.1 gg_id:280188 profile human microbiota antecubital fossa (inner elbow) skin clone nbt172g06
EU539660.1 gg_id:283327 profile human microbiota antecubital fossa (inner elbow) skin clone nbt243f12
EU434368.1 gg_id:276148 Pseudomonas lundensis str. a301
DQ453709.1 gg_id:156806 Pseudomonas pv. savastanoi str. ITM-317
EU539126.1 gg_id:279910 profile human microbiota antecubital fossa (inner elbow) skin clone nbt98f01
EF528261.1 gg_id:227324 Pseudomonas migulae AE2
EU647701.1 gg_id:276918 Pseudomonas mandelii str. REG46
GQ502786.1 gg_id:582124 Pseudomonas putida str. xyz-zjut
DQ465009.2 gg_id:227277 Pseudomonas sp. str. VTT E-052906
AY748893.1 gg_id:104631 Pseudomonas sp. N21.4
EU169190.1 gg_id:245659 Pseudomonas tolaasii str. B35

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| EU539837.1 | 285008 | 5287.2 | 6575.4 | 7377.6 | 5743.0 | 9208.4 | 11774.5 |
| EU540286.1 | 279871 | 850.1 | 1492.2 | 2007.9 | 533.8 | 5987.9 | 10755.0 |
| U81870.1 | 8646 | 4040.5 | 4814.3 | 4779.5 | 6249.3 | 6911.5 | 9165.2 |
| AY303300.1 | 129613 | 788.7 | 983.2 | 1316.7 | 376.4 | 5010.4 | 6706.8 |
| EU537958.1 | 282775 | 2710.9 | 2818.6 | 3014.3 | 2881.7 | 6969.5 | 8338.5 |
| FJ894406.1 | 573458 | 2687.6 | 3520.0 | 3638.5 | 3288.1 | 8872.5 | 12369.2 |
| AF100322.1 | 8680 | 371.8 | 575.0 | 1179.9 | 385.3 | 1246.0 | 3555.8 |
| EU536400.1 | 285545 | 4673.9 | 7415.7 | 6792.1 | 7554.0 | 9157.3 | 11307.9 |
| DQ071557.1 | 128217 | 1560.1 | 2783.7 | 1360.8 | 1084.2 | 6146.6 | 4593.4 |
| AJ889839.1 | 113774 | 739.0 | 1003.0 | 1782.1 | 1748.2 | 2917.9 | 5307.4 |
| EU538917.1 | 281421 | 947.6 | 1726.3 | 2640.0 | 2095.2 | 6880.5 | 11602.1 |
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| EU538578.1 | 284694 | 5756.2 | 4734.5 | 7965.8 | 5802.0 | 9390.1 | 11690.6 |
| EF645247.1 | 238269 | 303.1 | 621.9 | 1049.2 | 354.9 | 13527.3 | 2409.3 |
| EU540085.1 | 284259 | 5936.8 | 5902.9 | 5452.7 | 7629.1 | 9759.0 | 11859.8 |
| FJ894690.1 | 551928 | 613.8 | 1341.3 | 1368.5 | 1416.5 | 1650.1 | 9852.9 |
| EU536050.1 | 285952 | 14960.6 | 15192.0 | 9061.9 | 13723.7 | 16942.2 | 15726.2 |
| DQ318865.1 | 156534 | 555.7 | 754.6 | 1484.8 | 526.6 | 2214.5 | 4598.4 |
| EF489479.1 | 226767 | 5393.3 | 3256.4 | 11397.1 | 7631.4 | 5096.4 | 6451.8 |
| FJ894423.1 | 538102 | 16351.7 | 15340.0 | 12450.7 | 17084.4 | 21088.8 | 20968.5 |
| EU434397.1 | 276367 | 3315.2 | 4423.2 | 5682.2 | 4954.6 | 7885.5 | 12014.6 |
| GU177878.1 | 591085 | 5181.8 | 7124.0 | 9036.6 | 5062.5 | 14761.1 | 9868.5 |
| AF131104.1 | 8590 | 3960.7 | 3264.3 | 2647.3 | 5471.1 | 5861.5 | 5938.3 |
| EU539817.1 | 285462 | 1165.8 | 1531.4 | 2805.2 | 2023.1 | 4487.9 | 6033.7 |
| DQ377742.1 | 151735 | 2622.3 | 3376.6 | 3383.6 | 2953.2 | 6094.1 | 8445.0 |
| EU538358.1 | 280546 | 13634.5 | 14990.7 | 16697.4 | 10820.5 | 16673.5 | 17437.6 |
| FJ895027.1 | 573710 | 4721.3 | 4915.4 | 6182.4 | 4994.0 | 5964.8 | 9761.2 |
| FJ893564.1 | 549060 | 574.7 | 975.8 | 921.3 | 628.5 | 2801.9 | 7208.7 |
| EU535249.1 | 280188 | 15806.3 | 18851.8 | 16429.1 | 13106.2 | 22210.7 | 19547.2 |
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EU434396.1 gg_id:277610 Pseudomonas putida str. a317
AM905940.1 gg_id:239559 Pseudomonas sp. str. Ri83
FJ894079.1 gg_id:536394 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B1E; ear pu
EU538394.1 gg_id:280069 profile human microbiota antecubital fossa (inner elbow) skin clone nbt88g02
FJ418774.1 gg_id:366431 Pseudomonas syringae pv. tomato str. 2
EU539823.1 gg_id:286118 profile human microbiota antecubital fossa (inner elbow) skin clone nbt105f04
FM955865.1 gg_id:554111 Pseudomonas sp. str. Asd M4-6
EU434384.1 gg_id:269895 Pseudomonas fluorescens str. a95
EU439421.1 gg_id:538528 Pseudomonas putida str. LH-S1
DQ404013.1 gg_id:152693 Pseudomonas sp. P2
EU539570.1 gg_id:283143 profile human microbiota antecubital fossa (inner elbow) skin clone nbt242b02
EU537095.1 gg_id:285520 profile human microbiota antecubital fossa (inner elbow) skin clone nbt220e06
DQ073452.1 gg_id:133085 Pseudomonas mosselii str. R10
D84004.1 gg_id:8606 Pseudomonas oryzihabitans str. IAM1568
EU537178.1 gg_id:285666 profile human microbiota antecubital fossa (inner elbow) skin clone nbt67h12
EU169158.1 gg_id:238186 Pseudomonas frederiksbergensis str. B62
EU538923.1 gg_id:284541 profile human microbiota antecubital fossa (inner elbow) skin clone nbt95c09
DQ264492.1 gg_id:141127 universal microarray broader than typical library when sampling subsurface groundw
DQ112333.1 gg_id:136213 Pseudomonas putida str. RW-28
AB334768.1 gg_id:238610 Pseudomonas veronii str. MPU43
FJ893939.1 gg_id:554355 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B1E; ear pu
AM495258.1 gg_id:252526 Pseudomonas putida str. INBP1
DQ177468.1 gg_id:140357 Pseudomonas sp. str. Tibet-IIA21
EU538277.1 gg_id:282428 profile human microbiota antecubital fossa (inner elbow) skin clone nbt84c03
EU855189.1 gg_id:307393 Pseudomonas fulva str. CTSP6
EU540081.1 gg_id:283910 profile human microbiota antecubital fossa (inner elbow) skin clone nbt245b09
AJ132993.1 gg_id:46263 Pseudomonas putida #HR9
EU538386.1 gg_id:279796 profile human microbiota antecubital fossa (inner elbow) skin clone nbt87h04
EU538956.1 gg_id:285202 profile human microbiota antecubital fossa (inner elbow) skin clone nbt96a03
FJ893421.1 gg_id:543846 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota WT1; ear p
DQ095909.1 gg_id:128213 Pseudomonas plecoglossicida str. S20
EU162042.1 gg_id:243921 Pseudomonas sp. str. B2
EU784140.1 gg_id:354316 Azotobacter sp. str. HY1141
DQ314545.1 gg_id:149377 Pseudomonas sp. str. BWDY-41
AY303255.1 gg_id:134368 Pseudomonas sp. str. ps10-14
EU373390.1 gg_id:275232 Pseudomonas synxantha str. HNR22
EU539911.1 gg_id:284759 profile human microbiota antecubital fossa (inner elbow) skin clone nbt107f10
AY914075.1 gg_id:113352 Pseudomonas sp. R-9
EU540114.1 gg_id:280008 profile human microbiota antecubital fossa (inner elbow) skin clone nbt245f04
EU538552.1 gg_id:284463 profile human microbiota antecubital fossa (inner elbow) skin clone nbt231f09
FJ893186.1 gg_id:533616 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota HM3; ear p

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| EU434396.1 | 277610 | 8941.2 | 9660.9 | 8727.2 | 7039.7 | 12571.3 | 12802.9 |
| AM905940.1 | 239559 | 431.7 | 526.5 | 1213.4 | 703.1 | 252.8 | 3202.5 |
| FJ894079.1 | 536394 | 6029.4 | 7416.0 | 8510.0 | 6290.1 | 10533.5 | 12838.9 |
| EU538394.1 | 280069 | 20251.0 | 18871.9 | 17646.5 | 17016.2 | 19887.3 | 18873.6 |
| FJ418774.1 | 366431 | 4721.8 | 4349.9 | 2271.3 | 6077.9 | 7950.9 | 7988.3 |
| EU539823.1 | 286118 | 5322.9 | 6409.2 | 6254.3 | 6099.1 | 8611.5 | 11713.6 |
| FM955865.1 | 554111 | 3592.6 | 5964.4 | 7828.6 | 6803.1 | 11570.4 | 10118.9 |
| EU434384.1 | 269895 | 460.8 | 1016.5 | 1414.0 | 875.5 | 3597.7 | 4381.8 |
| EU439421.1 | 538528 | 1755.1 | 2730.6 | 1604.5 | 2060.3 | 11546.7 | 4725.3 |
| DQ404013.1 | 152693 | 6305.4 | 6506.4 | 5888.3 | 6746.0 | 9486.4 | 7039.9 |
| EU539570.1 | 283143 | 728.0 | 1195.9 | 2099.0 | 1130.2 | 6061.6 | 9905.3 |
| EU537095.1 | 285520 | 3044.9 | 3736.9 | 3266.5 | 1715.6 | 5608.6 | 4787.5 |
| DQ073452.1 | 133085 | 1158.9 | 1620.8 | 3870.4 | 1914.1 | 7078.6 | 5046.2 |
| D84004.1 | 8606 | 4840.7 | 5290.3 | 3392.3 | 3051.1 | 8795.3 | 7965.4 |
| EU537178.1 | 285666 | 8659.3 | 10236.2 | 10780.2 | 9835.3 | 14639.7 | 16527.0 |
| EU169158.1 | 238186 | 4930.9 | 6174.3 | 5291.0 | 5830.8 | 9681.0 | 12641.9 |
| EU538923.1 | 284541 | 9505.7 | 4984.5 | 3605.7 | 8429.4 | 9404.1 | 9334.0 |
| DQ264492.1 | 141127 | 798.1 | 883.7 | 696.3 | 1696.6 | 2520.1 | 5268.7 |
| DQ112333.1 | 136213 | 1425.3 | 1888.3 | 4255.6 | 3071.7 | 9556.2 | 5713.5 |
| AB334768.1 | 238610 | 2835.3 | 3484.9 | 5336.8 | 4059.4 | 9151.8 | 12015.5 |
| FJ893939.1 | 554355 | 813.6 | 1820.3 | 1691.6 | 2058.1 | 2771.0 | 9299.3 |
| AM495258.1 | 252526 | 3569.9 | 4211.5 | 5687.5 | 4264.3 | 10423.7 | 9156.2 |
| DQ177468.1 | 140357 | 612.5 | 1207.8 | 2979.1 | 901.4 | 8788.9 | 10819.2 |
| EU538277.1 | 282428 | 833.9 | 1320.5 | 1840.9 | 1491.3 | 5034.7 | 11706.0 |
| EU855189.1 | 307393 | 539.4 | 1200.0 | 1630.5 | 1281.9 | 10063.9 | 6503.6 |
| EU540081.1 | 283910 | 2241.6 | 4198.7 | 2812.0 | 2077.9 | 7501.5 | 7594.8 |
| AJ132993.1 | 46263 | 3075.6 | 2961.0 | 4009.6 | 3218.1 | 10607.4 | 6200.4 |
| EU538386.1 | 279796 | 13385.9 | 14891.0 | 10812.9 | 11108.7 | 11447.8 | 12923.7 |
| EU538956.1 | 285202 | 221.3 | 481.0 | 997.4 | 287.2 | 2469.2 | 5898.1 |
| FJ893421.1 | 543846 | 2696.2 | 3200.5 | 3479.0 | 5520.1 | 3394.6 | 7881.6 |
| DQ095909.1 | 128213 | 848.6 | 997.9 | 3094.6 | 2416.0 | 6308.9 | 5625.3 |
| EU162042.1 | 243921 | 2876.5 | 2967.7 | 6566.6 | 3604.4 | 10856.1 | 5503.8 |
| EU784140.1 | 354316 | 258.4 | 491.2 | 721.0 | 295.5 | 9787.8 | 1055.7 |
| DQ314545.1 | 149377 | 5939.5 | 1594.4 | 2966.3 | 8016.7 | 2763.2 | 1761.2 |
| AY303255.1 | 134368 | 6136.0 | 5393.1 | 4143.4 | 5634.1 | 10133.0 | 11161.5 |
| EU373390.1 | 275232 | 2080.9 | 3176.8 | 4554.1 | 2690.8 | 5052.9 | 8458.8 |
| EU539911.1 | 284759 | 3800.2 | 6357.4 | 3953.1 | 4167.0 | 14123.5 | 9473.1 |
| AY914075.1 | 113352 | 5641.5 | 3123.6 | 2515.1 | 5206.5 | 9410.6 | 4218.3 |
| EU540114.1 | 280008 | 530.8 | 1311.1 | 2768.0 | 358.3 | 4005.5 | 7893.3 |
| EU538552.1 | 284463 | 9380.6 | 9879.8 | 7562.4 | 7612.2 | 13115.2 | 13090.3 |
| FJ893186.1 | 533616 | 7871.2 | 8225.8 | 4687.5 | 7711.7 | 11355.5 | 12463.6 |

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| s__unclassified | 1805 |

FJ607146.1 gg_id:508873 Pseudomonas syringae pv. cerasicola str. ICMP 13927
EU539816.1 gg_id:281090 profile human microbiota antecubital fossa (inner elbow) skin clone nbt105d08
AF094730.1 gg_id:73624 Pseudomonas fluorescens str. ATCC 17573
EU538185.1 gg_id:282597 profile human microbiota antecubital fossa (inner elbow) skin clone nbt81g10
FJ010624.1 gg_id:369190 Pseudomonas putida str. JD1
AY689050.1 gg_id:100645 Pseudomonas sp. str. 6C_10
EU538184.1 gg_id:280930 profile human microbiota antecubital fossa (inner elbow) skin clone nbt81g09
AF332355.1 gg_id:25543 biostimulation process clone T12-4
AB001446.1 gg_id:42258 Pseudomonas syringae pv. mori str. MAFF 302279 pv.
EU537054.1 gg_id:285303 profile human microbiota antecubital fossa (inner elbow) skin clone nbt219g02
FJ539000.1 gg_id:555737 Pseudomonas plecoglossicida str. PNP-Y8
EU540288.1 gg_id:281800 profile human microbiota antecubital fossa (inner elbow) skin clone nbt114a07
DQ455072.1 gg_id:156940 Pseudomonas monteilii str. VK58
EU538335.1 gg_id:280356 profile human microbiota antecubital fossa (inner elbow) skin clone nbt84a04
GU244412.1 gg_id:529178 Pseudomonas fulva str. 132
FJ787327.1 gg_id:567597 Pseudomonas fluorescens str. NPRs4
DQ536520.1 gg_id:160291 Pseudomonas trivialis str. BIHB 759
FJ529916.1 gg_id:559003 Pseudomonas plecoglossicida str. PNP-F5
FM210032.1 gg_id:347743 Pseudomonas lini str. T1P26
EU540133.1 gg_id:285657 profile human microbiota antecubital fossa (inner elbow) skin clone nbt245h09
EU586044.1 gg_id:271160 Pseudomonas mandelii str. REG45
EU534917.1 gg_id:286166 profile human skin microbiota ear punch biopsy female C57BL/6J mouse clone nbt21
GQ368179.1 gg_id:577495 Pseudomonas koreensis str. JDM-2
DQ313382.1 gg_id:180841 Pseudomonas putida str. PCL1759
FJ577648.1 gg_id:541223 Pseudomonas putida str. CB2-1
FJ193643.1 gg_id:331315 Genetic inventory 'LMA-MTF' spacecraft assembly clean room during Phoenix missior
GU372963.1 gg_id:564991 Pseudomonas putida str. BA-2 D-2
EU537224.1 gg_id:282390 profile human microbiota antecubital fossa (inner elbow) skin clone nbt68h09
AF511433.1 gg_id:65400 Pseudomonas fluorescens CCCO8
GQ073242.1 gg_id:402914 Topographical and Temporal Human Skin Microbiome skin palm clone nbw206g04c1
DQ095914.1 gg_id:136320 Pseudomonas mosselii
EU537429.1 gg_id:282749 profile human microbiota antecubital fossa (inner elbow) skin clone nbt78c06
AM689949.1 gg_id:223789 Pseudomonas sp. str. SPS-8
AB189452.1 gg_id:112760 Pseudomonas azotifigens str. 6H33b
FJ892875.1 gg_id:564952 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota HM1; ear p
GU198123.1 gg_id:579684 Pseudomonas fluorescens str. LMG 14673
EU111689.2 gg_id:511952 Pseudomonas migulae str. T8
EU535172.1 gg_id:281864 profile human microbiota antecubital fossa (inner elbow) skin clone nbt171h04
EU862561.1 gg_id:328338 Pseudomonas putida str. AB35
EF031069.1 gg_id:225677 Pseudomonas putida CA16
X95745.1 gg_id:8655 Pseudomonas avellanae str. P90

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| FJ607146.1 | 508873 | 432.1 | 880.1 | 2329.7 | 1121.5 | 3349.5 | 6412.4 |
| EU539816.1 | 281090 | 3606.2 | 3085.4 | 6082.4 | 3695.8 | 7829.6 | 8939.8 |
| AF094730.1 | 73624 | 2756.5 | 1305.8 | 2270.0 | 3468.0 | 5968.9 | 8497.8 |
| EU538185.1 | 282597 | 7391.8 | 7544.3 | 6404.7 | 7732.4 | 8746.8 | 11676.7 |
| FJ010624.1 | 369190 | 85.9 | 348.3 | 776.8 | 210.4 | 1906.5 | 685.4 |
| AY689050.1 | 100645 | 2761.6 | 4225.4 | 6648.7 | 5072.1 | 10214.4 | 13975.8 |
| EU538184.1 | 280930 | 3067.4 | 3753.3 | 5009.2 | 3044.7 | 3981.1 | 10180.7 |
| AF332355.1 | 25543 | 340.8 | 651.1 | 1364.4 | 566.9 | 4295.6 | 1310.7 |
| AB001446.1 | 42258 | 972.7 | 1311.8 | 2267.8 | 1559.5 | 2684.1 | 7742.1 |
| EU537054.1 | 285303 | 6242.4 | 7648.3 | 4525.9 | 4389.3 | 6252.3 | 9476.8 |
| FJ539000.1 | 555737 | 1885.8 | 2030.6 | 4795.9 | 3304.9 | 9098.5 | 7266.4 |
| EU540288.1 | 281800 | 3429.3 | 2968.9 | 3281.5 | 4236.3 | 7354.1 | 10464.9 |
| DQ455072.1 | 156940 | 9304.3 | 10761.4 | 13830.6 | 8565.8 | 15094.0 | 13270.1 |
| EU538335.1 | 280356 | 1904.2 | 2871.4 | 1576.4 | 1798.0 | 4346.8 | 10788.4 |
| GU244412.1 | 529178 | 407.0 | 930.5 | 1292.1 | 756.7 | 8549.5 | 4994.4 |
| FJ787327.1 | 567597 | 4821.1 | 4543.6 | 5636.3 | 7357.4 | 5086.6 | 6872.1 |
| DQ536520.1 | 160291 | 2423.1 | 2917.6 | 2509.2 | 2465.6 | 5470.3 | 7537.3 |
| FJ529916.1 | 559003 | 91.9 | 297.0 | 950.2 | 103.4 | 1658.9 | 382.5 |
| FM210032.1 | 347743 | 1189.1 | 1655.5 | 3437.7 | 3086.8 | 3501.2 | 9401.2 |
| EU540133.1 | 285657 | 3046.4 | 4710.8 | 2612.7 | 2865.0 | 6429.8 | 9703.9 |
| EU586044.1 | 271160 | 1995.1 | 2538.8 | 2937.0 | 3725.2 | 4725.0 | 8472.7 |
| EU534917.1 | 286166 | 3510.5 | 4219.3 | 5867.0 | 5118.6 | 4692.2 | 7671.8 |
| GQ368179.1 | 577495 | 643.6 | 1080.8 | 2661.4 | 1865.9 | 8791.2 | 5848.5 |
| DQ313382.1 | 180841 | 2033.7 | 2670.6 | 1226.0 | 2391.9 | 8342.1 | 6317.6 |
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| AF511433.1 | 65400 | 1972.4 | 2955.0 | 2931.6 | 2213.0 | 9748.1 | 6512.0 |
| GQ073242.1 | 402914 | 2860.2 | 1916.2 | 3861.9 | 3712.0 | 5680.2 | 4261.7 |
| DQ095914.1 | 136320 | 1578.9 | 1967.4 | 4549.5 | 2451.2 | 7130.3 | 5597.0 |
| EU537429.1 | 282749 | 11286.2 | 11242.6 | 5424.1 | 5502.5 | 12164.1 | 10975.0 |
| AM689949.1 | 223789 | 2159.6 | 2185.6 | 3282.1 | 1415.2 | 8184.0 | 6043.2 |
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| FJ892875.1 | 564952 | 7274.2 | 6921.3 | 5533.5 | 5462.3 | 5562.7 | 8693.9 |
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| EU111689.2 | 511952 | 506.0 | 1035.3 | 3027.7 | 1650.2 | 4077.6 | 12123.2 |
| EU535172.1 | 281864 | 7870.5 | 7664.7 | 7513.8 | 8828.4 | 13182.4 | 10820.1 |
| EU862561.1 | 328338 | 4887.3 | 4825.0 | 2773.6 | 7795.4 | 9589.0 | 9974.1 |
| EF031069.1 | 225677 | 308.9 | 638.3 | 1686.3 | 397.5 | 8945.6 | 4219.6 |
| X95745.1 | 8655 | 1075.6 | 1334.3 | 1802.7 | 918.1 | 3299.3 | 5007.1 |

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AM411071.1 gg_id:186172 Pseudomonas fulva str. Z67zhy
GU138382.1 gg_id:589341 Pseudomonas sp. str. THG 32
FJ894845.1 gg_id:561762 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota BME; ear p
EU434358.1 gg_id:271891 Pseudomonas libanensis str. a110
FJ894768.1 gg_id:546879 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota BME; ear p
D88521.1 gg_id:8531 Agrobacterium agile str. IAM12615
DQ482656.1 gg_id:158174 Pseudomonas putida str. Dsp-1
FJ894373.1 gg_id:558838 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B2E; ear pu
DQ482655.1 gg_id:158425 Pseudomonas putida str. Dsp-3
AJ583090.1 gg_id:94698 Pseudomonas fluorescens str. 62e
EU538021.1 gg_id:283538 profile human microbiota antecubital fossa (inner elbow) skin clone nbt225a09
AY581137.1 gg_id:102527 Pseudomonas fluorescens B15
AY242068.1 gg_id:102312 Pseudomonas pv. syringae str. FG11
EF526503.1 gg_id:218860 Pseudomonas putida str. NAPC3
AY730552.1 gg_id:105687 Pseudomonas fluorescens str. VH060479
AJ308311.1 gg_id:21401 Pseudomonas putida str. Biotype ICMP 13629; ATCC 17392
GU136489.1 gg_id:559336 Pseudomonas sp. str. DY1
EU538936.1 gg_id:280552 profile human microbiota antecubital fossa (inner elbow) skin clone nbt95e08
AF170731.1 gg_id:8771 Pseudomonas sp. str. QSSC1-9
FJ950635.1 gg_id:419521 Pseudomonas putida str. c315
FJ894174.1 gg_id:568497 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B1E; ear pu
FJ894365.1 gg_id:561847 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B2E; ear pu
EU537979.1 gg_id:283040 profile human microbiota antecubital fossa (inner elbow) skin clone nbt228d04
FJ894967.1 gg_id:544031 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota BME; ear p
DQ232737.1 gg_id:144324 Pseudomonas marginalis str. JH8
EU534713.1 gg_id:285416 profile human skin microbiota ear punch biopsy female C57BL/6J mouse clone nbt18
EU022591.1 gg_id:322456 Pseudomonas putida str. KBL2RM2
FJ893927.1 gg_id:540978 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B1E; ear pu
EU539515.1 gg_id:283300 profile human microbiota antecubital fossa (inner elbow) skin clone nbt104e09
AY303303.1 gg_id:131515 Pseudomonas sp. str. ps4-34
FJ894815.1 gg_id:540259 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota BME; ear p
EU540308.1 gg_id:284991 profile human microbiota antecubital fossa (inner elbow) skin clone nbt114h10
EU539830.1 gg_id:287180 profile human microbiota antecubital fossa (inner elbow) skin clone nbt105g10
GU186122.1 gg_id:558279 Pseudomonas mandelii str. IHB B 1384
AY267197.1 gg_id:107228 Pseudomonas fluorescens str. SK1
EU538366.1 gg_id:282513 profile human microbiota antecubital fossa (inner elbow) skin clone nbt87f02
EU169162.1 gg_id:254921 Pseudomonas fluorescens str. B59
AY450557.1 gg_id:108449 Pseudomonas putida str. Q
EU538477.1 gg_id:283326 profile human microbiota antecubital fossa (inner elbow) skin clone nbt230d10
EU538265.1 gg_id:286824 profile human microbiota antecubital fossa (inner elbow) skin clone nbt84a09
DQ232743.1 gg_id:144114 Pseudomonas marginalis str. JH15

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| FJ894845.1 | 561762 | 10291.1 | 9883.2 | 5431.7 | 12507.5 | 16072.4 | 15727.0 |
| EU434358.1 | 271891 | 2552.4 | 3572.6 | 3841.2 | 2932.4 | 8661.0 | 12165.9 |
| FJ894768.1 | 546879 | 1317.6 | 1931.0 | 3000.6 | 1084.3 | 7291.0 | 7563.8 |
| D88521.1 | 8531 | 818.2 | 671.4 | 683.5 | 910.8 | 3060.1 | 4633.9 |
| DQ482656.1 | 158174 | 866.5 | 1181.3 | 2713.2 | 2055.0 | 8110.4 | 6135.9 |
| FJ894373.1 | 558838 | 4316.4 | 5361.7 | 6994.7 | 4475.7 | 9210.3 | 13786.7 |
| DQ482655.1 | 158425 | 10160.3 | 9804.0 | 11011.7 | 6700.0 | 15943.0 | 9019.5 |
| AJ583090.1 | 94698 | 683.8 | 851.2 | 765.4 | 347.0 | 1836.3 | 6595.9 |
| EU538021.1 | 283538 | 6836.8 | 6173.0 | 5576.4 | 5586.6 | 9918.8 | 14465.5 |
| AY581137.1 | 102527 | 2032.5 | 2865.7 | 2408.0 | 2180.0 | 1276.6 | 6648.0 |
| AY242068.1 | 102312 | 1236.4 | 1763.0 | 2919.1 | 1871.4 | 5976.2 | 9624.7 |
| EF526503.1 | 218860 | 1267.7 | 1459.4 | 3222.6 | 2613.2 | 7255.2 | 5165.7 |
| AY730552.1 | 105687 | 4355.7 | 6086.7 | 2936.7 | 3461.8 | 6722.6 | 10775.0 |
| AJ308311.1 | 21401 | 2418.2 | 2986.4 | 2714.8 | 5632.0 | 6736.3 | 9851.1 |
| GU136489.1 | 559336 | 14197.2 | 14759.2 | 12127.0 | 11888.5 | 16927.6 | 14476.1 |
| EU538936.1 | 280552 | 5632.3 | 6580.5 | 6505.6 | 4948.9 | 7086.0 | 11661.2 |
| AF170731.1 | 8771 | 1947.8 | 1505.4 | 802.2 | 1152.4 | 1598.2 | 1763.8 |
| FJ950635.1 | 419521 | 469.7 | 642.4 | 1697.7 | 1611.2 | 2297.6 | 2699.1 |
| FJ894174.1 | 568497 | 4984.6 | 5458.9 | 4713.7 | 5727.2 | 7732.6 | 11179.0 |
| FJ894365.1 | 561847 | 9519.4 | 7071.6 | 4512.7 | 9613.2 | 11563.7 | 11048.3 |
| EU537979.1 | 283040 | 9670.0 | 9745.1 | 6892.0 | 10408.5 | 13666.5 | 13194.6 |
| FJ894967.1 | 544031 | 4737.0 | 4130.7 | 6633.6 | 5643.1 | 5586.1 | 11446.5 |
| DQ232737.1 | 144324 | 422.7 | 963.2 | 1153.3 | 699.4 | 2311.0 | 4517.4 |
| EU534713.1 | 285416 | 104.0 | 263.7 | 242.2 | 136.6 | 2431.6 | 2068.8 |
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| FJ893927.1 | 540978 | 5643.7 | 6371.4 | 6930.0 | 6067.7 | 8594.0 | 12344.9 |
| EU539515.1 | 283300 | 2141.6 | 2123.6 | 1457.3 | 1572.4 | 1583.6 | 3609.9 |
| AY303303.1 | 131515 | 907.4 | 1286.0 | 1902.4 | 1383.8 | 6550.2 | 9388.3 |
| FJ894815.1 | 540259 | 1761.6 | 2408.3 | 3203.9 | 4570.1 | 2775.1 | 7548.2 |
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| GU186122.1 | 558279 | 6920.7 | 5196.9 | 4638.1 | 6271.1 | 8428.1 | 8188.0 |
| AY267197.1 | 107228 | 2154.5 | 3318.8 | 3161.1 | 3200.6 | 6685.0 | 9906.6 |
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| DQ232743.1 | 144114 | 2182.5 | 2918.5 | 3225.0 | 2481.9 | 4791.2 | 7993.0 |

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GQ258636.1 gg_id:541859 Pseudomonas sp. SR3(2009) str. SR3
FJ892762.1 gg_id:553469 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota HM1; ear p
EU539376.1 gg_id:285962 profile human microbiota antecubital fossa (inner elbow) skin clone nbt237h04
EU169163.1 gg_id:238574 Pseudomonas fluorescens str. B69
EU535707.1 gg_id:281570 profile human microbiota antecubital fossa (inner elbow) skin clone nbt09h04
DQ377749.1 gg_id:153662 Pseudomonas mandelii PD 8
DQ338570.1 gg_id:146088 Pseudomonas putida str. B0
DQ659141.1 gg_id:171377 Pseudomonas putida str. L21
EU434460.1 gg_id:258724 Pseudomonas putida str. a235
AB175652.1 gg_id:168428 Azomonas agilis str. NCIB 11693
EU536367.1 gg_id:283644 profile human microbiota antecubital fossa (inner elbow) skin clone nbt62c04
EU221415.1 gg_id:246429 Pseudomonas thivervalensis str. L2S4
AY303310.1 gg_id:134447 Pseudomonas sp. str. ps6-14
EU538470.1 gg_id:286942 profile human microbiota antecubital fossa (inner elbow) skin clone nbt230c08
FJ184353.1 gg_id:318906 structure and physiology pyrene-degrading consortia growing biofilms model trickle c
EU143350.1 gg_id:248196 Pseudomonas sp. J10(2007) str. J10
EU538023.1 gg_id:284720 profile human microbiota antecubital fossa (inner elbow) skin clone nbt225a11
FJ894566.1 gg_id:569821 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B2E; ear pu
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AF131103.1 gg_id:8589 Pseudomonas putida str. MTB6
EU540027.1 gg_id:286084 profile human microbiota antecubital fossa (inner elbow) skin clone nbt111h08
EU661864.1 gg_id:282250 Pseudomonas putida str. AS04
EU037280.1 gg_id:252326 Pseudomonas sp. G3DM-33
FM209481.1 gg_id:325760 Pseudomonas jessenii str. T2P28
EU539345.1 gg_id:284699 profile human microbiota antecubital fossa (inner elbow) skin clone nbt237c04
GU198111.1 gg_id:590944 Pseudomonas fluorescens str. LMG 5833
NZ_ACXS01000064.1 gg_id:516354 Pseudomonas syringae pv. aesculi str. NCPPB3681
FJ982922.1 gg_id:468384 Pseudomonas putida str. ST13
AY622256.1 gg_id:103728 subsurface soil clone B-AU68
EF101982.1 gg_id:181819 Pseudomonas putida str. MRP03
EU414476.1 gg_id:270637 Pseudomonas gingeri str. SDLi-1
AF105390.1 gg_id:8640 Pseudomonas syringae 010297
EU534446.1 gg_id:281265 profile human skin microbiota ear punch biopsy female C57BL/6J mouse clone nbt17
EU921228.1 gg_id:325449 Pseudomonas mosselii str. BM-F1
AM111041.1 gg_id:140863 Pseudomonas sp. str. 7052
AB021397.1 gg_id:8571 Pseudomonas asplenii str. ATCC 23835T
U81871.1 gg_id:8619 Pseudomonas sp. str. BI*8
EU540265.1 gg_id:287024 profile human microbiota antecubital fossa (inner elbow) skin clone nbt113b08
EF208895.1 gg_id:201648 Pseudomonas putida str. N6
AY772474.1 gg_id:108548 Pseudomonas putida str. NA-1

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| DQ659141.1 | 171377 | 294.2 | 583.0 | 895.8 | 232.9 | 1573.7 | 1329.5 |
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| EU221415.1 | 246429 | 815.0 | 982.7 | 1653.1 | 1927.5 | 1977.7 | 5083.6 |
| AY303310.1 | 134447 | 69.3 | 224.1 | 532.0 | 111.2 | 4473.7 | 3827.3 |
| EU538470.1 | 286942 | 2963.5 | 4129.8 | 3040.1 | 4649.2 | 5657.2 | 11239.0 |
| FJ184353.1 | 318906 | 1125.2 | 1763.6 | 2355.9 | 588.3 | 1369.2 | 4546.9 |
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| EU538023.1 | 284720 | 2468.4 | 3544.5 | 5131.7 | 2473.2 | 7235.7 | 9889.6 |
| FJ894566.1 | 569821 | 2749.6 | 4343.3 | 4918.1 | 3053.0 | 8291.8 | 13087.4 |
| EU539344.1 | 285493 | 6362.5 | 9149.2 | 4907.6 | 8037.3 | 10869.9 | 14267.8 |
| AF131103.1 | 8589 | 1290.5 | 925.7 | 1506.6 | 2197.2 | 7977.8 | 2366.1 |
| EU540027.1 | 286084 | 8029.4 | 10158.9 | 9124.7 | 8801.4 | 11478.4 | 16620.2 |
| EU661864.1 | 282250 | 2218.6 | 3857.8 | 566.0 | 731.5 | 9046.9 | 5068.7 |
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| FM209481.1 | 325760 | 11066.6 | 7465.4 | 6533.6 | 10140.6 | 14973.4 | 12380.7 |
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| AB021397.1 | 8571 | 908.8 | 1431.7 | 5089.1 | 780.8 | 8230.5 | 8614.5 |
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| EF208895.1 | 201648 | 332.2 | 682.7 | 1135.4 | 376.3 | 6466.4 | 1319.4 |
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EU537846.1 gg_id:282839 profile human microbiota antecubital fossa (inner elbow) skin clone nbt225b08
EU708323.1 gg_id:332433 Pseudomonas fluorescens str. KDK8
FJ893314.1 gg_id:558000 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota WT1; ear p
EU540613.1 gg_id:282117 profile human microbiota antecubital fossa (inner elbow) skin clone nbt120f10
AM111035.1 gg_id:140925 Pseudomonas sp. str. 7039
Z76652.1 gg_id:8784 Pseudomonas agarici str. LMG 2112T ()
EU536980.1 gg_id:283484 profile human microbiota antecubital fossa (inner elbow) skin clone nbt218b02
DQ916132.1 gg_id:197450 Pseudomonas fluorescens str. Mst8.2
AB302395.1 gg_id:221239 Pseudomonas metavorans str. F-1
AY770691.1 gg_id:108393 Pseudomonas sp. str. FR1439
FJ894581.1 gg_id:543698 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B2E; ear pu
DQ095882.1 gg_id:128167 Pseudomonas plecoglossicida str. R18
FJ393302.1 gg_id:358881 Pseudomonas plecoglossicida str. TCCC11291
EU538458.1 gg_id:285690 profile human microbiota antecubital fossa (inner elbow) skin clone nbt230a11
GU391451.1 gg_id:539092 Pseudomonas sp. str. Gd3F
FM163468.1 gg_id:336095 Pseudomonas putida str. R20
EU540073.1 gg_id:282714 profile human microbiota antecubital fossa (inner elbow) skin clone nbt245a09
EU537170.1 gg_id:280032 profile human microbiota antecubital fossa (inner elbow) skin clone nbt67g04
EU540309.1 gg_id:286020 profile human microbiota antecubital fossa (inner elbow) skin clone nbt114h11
AF291818.2 gg_id:64506 Pseudomonas andersonii str. JB413844
NR_029050.1 gg_id:588905 Pseudomonas palleroniana str. CFBP 4389
EU538927.1 gg_id:286420 profile human microbiota antecubital fossa (inner elbow) skin clone nbt95d04
EU538035.1 gg_id:285467 profile human microbiota antecubital fossa (inner elbow) skin clone nbt225c07
GQ153646.1 gg_id:557138 Pseudomonas sp. str. ANT-2400 S10
EU538345.1 gg_id:284600 profile human microbiota antecubital fossa (inner elbow) skin clone nbt84e01
GU059580.1 gg_id:514857 Pseudomonas fluorescens str. 1206
EU539619.1 gg_id:286023 profile human microbiota antecubital fossa (inner elbow) skin clone nbt242g08
AF320991.1 gg_id:21815 Pseudomonas gingeri str. NCPPB 3147
EU538170.1 gg_id:281603 profile human microbiota antecubital fossa (inner elbow) skin clone nbt81c12
EU537893.1 gg_id:286152 profile human microbiota antecubital fossa (inner elbow) skin clone nbt226g10
EU538166.1 gg_id:286284 profile human microbiota antecubital fossa (inner elbow) skin clone nbt81c07
EU535097.1 gg_id:282669 profile human skin microbiota ear punch biopsy female C57BL/6J mouse clone nbt18
FM202487.1 gg_id:344499 Pseudomonas tolaasii str. IEXb
FJ893683.1 gg_id:549927 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota WT3; ear p
EU538981.1 gg_id:283406 profile human microbiota antecubital fossa (inner elbow) skin clone nbt97f11
EU539231.1 gg_id:286159 profile human microbiota antecubital fossa (inner elbow) skin clone nbt101f10
AF326379.1 gg_id:41675 Pseudomonas syringae
EU537885.1 gg_id:284937 profile human microbiota antecubital fossa (inner elbow) skin clone nbt226d10
FJ824120.1 gg_id:565263 Pseudomonas oryzihabitans str. KCB005

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| GQ900589.1 | 573886 | 2650.1 | 2589.4 | 3540.5 | 3597.5 | 7953.0 | 5258.6 |
| EU537846.1 | 282839 | 11677.1 | 10350.3 | 6842.0 | 10363.6 | 11277.1 | 12510.2 |
| EU708323.1 | 332433 | 38.8 | 176.7 | 353.3 | 152.4 | 2997.7 | 4281.3 |
| FJ893314.1 | 558000 | 2962.3 | 1359.1 | 2369.6 | 3721.0 | 7801.1 | 8915.0 |
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| DQ916132.1 | 197450 | 250.3 | 627.4 | 1295.9 | 466.0 | 2170.8 | 3962.9 |
| AB302395.1 | 221239 | 21618.4 | 22649.0 | 19970.7 | 17902.4 | 25750.9 | 22489.2 |
| AY770691.1 | 108393 | 129.4 | 413.4 | 705.4 | 327.4 | 3733.1 | 360.8 |
| FJ894581.1 | 543698 | 1630.9 | 2411.3 | 2926.3 | 2516.5 | 3504.0 | 10830.2 |
| DQ095882.1 | 128167 | 145.6 | 435.9 | 565.5 | 197.7 | 8028.2 | 442.6 |
| FJ393302.1 | 358881 | 756.7 | 1628.0 | 3861.6 | 2558.3 | 8557.5 | 6833.0 |
| EU538458.1 | 285690 | 3286.6 | 3549.4 | 3773.1 | 4767.4 | 5932.8 | 4173.9 |
| GU391451.1 | 539092 | 988.4 | 1410.1 | 2388.0 | 1605.7 | 5961.0 | 10507.3 |
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| EU540073.1 | 282714 | 7835.5 | 8525.1 | 7032.7 | 5661.0 | 9422.4 | 9804.2 |
| EU537170.1 | 280032 | 4368.6 | 4654.9 | 3786.0 | 5617.4 | 7554.1 | 11283.7 |
| EU540309.1 | 286020 | 8414.9 | 9859.3 | 12493.9 | 11332.0 | 18642.4 | 17125.2 |
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| EU538927.1 | 286420 | 3420.2 | 3722.6 | 3784.9 | 2506.4 | 5297.1 | 9374.1 |
| EU538035.1 | 285467 | 2269.9 | 3178.3 | 3689.5 | 2362.5 | 6768.5 | 10058.3 |
| GQ153646.1 | 557138 | 327.2 | 415.8 | 657.1 | 803.5 | 728.3 | 1080.9 |
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| GU059580.1 | 514857 | 1611.2 | 1360.0 | 2404.0 | 3601.7 | 5820.1 | 7103.4 |
| EU539619.1 | 286023 | 2795.5 | 3465.2 | 4222.6 | 3331.7 | 7904.6 | 13021.2 |
| AF320991.1 | 21815 | 136.5 | 463.3 | 2955.1 | 195.0 | 6316.1 | 4877.8 |
| EU538170.1 | 281603 | 4407.9 | 5144.1 | 5551.8 | 3762.7 | 9968.2 | 11924.9 |
| EU537893.1 | 286152 | 9280.8 | 8556.4 | 4850.3 | 9248.4 | 14820.3 | 13254.6 |
| EU538166.1 | 286284 | 5706.3 | 6044.8 | 6510.9 | 6618.5 | 10530.7 | 9963.0 |
| EU535097.1 | 282669 | 5488.6 | 4093.8 | 5264.6 | 8399.8 | 5840.2 | 16348.3 |
| FM202487.1 | 344499 | 5248.1 | 4177.4 | 7998.7 | 4576.7 | 7256.6 | 12253.2 |
| FJ893683.1 | 549927 | 4316.3 | 5399.3 | 6819.8 | 4397.0 | 8259.8 | 11308.7 |
| EU538981.1 | 283406 | 6191.3 | 5419.3 | 2919.5 | 7723.7 | 9318.4 | 12600.2 |
| EU539231.1 | 286159 | 1250.9 | 2468.9 | 2024.2 | 687.7 | 3651.2 | 6828.5 |
| AF326379.1 | 41675 | 192.4 | 400.9 | 915.8 | 423.9 | 1304.0 | 2809.1 |
| EU537885.1 | 284937 | 3268.7 | 2551.1 | 2373.7 | 4971.4 | 6888.4 | 7449.0 |
| FJ824120.1 | 565263 | 112.9 | 211.4 | 1690.5 | 144.0 | 1444.4 | 5065.4 |

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EU586046.1 gg_id:269929 Pseudomonas fluorescens str. REG59
EU536445.1 gg_id:283229 profile human microbiota antecubital fossa (inner elbow) skin clone nbt214a03
EU538028.1 gg_id:279841 profile human microbiota antecubital fossa (inner elbow) skin clone nbt225b04
EU535251.1 gg_id:280823 profile human microbiota antecubital fossa (inner elbow) skin clone nbt172g09
GQ032573.1 gg_id:406089 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
EU169150.1 gg_id:237348 Pseudomonas tolaasii str. B48
FN599522.1 gg_id:565116 Pseudomonas fulva str. YMC09/4/B4619
EU511892.1 gg_id:262376 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_aaf10f12
FJ950618.1 gg_id:440750 Pseudomonas fluorescens str. c120
EU538898.1 gg_id:280517 profile human microbiota antecubital fossa (inner elbow) skin clone nbt96e11
FJ893841.1 gg_id:553685 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B1E; ear pu
EU539842.1 gg_id:283035 profile human microbiota antecubital fossa (inner elbow) skin clone nbt106b04
DQ117554.1 gg_id:155221 structure (Citrullus vulgaris SCHARD.) -based approaches and terminal fragment leng
AJ576246.1 gg_id:88635 Pseudomonas fluorescens 10CW
FJ894143.1 gg_id:568601 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B1E; ear pu
FJ605386.1 gg_id:454217 Pseudomonas poae str. AceR-3
DQ178219.1 gg_id:140655 Pseudomonas mendocina str. PC1
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EU538115.1 gg_id:285323 profile human microbiota antecubital fossa (inner elbow) skin clone nbt82c09
FJ894501.1 gg_id:565829 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B2E; ear pu
DQ318864.1 gg_id:154493 Pseudomonas syringae str. 8534
EU537937.1 gg_id:280598 profile human microbiota antecubital fossa (inner elbow) skin clone nbt227f02
FJ976605.1 gg_id:559208 Pseudomonas putida
FJ893686.1 gg_id:574564 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota WT3; ear p
AB180734.1 gg_id:102043 Pseudomonas putida str. MT4
FJ950650.1 gg_id:467776 Pseudomonas putida str. d61
EU537214.1 gg_id:282093 profile human microbiota antecubital fossa (inner elbow) skin clone nbt68f04
EF016110.1 gg_id:177261 Pseudomonas sp. str. BJSX
FJ892925.1 gg_id:563436 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota HM2; ear p
FJ893603.1 gg_id:553179 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota WT3; ear p
EU434560.1 gg_id:271676 Pseudomonas fluorescens str. b33
AM229082.1 gg_id:147892 Pseudomonas fluorescens str. C7R12
EU539097.1 gg_id:284787 profile human microbiota antecubital fossa (inner elbow) skin clone nbt98c04
EU540304.1 gg_id:285316 profile human microbiota antecubital fossa (inner elbow) skin clone nbt114g10
AJ492827.1 gg_id:63919 Pseudomonas cannabina str. CFBP 2341
EU540573.1 gg_id:283457 profile human microbiota antecubital fossa (inner elbow) skin clone nbt120b02
EU537625.1 gg_id:283084 profile human microbiota antecubital fossa (inner elbow) skin clone nbt73g10
AM184090.1 gg_id:152763 Pseudomonas syringae str. 1
DQ084459.1 gg_id:128081 Pseudomonas fluorescens str. FLM05-1
AF137359.1 gg_id:8710 Pseudomonas fluorescens
AB167245.1 gg_id:107953 Pseudomonas syringae str. c121

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| EU586046.1 | 269929 | 3594.6 | 3494.4 | 6078.3 | 5326.3 | 9321.1 | 13703.6 |
| EU536445.1 | 283229 | 1522.1 | 2194.8 | 2138.1 | 2813.6 | 4229.9 | 10143.9 |
| EU538028.1 | 279841 | 2348.2 | 3397.8 | 3650.7 | 2363.7 | 5706.0 | 10279.6 |
| EU535251.1 | 280823 | 4504.4 | 6053.8 | 6308.8 | 5135.3 | 10647.3 | 12442.4 |
| GQ032573.1 | 406089 | 4962.1 | 5108.5 | 5212.1 | 5597.2 | 8336.3 | 10835.9 |
| EU169150.1 | 237348 | 3480.7 | 2621.7 | 5527.4 | 3240.1 | 8998.2 | 9879.4 |
| FN599522.1 | 565116 | 846.4 | 1586.5 | 1409.8 | 1230.6 | 6768.2 | 3720.4 |
| EU511892.1 | 262376 | 2526.6 | 4159.3 | 6817.5 | 3763.6 | 5291.0 | 10214.8 |
| FJ950618.1 | 440750 | 6566.7 | 6789.9 | 3473.2 | 4940.2 | 9317.5 | 8625.3 |
| EU538898.1 | 280517 | 5219.0 | 6173.3 | 6473.7 | 6441.7 | 9071.0 | 12780.3 |
| FJ893841.1 | 553685 | 2147.0 | 2747.8 | 5232.3 | 4205.2 | 6225.1 | 11223.7 |
| EU539842.1 | 283035 | 2695.9 | 3158.4 | 3779.8 | 2745.6 | 9722.4 | 12903.1 |
| DQ117554.1 | 155221 | 277.5 | 873.9 | 1270.2 | 1402.5 | 4249.5 | 4808.7 |
| AJ576246.1 | 88635 | 1289.3 | 1623.2 | 3139.2 | 2607.4 | 5950.1 | 11307.7 |
| FJ894143.1 | 568601 | 11644.1 | 13881.6 | 9190.7 | 8757.0 | 14534.5 | 14962.5 |
| FJ605386.1 | 454217 | 3744.7 | 2775.1 | 3819.4 | 4980.7 | 5806.9 | 10056.3 |
| DQ178219.1 | 140655 | 485.2 | 576.0 | 3150.1 | 1365.5 | 848.8 | 2293.1 |
| EU538548.1 | 284117 | 947.7 | 1820.0 | 2332.2 | 3084.1 | 2622.2 | 11013.9 |
| EU538115.1 | 285323 | 7536.7 | 7131.7 | 5443.4 | 8919.3 | 12054.3 | 13030.9 |
| FJ894501.1 | 565829 | 545.8 | 1566.7 | 2953.3 | 987.6 | 1246.6 | 7310.8 |
| DQ318864.1 | 154493 | 316.4 | 863.2 | 1516.6 | 475.0 | 2442.2 | 5675.7 |
| EU537937.1 | 280598 | 8213.4 | 11988.2 | 1516.3 | 3780.3 | 8981.3 | 8347.5 |
| FJ976605.1 | 559208 | 1043.9 | 1565.2 | 1962.7 | 571.5 | 9534.7 | 4462.1 |
| FJ893686.1 | 574564 | 3367.9 | 3757.9 | 3549.8 | 4198.3 | 6636.4 | 10345.3 |
| AB180734.1 | 102043 | 8205.1 | 9556.3 | 8697.0 | 8263.8 | 15528.6 | 13712.0 |
| FJ950650.1 | 467776 | 8422.0 | 9045.5 | 10044.8 | 7914.9 | 15696.5 | 10385.0 |
| EU537214.1 | 282093 | 8402.8 | 7269.1 | 6035.8 | 6766.6 | 12382.3 | 12082.5 |
| EF016110.1 | 177261 | 585.7 | 908.1 | 1283.9 | 615.6 | 5065.6 | 2518.3 |
| FJ892925.1 | 563436 | 21216.1 | 17933.4 | 19688.9 | 15529.9 | 22925.7 | 21912.4 |
| FJ893603.1 | 553179 | 2020.2 | 2362.0 | 3011.3 | 1543.3 | 3760.4 | 7362.5 |
| EU434560.1 | 271676 | 2324.5 | 3038.6 | 3929.3 | 3234.4 | 6659.6 | 9988.2 |
| AM229082.1 | 147892 | 636.2 | 675.7 | 1688.5 | 889.8 | 1008.8 | 2194.8 |
| EU539097.1 | 284787 | 479.5 | 803.1 | 2261.1 | 480.4 | 1927.1 | 6719.5 |
| EU540304.1 | 285316 | 15430.7 | 18797.9 | 15235.1 | 11524.4 | 20120.1 | 17675.8 |
| AJ492827.1 | 63919 | 499.8 | 961.1 | 833.0 | 317.9 | 2929.4 | 2682.4 |
| EU540573.1 | 283457 | 936.8 | 1207.5 | 2080.9 | 1018.4 | 5793.0 | 11233.9 |
| EU537625.1 | 283084 | 892.2 | 1334.7 | 2247.2 | 973.1 | 5326.3 | 10145.6 |
| AM184090.1 | 152763 | 96.5 | 280.0 | 1139.4 | 209.8 | 4331.7 | 6395.1 |
| DQ084459.1 | 128081 | 141.4 | 357.6 | 585.3 | 209.6 | 3958.5 | 4684.3 |
| AF137359.1 | 8710 | 2861.8 | 3147.8 | 4547.4 | 4010.6 | 11791.3 | 11166.3 |
| AB167245.1 | 107953 | 249.5 | 632.2 | 910.2 | 220.6 | 3005.7 | 3446.7 |

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EU169146.1 gg_id:245783 Pseudomonas brenneri str. B46
FJ893732.1 gg_id:548088 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota WT3; ear p
EU539860.1 gg_id:284811 profile human microbiota antecubital fossa (inner elbow) skin clone nbt106g03
EU169179.1 gg_id:253450 Pseudomonas fluorescens str. B73
DQ095893.1 gg_id:130252 Pseudomonas plecoglossicida str. S4
FJ950610.1 gg_id:425507 Pseudomonas sp. str. c156
AF064458.1 gg_id:8588 Pseudomonas monteilii str. CIP 104883
AY303311.1 gg_id:132103 Pseudomonas sp. str. ps6-16
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EU539954.1 gg_id:282412 profile human microbiota antecubital fossa (inner elbow) skin clone nbt108d06
EU111725.2 gg_id:558591 Pseudomonas migulae str. CT14
AF348508.1 gg_id:74250 Pseudomonas corrugata str. ND9L
AY625608.1 gg_id:106509 Pseudomonas sp. str. E2.2
EU538196.1 gg_id:283086 profile human microbiota antecubital fossa (inner elbow) skin clone nbt82e10
FJ588703.1 gg_id:565803 Pseudomonas fluorescens str. HDY-9
EU534971.1 gg_id:281416 profile human skin microbiota ear punch biopsy female C57BL/6J mouse clone nbt18
FJ893154.1 gg_id:549797 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota HM3; ear p
EF154270.1 gg_id:188602 Pseudomonas cannabina str. 30
EU239464.1 gg_id:253435 Pseudomonas putida str. XJUHX-1
AF447394.1 gg_id:33976 Pseudomonas putida str. DLL-E4
FJ894001.1 gg_id:570570 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B1E; ear pu
EU169171.1 gg_id:250792 Pseudomonas fluorescens str. B20
EU537043.1 gg_id:281302 profile human microbiota antecubital fossa (inner elbow) skin clone nbt219e06
AF112477.1 gg_id:8726 Azospirillum sp
AY303254.1 gg_id:133637 Pseudomonas sp. str. ps10-13
GQ260082.1 gg_id:545388 Pseudomonas fluorescens str. ICIRC97
EU538363.1 gg_id:280933 profile human microbiota antecubital fossa (inner elbow) skin clone nbt87d05
AY303243.1 gg_id:132705 Pseudomonas sp. str. pcs19
EU538992.1 gg_id:286283 profile human microbiota antecubital fossa (inner elbow) skin clone nbt98c10
EU538181.1 gg_id:280147 profile human microbiota antecubital fossa (inner elbow) skin clone nbt81f12
EU538555.1 gg_id:283206 profile human microbiota antecubital fossa (inner elbow) skin clone nbt231f12
AM933495.1 gg_id:321985 Pseudomonas antarctica FB1
EU535368.1 gg_id:286102 profile human microbiota antecubital fossa (inner elbow) skin clone nbt02b04
AJ012712.1 gg_id:8701 Pseudomonas borealis MA342
DQ536514.1 gg_id:160709 Pseudomonas trivialis str. BIHB 736
FJ892816.1 gg_id:567266 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota HM1; ear p
AM262973.1 gg_id:159153 Pseudomonas oryzihabitans str. IAM 1568
FJ005063.1 gg_id:351681 feasibility and indigenous moderate-thermophilic bioleaching which old Pb/Zn smeltir
FJ607150.1 gg_id:555195 Pseudomonas syringae pv. morsprunorum str. ICMP 4991

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| FJ893732.1 | 548088 | 11980.5 | 13020.4 | 7095.5 | 9654.6 | 12796.4 | 11415.8 |
| EU539860.1 | 284811 | 7547.6 | 3370.4 | 3682.3 | 6733.2 | 5687.6 | 5684.7 |
| EU169179.1 | 253450 | 944.9 | 1566.6 | 1425.4 | 444.6 | 5952.2 | 7573.7 |
| DQ095893.1 | 130252 | 1374.9 | 1486.2 | 2604.0 | 1605.1 | 9417.9 | 1519.4 |
| FJ950610.1 | 425507 | 8946.5 | 8283.0 | 4449.7 | 8466.9 | 11219.5 | 9908.9 |
| AF064458.1 | 8588 | 10688.1 | 9209.3 | 7316.5 | 8702.5 | 12600.3 | 9192.3 |
| AY303311.1 | 132103 | 82.1 | 232.7 | 522.5 | 86.3 | 5281.8 | 4519.1 |
| EU540402.1 | 283690 | 4228.7 | 5405.5 | 6820.5 | 4388.5 | 9266.4 | 11554.4 |
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| EU111725.2 | 558591 | 3108.6 | 4182.5 | 4280.5 | 4880.3 | 10360.4 | 14527.4 |
| AF348508.1 | 74250 | 193.5 | 415.3 | 838.6 | 289.2 | 1065.3 | 4988.3 |
| AY625608.1 | 106509 | 1186.3 | 1244.6 | 1797.1 | 2035.8 | 2998.5 | 8395.2 |
| EU538196.1 | 283086 | 1715.9 | 2307.5 | 4070.2 | 3952.9 | 2656.6 | 11328.4 |
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| EU534971.1 | 281416 | 216.8 | 714.1 | 1928.1 | 341.1 | 7510.4 | 8303.2 |
| FJ893154.1 | 549797 | 6772.7 | 6798.8 | 7192.0 | 8258.1 | 7365.3 | 8136.3 |
| EF154270.1 | 188602 | 5146.3 | 4187.6 | 2105.6 | 5008.5 | 6931.2 | 9508.1 |
| EU239464.1 | 253435 | 144.5 | 332.3 | 1065.7 | 1209.9 | 391.9 | 1514.8 |
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| FJ894001.1 | 570570 | 5172.9 | 6270.2 | 6226.1 | 5657.4 | 7454.2 | 10966.4 |
| EU169171.1 | 250792 | 190.4 | 403.7 | 1540.4 | 213.4 | 2018.4 | 4998.5 |
| EU537043.1 | 281302 | 481.9 | 919.1 | 1476.1 | 1234.8 | 2556.1 | 10132.8 |
| AF112477.1 | 8726 | 228.3 | 390.1 | 670.2 | 263.6 | 1251.7 | 4483.7 |
| AY303254.1 | 133637 | 4467.2 | 3898.7 | 2661.8 | 5655.0 | 4734.4 | 7441.3 |
| GQ260082.1 | 545388 | 4467.1 | 5875.9 | 5885.6 | 6496.9 | 6636.5 | 7756.2 |
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| EU538992.1 | 286283 | 17914.6 | 20881.9 | 16176.1 | 13837.5 | 21586.8 | 20362.0 |
| EU538181.1 | 280147 | 6983.6 | 5783.5 | 2705.8 | 6712.2 | 13985.9 | 13333.1 |
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EU536420.1 gg_id:283843 profile human microbiota antecubital fossa (inner elbow) skin clone nbt213f02
EU538972.1 gg_id:281795 profile human microbiota antecubital fossa (inner elbow) skin clone nbt96c06
EU888582.1 gg_id:310807 Pseudomonas syringae str. FR2_MS8c
EU539489.1 gg_id:281181 profile human microbiota antecubital fossa (inner elbow) skin clone nbt104b06
AY622219.1 gg_id:101900 Pseudomonas fluorescens str. DR54
AY303306.1 gg_id:135272 Pseudomonas sp. str. ps4-49
AY970952.1 gg_id:115366 Pseudomonas moraviensis str. 1B4
FJ893108.1 gg_id:546592 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota HM3; ear p
FJ893415.1 gg_id:552313 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota WT1; ear p
FJ405364.1 gg_id:368656 Pseudomonas sp. str. SPe
EU536909.1 gg_id:285991 profile human microbiota antecubital fossa (inner elbow) skin clone nbt223g07
EF194769.1 gg_id:202303 Pseudomonas plecoglossicida str. AT10
EF623836.1 gg_id:245159 Pseudomonas putida str. GIST-MRP44-1
EU538635.1 gg_id:283783 profile human microbiota antecubital fossa (inner elbow) skin clone nbt234c07
L28676.1 gg_id:8572 Pseudomonas putida str. mt-2 PaW1
AM933518.1 gg_id:309848 Pseudomonas antarctica FB27
EU540148.1 gg_id:283193 profile human microbiota antecubital fossa (inner elbow) skin clone nbt246b06
EU046271.1 gg_id:253171 Pseudomonas takelamaensis str. HR2
DQ981457.1 gg_id:203619 Pseudomonas fluorescens SB2
L37365.1 gg_id:8573 Pseudomonas putida str. F1
EU159479.1 gg_id:310066 Pseudomonas fluorescens str. A7
FJ972536.1 gg_id:433249 Pseudomonas fluorescens str. NO7
AB181497.1 gg_id:109263 wastewater biofilm clone HSN-95
EU537190.1 gg_id:286488 profile human microbiota antecubital fossa (inner elbow) skin clone nbt68b06
DQ076645.1 gg_id:131495 Pseudomonas sp. str. LDC-25
AY303320.1 gg_id:135251 Pseudomonas sp. str. ps6-47
AF494092.1 gg_id:67520 Burkholderia caryophylli str. YS13
AM411057.1 gg_id:191934 Pseudomonas sp. str. Z49zhy
EU008575.1 gg_id:257715 Pseudomonas putida str. PS13
EU439420.1 gg_id:547800 Pseudomonas putida str. LH-R1
AF094732.1 gg_id:47203 Pseudomonas fluorescens str. ATCC 49642
EU539155.1 gg_id:285112 profile human microbiota antecubital fossa (inner elbow) skin clone nbt101a08
EU540291.1 gg_id:284613 profile human microbiota antecubital fossa (inner elbow) skin clone nbt114b02
FJ893413.1 gg_id:547116 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota WT1; ear p
EF509497.1 gg_id:223307 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aerug
AB234274.1 gg_id:147927 Biotransformation Polychlorinated Dioxins Microbial Dynamics Sediment Microcosm
AF494091.1 gg_id:67521 Pseudomonas nitroreducens str. 0802

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| EU536420.1 | 283843 | 4027.9 | 5431.4 | 6590.4 | 4427.3 | 10400.5 | 12190.2 |
| EU538972.1 | 281795 | 2168.6 | 3331.1 | 1859.4 | 2056.4 | 3757.7 | 10318.4 |
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| EU539489.1 | 281181 | 6635.3 | 7529.8 | 6636.6 | 6388.1 | 11458.9 | 13494.4 |
| AY622219.1 | 101900 | 454.0 | 869.3 | 1640.9 | 776.5 | 1137.0 | 7907.3 |
| AY303306.1 | 135272 | 10492.7 | 11842.8 | 9645.1 | 9576.6 | 11168.9 | 14721.6 |
| AY970952.1 | 115366 | 108.8 | 290.0 | 1638.5 | 525.8 | 2447.6 | 8640.4 |
| FJ893108.1 | 546592 | 10102.2 | 10528.8 | 8621.3 | 8179.3 | 11377.0 | 14586.8 |
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| FJ405364.1 | 368656 | 728.5 | 1195.0 | 3175.7 | 543.8 | 3869.6 | 5972.3 |
| EU536909.1 | 285991 | 6513.5 | 4903.2 | 7257.1 | 6334.5 | 10742.1 | 12798.9 |
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| EU537190.1 | 286488 | 3465.0 | 4678.8 | 4971.2 | 3355.2 | 5691.1 | 10221.7 |
| DQ076645.1 | 131495 | 264.6 | 731.7 | 2463.5 | 255.8 | 6608.1 | 3293.3 |
| AY303320.1 | 135251 | 14371.6 | 12663.8 | 8347.5 | 12025.3 | 18725.1 | 19189.0 |
| AF494092.1 | 67520 | 8002.5 | 10024.4 | 6838.4 | 7286.2 | 10098.8 | 7996.2 |
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| EU439420.1 | 547800 | 2266.8 | 1955.5 | 3964.8 | 4147.8 | 7864.4 | 6412.0 |
| AF094732.1 | 47203 | 494.3 | 862.0 | 1852.3 | 867.1 | 4512.1 | 12157.6 |
| EU539155.1 | 285112 | 2044.8 | 2858.8 | 3316.2 | 2122.9 | 3311.7 | 8870.5 |
| EU540291.1 | 284613 | 2178.4 | 1413.4 | 2083.2 | 1657.3 | 3218.3 | 5525.6 |
| FJ893413.1 | 547116 | 1547.0 | 1195.5 | 1651.5 | 3488.1 | 7641.5 | 7885.1 |
| EF509497.1 | 223307 | 4259.4 | 3129.1 | 6624.7 | 5777.1 | 12647.1 | 7864.1 |
| AB234274.1 | 147927 | 3340.6 | 3908.6 | 7454.0 | 4320.2 | 7647.8 | 6780.9 |
| AF494091.1 | 67521 | 945.3 | 1735.9 | 879.5 | 985.3 | 7454.2 | 3285.0 |

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GQ231353.1 gg_id:583913 -stable isotope probing integrated metagenomics biphenyl dioxygenase genes polyc
AB088750.2 gg_id:78890 Pseudomonas resinovorans str. CA06
AB234275.1 gg_id:146760 Biotransformation Polychlorinated Dioxins Microbial Dynamics Sediment Microcosm
GU057052.1 gg_id:582539 Pseudomonas sp. str. VSR
AY486367.1 gg_id:202697 Pseudomonas aeruginosa str. AU4594
X06684.1 gg_id:8424 Pseudomonas aeruginosa str. DSM50071
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AF140011.1 gg_id:8525 Pseudomonas pseudoalcaligenes str. ML-A04
AY486371.1 gg_id:99682 Pseudomonas aeruginosa str. AU5056
FJ675201.1 gg_id:518305 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
FJ658037.1 gg_id:533358 Metalworking Fluids and Aerosols Metallurgy Plant metalworking fluid clone Winter_
DQ350823.1 gg_id:147528 Pseudomonas aeruginosa str. B13
FM992407.1 gg_id:574081 Pseudomonas sp. JPM-2009-2
AJ550306.1 gg_id:81887 Pseudomonas aeruginosa OK1
EF515555.1 gg_id:218565 Electricigen Enrichment MFC full-scale anaerobic bioreactor sludge treating brewery
GU217696.1 gg_id:536568 Pseudomonas sp. str. ljh-16
EF208965.1 gg_id:175605 Pseudomonas mendocina str. B6-1
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FJ226424.1 gg_id:356153 Pseudomonas aeruginosa str. NAPCC-1
EU195558.1 gg_id:237500 Pseudomonas aeruginosa str. LP8
FJ152919.1 gg_id:320016 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX4CE
AY947918.1 gg_id:141280 Synchrony and seasonality two temperate rivers USA: Massachusetts Ipswich River c
EF200115.1 gg_id:202547 mine sulfur-cycling assemblage subpermafrost fracture waters Arctic gold mines clon
DQ916277.2 gg_id:161990 Pseudomonas lindanilytica str. IPL-1
EU538163.1 gg_id:280131 profile human microbiota antecubital fossa (inner elbow) skin clone nbt81b11
EU274299.1 gg_id:251989 Azotobacter chroococcum str. AZO2
DQ149582.1 gg_id:160454 Pseudomonas aeruginosa str. HS-D38
GU391472.1 gg_id:572803 Pseudomonas fluorescens str. Gd2F
FJ169986.1 gg_id:344935 Pseudomonas sp. str. E505-11
AF140013.1 gg_id:23182 Pseudomonas pseudoalcaligenes str. ML-A09
GQ149776.1 gg_id:565857 Burkholderia cepacia str. BCC933
FJ675469.1 gg_id:531082 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
EU365515.1 gg_id:261544 Pseudomonas sp. str. BSs20085
EU600372.1 gg_id:271714 Pseudomonas poae str. RT5RP2

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| AB010851.1 | 8534 | 288.5 | 523.3 | 1405.6 | 670.4 | 3925.6 | 3046.8 |
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| AB088750.2 | 78890 | 372.1 | 581.4 | 321.4 | 235.3 | 6316.1 | 1940.6 |
| AB234275.1 | 146760 | 3467.8 | 2584.0 | 3562.9 | 4958.6 | 5857.9 | 4965.4 |
| GU057052.1 | 582539 | 1646.1 | 2252.9 | 1401.6 | 2669.7 | 11998.9 | 3509.2 |
| AY486367.1 | 202697 | 6600.7 | 5383.5 | 3268.1 | 9071.6 | 16830.6 | 10776.2 |
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| AF140011.1 | 8525 | 60.9 | 133.7 | 216.1 | 107.3 | 393.4 | 2278.8 |
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| FJ658037.1 | 533358 | 163.1 | 310.4 | 799.8 | 176.2 | 3290.5 | 1542.6 |
| DQ350823.1 | 147528 | 1202.6 | 838.4 | 1308.9 | 719.3 | 14961.8 | 8282.2 |
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| AJ550306.1 | 81887 | 4807.0 | 6247.5 | 2613.8 | 3581.9 | 9215.6 | 3726.6 |
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| GU217696.1 | 536568 | 5161.5 | 5132.4 | 7973.2 | 7525.0 | 9212.9 | 6298.7 |
| EF208965.1 | 175605 | 22.7 | 19.5 | 19.2 | 49.7 | 115.7 | 19.0 |
| EF179862.1 | 198175 | 8645.8 | 4618.0 | 7647.6 | 8371.0 | 12165.8 | 8730.0 |
| FJ556919.1 | 586137 | 3026.7 | 2618.9 | 4743.9 | 5057.1 | 11007.2 | 6312.0 |
| EU537862.1 | 281450 | 7952.2 | 7784.2 | 9240.0 | 7994.4 | 12718.6 | 13796.6 |
| EF511012.1 | 225088 | 1128.6 | 2001.2 | 1442.1 | 960.0 | 5911.2 | 4023.4 |
| AM293678.1 | 242660 | 576.0 | 1138.4 | 2470.1 | 1287.6 | 6908.3 | 5013.3 |
| DQ256334.1 | 142026 | 37.5 | 56.9 | 41.3 | 81.7 | 76.1 | 258.7 |
| EU370415.1 | 260507 | 4279.5 | 3982.3 | 5171.2 | 4146.8 | 10554.6 | 9102.2 |
| FJ226424.1 | 356153 | 10566.2 | 12507.0 | 3603.9 | 8559.7 | 19081.9 | 9904.0 |
| EU195558.1 | 237500 | 1373.9 | 1407.2 | 1752.8 | 1136.6 | 15687.6 | 7233.8 |
| FJ152919.1 | 320016 | 2715.9 | 1808.5 | 492.8 | 2086.7 | 3412.9 | 2359.1 |
| AY947918.1 | 141280 | 9621.7 | 5163.7 | 6673.3 | 9277.2 | 9822.4 | 7378.0 |
| EF200115.1 | 202547 | 8030.6 | 7076.4 | 5687.3 | 7335.5 | 14516.6 | 10685.4 |
| DQ916277.2 | 161990 | 1250.5 | 1280.9 | 1535.4 | 2476.4 | 3240.1 | 3864.4 |
| EU538163.1 | 280131 | 1389.4 | 2009.5 | 2422.6 | 2516.0 | 2731.6 | 9908.6 |
| EU274299.1 | 251989 | 1254.5 | 2114.7 | 2948.7 | 2333.3 | 4756.6 | 6123.9 |
| DQ149582.1 | 160454 | 11196.8 | 9885.3 | 7313.7 | 10643.6 | 17222.8 | 9001.6 |
| GU391472.1 | 572803 | 222.6 | 461.5 | 1063.7 | 159.2 | 1185.4 | 2017.0 |
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| GQ149776.1 | 565857 | 3278.9 | 3393.6 | 2737.1 | 3684.5 | 7817.7 | 11836.8 |
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EU434518.1 gg_id:265493 Pseudomonas fluorescens str. b225
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EF053508.2 gg_id:328163 Pseudomonas aeruginosa MCCB 103
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AM111047.1 gg_id:140795 Pseudomonas sp. str. 7070
FJ901022.1 gg_id:513124 Polymorphism microbial reservoirs water cut stage oil field clone G-68
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FJ976651.1 gg_id:450877 Pseudomonas aeruginosa str. DBT1BNH3
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EU428823.1 gg_id:262434 Pseudomonas aeruginosa str. RRLJH2

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| EU854429.1 | 309948 | 203.7 | 622.4 | 820.2 | 371.0 | 8965.2 | 7762.5 |
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| EU841537.1 | 324692 | 170.5 | 761.3 | 1343.7 | 359.8 | 6432.2 | 1883.2 |
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| GU395986.1 | 520012 | 672.0 | 477.7 | 1036.6 | 800.7 | 11208.7 | 1423.4 |
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| GQ388959.1 | 511710 | 5039.5 | 2952.9 | 6918.3 | 5736.5 | 7147.5 | 4729.6 |
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| FJ901022.1 | 513124 | 6980.0 | 7291.3 | 13338.8 | 6327.3 | 15730.8 | 10805.1 |
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| FJ889644.1 | 563629 | 20.2 | 33.7 | 32.2 | 41.1 | 739.4 | 1421.3 |
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| AB037561.1 | 74648 | 4987.7 | 4165.3 | 6988.9 | 5685.4 | 16902.8 | 7253.9 |
| AY770964.1 | 108340 | 509.8 | 913.6 | 1230.7 | 581.0 | 4049.3 | 4759.4 |
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| FJ009387.1 | 318773 | 9123.1 | 8243.9 | 4939.6 | 8766.9 | 16960.8 | 9690.7 |
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EU821343.1 gg_id:342183 Pseudomonas mendocina str. LM7
DQ530464.1 gg_id:164982 Pseudomonas sp. str. gap-f-39
AJ316017.1 gg_id:29570 Paederus melanurus endosymbiont
EF515488.1 gg_id:222712 Electricigen Enrichment MFC full-scale anaerobic bioreactor sludge treating brewery
FJ950669.1 gg_id:387747 Pseudomonas sp. str. d130
EU043330.1 gg_id:324324 Pseudomonas mendocina str. PASS3-slimb
DQ803319.1 gg_id:199647 human fecal clone RL311_aam23h11
EU169149.1 gg_id:245779 Pseudomonas tolaasii str. B37
DQ497784.1 gg_id:161169 Microbial within Ground Support Equipment and Flight Hardware Station's Internal
GU723305.1 gg_id:528277 Pseudomonas aeruginosa str. PSCMST2
EU373426.1 gg_id:265122 Pseudomonas aeruginosa str. YRR02
AJ550466.1 gg_id:83866 Pseudomonas alcaliphila
GQ388955.1 gg_id:511762 quality deterioration drinking system during serious red water outbreak clone J130
Z76666.1 gg_id:8520 Pseudomonas pseudoalcaligenes str. LMG 1225T ()
DQ095892.1 gg_id:134548 Pseudomonas plecoglossicida str. S3
AB021373.1 gg_id:8434 Pseudomonas resinovorans str. ATCC 14235T
AF094735.1 gg_id:73739 Pseudomonas oleovorans str. ATCC 8062
AF139996.1 gg_id:53457 Pseudomonas sp. str. ML-120
EF586018.1 gg_id:240439 Methanol-assimilating anaerobic solid waste digester fed methanol clone M35_D20_
AY486387.1 gg_id:105677 Pseudomonas pseudoalcaligenes str. AU4510
DQ279822.1 gg_id:144098 Pseudomonas sp. str. D14
AY689052.1 gg_id:100960 Pseudomonas sp. str. 6C_12
FJ901043.1 gg_id:549234 Polymorphism microbial reservoirs water cut stage oil field clone G-84
EF102842.1 gg_id:241788 Pseudomonas aeruginosa str. P-5-3
FJ853495.1 gg_id:539000 Pseudomonas aeruginosa str. ZSL-2
EF608177.1 gg_id:573436 Pseudomonas aeruginosa str. HT25
DQ459316.1 gg_id:157858 Pseudomonas aeruginosa str. NRRL B-14935
FM955874.1 gg_id:549837 Pseudomonas sp. str. Asd M6-6
AY953147.1 gg_id:115164 Pseudomonas otitidis str. MCC10330
EU272857.1 gg_id:363576 Pseudomonas aeruginosa str. MK50
DQ270690.1 gg_id:143958 Pseudomonas sp. B-2051
FN429930.1 gg_id:584843 Pseudomonas sp. C2(2009) str. C2
DQ984615.1 gg_id:253301 LY oil-contaminated soil clone LYC240
EU043329.1 gg_id:315956 Pseudomonas mendocina str. PASS3-bpib
EU857418.1 gg_id:314447 Pseudomonas putida str. BF-S5
FJ462715.1 gg_id:550332 Pseudomonas citronellolis str. YS-8
EF101781.1 gg_id:181146 Effect carbon source addition method on enrichment salicylate-degrading organisms
EU579530.1 gg_id:263193 Pseudomonas pseudoalcaligenes str. R32

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| FJ675189.1 | 526355 | 88.6 | 193.7 | 766.4 | 79.3 | 5335.6 | 471.2 |
| FJ358435.1 | 358990 | 944.7 | 1608.5 | 4081.8 | 2023.2 | 12946.6 | 8628.4 |
| DQ289071.1 | 144048 | 1582.1 | 1844.1 | 2107.7 | 2446.9 | 11812.7 | 5942.1 |
| EU821343.1 | 342183 | 800.0 | 549.4 | 875.9 | 581.0 | 6170.9 | 1967.6 |
| DQ530464.1 | 164982 | 1130.4 | 2125.7 | 3735.9 | 2033.6 | 13727.8 | 11876.1 |
| AJ316017.1 | 29570 | 39.3 | 54.2 | 171.9 | 109.5 | 3172.1 | 131.5 |
| EF515488.1 | 222712 | 3188.9 | 4246.3 | 4093.5 | 1844.8 | 8644.1 | 8479.3 |
| FJ950669.1 | 387747 | 6770.4 | 7494.8 | 6004.2 | 7100.9 | 9615.1 | 8023.2 |
| EU043330.1 | 324324 | 300.9 | 502.3 | 838.5 | 526.8 | 6042.3 | 2351.3 |
| DQ803319.1 | 199647 | 4039.1 | 3431.8 | 6425.2 | 4270.2 | 14572.3 | 9341.8 |
| EU169149.1 | 245779 | 2968.1 | 3562.1 | 2893.5 | 2882.3 | 5144.7 | 11551.2 |
| DQ497784.1 | 161169 | 504.6 | 208.4 | 252.1 | 192.0 | 953.1 | 1692.3 |
| GU723305.1 | 528277 | 3593.1 | 3501.0 | 4531.9 | 4243.0 | 15715.0 | 5989.8 |
| EU373426.1 | 265122 | 2813.2 | 3905.7 | 1682.5 | 2030.3 | 16362.6 | 6429.2 |
| AJ550466.1 | 83866 | 1404.7 | 1119.3 | 1535.6 | 1941.4 | 5926.0 | 4234.2 |
| GQ388955.1 | 511762 | 1751.6 | 1102.0 | 3288.9 | 1050.6 | 7005.8 | 4459.9 |
| Z76666.1 | 8520 | 129.5 | 232.1 | 446.3 | 134.4 | 3027.4 | 719.2 |
| DQ095892.1 | 134548 | 651.6 | 1480.1 | 1924.1 | 2535.6 | 6707.3 | 3756.3 |
| AB021373.1 | 8434 | 442.5 | 1433.7 | 2500.6 | 898.4 | 9967.3 | 3304.1 |
| AF094735.1 | 73739 | 622.4 | 493.3 | 1130.0 | 741.1 | 7321.5 | 5298.6 |
| AF139996.1 | 53457 | 1958.9 | 2714.7 | 1395.9 | 1662.3 | 4817.2 | 3646.9 |
| EF586018.1 | 240439 | 69.7 | 226.2 | 1290.4 | 225.3 | 1466.7 | 3336.5 |
| AY486387.1 | 105677 | 109.3 | 193.1 | 869.4 | 190.3 | 4190.0 | 3005.6 |
| DQ279822.1 | 144098 | 4496.5 | 4501.3 | 7803.0 | 4277.5 | 14962.7 | 6163.4 |
| AY689052.1 | 100960 | 683.9 | 1240.0 | 1470.2 | 1995.4 | 6347.7 | 6169.9 |
| FJ901043.1 | 549234 | 5211.6 | 3819.3 | 5017.9 | 5093.3 | 12988.6 | 6098.0 |
| EF102842.1 | 241788 | 4814.9 | 5153.0 | 3033.8 | 4637.2 | 10504.2 | 5685.3 |
| FJ853495.1 | 539000 | 3264.3 | 4971.2 | 1499.3 | 2391.0 | 14199.6 | 6016.8 |
| EF608177.1 | 573436 | 3917.8 | 4188.5 | 3252.7 | 3054.3 | 14067.2 | 6934.0 |
| DQ459316.1 | 157858 | 2213.2 | 2816.8 | 1873.4 | 2762.1 | 12577.4 | 5107.9 |
| FM955874.1 | 549837 | 2554.1 | 2345.0 | 1718.4 | 1625.6 | 3789.3 | 8035.2 |
| AY953147.1 | 115164 | 671.0 | 663.8 | 1389.8 | 811.9 | 12477.2 | 2050.5 |
| EU272857.1 | 363576 | 4760.5 | 4705.5 | 3770.8 | 4243.0 | 12928.9 | 6642.6 |
| DQ270690.1 | 143958 | 537.3 | 296.8 | 148.8 | 1088.1 | 659.9 | 859.1 |
| FN429930.1 | 584843 | 143.8 | 450.6 | 880.2 | 285.5 | 1524.4 | 1525.1 |
| DQ984615.1 | 253301 | 1690.8 | 1795.2 | 2913.3 | 2277.2 | 16369.2 | 6966.3 |
| EU043329.1 | 315956 | 280.3 | 465.1 | 666.6 | 266.8 | 6326.4 | 1775.6 |
| EU857418.1 | 314447 | 3601.9 | 3629.8 | 6287.5 | 4866.0 | 9721.1 | 6916.1 |
| FJ462715.1 | 550332 | 3515.6 | 3209.3 | 2756.5 | 4533.2 | 11733.3 | 7134.3 |
| EF101781.1 | 181146 | 5837.2 | 3023.4 | 9636.8 | 5712.0 | 8175.7 | 3967.9 |
| EU579530.1 | 263193 | 3875.6 | 3271.9 | 2369.3 | 3238.3 | 7662.5 | 3364.6 |

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EU841539.1 gg_id:321313 Pseudomonas sp. str. 418
EU937756.1 gg_id:304789 Pseudomonas sp. str. JG 13 Iti 9
GQ389015.1 gg_id:580124 quality deterioration drinking system during serious red water outbreak clone J63
AY748891.1 gg_id:104313 Pseudomonas aeruginosa N17.35
EU109736.1 gg_id:256066 Pseudomonas aeruginosa str. CR-25
EF091149.1 gg_id:248422 Pseudomonas sp. str. 19rlim
AJ278107.1 gg_id:66198 Pseudomonas sp. str. KI
FJ657973.1 gg_id:543148 Metalworking Fluids and Aerosols Metallurgy Plant metalworking fluid clone Winter_
AF139998.1 gg_id:53970 Pseudomonas sp. str. ML-124
EF509416.1 gg_id:220349 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aerug
X92133.1 gg_id:71972 Lake Elmenteita isolate 45E3
EU888911.1 gg_id:312742 Pseudomonas sp. str. CL-AP6
EU538380.1 gg_id:286403 profile human microbiota antecubital fossa (inner elbow) skin clone nbt88h01
DQ872929.1 gg_id:163170 Pseudomonas sp. str. BSL3
AF448033.1 gg_id:111937 Pseudomonas aeruginosa str. S1-1
FJ900979.1 gg_id:510176 Polymorphism microbial reservoirs water cut stage oil field clone G-15
EU535314.1 gg_id:280820 profile human microbiota antecubital fossa (inner elbow) skin clone nbt01e06
FJ901060.1 gg_id:509240 Polymorphism microbial reservoirs water cut stage oil field clone G-98
EU311211.1 gg_id:244918 Pseudomonas mendocina str. zyj1-4
GQ389188.1 gg_id:543389 quality deterioration drinking system during serious red water outbreak clone D60
GQ884172.1 gg_id:560075 Pseudomonas aeruginosa str. SH-P
AY738649.1 gg_id:150711 Pseudomonas putida str. HOT19
AF225956.1 gg_id:28841 Pseudomonas aeruginosa
FJ830845.1 gg_id:540820 Pseudomonas alcaligenes str. Y34
FJ674304.1 gg_id:526122 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
EU034723.1 gg_id:571092 Pseudomonas aeruginosa str. swu31-2
AF118398.2 gg_id:66758 Pseudomonas sp. str. AST1
FJ893914.1 gg_id:536878 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B1E; ear pu
AB037546.1 gg_id:47079 Pseudomonas aeruginosa str. #47
EU538530.1 gg_id:282256 profile human microbiota antecubital fossa (inner elbow) skin clone nbt231c12
L37366.1 gg_id:8488 Pseudomonas mendocina str. KR
DQ300317.1 gg_id:141270 Pseudomonas sp. str. L24
AF448038.1 gg_id:112197 Pseudomonas aeruginosa str. SCD-1
EU538383.1 gg_id:284088 profile human microbiota antecubital fossa (inner elbow) skin clone nbt87b06
DQ985230.1 gg_id:182210 Pseudomonas sp. str. Man1
GQ388928.1 gg_id:575928 quality deterioration drinking system during serious red water outbreak clone J105
FJ657941.1 gg_id:573409 Metalworking Fluids and Aerosols Metallurgy Plant metalworking fluid clone Winter_
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DQ837570.1 gg_id:166237 Pseudomonas sp. K1
EF011163.1 gg_id:173833 Pseudomonas aeruginosa str. PT2
EF509324.1 gg_id:221914 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aerug

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| EU841539.1 | 321313 | 112.7 | 287.1 | 385.5 | 196.2 | 163.5 | 363.8 |
| EU937756.1 | 304789 | 4213.8 | 5864.2 | 2077.7 | 3125.7 | 15243.5 | 7704.3 |
| GQ389015.1 | 580124 | 10987.3 | 6134.0 | 8698.3 | 10879.0 | 16696.5 | 11353.1 |
| AY748891.1 | 104313 | 93.1 | 161.3 | 314.4 | 437.8 | 6306.4 | 715.8 |
| EU109736.1 | 256066 | 1405.6 | 1217.5 | 4301.4 | 2776.1 | 16524.9 | 5720.9 |
| EF091149.1 | 248422 | 642.9 | 465.1 | 1085.1 | 531.1 | 4450.5 | 1252.0 |
| AJ278107.1 | 66198 | 2902.9 | 2352.6 | 1873.1 | 2687.8 | 8597.6 | 4947.4 |
| FJ657973.1 | 543148 | 7462.2 | 7807.4 | 4376.0 | 6655.8 | 13733.5 | 8578.6 |
| AF139998.1 | 53970 | 326.4 | 474.1 | 966.3 | 395.1 | 6027.3 | 4018.2 |
| EF509416.1 | 220349 | 1632.8 | 1717.8 | 882.4 | 1711.0 | 15432.8 | 6773.0 |
| X92133.1 | 71972 | 25.0 | 41.7 | 159.0 | 127.2 | 3916.6 | 628.2 |
| EU888911.1 | 312742 | 1406.7 | 2164.1 | 2219.1 | 1309.5 | 5189.8 | 7006.3 |
| EU538380.1 | 286403 | 3256.3 | 3547.9 | 3237.8 | 2617.0 | 13411.0 | 11258.2 |
| DQ872929.1 | 163170 | 3652.4 | 1276.8 | 1509.6 | 2128.2 | 9329.6 | 3075.8 |
| AF448033.1 | 111937 | 5538.5 | 6028.0 | 14227.6 | 6743.5 | 15353.4 | 10583.9 |
| FJ900979.1 | 510176 | 1502.2 | 1438.4 | 1773.2 | 2846.9 | 2506.6 | 3129.4 |
| EU535314.1 | 280820 | 8740.8 | 12007.6 | 6488.2 | 9377.2 | 10058.9 | 11376.5 |
| FJ901060.1 | 509240 | 2338.0 | 1556.4 | 5071.7 | 2904.9 | 8184.9 | 3850.9 |
| EU311211.1 | 244918 | 153.0 | 276.8 | 721.1 | 262.2 | 2947.2 | 1306.1 |
| GQ389188.1 | 543389 | 3851.7 | 5511.6 | 3343.9 | 4819.3 | 11205.3 | 8703.5 |
| GQ884172.1 | 560075 | 9628.8 | 9643.8 | 7959.6 | 8364.9 | 16300.1 | 11288.9 |
| AY738649.1 | 150711 | 2531.8 | 2970.7 | 4044.6 | 3161.0 | 8662.4 | 5671.6 |
| AF225956.1 | 28841 | 11229.5 | 8512.6 | 8321.6 | 11567.8 | 12146.6 | 10459.9 |
| FJ830845.1 | 540820 | 521.2 | 467.1 | 876.5 | 319.7 | 8670.3 | 4592.9 |
| FJ674304.1 | 526122 | 4049.1 | 3834.4 | 3482.6 | 2152.7 | 9920.4 | 4400.9 |
| EU034723.1 | 571092 | 4633.7 | 4580.0 | 3746.1 | 3787.0 | 14144.6 | 6582.7 |
| AF118398.2 | 66758 | 4180.0 | 4610.1 | 5331.2 | 2944.3 | 14594.7 | 6400.6 |
| FJ893914.1 | 536878 | 11805.7 | 11575.8 | 14397.3 | 9546.3 | 13889.3 | 17100.7 |
| AB037546.1 | 47079 | 4252.4 | 3610.0 | 6187.1 | 4720.2 | 11905.4 | 6229.7 |
| EU538530.1 | 282256 | 3967.3 | 4302.0 | 4131.5 | 5783.9 | 6928.8 | 10194.0 |
| L37366.1 | 8488 | 2515.2 | 1544.9 | 2140.8 | 3527.2 | 9876.3 | 4599.0 |
| DQ300317.1 | 141270 | 11713.3 | 12188.8 | 8329.7 | 12279.6 | 18117.9 | 12316.1 |
| AF448038.1 | 112197 | 12335.0 | 13351.8 | 9602.6 | 9903.8 | 15891.8 | 12375.2 |
| EU538383.1 | 284088 | 14136.4 | 15214.5 | 10680.5 | 12142.3 | 15760.5 | 12652.9 |
| DQ985230.1 | 182210 | 188.5 | 527.7 | 1857.4 | 370.6 | 681.6 | 1578.1 |
| GQ388928.1 | 575928 | 222.0 | 415.2 | 939.3 | 297.7 | 6065.8 | 3887.3 |
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| EU082809.1 | 245977 | 7471.9 | 6437.9 | 4750.3 | 2492.7 | 10645.8 | 11276.3 |
| DQ837570.1 | 166237 | 7077.3 | 5492.5 | 6704.2 | 8388.3 | 12904.4 | 9913.5 |
| EF011163.1 | 173833 | 5130.7 | 4888.6 | 7321.4 | 6686.3 | 15901.9 | 8365.6 |
| EF509324.1 | 221914 | 1110.1 | 1192.0 | 2859.3 | 2839.7 | 16244.1 | 3790.4 |

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FJ715961.1 gg_id:550759 Pseudomonas aeruginosa
GQ388981.1 gg_id:511565 quality deterioration drinking system during serious red water outbreak clone J30
EU286805.1 gg_id:257108 Pseudomonas sp. str. S3-3
DQ308541.1 gg_id:145218 Pseudomonas sp. L6
FJ184324.1 gg_id:319416 structure and physiology pyrene-degrading consortia growing biofilms model trickle c
FJ674967.1 gg_id:513753 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
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GQ222267.1 gg_id:552840 Pseudomonas reactans str. AS1
FJ901156.1 gg_id:541120 Polymorphism microbial reservoirs water cut stage oil field clone Z-85
Z76672.1 gg_id:70154 Pseudomonas aeruginosa str. DSM 50071T ()
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AY443041.1 gg_id:105353 Pseudomonas sp. str. HS5322
DQ420635.1 gg_id:151159 Pseudomonas aeruginosa str. PGSL 03
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EU939691.1 gg_id:309323 Pseudomonas sp. str. SC06
EU780001.1 gg_id:326591 Pseudomonas pseudoalcaligenes str. 23
EU252491.1 gg_id:237266 Pseudomonas sp. str. AM3
AB021419.1 gg_id:8561 Pseudomonas denitrificans str. IAM 12023
X92134.1 gg_id:43286 Lake Nakuru isolate 52N3
DQ140184.1 gg_id:139321 Pseudomonas sp. LJLP1-15
AM088480.1 gg_id:142278 Pseudomonas citronellolis str. BG 6903
FJ893386.1 gg_id:548779 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota WT1; ear p
EU308476.1 gg_id:357842 Pseudomonas sp str. TA022
AJ853507.1 gg_id:110023 landfill leachate clone GZKB12
AB088116.1 gg_id:78808 Pseudomonas thermaerum str. T1
FJ937924.1 gg_id:513078 Pseudomonas sp. str. LS197
FJ901066.1 gg_id:513913 Polymorphism microbial reservoirs water cut stage oil field clone G-104
EU661707.1 gg_id:283175 Pseudomonas aeruginosa str. NBRAJG91
FJ675280.1 gg_id:527897 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
GQ388992.1 gg_id:587812 quality deterioration drinking system during serious red water outbreak clone J40
AY699593.1 gg_id:106717 soil contaminated with polyaromatic hydrocarbons clone SAL2d7
EU931560.1 gg_id:336985 Pseudomonas aeruginosa str. ZFJ-5
DQ365584.1 gg_id:145159 Pseudomonas sp. str. GS08
GQ241352.1 gg_id:570943 Pseudomonas sp. str. C23
AF237678.1 gg_id:18018 Pseudomonas aeruginosa str. M2E
DQ481477.1 gg_id:157307 Pseudomonas putida str. VTs-34
EU536369.1 gg_id:285992 profile human microbiota antecubital fossa (inner elbow) skin clone nbt62e06

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| FJ715961.1 | 550759 | 6002.7 | 8169.9 | 6657.6 | 8565.0 | 13390.2 | 12016.3 |
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| EU286805.1 | 257108 | 828.0 | 1319.2 | 1608.9 | 1769.3 | 5363.3 | 4592.0 |
| DQ308541.1 | 145218 | 3476.4 | 3189.1 | 5765.6 | 4989.4 | 16922.9 | 6310.2 |
| FJ184324.1 | 319416 | 162.5 | 540.2 | 1688.8 | 1095.7 | 510.6 | 3807.5 |
| FJ674967.1 | 513753 | 7784.5 | 7314.5 | 5376.5 | 7700.0 | 16446.7 | 11081.5 |
| AB361591.1 | 267729 | 7865.6 | 6076.4 | 5262.7 | 9100.7 | 18523.2 | 11218.0 |
| GQ222267.1 | 552840 | 11819.0 | 11315.8 | 9311.9 | 12445.9 | 12708.6 | 12094.1 |
| FJ901156.1 | 541120 | 6104.4 | 6428.9 | 2490.6 | 6008.6 | 11927.7 | 5622.0 |
| Z76672.1 | 70154 | 1482.4 | 2678.5 | 1262.3 | 922.1 | 15249.2 | 5245.1 |
| AY264292.1 | 85816 | 6862.3 | 7219.8 | 3028.2 | 5592.5 | 16764.6 | 7544.8 |
| AY443041.1 | 105353 | 2669.2 | 2881.3 | 2073.8 | 2223.7 | 3880.0 | 4304.0 |
| DQ420635.1 | 151159 | 18909.3 | 18299.9 | 13751.1 | 16069.8 | 20948.0 | 16798.1 |
| AM697417.1 | 225569 | 54.9 | 105.2 | 135.6 | 105.3 | 315.5 | 1867.5 |
| EU539418.1 | 285673 | 2946.0 | 3419.6 | 5421.9 | 4199.1 | 4484.3 | 8551.5 |
| EU939691.1 | 309323 | 1914.9 | 1434.6 | 2542.7 | 2267.9 | 5296.2 | 4959.5 |
| EU780001.1 | 326591 | 6473.4 | 2665.7 | 2433.9 | 3948.6 | 12293.4 | 4280.3 |
| EU252491.1 | 237266 | 2188.5 | 1787.5 | 1676.3 | 2589.7 | 6001.8 | 3774.3 |
| AB021419.1 | 8561 | 3336.5 | 3406.8 | 1951.9 | 4332.1 | 11395.4 | 7825.4 |
| X92134.1 | 43286 | 1206.0 | 2269.6 | 1476.7 | 535.0 | 13848.3 | 1324.6 |
| DQ140184.1 | 139321 | 547.9 | 1125.3 | 3043.3 | 709.1 | 11041.1 | 1967.1 |
| AM088480.1 | 142278 | 752.3 | 1202.7 | 3092.7 | 3413.3 | 5036.9 | 4887.4 |
| FJ893386.1 | 548779 | 1061.4 | 1795.6 | 2683.6 | 1436.0 | 6244.9 | 11946.8 |
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| AJ853507.1 | 110023 | 2363.6 | 3390.8 | 2415.2 | 2266.4 | 4165.2 | 3212.4 |
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| GQ388992.1 | 587812 | 8960.0 | 10137.5 | 9761.7 | 8431.0 | 16272.8 | 11422.4 |
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FJ494693.1 gg_id:512429 Pseudomonas putida str. SY45
EU536306.1 gg_id:283773 profile human microbiota antecubital fossa (inner elbow) skin clone nbt62c10
NZ_ABZR01000729.1 gg_id:569411 Pseudomonas syringae pv. oryzae str. 1_6
EU214613.1 gg_id:328976 Pseudomonas fluorescens yb126
EU734169.1 gg_id:461530 Pseudomonas plecoglossicida
AM410631.1 gg_id:177686 Pseudomonas fluorescens str. 9zhy
EU537179.1 gg_id:284941 profile human microbiota antecubital fossa (inner elbow) skin clone nbt68a03
FJ892842.1 gg_id:559778 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota HM1; ear p
EF051575.2 gg_id:198685 Pseudomonas putida str. T7-5
FJ607147.1 gg_id:513959 Pseudomonas syringae pv. actinidiae str. ICMP 9853
EF515714.1 gg_id:223417 Electricigen Enrichment MFC full-scale anaerobic bioreactor sludge treating brewery
AY206685.1 gg_id:82206 Pseudomonas jessenii str. PS06
EU535797.1 gg_id:282047 profile human microbiota antecubital fossa (inner elbow) skin clone nbt10h06
FJ894178.1 gg_id:540187 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B2E; ear pu
AY267192.1 gg_id:106450 Pseudomonas veronii str. 16-6A
AY970951.1 gg_id:115314 Pseudomonas vranovensis str. 2B2
DQ868767.1 gg_id:165580 Pseudomonas tuomuerense str. Yuhua Xin
GQ200823.1 gg_id:533247 Pseudomonas plecoglossicida str. SP8
AY054374.1 gg_id:105822 Pseudomonas pavonaceae
EU538192.1 gg_id:282127 profile human microbiota antecubital fossa (inner elbow) skin clone nbt82b02
EF561642.1 gg_id:228381 Pseudomonas veronii str. T1/1
AF074383.1 gg_id:8628 Pseudomonas migulae str. CIP 105470
FJ894073.1 gg_id:534048 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B1E; ear pu
EU540285.1 gg_id:282167 profile human microbiota antecubital fossa (inner elbow) skin clone nbt113h06
GU185861.1 gg_id:577433 Pseudomonas koreensis str. PBRs7
EU797470.1 gg_id:350105 sediment station DBSE Northern Bering Sea clone 130D73
AY622320.1 gg_id:102554 Pseudomonas putida str. AS90
EF011017.1 gg_id:362986 Pseudomonas putida str. WP090
FM864215.1 gg_id:362580 Pseudomonas tolaasii str. LPPA 532
EU826028.1 gg_id:333541 Pseudomonas putida str. SRI156
EU538858.1 gg_id:284602 profile human microbiota antecubital fossa (inner elbow) skin clone nbt95c02
GU391485.1 gg_id:537184 Pseudomonas sp. str. Pd1T
FJ894574.1 gg_id:555704 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B2E; ear pu
EU536488.1 gg_id:285516 profile human microbiota antecubital fossa (inner elbow) skin clone nbt214f08
FJ893512.1 gg_id:572521 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota WT2; ear p
EU538922.1 gg_id:281466 profile human microbiota antecubital fossa (inner elbow) skin clone nbt95c04
EU620069.1 gg_id:269290 Pseudomonas putida str. GNA5
EU434528.1 gg_id:264077 Pseudomonas fluorescens str. b338

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| GU354317.1 | 523150 | 2577.0 | 2910.7 | 4426.7 | 2370.6 | 9839.1 | 6202.4 |
| AY866408.1 | 111749 | 716.0 | 941.4 | 2330.8 | 485.8 | 5217.0 | 5887.7 |
| AY308050.1 | 88404 | 7406.3 | 6021.4 | 7136.1 | 10009.3 | 8888.6 | 10611.6 |
| FJ494693.1 | 512429 | 3060.7 | 3718.8 | 5033.0 | 3712.1 | 10760.7 | 8311.1 |
| EU536306.1 | 283773 | 5300.4 | 7507.5 | 4436.8 | 5587.6 | 12095.7 | 8219.3 |
| NZ_ABZR01000729.1 | 569411 | 89.7 | 275.1 | 1127.2 | 255.3 | 75.8 | 744.9 |
| EU214613.1 | 328976 | 8574.7 | 6439.2 | 8050.2 | 8706.9 | 8494.2 | 10277.2 |
| EU734169.1 | 461530 | 6985.2 | 7483.1 | 7590.5 | 7215.6 | 16125.1 | 12560.8 |
| AM410631.1 | 177686 | 985.3 | 1429.5 | 2854.7 | 2692.6 | 5360.5 | 7301.3 |
| EU537179.1 | 284941 | 7566.6 | 5592.5 | 4856.5 | 5891.0 | 8544.5 | 11333.0 |
| FJ892842.1 | 559778 | 10383.0 | 8114.5 | 16080.4 | 11820.8 | 10586.9 | 10958.2 |
| EF051575.2 | 198685 | 886.9 | 1091.8 | 2279.8 | 2130.5 | 8324.9 | 5848.5 |
| FJ607147.1 | 513959 | 159.1 | 403.6 | 928.4 | 353.5 | 671.6 | 3311.6 |
| EF515714.1 | 223417 | 1213.6 | 1690.1 | 3320.8 | 929.2 | 1472.8 | 2857.1 |
| AY206685.1 | 82206 | 1138.7 | 1483.3 | 2482.4 | 2840.8 | 8716.5 | 8206.3 |
| EU535797.1 | 282047 | 3927.6 | 3630.6 | 8360.7 | 4250.9 | 4149.3 | 8371.6 |
| FJ894178.1 | 540187 | 3378.3 | 3994.7 | 5186.6 | 3909.6 | 8285.9 | 12626.0 |
| AY267192.1 | 106450 | 3521.2 | 4248.7 | 5709.9 | 4608.7 | 6572.6 | 10669.1 |
| AY970951.1 | 115314 | 360.5 | 947.6 | 1215.4 | 342.7 | 5619.9 | 3190.8 |
| DQ868767.1 | 165580 | 81.9 | 100.0 | 306.4 | 111.0 | 1129.0 | 2056.9 |
| GQ200823.1 | 533247 | 1103.9 | 1286.5 | 2309.8 | 1054.1 | 8053.3 | 5291.4 |
| AY054374.1 | 105822 | 4575.3 | 4414.6 | 5826.7 | 4389.1 | 7605.0 | 7438.0 |
| EU538192.1 | 282127 | 12461.7 | 11043.8 | 6428.7 | 11209.8 | 17289.3 | 15369.4 |
| EF561642.1 | 228381 | 2588.4 | 3034.0 | 3953.9 | 3276.6 | 5926.8 | 9726.4 |
| AF074383.1 | 8628 | 505.9 | 1118.3 | 3178.3 | 2184.2 | 4228.4 | 12285.7 |
| FJ894073.1 | 534048 | 1572.3 | 2183.7 | 2296.1 | 1576.4 | 3693.2 | 4161.8 |
| EU540285.1 | 282167 | 9892.8 | 10439.8 | 7722.6 | 12382.0 | 14235.9 | 13545.1 |
| GU185861.1 | 577433 | 716.4 | 1133.0 | 2394.4 | 1947.5 | 6417.9 | 5681.7 |
| EU797470.1 | 350105 | 1475.7 | 1559.5 | 2097.2 | 3877.1 | 8481.0 | 6896.9 |
| AY622320.1 | 102554 | 767.7 | 999.0 | 1570.0 | 766.0 | 5768.2 | 4712.9 |
| EF011017.1 | 362986 | 416.2 | 461.7 | 1274.5 | 366.6 | 6536.4 | 479.2 |
| FM864215.1 | 362580 | 148.1 | 444.4 | 1512.3 | 1118.7 | 1938.6 | 4119.1 |
| EU826028.1 | 333541 | 187.2 | 503.2 | 1314.7 | 754.8 | 10477.5 | 1693.8 |
| EU538858.1 | 284602 | 2390.2 | 3718.3 | 5139.1 | 2451.4 | 7374.8 | 10528.4 |
| GU391485.1 | 537184 | 1196.4 | 2520.7 | 4122.0 | 1933.8 | 8980.7 | 10438.8 |
| FJ894574.1 | 555704 | 12466.3 | 10666.8 | 9391.4 | 12911.1 | 18316.1 | 16843.5 |
| EU536488.1 | 285516 | 3279.5 | 3669.9 | 6476.1 | 5656.0 | 8658.2 | 11283.0 |
| FJ893512.1 | 572521 | 2598.7 | 2645.5 | 4282.6 | 4430.4 | 5167.9 | 9563.5 |
| EU538922.1 | 281466 | 571.0 | 898.2 | 2556.9 | 425.6 | 767.2 | 6267.0 |
| EU620069.1 | 269290 | 15772.3 | 16364.8 | 15137.5 | 14966.1 | 21393.0 | 18237.0 |
| EU434528.1 | 264077 | 2762.8 | 3131.2 | 4553.3 | 3986.2 | 5480.6 | 10834.7 |

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DQ473439.1 gg_id:157065 Pseudomonas fluorescens str. Pf29A
EU538750.1 gg_id:281718 profile human microbiota antecubital fossa (inner elbow) skin clone nbt236a07
X99541.1 gg_id:8521 Pseudomonas anguilliseptica str. 1123/5
EU434493.1 gg_id:261872 Pseudomonas fluorescens str. b361
DQ117553.1 gg_id:138228 structure (Citrullus vulgaris SCHARD.) -based approaches and terminal fragment len
AY690672.1 gg_id:98925 Pseudomonas sp. str. GC06
FM213380.2 gg_id:335840 Pseudomonas antarctica str. KJPB54
EU460330.1 gg_id:301237 polar bear feces clone PB1_aai26f10
EU539906.1 gg_id:284493 profile human microbiota antecubital fossa (inner elbow) skin clone nbt107f04
EU538024.1 gg_id:280553 profile human microbiota antecubital fossa (inner elbow) skin clone nbt225a12
FJ893055.1 gg_id:566846 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota HM2; ear p
AM689948.1 gg_id:217808 Pseudomonas sp. str. SBC-3
AM933517.1 gg_id:340813 Pseudomonas migulae FB26
AJ308306.1 gg_id:37605 Pseudomonas fluorescens str. Biotype F ICMP 13616; ATCC 12983
EF428993.1 gg_id:217131 Pseudomonas sp. str. GIST-WP4s2
EU536354.1 gg_id:284460 profile human microbiota antecubital fossa (inner elbow) skin clone nbt61e08
FJ405303.1 gg_id:360957 Edwardsiella tarda str. K14
AY741159.1 gg_id:170404 Pseudomonas fulva str. S29
FJ675430.1 gg_id:532272 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
AJ132994.1 gg_id:201265 Pseudomonas sp H171
AJ299216.1 gg_id:25364 Pseudomonas mevalonii str. M
FJ893123.1 gg_id:539941 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota HM3; ear p
DQ279335.1 gg_id:141206 Dynamic during maturation Tuber magnatum Pico ascoma Pseudomonas clone TM1
FJ950541.1 gg_id:416614 Pseudomonas putida str. c252
AF534212.1 gg_id:60329 soil clone Phe41
EU536746.1 gg_id:286175 profile human microbiota antecubital fossa (inner elbow) skin clone nbt250c09
NR_029051.1 gg_id:581450 Pseudomonas salomonii str. CFBP 2022
EU540306.1 gg_id:283879 profile human microbiota antecubital fossa (inner elbow) skin clone nbt114h04
FJ893304.1 gg_id:538132 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota WT1; ear p
AY091631.1 gg_id:123196 Pseudomonas sp. str. PH-05
EU071502.1 gg_id:238253 and resistance microorganisms European clean room ESTEC HYDRA facility clone EHF
EU538018.1 gg_id:282396 profile human microbiota antecubital fossa (inner elbow) skin clone nbt225a06
AY538264.1 gg_id:111611 Pseudomonas fluorescens str. PC20
X86623.1 gg_id:8602 Pseudomonas sp str. 2E-14 2A
EU538325.1 gg_id:285758 profile human microbiota antecubital fossa (inner elbow) skin clone nbt83d10
EU537274.1 gg_id:282810 profile human microbiota antecubital fossa (inner elbow) skin clone nbt72c03
DQ318866.1 gg_id:156064 Pseudomonas pv. syringae str. NCPPB 281; 8511
FJ950621.1 gg_id:434785 Pseudomonas putida str. c144
EU834281.1 gg_id:324211 Pseudomonas brassicacearum str. DS67
FJ894807.1 gg_id:544342 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota BME; ear p
FJ893018.1 gg_id:534589 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota HM2; ear p

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| DQ473439.1 | 157065 | 927.5 | 967.5 | 2112.4 | 1023.5 | 1746.7 | 4393.6 |
| EU538750.1 | 281718 | 11033.1 | 10521.6 | 10629.9 | 10043.1 | 13754.0 | 13648.8 |
| X99541.1 | 8521 | 2533.6 | 2415.7 | 5176.5 | 5164.9 | 5162.8 | 5610.6 |
| EU434493.1 | 261872 | 2323.8 | 3024.6 | 3861.7 | 3029.6 | 6569.9 | 9997.0 |
| DQ117553.1 | 138228 | 1081.3 | 1636.0 | 6164.6 | 3963.3 | 6285.1 | 11607.9 |
| AY690672.1 | 98925 | 2929.7 | 1446.3 | 5887.4 | 4118.9 | 3838.3 | 4690.2 |
| FM213380.2 | 335840 | 3264.5 | 4464.9 | 5671.2 | 4515.1 | 9463.9 | 16386.6 |
| EU460330.1 | 301237 | 3655.5 | 5566.0 | 5706.8 | 2813.5 | 10508.3 | 9928.8 |
| EU539906.1 | 284493 | 839.0 | 1215.7 | 2603.9 | 635.1 | 3633.0 | 3953.8 |
| EU538024.1 | 280553 | 3274.6 | 3976.8 | 5012.1 | 4268.0 | 8960.9 | 13573.1 |
| FJ893055.1 | 566846 | 1676.7 | 2346.4 | 1347.9 | 4370.8 | 2949.2 | 6761.7 |
| AM689948.1 | 217808 | 51.8 | 371.0 | 682.7 | 124.9 | 5448.1 | 3737.2 |
| AM933517.1 | 340813 | 666.9 | 1581.3 | 3787.2 | 2295.9 | 7356.1 | 11711.7 |
| AJ308306.1 | 37605 | 624.4 | 906.2 | 1031.7 | 306.4 | 3382.0 | 3994.0 |
| EF428993.1 | 217131 | 176.9 | 419.6 | 120.0 | 153.7 | 399.3 | 1614.9 |
| EU536354.1 | 284460 | 136.8 | 363.6 | 1686.8 | 282.1 | 8037.4 | 10045.5 |
| FJ405303.1 | 360957 | 481.8 | 1356.9 | 2883.4 | 2449.6 | 3371.2 | 10598.5 |
| AY741159.1 | 170404 | 516.6 | 544.2 | 1342.9 | 777.2 | 6086.3 | 2240.6 |
| FJ675430.1 | 532272 | 784.9 | 529.9 | 1271.7 | 602.5 | 3762.3 | 2645.8 |
| AJ132994.1 | 201265 | 629.6 | 1339.6 | 2144.3 | 1227.2 | 3885.2 | 4166.0 |
| AJ299216.1 | 25364 | 1281.1 | 2261.9 | 1810.5 | 2105.0 | 4501.6 | 7626.3 |
| FJ893123.1 | 539941 | 894.0 | 1989.4 | 1276.1 | 504.2 | 5171.1 | 9322.8 |
| DQ279335.1 | 141206 | 4903.2 | 4892.7 | 7934.1 | 6271.1 | 12178.0 | 10507.2 |
| FJ950541.1 | 416614 | 3940.7 | 4007.0 | 2503.2 | 3817.1 | 10710.1 | 5375.2 |
| AF534212.1 | 60329 | 3647.0 | 3049.0 | 2268.2 | 3015.1 | 4806.5 | 3516.2 |
| EU536746.1 | 286175 | 4626.4 | 5738.0 | 5400.3 | 4220.1 | 10614.2 | 13025.8 |
| NR_029051.1 | 581450 | 207.9 | 560.7 | 1641.4 | 1091.1 | 1586.0 | 5127.1 |
| EU540306.1 | 283879 | 1352.0 | 1972.5 | 2605.4 | 2264.9 | 6138.6 | 12715.4 |
| FJ893304.1 | 538132 | 6197.0 | 9935.9 | 6805.2 | 6164.0 | 10750.2 | 13067.9 |
| AY091631.1 | 123196 | 1152.0 | 2016.8 | 4093.7 | 2623.7 | 7334.5 | 11568.9 |
| EU071502.1 | 238253 | 4501.1 | 3042.0 | 5448.8 | 4999.8 | 7747.1 | 7000.0 |
| EU538018.1 | 282396 | 7365.2 | 5873.1 | 4715.5 | 6622.2 | 6827.3 | 10953.3 |
| AY538264.1 | 111611 | 579.6 | 1207.9 | 2112.0 | 2148.2 | 4455.0 | 6807.7 |
| X86623.1 | 8602 | 1284.7 | 2193.8 | 2215.3 | 974.6 | 9723.8 | 4066.7 |
| EU538325.1 | 285758 | 1067.0 | 1832.1 | 2718.2 | 2169.9 | 5818.5 | 12161.3 |
| EU537274.1 | 282810 | 3823.8 | 4781.5 | 3075.0 | 1936.9 | 4478.9 | 10597.2 |
| DQ318866.1 | 156064 | 517.9 | 774.0 | 1699.6 | 529.6 | 2520.1 | 6380.0 |
| FJ950621.1 | 434785 | 2605.7 | 3420.1 | 3042.7 | 4800.5 | 6180.5 | 6167.2 |
| EU834281.1 | 324211 | 577.9 | 796.6 | 1482.8 | 582.0 | 1621.4 | 4761.6 |
| FJ894807.1 | 544342 | 1865.7 | 2710.6 | 2250.1 | 2189.6 | 3652.3 | 9472.1 |
| FJ893018.1 | 534589 | 4113.8 | 5577.6 | 6609.8 | 4018.6 | 7797.9 | 10855.0 |

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FJ892869.1 gg_id:560497 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota HM1; ear p
EF102848.1 gg_id:238201 Pseudomonas putida str. N-5-143XBH
EU537051.1 gg_id:280037 profile human microbiota antecubital fossa (inner elbow) skin clone nbt219f07
DQ282185.1 gg_id:144955 Pseudomonas fluorescens str. PGN-1
EU536280.1 gg_id:280556 profile human microbiota antecubital fossa (inner elbow) skin clone nbt62a02
AY321588.1 gg_id:88851 Pseudomonas fluorescens str. CCUG32456A
EU539168.1 gg_id:280377 profile human microbiota antecubital fossa (inner elbow) skin clone nbt102a09
EF428995.1 gg_id:216433 Pseudomonas fluorescens
EU538158.1 gg_id:285771 profile human microbiota antecubital fossa (inner elbow) skin clone nbt81a05
EU538367.1 gg_id:284298 profile human microbiota antecubital fossa (inner elbow) skin clone nbt87f04
DQ234206.2 gg_id:143653 determined library mangrove clone DS123
FJ894557.1 gg_id:565334 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B2E; ear pu
FJ894984.1 gg_id:560160 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota BME; ear p
EU538332.1 gg_id:286926 profile human microbiota antecubital fossa (inner elbow) skin clone nbt83g07
FJ799903.2 gg_id:556353 Proteus vulgaris str. 4Bi
EU537643.1 gg_id:285279 profile human microbiota antecubital fossa (inner elbow) skin clone nbt74h03
GU191929.1 gg_id:588639 Pseudomonas putida str. SB 3051
GU191927.1 gg_id:584485 Pseudomonas monteilii str. SB 3078
FJ894054.1 gg_id:566587 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B1E; ear pu
AY472116.1 gg_id:99985 Pseudomonas fluorescens
Z76654.1 gg_id:8607 Pseudomonas amygdali str. LMG 2123T ()
NR_025174.1 gg_id:564254 Pseudomonas extremorientalis str. KMM 3447
EU538955.1 gg_id:284428 profile human microbiota antecubital fossa (inner elbow) skin clone nbt95h10
GQ169380.1 gg_id:588287 Pseudomonas thivervalensis str. IEHa
GQ900590.1 gg_id:574251 Pseudomonas putida str. MPR 4
EU539535.1 gg_id:283940 profile human microbiota antecubital fossa (inner elbow) skin clone nbt241d05
EF194768.1 gg_id:203364 Pseudomonas putida str. PM1
EU538937.1 gg_id:282205 profile human microbiota antecubital fossa (inner elbow) skin clone nbt95e09
EU536583.1 gg_id:282830 profile human microbiota antecubital fossa (inner elbow) skin clone nbt63c09
EU118771.1 gg_id:236931 Pseudomonas lutea str. AGL 2
EU538944.1 gg_id:283825 profile human microbiota antecubital fossa (inner elbow) skin clone nbt95f09
EF061900.1 gg_id:189806 Pseudomonas sp. str. M191
FJ950560.1 gg_id:429741 Pseudomonas putida str. c53
FJ894025.1 gg_id:554071 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B1E; ear pu
NR_028987.1 gg_id:542667 Pseudomonas trivialis str. P 513/19; DSM 14937; LMG 21464
EU538393.1 gg_id:282501 profile human microbiota antecubital fossa (inner elbow) skin clone nbt88f02
FJ424813.1 gg_id:364673 Pseudomonas sp. str. MS-3
EF010981.1 gg_id:184602 Pseudomonas putida str. PM15
FJ893331.1 gg_id:564098 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota WT1; ear p
AJ871471.1 gg_id:110332 Pseudomonas luteola CP155-2
AF430121.1 gg_id:66816 Pseudomonas sp. str. VKM B-2265 dcm4

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| FJ892869.1 | 560497 | 13545.1 | 12497.8 | 10633.8 | 10886.8 | 12949.0 | 12065.7 |
| EF102848.1 | 238201 | 2568.7 | 2295.0 | 4557.7 | 4486.4 | 7091.8 | 7141.3 |
| EU537051.1 | 280037 | 7499.4 | 6483.0 | 5595.7 | 6439.9 | 9521.1 | 11728.1 |
| DQ282185.1 | 144955 | 804.7 | 1447.9 | 2780.4 | 371.5 | 4977.1 | 9768.8 |
| EU536280.1 | 280556 | 5673.9 | 7570.3 | 7180.5 | 5423.5 | 7757.6 | 11682.9 |
| AY321588.1 | 88851 | 5947.4 | 4976.1 | 2970.2 | 6369.1 | 16937.1 | 13211.5 |
| EU539168.1 | 280377 | 12203.6 | 12522.6 | 8402.8 | 11602.4 | 16882.5 | 16419.8 |
| EF428995.1 | 216433 | 2015.1 | 2086.5 | 4791.9 | 4030.6 | 8919.2 | 7178.9 |
| EU538158.1 | 285771 | 4406.4 | 3138.9 | 5314.4 | 4807.9 | 5568.9 | 10950.5 |
| EU538367.1 | 284298 | 7328.5 | 4174.7 | 4000.9 | 4183.6 | 6773.3 | 8631.0 |
| DQ234206.2 | 143653 | 6365.7 | 3053.5 | 6833.6 | 7825.0 | 2470.9 | 5601.7 |
| FJ894557.1 | 565334 | 8603.5 | 8942.3 | 7433.4 | 8296.8 | 13293.0 | 13789.2 |
| FJ894984.1 | 560160 | 8211.4 | 10375.0 | 9688.0 | 7231.5 | 12603.7 | 15725.2 |
| EU538332.1 | 286926 | 14262.7 | 11836.0 | 6761.6 | 12715.0 | 16591.9 | 13075.5 |
| FJ799903.2 | 556353 | 1570.7 | 1247.1 | 8363.6 | 3190.2 | 2733.7 | 3055.1 |
| EU537643.1 | 285279 | 4013.3 | 5842.4 | 3924.7 | 3307.7 | 12042.2 | 8926.7 |
| GU191929.1 | 588639 | 1222.8 | 1432.4 | 2653.7 | 2831.7 | 4845.4 | 6163.4 |
| GU191927.1 | 584485 | 2449.0 | 2150.7 | 4498.3 | 4607.8 | 7353.4 | 6996.7 |
| FJ894054.1 | 566587 | 6218.1 | 7740.6 | 8318.9 | 5931.8 | 10597.6 | 11902.8 |
| AY472116.1 | 99985 | 1040.4 | 1949.9 | 2063.7 | 1188.3 | 8999.4 | 16223.5 |
| Z76654.1 | 8607 | 2063.3 | 1991.7 | 5852.3 | 2647.3 | 4060.7 | 4352.4 |
| NR_025174.1 | 564254 | 2168.4 | 1546.3 | 2502.0 | 3977.3 | 4558.9 | 8500.1 |
| EU538955.1 | 284428 | 198.2 | 447.7 | 1182.1 | 329.2 | 7116.1 | 8012.6 |
| GQ169380.1 | 588287 | 197.6 | 741.4 | 1538.9 | 1368.7 | 631.9 | 3975.8 |
| GQ900590.1 | 574251 | 3985.6 | 4043.2 | 6474.0 | 5722.8 | 8957.8 | 8799.6 |
| EU539535.1 | 283940 | 6119.0 | 5469.2 | 2288.0 | 2523.5 | 6965.7 | 8688.3 |
| EF194768.1 | 203364 | 5580.3 | 4264.9 | 1282.1 | 5374.8 | 8103.0 | 5361.1 |
| EU538937.1 | 282205 | 1902.8 | 2894.8 | 2814.1 | 2080.1 | 4806.6 | 11584.2 |
| EU536583.1 | 282830 | 507.9 | 1192.3 | 2316.2 | 697.3 | 9980.3 | 9228.3 |
| EU118771.1 | 236931 | 326.2 | 960.4 | 3677.6 | 1320.0 | 4232.4 | 4502.5 |
| EU538944.1 | 283825 | 2285.6 | 2989.9 | 1957.8 | 1546.0 | 2857.9 | 2983.1 |
| EF061900.1 | 189806 | 95.1 | 312.2 | 507.3 | 103.6 | 1303.4 | 1594.0 |
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| NR_028987.1 | 542667 | 1095.1 | 1332.0 | 2036.3 | 1518.2 | 5659.9 | 8595.8 |
| EU538393.1 | 282501 | 16015.2 | 18570.3 | 15913.9 | 12665.4 | 19866.3 | 18560.8 |
| FJ424813.1 | 364673 | 981.7 | 895.6 | 1792.0 | 1123.3 | 1001.1 | 3597.9 |
| EF010981.1 | 184602 | 88.6 | 288.0 | 1053.0 | 161.9 | 1484.1 | 694.2 |
| FJ893331.1 | 564098 | 4303.9 | 6356.8 | 5523.2 | 5716.8 | 10128.8 | 13162.6 |
| AJ871471.1 | 110332 | 5905.0 | 7080.1 | 4594.5 | 5689.0 | 13920.2 | 9079.6 |
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EF062805.1 gg_id:202317 Pseudomonas sp. str. MY1410
AJ534672.1 gg_id:75843 ground water deep-well injection disposal site radioactive wastes Tomsk-7 clone S15A
AM111045.1 gg_id:140916 Pseudomonas sp. str. 7065
FN646596.1 gg_id:557247 Pseudomonas sp. SS-2009-PA4 str. PA4
AJ249382.1 gg_id:22698 Pseudomonas frederiksbergensis str. JAJ28
EU539350.1 gg_id:283152 profile human microbiota antecubital fossa (inner elbow) skin clone nbt237c09
EU538914.1 gg_id:285813 profile human microbiota antecubital fossa (inner elbow) skin clone nbt95a08
GU272230.1 gg_id:548694 library dichlorvos treatment rape phyllosphere clone TF19
EU348741.1 gg_id:272086 Pseudomonas putida soil
EU537111.1 gg_id:279820 profile human microbiota antecubital fossa (inner elbow) skin clone nbt67a05
EU538710.1 gg_id:286594 profile human microbiota antecubital fossa (inner elbow) skin clone nbt235e05
AB440177.1 gg_id:535106 Pseudomonas costantinii
EU536997.1 gg_id:280285 profile human microbiota antecubital fossa (inner elbow) skin clone nbt218e01
FJ893409.1 gg_id:569655 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota WT1; ear p
EU535778.1 gg_id:283503 profile human microbiota antecubital fossa (inner elbow) skin clone nbt10f10
AF320987.1 gg_id:72973 Pseudomonas reactans str. NCPPB 1311
AF511511.1 gg_id:65394 Pseudomonas syringae SaU8
FJ607148.1 gg_id:573718 Pseudomonas syringae pv. papulans str. ICMP 4044
DQ095887.1 gg_id:134099 Pseudomonas plecoglossicida str. R25
FJ893902.1 gg_id:560794 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B1E; ear pu
GQ497248.1 gg_id:544313 Pseudomonas sp. str. F2-2
AM933508.1 gg_id:324712 Pseudomonas antarctica FB16
EU538247.1 gg_id:286083 profile human microbiota antecubital fossa (inner elbow) skin clone nbt83g04
AY303293.1 gg_id:131271 Pseudomonas sp. str. ps4-16
EU538994.1 gg_id:286958 profile human microbiota antecubital fossa (inner elbow) skin clone nbt98f12
AY622264.1 gg_id:99494 subsurface soil clone S-A1
AB021381.1 gg_id:8570 Pseudomonas fuscovaginae str. MAFF 301177T
AJ297354.1 gg_id:70736 Pseudomonas sp. str. FAIR/BE/F/GH39
AY771716.1 gg_id:108690 Pseudomonas aeruginosa str. S2-77
FJ892791.1 gg_id:574101 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota HM1; ear p
DQ084462.1 gg_id:134086 Pseudomonas sp. str. CSS-1
EU537986.1 gg_id:282145 profile human microbiota antecubital fossa (inner elbow) skin clone nbt228e02
DQ119111.1 gg_id:132307 Pseudomonas putida
DQ095885.1 gg_id:129354 Pseudomonas monteilii str. R23
AY690691.1 gg_id:99958 Pseudomonas sp. str. MaT03
FJ465156.2 gg_id:575465 Pseudomonas fluorescens str. FY32
AB126621.2 gg_id:104655 Pseudomonas japonica str. IAM 15071
AB060137.1 gg_id:62341 Pseudomonas cremoricolorata str. IAM 1541T
EU537931.1 gg_id:285392 profile human microbiota antecubital fossa (inner elbow) skin clone nbt227e04
AM495723.1 gg_id:217056 Pseudomonas syringae str. ISF FR1

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| EU538637.1 | 283995 | 2584.8 | 3549.6 | 5061.9 | 2696.4 | 4458.0 | 9943.1 |
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| AJ534672.1 | 75843 | 10070.9 | 9194.4 | 8954.3 | 11339.1 | 19162.3 | 15670.2 |
| AM111045.1 | 140916 | 12903.0 | 13375.3 | 6564.7 | 11916.5 | 11189.5 | 9267.4 |
| FN646596.1 | 557247 | 1104.6 | 1852.8 | 2211.6 | 1566.2 | 7658.4 | 6120.9 |
| AJ249382.1 | 22698 | 1149.2 | 1659.3 | 2310.3 | 2584.3 | 4421.0 | 6636.9 |
| EU539350.1 | 283152 | 2014.5 | 3231.4 | 5934.6 | 2242.1 | 4024.8 | 9387.7 |
| EU538914.1 | 285813 | 178.9 | 326.9 | 539.8 | 269.4 | 447.4 | 4663.3 |
| GU272230.1 | 548694 | 7434.5 | 6895.7 | 5069.1 | 6771.5 | 6082.6 | 6256.1 |
| EU348741.1 | 272086 | 3452.9 | 3360.1 | 2651.8 | 5840.2 | 8641.6 | 8854.1 |
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| EU538710.1 | 286594 | 3117.3 | 4162.1 | 3400.0 | 4950.4 | 10290.7 | 10533.2 |
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| FJ893409.1 | 569655 | 1727.0 | 2523.6 | 2805.5 | 3071.7 | 3430.2 | 9683.3 |
| EU535778.1 | 283503 | 1039.8 | 1729.9 | 1852.0 | 520.2 | 4656.7 | 6513.9 |
| AF320987.1 | 72973 | 6785.3 | 5918.8 | 4438.5 | 5275.7 | 10384.8 | 12750.3 |
| AF511511.1 | 65394 | 8603.4 | 7606.0 | 5801.2 | 6325.0 | 7201.6 | 6707.1 |
| FJ607148.1 | 573718 | 114.9 | 234.8 | 745.3 | 351.8 | 458.5 | 1769.9 |
| DQ095887.1 | 134099 | 184.6 | 407.6 | 473.9 | 202.9 | 5269.9 | 390.2 |
| FJ893902.1 | 560794 | 3515.2 | 4407.6 | 5308.6 | 3936.3 | 5858.5 | 11627.8 |
| GQ497248.1 | 544313 | 3831.1 | 3389.7 | 6016.0 | 4667.9 | 6038.0 | 7826.6 |
| AM933508.1 | 324712 | 1091.6 | 1813.6 | 3140.5 | 1984.7 | 9210.4 | 9715.8 |
| EU538247.1 | 286083 | 4042.2 | 5593.3 | 6626.5 | 4019.4 | 8892.7 | 11174.0 |
| AY303293.1 | 131271 | 564.7 | 1221.7 | 2175.0 | 672.8 | 7532.5 | 12455.5 |
| EU538994.1 | 286958 | 3507.7 | 4180.7 | 2058.0 | 2135.0 | 8362.7 | 5893.4 |
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| AB021381.1 | 8570 | 529.9 | 1100.6 | 1474.5 | 308.6 | 7382.8 | 6233.8 |
| AJ297354.1 | 70736 | 1043.5 | 614.1 | 592.6 | 276.7 | 2207.0 | 4223.1 |
| AY771716.1 | 108690 | 64.8 | 93.0 | 411.8 | 94.7 | 1384.1 | 3459.5 |
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| DQ084462.1 | 134086 | 337.7 | 723.0 | 2932.9 | 1161.3 | 7137.8 | 10204.3 |
| EU537986.1 | 282145 | 773.2 | 1173.1 | 1995.3 | 987.1 | 4043.9 | 5928.9 |
| DQ119111.1 | 132307 | 2879.7 | 3762.9 | 5348.9 | 3777.4 | 6306.4 | 6870.9 |
| DQ095885.1 | 129354 | 9062.7 | 10065.9 | 6355.3 | 8947.9 | 11861.9 | 11922.3 |
| AY690691.1 | 99958 | 212.9 | 376.0 | 1181.7 | 150.7 | 4688.0 | 5911.6 |
| FJ465156.2 | 575465 | 313.4 | 783.6 | 689.7 | 258.7 | 6789.8 | 5947.1 |
| AB126621.2 | 104655 | 947.9 | 963.5 | 1257.7 | 786.7 | 8483.6 | 7053.1 |
| AB060137.1 | 62341 | 1519.1 | 1323.1 | 1966.1 | 652.8 | 5252.7 | 3461.5 |
| EU537931.1 | 285392 | 11867.8 | 15163.0 | 10693.6 | 8367.9 | 13333.2 | 12184.3 |
| AM495723.1 | 217056 | 798.1 | 1817.6 | 1020.2 | 483.0 | 5205.8 | 4740.0 |

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EU169178.1 gg_id:252479 Pseudomonas tolaasii str. B14
EU877078.1 gg_id:345765 Pseudomonas putida str. EC1_2004
EU118779.1 gg_id:251758 Pseudomonas putida str. AGL 13
FJ893746.1 gg_id:538659 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota WT3; ear p
AM184286.1 gg_id:161051 Pseudomonas putida str. WAB1947
AY303292.1 gg_id:130388 Pseudomonas sp. str. ps4-14
EU540490.1 gg_id:280406 profile human microbiota antecubital fossa (inner elbow) skin clone nbt116d09
NZ_AAXR01000013.1 gg_id:209007 Pseudomonas putida str. GB-1
DQ536512.1 gg_id:160564 Pseudomonas trivialis str. BIHB 728
EU539847.1 gg_id:285307 profile human microbiota antecubital fossa (inner elbow) skin clone nbt106c11
EU215454.1 gg_id:367789 Pseudomonas sp. str. PTPbra-1
EU538932.1 gg_id:286172 profile human microbiota antecubital fossa (inner elbow) skin clone nbt95e02
EU538389.1 gg_id:282624 profile human microbiota antecubital fossa (inner elbow) skin clone nbt88b06
EU538933.1 gg_id:284429 profile human microbiota antecubital fossa (inner elbow) skin clone nbt95e03
AB504737.2 gg_id:543903 Pseudomonas syringae str. CP001
FJ893378.1 gg_id:543253 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota WT1; ear p
FJ894829.1 gg_id:567640 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota BME; ear p
EU539348.1 gg_id:286481 profile human microbiota antecubital fossa (inner elbow) skin clone nbt237c07
AY856844.1 gg_id:110621 Pseudomonas sp. str. 38
EU540292.1 gg_id:283763 profile human microbiota antecubital fossa (inner elbow) skin clone nbt114b08
EU540256.1 gg_id:282554 profile human microbiota antecubital fossa (inner elbow) skin clone nbt248b08
EU465095.1 gg_id:289664 African elephant feces clone AFYEL_aaj68a05
DQ279334.1 gg_id:143425 Dynamic during maturation Tuber magnatum Pico ascoma Pseudomonas clone TM1
FJ807483.1 gg_id:537835 Pseudomonas fulva str. TY16
EU539850.1 gg_id:284339 profile human microbiota antecubital fossa (inner elbow) skin clone nbt106d09
AY491973.1 gg_id:99308 Pseudomonas putida str. 1290
FJ005054.1 gg_id:326078 Pseudomonas grimontii str. R1
DQ365566.1 gg_id:149449 Pseudomonas poae str. JA01
FJ894067.1 gg_id:544310 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B1E; ear pu
EF079867.1 gg_id:174369 Pseudomonas sp. str. MY1412
EU537635.1 gg_id:284554 profile human microbiota antecubital fossa (inner elbow) skin clone nbt74c03
EU708321.1 gg_id:309775 Pseudomonas pv. syringae str. BBK3
FJ894204.1 gg_id:535083 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B2E; ear pu
EU538377.1 gg_id:287065 profile human microbiota antecubital fossa (inner elbow) skin clone nbt88d09
EU536974.1 gg_id:285745 profile human microbiota antecubital fossa (inner elbow) skin clone nbt217h10
EF529516.1 gg_id:225502 Pseudomonas putida str. CM5001
EU538675.1 gg_id:285670 profile human microbiota antecubital fossa (inner elbow) skin clone nbt235a04
EU538346.1 gg_id:285713 profile human microbiota antecubital fossa (inner elbow) skin clone nbt84e03
FJ893112.1 gg_id:543418 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota HM3; ear p
EU482040.1 gg_id:259836 Pseudomonas sp. str. KSH3
AM259177.1 gg_id:198385 Pseudomonas fluorescens pdm

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| EU169178.1 | 252479 | 651.8 | 1057.8 | 2193.7 | 923.4 | 5451.6 | 10679.8 |
| EU877078.1 | 345765 | 6600.3 | 5387.4 | 5297.8 | 8441.6 | 8905.0 | 11868.4 |
| EU118779.1 | 251758 | 3420.8 | 4045.4 | 4971.7 | 4327.4 | 7614.6 | 7188.0 |
| FJ893746.1 | 538659 | 7110.2 | 6851.1 | 6720.8 | 7505.8 | 8665.7 | 11762.9 |
| AM184286.1 | 161051 | 790.2 | 1098.8 | 3187.9 | 3907.4 | 8466.2 | 5167.1 |
| AY303292.1 | 130388 | 319.1 | 1062.7 | 2299.3 | 1176.8 | 3190.0 | 10719.7 |
| EU540490.1 | 280406 | 9456.2 | 10953.3 | 14077.2 | 9835.2 | 13004.7 | 12197.9 |
| NZ_AAXR01000013.1 | 209007 | 2389.3 | 3606.5 | 1047.3 | 1773.1 | 1947.8 | 2043.7 |
| DQ536512.1 | 160564 | 4789.4 | 3921.7 | 3966.9 | 7715.8 | 4580.8 | 9619.1 |
| EU539847.1 | 285307 | 6747.5 | 9733.1 | 8739.9 | 6353.1 | 15016.0 | 13463.4 |
| EU215454.1 | 367789 | 6613.8 | 6294.3 | 4110.5 | 6806.7 | 9916.1 | 8892.3 |
| EU538932.1 | 286172 | 384.5 | 1111.3 | 1714.7 | 478.3 | 3975.7 | 6192.2 |
| EU538389.1 | 282624 | 8821.5 | 8865.1 | 4103.5 | 7033.3 | 6800.0 | 9883.0 |
| EU538933.1 | 284429 | 13586.1 | 13480.7 | 18422.8 | 11072.8 | 18492.3 | 16044.5 |
| AB504737.2 | 543903 | 687.7 | 1667.5 | 2510.3 | 2214.2 | 979.6 | 5736.5 |
| FJ893378.1 | 543253 | 18736.1 | 13794.5 | 9532.0 | 16616.9 | 17088.2 | 14649.3 |
| FJ894829.1 | 567640 | 639.6 | 1156.4 | 1773.0 | 1119.0 | 4100.6 | 11047.2 |
| EU539348.1 | 286481 | 5369.6 | 6634.9 | 6722.9 | 5664.9 | 9296.0 | 12182.8 |
| AY856844.1 | 110621 | 384.0 | 386.5 | 246.2 | 841.6 | 892.5 | 1695.6 |
| EU540292.1 | 283763 | 8101.3 | 7368.1 | 6575.4 | 7040.1 | 7664.6 | 11807.8 |
| EU540256.1 | 282554 | 3505.3 | 4205.2 | 3244.2 | 5107.2 | 9678.5 | 7329.6 |
| EU465095.1 | 289664 | 18881.6 | 10914.6 | 23538.6 | 16901.1 | 8128.5 | 12071.5 |
| DQ279334.1 | 143425 | 307.6 | 397.8 | 629.1 | 443.3 | 1033.3 | 3764.7 |
| FJ807483.1 | 537835 | 3618.4 | 3660.1 | 5406.8 | 4286.1 | 10183.8 | 7655.1 |
| EU539850.1 | 284339 | 12453.0 | 10313.6 | 9584.0 | 11056.7 | 15453.6 | 15075.2 |
| AY491973.1 | 99308 | 1463.4 | 1067.3 | 2693.1 | 1468.6 | 666.0 | 2149.2 |
| FJ005054.1 | 326078 | 1373.0 | 1498.0 | 1628.0 | 1431.5 | 2774.5 | 3848.1 |
| DQ365566.1 | 149449 | 2477.3 | 1840.7 | 3009.2 | 4110.9 | 5246.6 | 10187.5 |
| FJ894067.1 | 544310 | 18498.8 | 18023.5 | 8646.0 | 14671.9 | 18920.5 | 17437.6 |
| EF079867.1 | 174369 | 6003.0 | 4773.7 | 4971.2 | 6537.5 | 11697.3 | 13225.1 |
| EU537635.1 | 284554 | 2246.1 | 3464.9 | 2733.7 | 2773.4 | 5517.1 | 7441.2 |
| EU708321.1 | 309775 | 5529.9 | 5816.6 | 3857.5 | 5127.1 | 6885.2 | 4757.9 |
| FJ894204.1 | 535083 | 15925.8 | 15301.1 | 16200.7 | 14224.7 | 19742.0 | 17659.1 |
| EU538377.1 | 287065 | 286.6 | 866.2 | 2234.5 | 380.8 | 678.6 | 7228.1 |
| EU536974.1 | 285745 | 116.6 | 420.2 | 1111.0 | 124.9 | 4002.3 | 7978.4 |
| EF529516.1 | 225502 | 10444.6 | 8641.4 | 6143.2 | 7170.6 | 8510.5 | 7372.9 |
| EU538675.1 | 285670 | 1652.1 | 3446.1 | 5073.4 | 2490.6 | 4524.2 | 10476.8 |
| EU538346.1 | 285713 | 153.8 | 463.6 | 523.1 | 154.4 | 2813.6 | 2995.8 |
| FJ893112.1 | 543418 | 6654.6 | 6720.4 | 4173.2 | 7569.3 | 11910.4 | 11919.0 |
| EU482040.1 | 259836 | 260.2 | 585.1 | 1417.4 | 212.4 | 8738.6 | 9840.6 |
| AM259177.1 | 198385 | 4400.0 | 3144.9 | 4666.8 | 3951.3 | 11282.9 | 9299.8 |

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EU215446.1 gg_id:363719 Pseudomonas fluorescens str. PTPf-1
EU539695.1 gg_id:284796 profile human microbiota antecubital fossa (inner elbow) skin clone nbt244c07
FJ894864.1 gg_id:552364 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota BME; ear p
AY263475.1 gg_id:82913 Pseudomonas sp. WE7#2b
EU536231.1 gg_id:279948 profile human microbiota antecubital fossa (inner elbow) skin clone nbt61c07
EU545156.1 gg_id:272623 Pseudomonas congelans str. SS157
DQ086781.1 gg_id:128180 Pseudomonas fluorescens str. SKIN2
GU198113.1 gg_id:589242 Pseudomonas fluorescens str. LMG 5849
EU834261.1 gg_id:345741 Pseudomonas plecoglossicida str. DS39
AY271793.1 gg_id:109330 Pseudomonas fluorescens str. VKM B-2168
FJ894374.1 gg_id:539676 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B2E; ear pu
AY456712.1 gg_id:100571 Pseudomonas sp. str. SBW25
GU391452.1 gg_id:563866 Pseudomonas sp. str. Gd1T
EU535434.1 gg_id:280220 profile human microbiota antecubital fossa (inner elbow) skin clone nbt02h02
FJ950619.1 gg_id:389167 Pseudomonas putida str. c141
FJ976589.1 gg_id:572088 Pseudomonas putida str. LCR80
EU539815.1 gg_id:280992 profile human microbiota antecubital fossa (inner elbow) skin clone nbt105c12
EU221400.1 gg_id:256776 Pseudomonas thivervalensis str. H2P1
AF094738.1 gg_id:24808 Pseudomonas putida str. ATCC 17472
AM111028.1 gg_id:140966 Pseudomonas sp. str. 7028
EU537168.1 gg_id:285451 profile human microbiota antecubital fossa (inner elbow) skin clone nbt67g02
EF682071.1 gg_id:348246 Pseudomonas putida str. DN1.2
AY259924.1 gg_id:91834 Pseudomonas filiscindens str. ATCC BAA-697
DQ313381.1 gg_id:190384 Pseudomonas putida str. PCL1758
EU439423.1 gg_id:536092 Pseudomonas putida str. QR2
EU538074.1 gg_id:279760 profile human microbiota antecubital fossa (inner elbow) skin clone nbt81f06
AB507253.1 gg_id:593521 Pseudomonas putida str. Pes207
EU822884.1 gg_id:328707 Pseudomonas fluorescens str. MXX08012001
AM110075.2 gg_id:257086 Pseudomonas sp. str. Ri71
AB046996.1 gg_id:106916 Pseudomonas fulva str. AJ 2129
EU538204.1 gg_id:281728 profile human microbiota antecubital fossa (inner elbow) skin clone nbt82h11
EF459522.1 gg_id:207295 Pseudomonas graminis KFC-45
AY047218.1 gg_id:17462 Pseudomonas migulae
AB302401.1 gg_id:222217 Pseudomonas cinnamophila str. C-17
EU169169.1 gg_id:251990 Pseudomonas aurantiaca str. B23
EU647702.1 gg_id:272669 Pseudomonas mediterranea str. REG60
EU538388.1 gg_id:279923 profile human microbiota antecubital fossa (inner elbow) skin clone nbt88a06
EU179737.1 gg_id:244818 Pseudomonas putida str. MG-Y2
AB110608.1 gg_id:104753 Pseudomonas putida str. KF751
DQ095884.1 gg_id:128118 Pseudomonas plecoglossicida str. R21
EU537624.1 gg_id:283531 profile human microbiota antecubital fossa (inner elbow) skin clone nbt73g03

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| EU215446.1 | 363719 | 5333.3 | 3220.8 | 987.2 | 2710.7 | 2409.8 | 4681.8 |
| EU539695.1 | 284796 | 1738.3 | 2950.5 | 1915.4 | 2140.3 | 6651.2 | 5967.4 |
| FJ894864.1 | 552364 | 3689.6 | 4330.1 | 3713.5 | 5319.9 | 5174.7 | 12839.0 |
| AY263475.1 | 82913 | 5639.4 | 8358.5 | 6259.7 | 6125.7 | 9032.6 | 8733.2 |
| EU536231.1 | 279948 | 735.5 | 1461.3 | 988.2 | 527.0 | 5995.4 | 7498.3 |
| EU545156.1 | 272623 | 202.6 | 438.2 | 983.5 | 449.6 | 5399.6 | 4195.2 |
| DQ086781.1 | 128180 | 320.1 | 985.1 | 2166.6 | 1096.6 | 2889.4 | 9994.0 |
| GU198113.1 | 589242 | 463.4 | 1145.2 | 1796.7 | 1531.5 | 2520.4 | 7829.4 |
| EU834261.1 | 345741 | 2362.8 | 1953.0 | 2063.5 | 4650.3 | 6019.4 | 3256.3 |
| AY271793.1 | 109330 | 775.9 | 1604.5 | 3561.6 | 2662.0 | 4011.3 | 11892.6 |
| FJ894374.1 | 539676 | 5342.1 | 6430.4 | 6349.3 | 6079.0 | 7616.2 | 11593.8 |
| AY456712.1 | 100571 | 890.7 | 1552.6 | 2573.8 | 1890.8 | 3908.4 | 8506.7 |
| GU391452.1 | 563866 | 3394.8 | 4629.3 | 4558.1 | 4901.1 | 8605.7 | 11264.4 |
| EU535434.1 | 280220 | 4293.0 | 4510.0 | 5793.7 | 4788.3 | 11239.5 | 11895.8 |
| FJ950619.1 | 389167 | 282.5 | 505.9 | 1183.5 | 798.4 | 2353.1 | 3758.1 |
| FJ976589.1 | 572088 | 1546.1 | 1195.5 | 1755.3 | 3025.4 | 6592.9 | 4757.0 |
| EU539815.1 | 280992 | 2484.3 | 3201.2 | 4167.8 | 2659.6 | 2966.6 | 8388.7 |
| EU221400.1 | 256776 | 71.2 | 235.3 | 690.7 | 118.2 | 367.6 | 2130.9 |
| AF094738.1 | 24808 | 218.7 | 392.5 | 1310.2 | 202.8 | 2107.0 | 2880.2 |
| AM111028.1 | 140966 | 130.6 | 179.8 | 96.2 | 528.8 | 967.8 | 565.2 |
| EU537168.1 | 285451 | 6529.1 | 7471.0 | 4689.0 | 6891.3 | 8633.0 | 10743.0 |
| EF682071.1 | 348246 | 252.9 | 389.6 | 455.3 | 259.5 | 241.4 | 2486.3 |
| AY259924.1 | 91834 | 7223.7 | 6036.2 | 11204.1 | 7059.4 | 11047.9 | 9771.8 |
| DQ313381.1 | 190384 | 3634.2 | 3713.8 | 5655.6 | 5010.4 | 9824.9 | 8488.3 |
| EU439423.1 | 536092 | 3078.2 | 4214.0 | 6018.3 | 4052.7 | 8543.6 | 8020.6 |
| EU538074.1 | 279760 | 2800.6 | 3584.8 | 3369.2 | 4799.5 | 9732.2 | 11038.1 |
| AB507253.1 | 593521 | 4556.3 | 5756.7 | 7069.8 | 6938.2 | 9224.5 | 9464.2 |
| EU822884.1 | 328707 | 238.5 | 451.8 | 565.8 | 191.0 | 7027.3 | 6323.5 |
| AM110075.2 | 257086 | 3076.8 | 2528.8 | 3341.1 | 3781.5 | 4492.8 | 6551.2 |
| AB046996.1 | 106916 | 361.2 | 802.3 | 1865.3 | 459.3 | 8030.2 | 5859.2 |
| EU538204.1 | 281728 | 7629.8 | 6147.7 | 3780.8 | 8227.7 | 11346.3 | 11619.0 |
| EF459522.1 | 207295 | 56.9 | 151.6 | 441.3 | 114.0 | 538.0 | 600.2 |
| AY047218.1 | 17462 | 503.9 | 1066.7 | 902.9 | 998.2 | 2195.2 | 9349.0 |
| AB302401.1 | 222217 | 7219.9 | 7646.8 | 4244.3 | 6020.7 | 11068.3 | 9004.3 |
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| EU538388.1 | 279923 | 1452.3 | 2181.8 | 1069.8 | 1572.9 | 6791.7 | 6105.8 |
| EU179737.1 | 244818 | 1056.8 | 1686.6 | 1412.0 | 567.4 | 4841.4 | 2944.8 |
| AB110608.1 | 104753 | 418.8 | 532.1 | 1628.3 | 1258.7 | 1983.7 | 1369.2 |
| DQ095884.1 | 128118 | 1347.2 | 2607.9 | 793.2 | 904.0 | 8702.4 | 2963.9 |
| EU537624.1 | 283531 | 4554.2 | 5518.7 | 5593.9 | 4184.6 | 9580.5 | 11681.5 |

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| s__unclassified | 17307 |
| s__unclassified | 15946 |
| s__unclassified | 16043 |
| s__Anodontia fragilis gill symbiont | 2417 |
| s__endosymbiont of Riftia pachyptila | 2403 |
| s__Loripes lacteus gill symbiont | 2451 |
| s__unclassified | 1040 |
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| s__unclassified | 1234 |
| s__unclassified | 1517 |
| s__unclassified | 1762 |
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| s__unclassified | 2387 |
| s__unclassified | 2411 |
| s__unclassified | 2462 |
| s__unclassified | 2482 |
| s__unclassified | 2558 |
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EF062806.1 gg_id:188482 Pseudomonas sp. str. MY1416
AY303305.1 gg_id:130588 Pseudomonas sp. str. ps4-45
EU169168.1 gg_id:244420 Pseudomonas lini str. B25
EF513773.1 gg_id:220219 Pseudomonas putida str. JB-1
DQ536517.1 gg_id:159873 Pseudomonas trivialis str. BIHB 747
EU647538.1 gg_id:282969 recovered Xidatan Tanggula and Yuzhufeng glaciers glacial snow glacier Tin Plateau c
EU536806.1 gg_id:283384 profile human microbiota antecubital fossa (inner elbow) skin clone nbt222a08
EU101096.1 gg_id:252064 Sulfide/oxygen supply ratio predicts outcome competition among sulfur-oxidizing wa
EU464759.1 gg_id:294113 Hartmann's mountain zebra feces clone AFZEB_aaj70c09
DQ824715.1 gg_id:192521 human fecal clone RL185_aaj72b08
EU252490.1 gg_id:236335 Pseudomonas sp. AM2(2007) str. AM2
EF608541.1 gg_id:234990 predatory Poecilus chalcites their response lab rearing and antibiotic treatment diges
AM403206.1 gg_id:172703 Nitrate-reducing and Denitrifying Marine Aqua Biofilter marine aqua
DQ824723.1 gg_id:194608 human fecal clone RL185_aaj72c07
DQ339144.1 gg_id:149280 Pseudomonas pohangensis str. H3-R18
EU143343.1 gg_id:238940 Salinisphaera sp. str. C1
GU452539.1 gg_id:528872 Salinisphaera sp. str. T31B1
EF988634.1 gg_id:235478 Salinisphaera dokdoensis str. CL-ES53
AJ421425.1 gg_id:64239 Salinisphaera shabanensis str. E1L3A
EU740416.1 gg_id:464939 Salinisphaera hydrothermalis str. EPR70
DQ015776.1 gg_id:139798 Antarctic lake water clone ELB25-046
EF157203.1 gg_id:244546 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon
FJ752438.1 gg_id:530747 endosymbionts Loripes lacteus and Anodontia fragilis gill symbiont clone 2A
U77478.1 gg_id:7623 endosymbiont Riftia pachyptila
FJ752447.1 gg_id:517886 endosymbionts and Anodontia fragilis Loripes lacteus gill symbiont clone 2C
AY542558.1 gg_id:113155 Gulf Mexico seafloor sediment clone GoM GB425 12B-13
AM883183.1 gg_id:337155 Endosymbioses between and deep-sea siboglinid tubeworms arctic cold seep (Haak
DQ394953.1 gg_id:152604 harbor sediment clone VHS-B3-62
AB530204.1 gg_id:586339 Monitoring Suez and Tokyo bays based on analyses marine sediment clone Tokyo..Ba
AM040102.1 gg_id:148469 sandy sediments clone Sylt 6
AB189713.2 gg_id:104039 Ifremeria nautilei gill symbiont
AF165909.1 gg_id:7577 Escarpia spicata endosymbiont 'Alvin #2837' Alvin #2837 endosymbiont
X84980.1 gg_id:7606 Lucina pectinata gill symbiont
EU488600.1 gg_id:535578 lucinid bivalve- symbiotic system: significance geochemical habitat on and gill symbio
U62131.1 gg_id:32280 Solemya terraeregina gill symbiont
AM236336.1 gg_id:169677 thiotrophic endosymbiont Lucinoma aff. kazani
U77480.1 gg_id:7624 endosymbiont Ridgeia piscesae
AY129089.1 gg_id:81760 Seepiophila jonesi symbiont
L25707.1 gg_id:7583 Lucina floridana gill symbiont
EF646140.1 gg_id:241188 Potential interactions particle- anammox and archaeal partners namibian Namibian u
AB073120.1 gg_id:67480 Endosymbiont Lamellibrachia satsuma clone TUB163

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| EF062806.1 | 188482 | 1363.8 | 1336.1 | 2219.2 | 770.1 | 5606.7 | 5983.9 |
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| EU169168.1 | 244420 | 1313.8 | 1660.3 | 2171.5 | 1294.7 | 1965.5 | 2705.6 |
| EF513773.1 | 220219 | 5300.4 | 4332.8 | 5474.0 | 7028.3 | 7012.0 | 8872.0 |
| DQ536517.1 | 159873 | 4090.9 | 4367.4 | 3755.7 | 3889.6 | 7896.2 | 9469.7 |
| EU647538.1 | 282969 | 759.2 | 1785.2 | 1713.7 | 437.0 | 7600.8 | 3520.2 |
| EU536806.1 | 283384 | 1417.4 | 2385.7 | 3539.8 | 1325.5 | 5708.9 | 8926.6 |
| EU101096.1 | 252064 | 6764.6 | 3060.9 | 6955.1 | 5709.1 | 7342.5 | 6930.3 |
| EU464759.1 | 294113 | 767.3 | 879.0 | 1398.9 | 897.4 | 3943.9 | 2714.0 |
| DQ824715.1 | 192521 | 15807.1 | 17461.7 | 13137.3 | 14020.6 | 21315.4 | 16963.9 |
| EU252490.1 | 236335 | 3794.8 | 3858.5 | 3719.2 | 5399.7 | 7980.1 | 6326.9 |
| EF608541.1 | 234990 | 459.9 | 831.8 | 951.3 | 1510.2 | 2849.0 | 2354.7 |
| AM403206.1 | 172703 | 201.7 | 302.7 | 1107.4 | 316.6 | 4993.0 | 3922.6 |
| DQ824723.1 | 194608 | 5041.9 | 7082.7 | 5414.2 | 4524.7 | 10087.6 | 8904.7 |
| DQ339144.1 | 149280 | 1858.7 | 2330.7 | 11275.3 | 5050.6 | 13191.1 | 9107.1 |
| EU143343.1 | 238940 | 9734.9 | 4970.8 | 8093.3 | 8317.0 | 7761.8 | 5411.1 |
| GU452539.1 | 528872 | 2787.8 | 1886.9 | 3540.4 | 4394.0 | 2591.5 | 1244.8 |
| EF988634.1 | 235478 | 672.0 | 862.3 | 518.2 | 262.5 | 4079.5 | 2393.3 |
| AJ421425.1 | 64239 | 26.4 | 64.1 | 53.2 | 80.7 | 572.0 | 321.1 |
| EU740416.1 | 464939 | 6182.0 | 5026.4 | 7253.3 | 5845.1 | 8050.0 | 5256.1 |
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| FJ752447.1 | 517886 | 5171.5 | 3875.7 | 5519.0 | 3471.3 | 865.4 | 3367.4 |
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| AB189713.2 | 104039 | 1164.6 | 2113.9 | 2053.9 | 1793.0 | 1984.4 | 3785.1 |
| AF165909.1 | 7577 | 1379.6 | 3127.8 | 4762.0 | 2242.7 | 4098.2 | 4292.7 |
| X84980.1 | 7606 | 239.3 | 456.6 | 907.2 | 540.6 | 1255.9 | 143.6 |
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| AM236336.1 | 169677 | 195.4 | 303.4 | 733.1 | 278.6 | 1399.6 | 1885.8 |
| U77480.1 | 7624 | 3277.2 | 2402.6 | 4083.0 | 2429.5 | 639.9 | 2636.7 |
| AY129089.1 | 81760 | 4371.6 | 2275.2 | 4875.1 | 4614.4 | 2181.5 | 3658.2 |
| L25707.1 | 7583 | 2436.9 | 1967.5 | 1427.5 | 1242.8 | 1865.7 | 834.5 |
| EF646140.1 | 241188 | 4032.9 | 4298.8 | 3319.1 | 3414.9 | 5889.1 | 5980.6 |
| AB073120.1 | 67480 | 6314.7 | 5501.9 | 7629.5 | 5071.4 | 7510.8 | 6794.9 |

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| k__Bacteria | k__Bacteria | p__Proteobacteria | c__Gammaproteobacteria |
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| o__Thiotrichales | f__Endoecteinascidiaceae |
| o__Thiotrichales | f__Endoecteinascidiaceae |
| o__Thiotrichales | f__Francisellaceae |
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g__Thiohalomonas
g__Thiohalorhabdus
g__Thiohalorhabdus
g__Candidatus Endoecteinascidia
g__unclassified
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g__Francisella
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| s__Thiohalomonas denitrificans | 2658 |
| s__Thiohalomonas denitrificans | 2789 |
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| s__Thiohalorhabdus denitrificans | 3209 |
| s__unclassified | 3097 |
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| s__Francisella endosymbiont of Dermacentor variabilis | 3861 |
| s__Francisella noatunensis | 3470 |
| s__Francisella philomiragia | 3508 |
| s__Francisella philomiragia | 3843 |
| s__unclassified | 3607 |
| s__unclassified | 3763 |
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| s__unclassified | 3308 |
| s__unclassified | 3452 |
| s__unclassified | 3457 |
| s__unclassified | 3750 |
| s__unclassified | 3760 |
| s__unclassified | 3862 |

L25711.1 gg_id:7585 Anodontia phillipiana gill symbiont
AF165908.1 gg_id:7619 Escarpia spicata endosymbiont 'Alvin #2839' Alvin #2839 endosymbiont
L25712.1 gg_id:7640 Codakia costata gill symbiont
L01575.1 gg_id:7575 Thyasira flexuosa gill symbiont
EU487821.1 gg_id:545897 lucinid bivalve- symbiotic system: significance geochemical habitat on and gill symbi
EU487848.1 gg_id:571610 lucinid bivalve- symbiotic system: significance geochemical habitat on and gill symbi
EU487790.1 gg_id:538251 lucinid bivalve- symbiotic system: significance geochemical habitat on and gill symbi
AF420355.1 gg_id:74333 hydrothermal sediment clone AF420355
DQ394903.1 gg_id:154047 harbor sediment clone VHS-B1-30
AY129088.1 gg_id:81293 unclassified escarpiid symbiont
DQ513106.1 gg_id:160275 Microbial life fluids ridge flank crustal fluid clone FS275-64B-03
EU487817.1 gg_id:569845 lucinid bivalve- symbiotic system: significance geochemical habitat on and gill symbi
EU487849.1 gg_id:557080 lucinid bivalve- symbiotic system: significance geochemical habitat on and gill symbi
EU290681.1 gg_id:241066 microbial structure biogeochemical contrasting shelf sediments Namibian upwelling
AF170359.1 gg_id:7586 Dechloromarinus chlorophilus str. NSS
X84979.1 gg_id:7598 Codakia orbicularis gill symbiont
EU580679.1 gg_id:269980 Autotrophic Thiomicrospira denitrificans-Like Catalyst Coupled Denitrification and Su
AM882519.1 gg_id:331064 Structure along hydrocarbon contamination coastal sediment oil polluted water pet
EU287120.1 gg_id:235979 Pacific arctic surface sediment clone P13-27
EF117913.1 gg_id:198462 Thiohalomonas denitrificans str. HLD 14
DQ836238.1 gg_id:168486 Thiohalomonas nitratireducens str. HRHd 3sp
EF455919.1 gg_id:217101 Thiohalomonas denitrificans str. HLD 15
EU374712.1 gg_id:274344 Thiohalorhabdus denitrificans str. HLD 10
EU246256.1 gg_id:255672 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-P5-H08
AY054370.1 gg_id:105206 marine ascidian symbiont clone AY054370
GQ346935.1 gg_id:561050 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
AY805307.1 gg_id:124180 Dermacentor variabilis symbiont
AY243027.1 gg_id:84287 Francisella philomiragia str. 2669
L26085.1 gg_id:7731 Francisella philomiragia
AJ698862.1 gg_id:112014 Francisella philomiragia str. ATCC 25015
Z21931.1 gg_id:7757 Francisella tularensis str. lvs ATCC 6223 FSC 155
EF153479.1 gg_id:208502 Francisella philomiragia str. DSM 7535
AM403242.1 gg_id:192162 Francisella piscicida str. 2006-Chile
AB001522.1 gg_id:7749 Ornithodoros moubata symbiote B
EU924183.1 gg_id:323152 sequences ticks USA: south-central Pennsylvania clone DA2
FJ425613.1 gg_id:365486 communnities healthy and diseased colonies Caribbean coral Montastrea faveolata C
FJ202233.1 gg_id:340201 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k
FJ202510.1 gg_id:319177 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k
FJ202975.1 gg_id:314000 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k
FJ202678.1 gg_id:337559 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k
FJ202250.1 gg_id:330874 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k

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|---|---|---|---|---|---|---|---|
| L25711.1 | 7585 | 728.3 | 387.3 | 1131.1 | 1762.0 | 1264.3 | 1381.1 |
| AF165908.1 | 7619 | 10648.2 | 12701.8 | 552.5 | 9237.1 | 2559.5 | 3240.0 |
| L25712.1 | 7640 | 904.6 | 1473.9 | 1890.2 | 1342.7 | 1245.9 | 3789.5 |
| L01575.1 | 7575 | 936.7 | 616.4 | 353.2 | 609.8 | 354.9 | 276.2 |
| EU487821.1 | 545897 | 9558.7 | 7993.3 | 7263.2 | 9919.9 | 11866.5 | 12578.6 |
| EU487848.1 | 571610 | 16365.1 | 16425.4 | 8004.2 | 12161.8 | 14005.1 | 10396.1 |
| EU487790.1 | 538251 | 13778.9 | 13412.1 | 5437.8 | 9545.3 | 11762.6 | 7927.8 |
| AF420355.1 | 74333 | 227.3 | 820.4 | 1648.9 | 262.4 | 261.1 | 272.2 |
| DQ394903.1 | 154047 | 9118.3 | 9065.6 | 4430.0 | 6308.4 | 5378.2 | 4503.3 |
| AY129088.1 | 81293 | 5197.9 | 3422.5 | 1218.9 | 3868.7 | 2673.2 | 2186.5 |
| DQ513106.1 | 160275 | 2778.5 | 3476.2 | 3616.2 | 3227.8 | 3120.2 | 3024.3 |
| EU487817.1 | 569845 | 11287.8 | 11680.6 | 11043.8 | 8183.3 | 14204.7 | 10954.8 |
| EU487849.1 | 557080 | 8547.8 | 10527.8 | 3326.8 | 6484.3 | 5984.0 | 5557.8 |
| EU290681.1 | 241066 | 3193.8 | 3695.0 | 4315.6 | 2443.2 | 3481.0 | 3436.2 |
| AF170359.1 | 7586 | 1716.6 | 1526.5 | 2898.2 | 931.4 | 3237.2 | 1856.2 |
| X84979.1 | 7598 | 420.6 | 1526.4 | 2266.8 | 130.6 | 143.8 | 1377.6 |
| EU580679.1 | 269980 | 9075.6 | 8466.7 | 11940.5 | 11804.5 | 14484.5 | 11752.8 |
| AM882519.1 | 331064 | 1508.5 | 3197.3 | 4618.4 | 1961.3 | 4497.0 | 5014.2 |
| EU287120.1 | 235979 | 1502.3 | 1025.7 | 1836.1 | 2287.6 | 1289.0 | 2120.0 |
| EF117913.1 | 198462 | 168.2 | 698.9 | 2329.5 | 439.5 | 3475.0 | 290.2 |
| DQ836238.1 | 168486 | 597.3 | 1260.0 | 2449.8 | 1176.9 | 948.8 | 1682.3 |
| EF455919.1 | 217101 | 2456.4 | 3609.0 | 5900.5 | 3111.0 | 8180.5 | 5731.6 |
| EU374712.1 | 274344 | 42.2 | 58.4 | 43.4 | 44.1 | 57.6 | 44.2 |
| EU246256.1 | 255672 | 4087.8 | 5974.2 | 8472.1 | 3961.0 | 11898.7 | 9275.1 |
| AY054370.1 | 105206 | 291.9 | 442.5 | 506.4 | 292.7 | 750.5 | 750.9 |
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| AY805307.1 | 124180 | 315.0 | 942.0 | 922.8 | 785.1 | 2711.6 | 2508.6 |
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| AM403242.1 | 192162 | 799.0 | 2100.3 | 2180.9 | 1903.3 | 8631.4 | 3704.2 |
| AB001522.1 | 7749 | 1567.2 | 2106.7 | 2451.3 | 2748.6 | 5792.4 | 4136.6 |
| EU924183.1 | 323152 | 4303.2 | 6487.2 | 1779.5 | 3997.5 | 3259.0 | 3661.3 |
| FJ425613.1 | 365486 | 12838.8 | 11658.4 | 5043.2 | 6967.1 | 7764.1 | 5899.9 |
| FJ202233.1 | 340201 | 726.3 | 912.1 | 1118.9 | 635.9 | 955.4 | 1113.2 |
| FJ202510.1 | 319177 | 9586.0 | 11038.7 | 10768.6 | 7157.4 | 10731.4 | 9035.0 |
| FJ202975.1 | 314000 | 3271.9 | 3619.3 | 4456.6 | 2478.3 | 4521.4 | 4235.7 |
| FJ202678.1 | 337559 | 3798.2 | 5205.3 | 7888.6 | 2701.8 | 7574.4 | 6431.2 |
| FJ202250.1 | 330874 | 8638.2 | 7844.0 | 5391.2 | 5204.6 | 8664.2 | 6797.8 |

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DQ889939.1 gg_id:173408 natural product producing octocoral Erythropodium caribaeorum Thiotrichales clone
AY102612.1 gg_id:64552 Caedibacter taeniospiralis
FJ202512.1 gg_id:350687 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k
AB176554.1 gg_id:98992 Thiotrichales CML28
DQ660912.1 gg_id:225063 Methylophaga sp. str. DMS002
AY128533.1 gg_id:86185 Methylophaga natronica str. Bur2
EU328072.1 gg_id:278985 dynamics during bioremediation crude oil contaminated moderate saline soil clone Y
DQ400508.1 gg_id:160152 Methylophaga marina str. KM5
FJ172066.1 gg_id:333882 Microbial athalassohaline Tirez lagoon (Spain) water clone MJW9
AF384373.1 gg_id:66020 Methylophaga alcalica str. M39
AY694421.1 gg_id:99935 Methylophaga murata str. Kr3
EU287295.1 gg_id:254176 Pacific arctic surface sediment clone S11-112
AY375062.1 gg_id:97463 deep sea sediment clone B92
EU287249.1 gg_id:246106 Pacific arctic surface sediment clone S11-66
EU287255.1 gg_id:239634 Pacific arctic surface sediment clone S11-72
AJ704666.1 gg_id:109271 marine sediment clone HMMVCen-13
EU236405.1 gg_id:290767 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg92D11
EU287300.1 gg_id:255354 Pacific arctic surface sediment clone S11-117
FJ155021.1 gg_id:353468 seasonal fluctuation coastal Bohai Bay sequencing and RFLP soil clone D21
DQ521546.1 gg_id:191569 Antarctic lake ice cover clone ANTLV7_H05
AY212648.1 gg_id:99225 water 20 m upstream manure clone 195up
GQ007716.1 gg_id:501947 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
AY542557.1 gg_id:113736 Gulf Mexico seafloor sediment clone GoM GB425 12B-8
EU919781.1 gg_id:340144 Kongsfjorden western Spitsbergen Svalbard ocean water clone b59
EU287118.1 gg_id:257905 Pacific arctic surface sediment clone P13-25
AY375084.1 gg_id:97200 deep sea sediment clone B132
AF532772.1 gg_id:60454 marine sediment clone Limfjorden L22
AF035956.1 gg_id:7511 Beggiatoa sp. 'Bay Concepcion' str. Bay Concepcion 'Bay
FJ875195.1 gg_id:573955 Coexistence Beggiatoa spp. Epsilonproteobacteria and Fusibacter organically-enriche
AF532775.1 gg_id:60451 marine sediment clone Limfjorden L9
AY580013.1 gg_id:111119 Beggiatoa sp. 'Carmel Canyon' Carmel Canyon
AY883933.1 gg_id:137953 Juan de Fuca filamentous
AF532774.1 gg_id:60452 marine sediment clone Limfjorden L8
AB108786.1 gg_id:84651 marine sediment clone Tokyo Bay D
AF532773.1 gg_id:60453 marine sediment clone Limfjorden L6
FM203381.1 gg_id:432832 Biogeography filamentous and epsilonproteobacterial ectosymbionts vent shrimp e
FM203400.1 gg_id:407753 Biogeography filamentous and epsilonproteobacterial ectosymbionts vent shrimp e
EU086765.1 gg_id:286899 Siboglinum fiordicum and Endosymbionts Siboglinidae (Annelida) Norway: Ypsesund
EU086760.1 gg_id:285854 Siboglinum fiordicum and Endosymbionts Siboglinidae (Annelida) Norway: Ypsesund
EU491817.1 gg_id:271093 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39
FJ497604.1 gg_id:533041 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun

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| DQ889939.1 | 173408 | 1016.5 | 1578.6 | 2194.4 | 443.2 | 2148.9 | 897.7 |
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| FJ202512.1 | 350687 | 10796.9 | 11647.1 | 13839.9 | 10850.1 | 18097.6 | 12283.4 |
| AB176554.1 | 98992 | 16.8 | 19.4 | 12.0 | 38.9 | 51.3 | 16.4 |
| DQ660912.1 | 225063 | 2102.0 | 2270.5 | 2210.1 | 1684.6 | 2723.5 | 3677.7 |
| AY128533.1 | 86185 | 3051.1 | 2960.4 | 2963.0 | 3056.0 | 1268.9 | 1648.8 |
| EU328072.1 | 278985 | 1127.1 | 1879.8 | 4776.9 | 1301.2 | 1997.4 | 2423.1 |
| DQ400508.1 | 160152 | 2379.9 | 2430.4 | 1606.2 | 2157.5 | 1998.0 | 4777.4 |
| FJ172066.1 | 333882 | 1171.7 | 919.6 | 1679.0 | 772.2 | 1693.7 | 1178.7 |
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| AY694421.1 | 99935 | 8363.7 | 9026.5 | 4012.4 | 7352.7 | 7521.5 | 5178.0 |
| EU287295.1 | 254176 | 6850.2 | 7006.8 | 7402.9 | 5803.3 | 5522.0 | 5285.9 |
| AY375062.1 | 97463 | 3547.8 | 3429.2 | 4705.8 | 3310.3 | 4690.7 | 3432.5 |
| EU287249.1 | 246106 | 756.7 | 1944.1 | 3675.6 | 1927.6 | 2493.0 | 2414.1 |
| EU287255.1 | 239634 | 2531.8 | 2794.9 | 9592.1 | 5547.6 | 3753.1 | 5746.6 |
| AJ704666.1 | 109271 | 225.0 | 154.5 | 92.6 | 878.6 | 74.5 | 44.2 |
| EU236405.1 | 290767 | 3033.5 | 4354.0 | 5187.0 | 4723.9 | 3481.2 | 4596.8 |
| EU287300.1 | 255354 | 1770.2 | 1688.5 | 4036.3 | 3133.9 | 1872.3 | 1304.2 |
| FJ155021.1 | 353468 | 991.7 | 744.8 | 1229.8 | 3347.4 | 1322.1 | 1828.7 |
| DQ521546.1 | 191569 | 517.6 | 584.8 | 2301.5 | 1424.4 | 1365.3 | 1523.8 |
| AY212648.1 | 99225 | 1988.7 | 1327.9 | 2141.3 | 2984.9 | 1437.5 | 2071.5 |
| GQ007716.1 | 501947 | 3982.3 | 4755.0 | 3759.2 | 4215.4 | 5463.1 | 5716.7 |
| AY542557.1 | 113736 | 3438.9 | 3955.7 | 4042.4 | 3641.9 | 5529.9 | 5291.0 |
| EU919781.1 | 340144 | 10094.0 | 9076.1 | 6596.7 | 6791.6 | 5614.6 | 5955.6 |
| EU287118.1 | 257905 | 7200.1 | 7194.6 | 6702.7 | 8486.5 | 10100.4 | 9291.2 |
| AY375084.1 | 97200 | 17699.0 | 18141.5 | 13305.3 | 15601.2 | 22976.0 | 16405.9 |
| AF532772.1 | 60454 | 5057.2 | 5184.1 | 7631.3 | 6027.3 | 6670.5 | 7227.0 |
| AF035956.1 | 7511 | 1654.9 | 1680.7 | 3193.6 | 2049.5 | 1778.5 | 2867.6 |
| FJ875195.1 | 573955 | 5579.3 | 6850.4 | 8162.0 | 8720.3 | 11476.4 | 7832.0 |
| AF532775.1 | 60451 | 4039.0 | 5641.9 | 3832.4 | 5661.4 | 3906.6 | 3269.0 |
| AY580013.1 | 111119 | 4195.6 | 4869.7 | 4876.9 | 3269.8 | 4026.1 | 3851.8 |
| AY883933.1 | 137953 | 34.1 | 43.2 | 99.7 | 65.6 | 86.0 | 180.0 |
| AF532774.1 | 60452 | 16052.1 | 13449.6 | 10556.9 | 12531.0 | 14748.8 | 13074.3 |
| AB108786.1 | 84651 | 5100.7 | 6686.7 | 10228.5 | 7559.7 | 9430.1 | 5402.0 |
| AF532773.1 | 60453 | 839.3 | 1665.9 | 1001.3 | 1131.2 | 2487.9 | 2855.5 |
| FM203381.1 | 432832 | 319.8 | 1431.1 | 530.9 | 167.8 | 147.5 | 99.8 |
| FM203400.1 | 407753 | 2036.2 | 1409.1 | 1917.2 | 1547.9 | 1001.0 | 3143.7 |
| EU086765.1 | 286899 | 5823.0 | 6283.2 | 2791.5 | 3640.1 | 4869.6 | 3660.7 |
| EU086760.1 | 285854 | 2830.2 | 2529.3 | 8508.8 | 3492.0 | 8650.0 | 6046.2 |
| EU491817.1 | 271093 | 9058.9 | 5536.4 | 14977.6 | 12084.6 | 8906.7 | 10810.7 |
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|---|---|
| s__gamma proteobacterium endosymbiont of Siboglinum fiordicum | 3067 |
| s__gamma proteobacterium endosymbiont of Siboglinum fiordicum | 3288 |
| s__unclassified | 1649 |
| s__unclassified | 2313 |
| s__unclassified | 2315 |
| s__unclassified | 2343 |
| s__unclassified | 2344 |
| s__unclassified | 2365 |
| s__unclassified | 2389 |
| s__unclassified | 2431 |
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| s__unclassified | 2487 |
| s__unclassified | 2490 |
| s__unclassified | 2535 |
| s__unclassified | 2540 |
| s__unclassified | 2550 |
| s__unclassified | 2628 |
| s__unclassified | 2688 |
| s__unclassified | 2690 |
| s__unclassified | 2707 |
| s__unclassified | 2710 |
| s__unclassified | 2752 |
| s__unclassified | 2798 |
| s__unclassified | 2807 |
| s__unclassified | 2852 |
| s__unclassified | 2878 |
| s__unclassified | 2939 |
| s__unclassified | 2952 |
| s__unclassified | 2953 |
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| s__unclassified | 3041 |
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| s__unclassified | 3110 |
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| s__unclassified | 3145 |
| s__unclassified | 3180 |
| s__unclassified | 3276 |
| s__unclassified | 3290 |

EU086767.1 gg_id:280842 Siboglinum fiordicum and Endosymbionts Siboglinidae (Annelida) Norway: Skoge Inle
EU491836.1 gg_id:263959 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39
EU592359.1 gg_id:581185 Seasonal changes Salton Sea hypersaline water clone SSW84Ap
AB252051.1 gg_id:170060 Oligobrachia mashikoi endosymbiont
FN397818.1 gg_id:421635 geomicrobiological investigation sediments Gulf Cadiz GeoB 9072-1 anoxic sub-surfa
EU617743.1 gg_id:311740 Seasonal variation microbial Yel Sea sediment clone D13S-152
AB476179.1 gg_id:559576 Compositional and functional transition epibiotic microbial hydrothermal vent galath
EU265784.1 gg_id:273851 epibiotic assemblage recently described Yeti Kiwa hirsuta ( Kiwidae) surface crab hyc
DQ351782.1 gg_id:149662 Microbial Adherent Sediment Particles Heavy Metal Contaminated North Sea Surfac
AB440173.1 gg_id:546279 Farming and harvesting filamentous vent- galatheid crab (Decapoda; Anomura) vent
AM883178.1 gg_id:349801 Endosymbioses between and deep-sea siboglinid tubeworms arctic cold seep (Haak
EU652549.1 gg_id:278683 Seasonal variation microbial Yel Sea sediment clone A8S-100
FJ712487.1 gg_id:522744 and Archaea Gas Hydrate Sediments (East Sea) Kazan Mud Volcano Anaximander Mo
AY922216.1 gg_id:114239 whalefall clone 131703
AB476177.1 gg_id:535260 Compositional and functional transition epibiotic microbial hydrothermal vent galath
EU617742.1 gg_id:317335 Seasonal variation microbial Yel Sea sediment clone D13S-1
EF687220.1 gg_id:280984 Biogeochemistry iron- and sulfur-precipitating microbial mats (Nile Mediterranean) ir
FJ712552.1 gg_id:520020 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) K
DQ925898.1 gg_id:254275 Microbes and Thermal Gradients Temperature Hydrothermal Chimneys hydrotherm
AM176844.1 gg_id:160888 Recovery mangrove sediment clone SZB76
AB239761.1 gg_id:148717 isotopic evidence ectosymbiosis between filamentous and stalked barnacle (Cirriped
EU652547.1 gg_id:277645 Seasonal variation microbial Yel Sea sediment clone C8S-96
AB271123.1 gg_id:165803 Oligobrachia mashikoi endosymbiont E
AY225630.1 gg_id:98216 Mid-Atlantic Ridge hydrothermal sediment clone AT-s43
AY531559.1 gg_id:107157 Indian Ocean hydrothermal vent clone SF_C7-H11
FJ905702.1 gg_id:555129 s Tonga-Kermadec iron oxide sediments Volcano 1 Tonga Arc clone V1F22b
FM242244.1 gg_id:345341 sequences sediment clone 81 T0h-oil
EU707297.1 gg_id:349336 sulfur oxidizing Wadden Sea sediments Janssand intertidal sandy sediment 0 3 cm de
EU025026.1 gg_id:252006 Leucothrix mucor str. LJS0601
EU265790.1 gg_id:260040 epibiotic assemblage recently described Yeti Kiwa hirsuta ( Kiwidae) surface crab hyc
DQ925906.1 gg_id:249236 Microbes and Thermal Gradients Temperature Hydrothermal Chimneys hydrotherm
AJ441234.1 gg_id:57450 hydrothermal vent polychaete mucous clone P. palm A 79
FJ712548.1 gg_id:527446 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) K
AB476202.1 gg_id:559867 Compositional and functional transition epibiotic microbial hydrothermal vent galath
AM883179.1 gg_id:350065 Endosymbioses between and deep-sea siboglinid tubeworms arctic cold seep (Haak
AM040128.1 gg_id:145294 sandy sediments clone Sylt 32
AY327876.2 gg_id:89122 surface vent snail foot clone SF_C7-E4
EU491039.1 gg_id:272243 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount South Rift X
EU265791.1 gg_id:267469 epibiotic assemblage recently described Yeti Kiwa hirsuta ( Kiwidae) surface crab hyc
EU555124.1 gg_id:260421 Microbial Sulfide Hydrothermal Vent Field Juan de Fuca Ridge Dudley hydrothermal
EU652546.1 gg_id:278109 Seasonal variation microbial Yel Sea sediment clone B8S-13

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| EU086767.1 | 280842 | 864.9 | 780.3 | 2134.8 | 710.7 | 1822.2 | 1431.9 |
| EU491836.1 | 263959 | 4372.6 | 3910.7 | 5597.9 | 4844.8 | 7167.6 | 5879.2 |
| EU592359.1 | 581185 | 3641.2 | 1202.9 | 4500.5 | 2405.5 | 4843.9 | 3599.3 |
| AB252051.1 | 170060 | 774.8 | 817.3 | 2498.9 | 1218.7 | 3748.6 | 3026.3 |
| FN397818.1 | 421635 | 7746.2 | 5856.9 | 7089.6 | 6858.6 | 9426.6 | 9094.5 |
| EU617743.1 | 311740 | 6670.9 | 6290.1 | 6028.5 | 4986.4 | 7020.1 | 5385.4 |
| AB476179.1 | 559576 | 1435.6 | 2124.0 | 2568.6 | 1848.8 | 3180.1 | 4075.6 |
| EU265784.1 | 273851 | 36.9 | 47.2 | 44.3 | 72.1 | 98.3 | 34.5 |
| DQ351782.1 | 149662 | 6992.9 | 6695.5 | 6491.3 | 6661.9 | 7795.3 | 8260.4 |
| AB440173.1 | 546279 | 578.2 | 348.6 | 446.8 | 331.9 | 168.8 | 122.9 |
| AM883178.1 | 349801 | 6860.5 | 2984.4 | 6559.5 | 7611.3 | 4986.3 | 5286.4 |
| EU652549.1 | 278683 | 3578.1 | 3625.1 | 2709.1 | 4259.1 | 5645.7 | 4670.4 |
| FJ712487.1 | 522744 | 4542.7 | 3394.7 | 3021.6 | 4124.6 | 2426.9 | 1693.4 |
| AY922216.1 | 114239 | 2378.9 | 3022.9 | 1171.9 | 1159.2 | 5088.6 | 4886.4 |
| AB476177.1 | 535260 | 1251.7 | 1251.1 | 2553.4 | 3490.4 | 1828.5 | 2097.8 |
| EU617742.1 | 317335 | 4238.8 | 2581.1 | 2399.8 | 3917.5 | 3671.0 | 2840.8 |
| EF687220.1 | 280984 | 5065.0 | 4307.6 | 3570.4 | 3746.4 | 3584.3 | 5594.4 |
| FJ712552.1 | 520020 | 2816.0 | 2165.5 | 1589.0 | 2084.8 | 3314.3 | 3096.4 |
| DQ925898.1 | 254275 | 4310.9 | 2944.7 | 4456.4 | 2633.3 | 3242.7 | 5834.3 |
| AM176844.1 | 160888 | 113.2 | 146.0 | 241.6 | 132.9 | 119.8 | 301.8 |
| AB239761.1 | 148717 | 4270.2 | 3704.6 | 3129.6 | 4243.6 | 4961.2 | 2858.3 |
| EU652547.1 | 277645 | 6630.3 | 4902.5 | 3283.9 | 6336.5 | 5975.2 | 6768.8 |
| AB271123.1 | 165803 | 464.7 | 554.9 | 1133.2 | 211.1 | 1627.4 | 474.0 |
| AY225630.1 | 98216 | 7261.7 | 3647.7 | 5847.7 | 7653.1 | 5548.5 | 8562.1 |
| AY531559.1 | 107157 | 408.7 | 458.7 | 1936.2 | 488.1 | 427.0 | 632.7 |
| FJ905702.1 | 555129 | 1895.7 | 1193.4 | 2105.4 | 2545.0 | 1495.8 | 1448.6 |
| FM242244.1 | 345341 | 2026.5 | 2361.0 | 3630.2 | 3020.4 | 3333.5 | 3093.2 |
| EU707297.1 | 349336 | 3670.4 | 2862.1 | 5064.4 | 4004.5 | 5364.4 | 3289.3 |
| EU025026.1 | 252006 | 1660.0 | 2221.8 | 2948.4 | 2780.6 | 2080.6 | 3645.0 |
| EU265790.1 | 260040 | 5729.1 | 5427.4 | 5802.7 | 6394.2 | 11426.7 | 7100.9 |
| DQ925906.1 | 249236 | 5475.6 | 1814.7 | 3702.7 | 5206.0 | 3932.1 | 1630.2 |
| AJ441234.1 | 57450 | 111.5 | 207.7 | 89.0 | 214.5 | 331.3 | 104.4 |
| FJ712548.1 | 527446 | 4867.2 | 4915.0 | 5004.3 | 5930.1 | 9265.7 | 8986.4 |
| AB476202.1 | 559867 | 6185.7 | 5163.1 | 7825.9 | 8117.2 | 7193.7 | 9592.3 |
| AM883179.1 | 350065 | 7321.4 | 4035.9 | 3614.7 | 8232.9 | 2371.3 | 2132.3 |
| AM040128.1 | 145294 | 1087.6 | 702.5 | 1094.6 | 991.0 | 3204.7 | 2739.1 |
| AY327876.2 | 89122 | 1017.1 | 863.1 | 522.4 | 810.6 | 1347.8 | 1012.4 |
| EU491039.1 | 272243 | 2425.8 | 2136.1 | 2615.5 | 1211.9 | 591.8 | 401.2 |
| EU265791.1 | 267469 | 2643.0 | 2210.3 | 2182.8 | 2500.3 | 3359.9 | 2884.9 |
| EU555124.1 | 260421 | 424.1 | 230.1 | 498.5 | 1113.7 | 415.3 | 654.7 |
| EU652546.1 | 278109 | 3419.4 | 2799.0 | 4603.4 | 5896.5 | 5519.3 | 5048.8 |

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|---|---|---|---|
| k__Bacteria | k__Bacteria | p__Proteobacteria | c__Gammaproteobacteria |
| k__Bacteria | k__Bacteria | p__Proteobacteria | c__Gammaproteobacteria |
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g__Leucothrix
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g__sfE

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| s__unclassified | 3297 |
| s__Thioploca ingrica | 3718 |
| s__Thiothrix eikelboomii | 2732 |
| s__Thiothrix flexilis | 2447 |
| s__Thiothrix fructosivorans | 2427 |
| s__unclassified | 2328 |
| s__unclassified | 2369 |
| s__unclassified | 2459 |
| s__unclassified | 2575 |
| s__unclassified | 2621 |
| s__unclassified | 2917 |
| s__unclassified | 3031 |
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| s__unclassified | 3238 |
| s__unclassified | 2353 |
| s__unclassified | 3071 |
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| s__unclassified | 3447 |
| s__unclassified | 3469 |
| s__unclassified | 3492 |
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| s__unclassified | 2473 |
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| s__unclassified | 2597 |
| s__unclassified | 2884 |
| s__unclassified | 2968 |
| s__unclassified | 2307 |
| s__unclassified | 2950 |
| s__unclassified | 3463 |
| s__unclassified | 4046 |

EU491688.1 gg_id:261914 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39
AB263619.1 gg_id:178235 Thioploca sp. 'Lake Ogawara'
AB042542.1 gg_id:18561 Thiothrix eikelboomii str. COM-
AB042544.1 gg_id:37302 Thiothrix flexilis str. EJ1M-B
GU269554.1 gg_id:546547 Thiothrix fructosivorans str. Q
FJ769459.1 gg_id:513774 Changes Methanogenic Microbial After Sludge Pre-treatment full-scale municipal ana
AM490765.1 gg_id:586481 Linking and functional nutrient spiraling mats (USA) microbial mat sulfidic cave sprir
DQ413126.1 gg_id:151073 Microbial -dependent and Approaches Anaerobic/Aerobic SBR Reactor EBPR sludge
AB042537.1 gg_id:18257 Thiothrix disciformis str. B2-8
DQ067608.1 gg_id:138619 Thiothrix sp. str. FBR0112
FM165205.1 gg_id:544166 Succession structure biotrickling filter treating loads H2S terminal restriction fragme
FM174321.1 gg_id:565016 biotrickling filter treating loads H2S biology tools clone H2SRC112
FM174322.1 gg_id:564802 biotrickling filter treating loads H2S biology tools clone H2SRC127
U32940.1 gg_id:7656 "Thiothrix ramosa"
L79961.1 gg_id:135216 Thiothrix unzii str. A1; ATCC 49747
AB166732.1 gg_id:99902 Thiothrix sp. str. KRN-B2
AY510242.1 gg_id:110102 microbial mat cave sulfidic spring clone LKC3_156.41
DQ676306.1 gg_id:219763 Archaeal sediment and plankton freshwater pond suboxic freshwater-pond clone M
EU662352.1 gg_id:566153 Productivity- Chemolithoautotrophically Based Sulfidic Karst Systems microbial mat
AF110276.1 gg_id:81307 Beggiatoa sp. str. MS-81-1c
GQ441309.1 gg_id:568660 and dynamic mat present vs. active nitrogen-fixing microorganisms marine microbia
GU117706.1 gg_id:552714 Beggiatoa sp. Arauama I
FJ516903.1 gg_id:562971 semiarid 'Tablas de Daimiel National Park' wetland (Central Spain) unravelled upper s
EF428583.1 gg_id:255153 Beggiatoa sp. 'Chiprana'
AF110275.1 gg_id:81842 Beggiatoa sp. str. AA5A
EU015402.1 gg_id:241048 Beggiatoa sp. str. LPN
AF110274.1 gg_id:81779 Beggiatoa alba str. B18LD; ATCC 33555
AF110277.1 gg_id:81107 Beggiatoa sp. str. MS-81-6
AM259850.1 gg_id:212023 Spatial sponge- Mediterranean Tethya aurantium sponge cortex clone TAA-10-90
EU491871.1 gg_id:261085 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39
FJ542932.1 gg_id:511554 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone B
EF471637.1 gg_id:269523 Fast Screening and Estuarine Operon Libraries whole surface water Chesapeake Bay
GU230347.1 gg_id:568157 Multilevel approach along Rio de la Plata-South Atlantic Ocean coastal sediment clo
FJ905691.1 gg_id:575131 s Tonga-Kermadec iron oxide chimney-like structure on Volcano 19 Tonga Arc clone V
DQ988300.1 gg_id:193694 Microbial lab-scale A1-A2-O fixed biofilm system coking wastewater treatment with
DQ451463.1 gg_id:156946 forest soil clone FAC24
EU369126.1 gg_id:346345 libraries oyster shell clone MBIOS-10
EU335403.1 gg_id:252003 Changes microbial metabolic and along hydrogeochemically variable profile unsatura
EU104116.1 gg_id:336069 Evidence Comamonadaceae determinants settling performance activated sludge clo
EU800820.1 gg_id:327533 It's all ranking aquatic Delaware Bay NJ clone 2C229038
AB013257.1 gg_id:8011 deep-sea sediment clone NKB5

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|---|---|---|---|---|---|---|---|
| EU491688.1 | 261914 | 1178.1 | 1423.5 | 1396.1 | 2456.0 | 624.5 | 1039.6 |
| AB263619.1 | 178235 | 34.2 | 146.1 | 124.9 | 83.0 | 536.8 | 185.2 |
| AB042542.1 | 18561 | 5804.2 | 7438.9 | 6091.0 | 4378.8 | 7475.6 | 5846.5 |
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| GU269554.1 | 546547 | 668.3 | 830.3 | 1687.4 | 895.5 | 2564.7 | 1566.7 |
| FJ769459.1 | 513774 | 1504.7 | 1582.1 | 5082.2 | 2165.6 | 9951.3 | 4907.2 |
| AM490765.1 | 586481 | 187.6 | 441.8 | 946.3 | 139.4 | 855.2 | 1539.2 |
| DQ413126.1 | 151073 | 986.2 | 1243.2 | 1721.9 | 961.9 | 1055.2 | 1550.2 |
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| FM165205.1 | 544166 | 6213.5 | 4310.4 | 6949.1 | 6152.2 | 7845.3 | 8886.5 |
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| L79961.1 | 135216 | 94.1 | 104.4 | 815.5 | 185.2 | 204.4 | 396.2 |
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FM242254.1 gg_id:356042 sequences sediment clone 22 T0h-oil
FJ202937.1 gg_id:334435 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k
EU369130.1 gg_id:333009 libraries oyster shell clone MBIOS-14
FN396657.1 gg_id:539488 constant flux thermophilic cold seabed Arctic marine surface sediment clone s5_0_I_
AM882547.1 gg_id:333792 Structure along hydrocarbon contamination coastal sediment oil polluted water pet
EU050800.1 gg_id:243549 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_03_88
AJ240989.1 gg_id:7567 Norway:(Svalbard)Hornsund clone Sva0318
FJ545579.1 gg_id:552276 Diveristy Seawater and Sediment Northern North Yel Sea sediment clone S2-59
EF632659.1 gg_id:251374 Unique microbial contrasting aquatic altitude Andean Altiplano (northern Chile) sedir
FJ712446.1 gg_id:532489 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) K
EU050802.1 gg_id:255117 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_01_06
EU734980.1 gg_id:327786 assemblages sediment station DBSE Northern Bering Sea clone 074B2
DQ351809.1 gg_id:146146 Microbial Adherent Sediment Particles Heavy Metal Contaminated North Sea Surfac
GQ259302.1 gg_id:584388 Microbial activities coastal marine sediments and water column Svalbard surface se
AM176874.1 gg_id:161459 Recovery mangrove sediment clone SZB41
DQ015812.1 gg_id:140611 Antarctic lake water clone ELB16-159
AM997958.1 gg_id:539642 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A
AF452606.1 gg_id:63851 hypersaline Mono Lake clone ML1218M-31
FJ425594.1 gg_id:369412 communnities healthy and diseased colonies Caribbean coral Montastrea faveolata cl
CU467479.1 gg_id:337214 Prokaryotic Tunisian saltern Saltern solar multipond clone
AY536224.1 gg_id:101210 host gut clone LAgut--P12
FJ712536.1 gg_id:515895 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) K
AB015252.1 gg_id:7561 deepest cold-seep area Japan Trench clone JTB148 proteobacterium
FM179868.1 gg_id:333458 Biogeochemical processes microbial Gullfaks and Tommeliten methane seeps (Nortl
CU467466.1 gg_id:352266 Prokaryotic Tunisian saltern Saltern solar multipond clone
FJ152643.1 gg_id:310058 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX1A_
DQ351787.1 gg_id:145050 Microbial Adherent Sediment Particles Heavy Metal Contaminated North Sea Surfac
EU592402.1 gg_id:578072 Seasonal changes Salton Sea hypersaline water clone SSW11Ap
FJ264563.1 gg_id:352025 Manganese and Iron Dependent Anaerobic Oxidation Methane methane seep sedime
EU287251.1 gg_id:256806 Pacific arctic surface sediment clone S11-68
DQ833465.1 gg_id:171373 detected analyses depth sediment Guanting Reservoir clone 5-7
FJ152993.1 gg_id:330383 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX4CI
DQ394977.1 gg_id:155915 harbor sediment clone VHS-B4-12
FJ205342.1 gg_id:550486 Prokaryotic deep-sea hydrothermal region East Lau Spreading Centre deep marine se
FM242255.1 gg_id:311786 sequences sediment clone 12 T0h-oil
DQ330799.1 gg_id:159131 Guerrero Negro hypersaline microbial mat clone 02D2Z21
AB294963.1 gg_id:225004 -dependent & analyses hydrothermal system off Taketomi Island Japan microbial ma
DQ811839.1 gg_id:164052 mangrove soil clone MSB-3C10
AJ504486.1 gg_id:62635 sewage sludge clone
CU922396.1 gg_id:567904 Towards definition core microorganisms involved digestion mesophilic anaerobic dig

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| EU369130.1 | 333009 | 5030.5 | 5669.3 | 3459.6 | 4360.3 | 6656.3 | 5924.9 |
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| AM882547.1 | 333792 | 3476.5 | 4156.7 | 2666.5 | 2787.6 | 2107.1 | 2932.3 |
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| EF632659.1 | 251374 | 11749.9 | 9887.6 | 6123.0 | 7380.4 | 7917.5 | 8727.3 |
| FJ712446.1 | 532489 | 9104.2 | 7215.4 | 6194.9 | 9404.9 | 11357.7 | 8910.7 |
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| EU734980.1 | 327786 | 478.0 | 1093.4 | 770.4 | 421.4 | 471.8 | 484.0 |
| DQ351809.1 | 146146 | 5299.0 | 3416.7 | 5797.9 | 3124.6 | 4006.4 | 3981.1 |
| GQ259302.1 | 584388 | 1091.7 | 530.2 | 205.3 | 828.3 | 984.1 | 424.1 |
| AM176874.1 | 161459 | 2088.8 | 1626.6 | 589.1 | 635.9 | 650.9 | 653.2 |
| DQ015812.1 | 140611 | 4522.2 | 3473.5 | 2347.5 | 4649.2 | 1389.7 | 2664.8 |
| AM997958.1 | 539642 | 6841.0 | 6438.9 | 3567.3 | 5330.7 | 6215.5 | 5262.6 |
| AF452606.1 | 63851 | 2041.1 | 2105.1 | 2342.7 | 2887.1 | 4291.2 | 5608.2 |
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| FJ152643.1 | 310058 | 2063.2 | 3329.2 | 1345.7 | 2297.1 | 6592.6 | 5724.9 |
| DQ351787.1 | 145050 | 11242.5 | 5773.5 | 12652.1 | 9921.2 | 7188.2 | 7320.3 |
| EU592402.1 | 578072 | 5220.0 | 3844.0 | 1176.8 | 6017.3 | 6852.0 | 6811.3 |
| FJ264563.1 | 352025 | 14484.8 | 13902.2 | 16330.7 | 14802.9 | 14384.3 | 15146.8 |
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FJ623384.1 gg_id:578673 Efficient polyhydroxyalkanoates production waste-activated submitted process seque
AM086102.1 gg_id:150497 Abundance and archaea mesotrophic Lake Kinneret lake profundal sediment clone c
FJ623328.1 gg_id:512280 Efficient polyhydroxyalkanoates production waste-activated submitted process seque
FJ623281.1 gg_id:580719 Efficient polyhydroxyalkanoates production waste-activated submitted process seque
AF314424.1 gg_id:29624 aerobic phosphorus-removal ecosystem clone PHOS-HE54
FJ623291.1 gg_id:578684 Efficient polyhydroxyalkanoates production waste-activated submitted process seque
FJ356056.1 gg_id:365992 Targeted FACS enrichment groups lab scale systems anaerobic:aerobic lab-scale EBPF
FM242366.1 gg_id:343417 sequences sediment clone 87 T9d+oil
FJ623332.1 gg_id:560016 Efficient polyhydroxyalkanoates production waste-activated submitted process seque
DQ413125.1 gg_id:155504 Microbial -dependent and Approaches Anaerobic/Aerobic SBR Reactor EBPR sludge
EU529733.1 gg_id:276817 FACS SBR EBPR system clone H68
AF361093.1 gg_id:58384 activated sludge clone SBRQ196
FJ623365.1 gg_id:512667 Efficient polyhydroxyalkanoates production waste-activated submitted process seque
FJ437975.1 gg_id:554795 Benthic okenone production Fayetteville New York Green Lake surface sediments 16.
EU529718.1 gg_id:274411 FACS SBR EBPR system clone H3
DQ228657.1 gg_id:144957 Microbial colonizing mineral surfaces within sulfide-microbial incubator clone CH2b5
EU236368.1 gg_id:295225 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg91E8
FJ197389.1 gg_id:343119 deep Pacific Ocean and Eastern Mediterranean Sea sediment clone ALVIN24a_5F_FL
FJ416083.1 gg_id:367767 sediments sediment station NEC5 Northern Bering Sea clone 020K31
EU491472.1 gg_id:274559 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X4 clone
EU652542.1 gg_id:278509 Seasonal variation microbial Yel Sea sediment clone C8S-35
AB250579.1 gg_id:160900 and ecology Grotta Azzurra Palinuro Cape (Salerno Italy) microbial mat clone #6-4
FJ712512.1 gg_id:529452 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) K
FJ497283.1 gg_id:575773 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun
EU287240.1 gg_id:236488 Pacific arctic surface sediment clone S11-57
AB015583.1 gg_id:7578 deep-sea sediment clone BD7-8
EU491479.1 gg_id:263853 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X4 clone
AJ620496.1 gg_id:305646 Olavius 3 endosymbiont O. algarvensis Individual 2
GQ064429.1 gg_id:419799 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw7
DQ013306.1 gg_id:136353 Manjusharmella aquatica str. GPTSA-6
GQ062984.1 gg_id:385334 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw96c02c
EF679186.1 gg_id:254988 sewage anaerobic sludge mediator-less MFC clone ASP-21
GQ060276.1 gg_id:372558 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
AB286529.1 gg_id:207647 Reducing production and domination comamonadaceae reducing oxygen supply was
GQ060660.1 gg_id:438403 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw03g09
GQ062191.1 gg_id:455804 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
GQ062255.1 gg_id:374917 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
AB286547.1 gg_id:203983 Reducing production and domination comamonadaceae reducing oxygen supply was
AF406529.1 gg_id:60643 bacterioplankton clone AEGEAN_165
GQ337214.1 gg_id:552282 Hydrography shapes biogeography deep Arctic Ocean water depth 400m clone CB13
GQ350551.1 gg_id:535210 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich

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| EU287240.1 | 236488 | 487.1 | 1106.8 | 2736.4 | 414.6 | 510.8 | 1716.2 |
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| AB286529.1 | 207647 | 1092.3 | 2432.6 | 6986.0 | 4867.7 | 7536.2 | 6364.2 |
| GQ060660.1 | 438403 | 7069.8 | 6404.8 | 10330.7 | 9502.5 | 5757.6 | 8013.4 |
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AF257292.2 gg_id:27722 marine clone DHB-2
DQ300596.1 gg_id:147780 microbial ocean's interior amplicon single fosmid library pool 130m depth HOT static
AF406536.1 gg_id:60638 bacterioplankton clone AEGEAN_243
AACY01030334.1 gg_id:99301 Sargasso Sea
AB186988.1 gg_id:103264 Mariana trough hydrothermal vent water 0.2micro-m filterable fraction clone MT-NE
FJ826243.1 gg_id:510441 Succession during spring diatom bloom Sea filtered surface sea water contrasting nor
GQ348876.1 gg_id:581691 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
AY700614.1 gg_id:109443 Australia: Great Barrier Reef clone PDB-OTU7
EF571905.1 gg_id:230907 Coco's Island site 23 marine clone S23_4
EU491486.1 gg_id:270695 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X4 clone
EU287407.1 gg_id:241556 Pacific arctic surface sediment clone S26-107
FJ873329.1 gg_id:539933 Vertical and archaea methane-rich cold seep located base sediments Okhotsk Sea clo
EU817105.1 gg_id:345886 Biological Haliclona (gellius) sp.: Sponge and Microbial Symbionts Pacific Ocean 13 m
EU652530.1 gg_id:278243 Seasonal variation microbial Yel Sea sediment clone C8S-47
GQ347341.1 gg_id:592135 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
GQ348494.1 gg_id:541236 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
GQ350244.1 gg_id:571396 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
GQ347632.1 gg_id:548782 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
FJ628318.1 gg_id:588621 transition and zone within near-shore basin: brackish water anoxic fjord Nitinat Lake
FJ203248.1 gg_id:351002 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c
FJ203316.1 gg_id:314846 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c
FJ959819.1 gg_id:558909 bottlenose dolphin upper respiratory tract blowhole clone D8A8_170
FJ203252.1 gg_id:309645 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c
AB212895.1 gg_id:132694 The Mini plant Run 6 of the Nippon Steel Research and Engineering Center clone nsm
AM935318.1 gg_id:556062 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
DQ337067.1 gg_id:146995 subsurface water clone EV818SWSAP22
GU208326.1 gg_id:568293 Study on Sediment Dongping Lake sediment clone Se2-23
AM935235.1 gg_id:552890 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
EF608532.1 gg_id:231765 predatory Poecilus chalcites their response lab rearing and antibiotic treatment diges
FJ612598.1 gg_id:511469 Orbus hercynius str. CN3
DQ837611.1 gg_id:173383 structures honeybee intestines and their response insecticidal proteins gut clone HB
AY942754.1 gg_id:147853 but species richness marine sponge Cymbastela concentrica clone Cc007
EF076133.1 gg_id:240090 Sponge- microorganisms: ecology and biotechnological potential Bahamas: Little San
GU118596.1 gg_id:548103 Threatened Corals Provide Microbial Habitats clone Mfav_B05
EU799507.1 gg_id:339161 It's all ranking aquatic Newport Harbour RI clone 1C227115
EU799990.1 gg_id:309275 It's all ranking aquatic Newport Harbour RI clone 1C227670
EU799493.1 gg_id:333893 It's all ranking aquatic Newport Harbour RI clone 1C227099
GQ441315.1 gg_id:554466 and dynamic mat present vs. active nitrogen-fixing microorganisms marine microbia
EF632661.1 gg_id:253267 Unique microbial contrasting aquatic altitude Andean Altiplano (northern Chile) sedir
DQ269079.1 gg_id:199419 marine macro-alga surface clone DPC097
CU466822.1 gg_id:328710 Evry wastewater treatment plant anoxic basin clone

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| AACY01030334.1 | 99301 | 10140.4 | 10867.5 | 10881.3 | 9321.4 | 15010.1 | 6167.2 |
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| FJ826243.1 | 510441 | 16888.5 | 15276.7 | 9254.1 | 13181.7 | 14272.3 | 13431.2 |
| GQ348876.1 | 581691 | 4097.2 | 4373.4 | 5511.9 | 9186.9 | 3612.6 | 4744.0 |
| AY700614.1 | 109443 | 9303.9 | 8377.9 | 7879.4 | 8466.8 | 11727.5 | 9278.3 |
| EF571905.1 | 230907 | 1406.4 | 1586.0 | 428.6 | 1250.7 | 2294.6 | 2131.2 |
| EU491486.1 | 270695 | 8216.5 | 7741.2 | 8187.9 | 8392.3 | 9435.8 | 10882.4 |
| EU287407.1 | 241556 | 8775.7 | 7028.5 | 8229.0 | 8190.8 | 9479.7 | 8168.5 |
| FJ873329.1 | 539933 | 779.7 | 860.5 | 887.8 | 1171.0 | 1095.0 | 436.1 |
| EU817105.1 | 345886 | 510.9 | 667.1 | 2480.7 | 791.9 | 2120.2 | 925.5 |
| EU652530.1 | 278243 | 11683.5 | 9474.6 | 3972.0 | 7147.5 | 8629.9 | 6526.8 |
| GQ347341.1 | 592135 | 5654.6 | 5080.6 | 10445.9 | 4619.9 | 4745.0 | 3910.3 |
| GQ348494.1 | 541236 | 4187.4 | 3843.2 | 2832.9 | 2198.5 | 14441.7 | 5825.5 |
| GQ350244.1 | 571396 | 7017.0 | 7821.5 | 4243.4 | 4215.7 | 4767.9 | 4991.4 |
| GQ347632.1 | 548782 | 3972.6 | 4299.7 | 4653.8 | 4162.0 | 6135.9 | 3885.7 |
| FJ628318.1 | 588621 | 4844.9 | 5885.2 | 3789.7 | 3277.3 | 10455.4 | 6847.0 |
| FJ203248.1 | 351002 | 8035.7 | 8154.7 | 7105.4 | 8067.1 | 9926.9 | 7653.3 |
| FJ203316.1 | 314846 | 11749.3 | 11135.1 | 8442.0 | 12174.4 | 12674.9 | 12340.0 |
| FJ959819.1 | 558909 | 3376.1 | 3545.9 | 3835.7 | 5135.9 | 6257.4 | 3966.3 |
| FJ203252.1 | 309645 | 2649.4 | 2470.4 | 2705.6 | 3705.8 | 4521.4 | 3395.0 |
| AB212895.1 | 132694 | 189.3 | 237.3 | 1036.1 | 446.6 | 1837.8 | 634.4 |
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| DQ337067.1 | 146995 | 4261.0 | 3790.9 | 3873.4 | 2870.5 | 7149.8 | 6189.5 |
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| FJ612598.1 | 511469 | 3576.3 | 4279.9 | 4080.1 | 2793.8 | 5977.3 | 4844.5 |
| DQ837611.1 | 173383 | 35.5 | 40.7 | 30.3 | 51.1 | 65.0 | 29.5 |
| AY942754.1 | 147853 | 205.3 | 350.3 | 338.6 | 271.5 | 78.2 | 149.0 |
| EF076133.1 | 240090 | 3526.3 | 3945.1 | 7576.4 | 3789.9 | 5913.8 | 6149.8 |
| GU118596.1 | 548103 | 7573.0 | 5708.3 | 10459.1 | 10905.1 | 8961.2 | 7221.9 |
| EU799507.1 | 339161 | 3403.0 | 3302.2 | 6249.3 | 3700.1 | 8428.9 | 8164.4 |
| EU799990.1 | 309275 | 6563.9 | 6618.2 | 1984.8 | 2636.5 | 6731.7 | 7530.1 |
| EU799493.1 | 333893 | 8497.8 | 7655.3 | 6013.3 | 7670.6 | 7825.4 | 7996.2 |
| GQ441315.1 | 554466 | 3137.8 | 4473.2 | 3132.5 | 2313.7 | 2317.2 | 4059.8 |
| EF632661.1 | 253267 | 2606.5 | 2931.4 | 1020.5 | 3737.3 | 3094.6 | 2886.2 |
| DQ269079.1 | 199419 | 510.2 | 921.0 | 545.8 | 847.6 | 476.3 | 1847.8 |
| CU466822.1 | 328710 | 3542.5 | 3111.2 | 3418.2 | 1471.3 | 2553.2 | 6953.9 |

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FJ444714.1 gg_id:585507 Cotton Rhizosphere cotton rhizosphere clone 4h-1
EF092261.1 gg_id:268390 Persistent Axinella corrugata clone BH1_G11
AJ581350.1 gg_id:92419 Mediterranean sponge clone E01-9C-15
AB286554.1 gg_id:204859 Reducing production and domination comamonadaceae reducing oxygen supply was
FJ940806.1 gg_id:388951 Aeromonas punctata str. 4pM30
DQ270618.1 gg_id:144237 hydrothermal carbonate chimney clone LC1133B-43
FJ497530.1 gg_id:592807 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun
FJ655515.1 gg_id:583817 symbiont
EU735652.1 gg_id:356150 archaeal structures oil contaminated and soils China pristine soil Jidong Oilfield clone
AY292922.1 gg_id:101121 Vibrio fischeri EM17
DQ026824.1 gg_id:227498 Vibrio fischeri str. PP3
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AY628647.1 gg_id:103863 Vibrio wodanis
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AB497068.1 gg_id:546558 Aliivibrio logei str. 11-2
EU185820.1 gg_id:398431 Aliivibrio logei str. WHSW1
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EU257749.1 gg_id:551220 Aliivibrio logei AV05/2007
AY292928.1 gg_id:102104 Vibrio logei str. SL101
EU091322.1 gg_id:314982 Aliivibrio salmonicida PB3-7rrnB
DQ642809.1 gg_id:161003 Vibrio sp. 6(2006)
EU091324.1 gg_id:317079 Aliivibrio salmonicida PB1-8rrnB
EU091323.1 gg_id:304361 Aliivibrio salmonicida PB1-8rrnA
AY292929.1 gg_id:102250 Vibrio logei str. Srond101401
FJ654064.1 gg_id:511531 Coral Reef Fish Feces and Gut Microbial Assemblages gut contents distal intestine clo
Z19105.1 gg_id:9129 Melanocetus johnsoni symbiont
AY576761.1 gg_id:139186 Photobacterium sp. str. 26III/A02/220
AY745814.1 gg_id:108596 Vibrio sp. str. JL-73
Z19106.1 gg_id:9131 Cryptosaras couesi symbiont
NR_025574.1 gg_id:535720 Grimontia hollisae str. 75-80; LMG 17719
AY292951.1 gg_id:107197 Photobacterium leiognathi str. SN2B
EF635307.1 gg_id:246572 Photobacterium subsp. damselae HQ061227-1
AY642160.1 gg_id:111666 Photobacterium phosphoreum str. NZ-11D
AY642161.1 gg_id:111692 Photobacterium phosphoreum str. calba.1.1
AY204488.1 gg_id:103923 Photobacterium leiognathi str. gachl1.1
D25309.1 gg_id:9154 Photobacterium leiognathi str. ATCC25521
AY341442.1 gg_id:106555 Photobacterium mandapamensis str. ATCC 33981
DQ978988.1 gg_id:183456 Photobacterium sp. S-7
DQ219367.1 gg_id:142286 Photobacterium sp. str. 2220
DQ534014.1 gg_id:160550 Photobacterium lutimaris str. DF-42

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| AJ581350.1 | 92419 | 52.8 | 98.2 | 275.6 | 81.6 | 316.7 | 85.9 |
| AB286554.1 | 204859 | 77.3 | 214.9 | 100.2 | 94.6 | 262.2 | 117.4 |
| FJ940806.1 | 388951 | 181.5 | 229.4 | 637.9 | 204.3 | 370.8 | 521.6 |
| DQ270618.1 | 144237 | 788.9 | 554.8 | 384.2 | 1976.6 | 238.5 | 1229.1 |
| FJ497530.1 | 592807 | 7074.6 | 7615.5 | 4632.6 | 9170.2 | 6966.4 | 6124.3 |
| FJ655515.1 | 583817 | 2686.0 | 2884.2 | 1993.1 | 3143.1 | 3715.2 | 3281.6 |
| EU735652.1 | 356150 | 5599.2 | 6725.3 | 9500.0 | 4545.6 | 7915.4 | 6563.9 |
| AY292922.1 | 101121 | 1861.4 | 1547.4 | 2231.7 | 2940.9 | 5089.1 | 2396.6 |
| DQ026824.1 | 227498 | 204.7 | 288.1 | 1084.6 | 403.3 | 1250.9 | 541.4 |
| CP000020.1 | 129275 | 7403.3 | 10497.7 | 2181.2 | 1545.0 | 4535.0 | 2587.8 |
| AY628647.1 | 103863 | 385.0 | 483.6 | 878.4 | 439.9 | 408.2 | 386.3 |
| DQ146991.1 | 146962 | 324.1 | 342.0 | 821.1 | 396.0 | 1887.0 | 546.4 |
| AB497068.1 | 546558 | 65.7 | 100.4 | 549.9 | 158.7 | 95.0 | 256.7 |
| EU185820.1 | 398431 | 102.8 | 93.4 | 312.4 | 226.5 | 97.8 | 132.7 |
| AY292934.1 | 106476 | 43.2 | 47.4 | 67.2 | 60.2 | 201.7 | 83.7 |
| EU862333.1 | 580068 | 378.3 | 454.6 | 772.0 | 520.8 | 1197.9 | 955.0 |
| EU257749.1 | 551220 | 385.7 | 398.7 | 273.1 | 395.5 | 402.9 | 298.9 |
| AY292928.1 | 102104 | 765.5 | 999.1 | 809.5 | 755.3 | 3153.5 | 2598.5 |
| EU091322.1 | 314982 | 533.3 | 619.8 | 1789.2 | 678.5 | 900.8 | 1136.5 |
| DQ642809.1 | 161003 | 9914.7 | 7940.4 | 5331.6 | 8749.5 | 8722.0 | 6976.7 |
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| EU091323.1 | 304361 | 6165.3 | 5405.7 | 7438.9 | 6576.4 | 6526.8 | 5707.3 |
| AY292929.1 | 102250 | 33.1 | 53.2 | 69.3 | 113.3 | 124.3 | 53.9 |
| FJ654064.1 | 511531 | 1576.6 | 1559.1 | 2611.3 | 1317.8 | 2784.7 | 3987.0 |
| Z19105.1 | 9129 | 532.5 | 384.8 | 541.7 | 601.6 | 463.8 | 701.8 |
| AY576761.1 | 139186 | 7141.9 | 7422.6 | 3348.9 | 7266.8 | 9227.8 | 8414.6 |
| AY745814.1 | 108596 | 757.2 | 785.0 | 1396.0 | 911.3 | 1136.3 | 611.0 |
| Z19106.1 | 9131 | 59.3 | 121.2 | 248.6 | 138.9 | 91.9 | 111.3 |
| NR_025574.1 | 535720 | 1693.7 | 2791.4 | 3439.6 | 4219.1 | 5618.7 | 6549.4 |
| AY292951.1 | 107197 | 113.4 | 225.6 | 218.8 | 113.2 | 1280.7 | 233.4 |
| EF635307.1 | 246572 | 495.9 | 188.5 | 691.5 | 454.4 | 343.7 | 107.5 |
| AY642160.1 | 111666 | 437.7 | 513.9 | 1135.3 | 1225.3 | 1884.0 | 774.9 |
| AY642161.1 | 111692 | 148.4 | 283.3 | 1459.6 | 272.4 | 1981.6 | 630.8 |
| AY204488.1 | 103923 | 536.8 | 997.0 | 737.1 | 349.6 | 676.1 | 492.9 |
| D25309.1 | 9154 | 1221.9 | 1268.1 | 1976.6 | 872.1 | 2717.2 | 1215.5 |
| AY341442.1 | 106555 | 278.9 | 671.7 | 248.7 | 608.9 | 230.0 | 199.2 |
| DQ978988.1 | 183456 | 3452.1 | 3856.8 | 4161.2 | 3305.6 | 2549.3 | 2796.2 |
| DQ219367.1 | 142286 | 6209.9 | 8028.3 | 7928.9 | 4641.3 | 7475.6 | 7196.3 |
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AY345892.1 gg_id:92198 Photobacterium phosphoreum AK7
NC_006370.1 gg_id:129245 Photobacterium profundum str. SS9
AY642169.1 gg_id:111940 Photobacterium phosphoreum str. calba.5.1
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AB166848.1 gg_id:102935 Photobacterium phosphoreum str. 127-1
AB000278.1 gg_id:9163 Photobacterium iliopiscarium str. ATCC51760
EF067913.1 gg_id:245715 endolithic microbes marine basalts aerobic enrichment s innoculated basalt Brown B
DQ085397.1 gg_id:131693 Photococcus caeruleum str. BC1
FJ467295.1 gg_id:535616 Photobacterium sp. str. QD-1A
DQ317679.1 gg_id:160104 Photobacterium sp. str. OIM3
NC_006370.1 gg_id:129232 Photobacterium profundum str. SS9
AJ630156.2 gg_id:160207 Photobacterium sp. str. J11
GQ386817.1 gg_id:582886 Photobacterium sp. str. CAIM 1206
NC_006370.1 gg_id:129243 Photobacterium profundum str. SS9
EU652566.1 gg_id:279374 Seasonal variation microbial Yel Sea sediment clone C8S-173
AM279735.1 gg_id:160832 Salinivibrio aegyptiaca subsp. sharmensis str. BbAG
EF541484.2 gg_id:254905 Vibrio taiwanensis
DQ513033.1 gg_id:160210 Microbial life fluids ridge flank crustal fluid clone FS142-3B-02
AY551089.1 gg_id:102788 Ferrania halotolerans str. MACL01
DQ289936.1 gg_id:171395 Microbial Carbon and Nitrogen Cycling Sediments South Atlantic Bight Permeable Sh
GU061990.1 gg_id:579828 and function microbial mesoscale eddy perturbations South China Sea clone S-DCM-
FJ457453.1 gg_id:549933 Photobacterium sp. str. S2545
GU061981.1 gg_id:589490 and function microbial mesoscale eddy perturbations South China Sea clone S-DCM-
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DQ146972.1 gg_id:147578 Vibrio sp. str. V031
DQ923438.1 gg_id:176420 Vibrio sp. W-4
AY960847.1 gg_id:114914 Photobacterium ganghwensis str. FR1311
EU153251.1 gg_id:243117 Photobacterium sp. str. P16011A
GQ231487.1 gg_id:582132 Vibrio natriegens str. T5
DQ097523.1 gg_id:134295 Vibrio litoralis str. mano22D
AY911397.1 gg_id:112495 Vibrio harveyi str. SW-4
AY292927.1 gg_id:101945 Vibrio lentus str. SI01
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AB470928.1 gg_id:559639 Vibrio sp. str. r17
EU931029.1 gg_id:355127 Vibrio vulnificus str. L1
AY264923.1 gg_id:105451 Vibrio harveyi str. ACMM 642

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| AY888014.1 | 140446 | 58.5 | 107.5 | 1326.4 | 417.9 | 1580.9 | 718.6 |
| AY642168.1 | 112325 | 454.3 | 640.5 | 1736.2 | 1317.1 | 2888.6 | 883.2 |
| AB003191.1 | 9160 | 720.9 | 679.5 | 1364.3 | 442.4 | 989.5 | 785.5 |
| AY345892.1 | 92198 | 419.0 | 523.7 | 1044.7 | 1122.0 | 777.2 | 751.6 |
| NC_006370.1 | 129245 | 1488.7 | 1904.7 | 2674.4 | 2164.7 | 2484.8 | 1385.2 |
| AY642169.1 | 111940 | 428.2 | 392.2 | 1287.3 | 1263.2 | 2151.4 | 693.5 |
| AB457049.1 | 348164 | 3015.6 | 4284.3 | 9428.2 | 6752.0 | 6426.9 | 2968.3 |
| AB166848.1 | 102935 | 300.5 | 400.9 | 475.8 | 368.4 | 1801.4 | 471.4 |
| AB000278.1 | 9163 | 2863.9 | 3082.2 | 4370.3 | 4095.7 | 6149.7 | 4529.5 |
| EF067913.1 | 245715 | 2453.9 | 2280.8 | 3176.7 | 1973.2 | 2219.5 | 2084.6 |
| DQ085397.1 | 131693 | 1092.3 | 1340.1 | 1607.0 | 1957.5 | 742.1 | 1122.6 |
| FJ467295.1 | 535616 | 87.4 | 129.2 | 618.1 | 409.6 | 1319.1 | 280.8 |
| DQ317679.1 | 160104 | 154.4 | 376.4 | 859.2 | 261.3 | 544.8 | 552.8 |
| NC_006370.1 | 129232 | 147.7 | 295.5 | 1184.2 | 411.2 | 769.9 | 644.0 |
| AJ630156.2 | 160207 | 36.3 | 77.3 | 205.5 | 73.2 | 110.4 | 57.5 |
| GQ386817.1 | 582886 | 515.7 | 837.8 | 991.5 | 611.0 | 1473.7 | 928.5 |
| NC_006370.1 | 129243 | 11539.6 | 13740.0 | 9327.5 | 10433.7 | 12871.4 | 10994.3 |
| EU652566.1 | 279374 | 3845.6 | 4848.4 | 4600.6 | 2637.5 | 6696.5 | 3790.9 |
| AM279735.1 | 160832 | 13.6 | 20.4 | 28.2 | 49.0 | 68.3 | 17.8 |
| EF541484.2 | 254905 | 1228.0 | 2862.3 | 1962.7 | 1955.7 | 389.0 | 949.3 |
| DQ513033.1 | 160210 | 21.2 | 21.7 | 24.7 | 63.8 | 58.1 | 39.0 |
| AY551089.1 | 102788 | 1045.3 | 1006.7 | 3622.2 | 1057.4 | 776.2 | 1616.4 |
| DQ289936.1 | 171395 | 1536.3 | 1451.6 | 2119.7 | 1968.1 | 1105.0 | 1032.2 |
| GU061990.1 | 579828 | 652.4 | 680.2 | 2642.8 | 1380.0 | 1600.0 | 883.1 |
| FJ457453.1 | 549933 | 3491.5 | 4145.8 | 3125.1 | 4647.5 | 7255.1 | 5436.4 |
| GU061981.1 | 589490 | 3452.9 | 2663.6 | 3489.0 | 3891.0 | 3419.4 | 4084.1 |
| AB470940.1 | 567653 | 3925.1 | 4975.5 | 6333.0 | 3820.0 | 5730.9 | 5321.5 |
| DQ146972.1 | 147578 | 793.0 | 831.0 | 1170.2 | 965.2 | 3526.9 | 2020.4 |
| DQ923438.1 | 176420 | 10743.9 | 10297.2 | 7845.7 | 9436.4 | 15995.8 | 11648.0 |
| AY960847.1 | 114914 | 266.8 | 422.9 | 766.0 | 477.9 | 159.5 | 448.6 |
| EU153251.1 | 243117 | 174.1 | 408.7 | 1909.7 | 387.3 | 563.1 | 679.5 |
| GQ231487.1 | 582132 | 630.6 | 800.4 | 2260.5 | 289.6 | 351.7 | 482.6 |
| DQ097523.1 | 134295 | 4521.6 | 4108.9 | 3740.1 | 4924.3 | 6191.6 | 6758.4 |
| AY911397.1 | 112495 | 6874.0 | 8998.8 | 3606.6 | 4869.8 | 8389.8 | 5200.6 |
| AY292927.1 | 101945 | 159.9 | 462.3 | 1147.8 | 459.3 | 835.2 | 479.1 |
| NC_004603.1 | 128967 | 74.5 | 246.9 | 275.5 | 111.2 | 79.8 | 767.7 |
| AB470928.1 | 559639 | 2134.0 | 1390.0 | 2507.8 | 1388.4 | 1597.4 | 751.6 |
| EU931029.1 | 355127 | 1620.8 | 1600.1 | 2114.7 | 1497.6 | 930.1 | 1459.0 |
| AY264923.1 | 105451 | 477.5 | 475.7 | 1708.6 | 4148.4 | 989.0 | 2606.2 |

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DQ068938.1 gg_id:128050 Vibrio natriegens str. ATCC 14048
EF584019.1 gg_id:233630 Vibrio sp. str. BISLNTS2
FJ457542.1 gg_id:540493 Vibrio sp. str. S3705
AY373027.1 gg_id:94344 Vibrio alginolyticus
NZ_ACFN01000056.1 gg_id:589213 Vibrio parahaemolyticus str. AQ4037
X56580.1 gg_id:9213 Vibrio parahaemolyticus str. ATCC 17802
EU854949.1 gg_id:327660 Vibrio sp. 7A3
NZ_ACFN01000122.1 gg_id:585208 Vibrio parahaemolyticus str. AQ4037
FJ457344.1 gg_id:543817 Vibrio sp. str. S844
AJ874352.1 gg_id:110401 Vibrio natriegens str. 01/097
AJ560649.1 gg_id:102693 Vibrio pomeroyi
EU660313.1 gg_id:295179 Vibrio parahaemolyticus str. V11
EU022572.1 gg_id:249726 Vibrio sp. str. 09022
EU854919.1 gg_id:325753 Vibrio sp. 6H5
AY770723.1 gg_id:109758 sea urchin Paracentrotus lividus clone PlS52
FJ465010.1 gg_id:553472 Vibrio sp. str. HB-1
FM204864.1 gg_id:362393 Vibrio rotiferianus str. LPD 1-1-86
EU931113.1 gg_id:317447 Vibrio breoganii str. RD 2B2
AJ874353.1 gg_id:110903 Vibrio natriegens str. 01/252
FJ952771.1 gg_id:409574 Vibrio sp. str. 1ta7
GQ180184.1 gg_id:585556 Vibrio harveyi str. LA08007
EF467290.1 gg_id:218679 Vibrio parahaemolyticus str. VF
AM159568.1 gg_id:184396 Vibrio sp. str. F 27
DQ814117.1 gg_id:165805 zebrafish digestive tract clone aab60b01
EU884928.1 gg_id:325564 microbial hindgut chamber Pomacanthus sexstriatus GI tract clone A3B7
DQ079634.1 gg_id:128193 Vibrio alginolyticus str. NA0302
EU854921.1 gg_id:331930 Vibrio sp. 6F1
AY264922.1 gg_id:105294 Vibrio harveyi str. ACMM 131
EU333880.1 gg_id:274586 Vibrio sp. str. K22-41
EF199917.1 gg_id:202707 Vibrio sp. str. DH147
EU854922.1 gg_id:315723 Vibrio sp. 6E11
DQ304558.1 gg_id:143830 Vibrio harveyi str. XVP5
AB257333.2 gg_id:178521 Vibrio fortis str. Do-47
EF542800.1 gg_id:218383 Vibrio alginolyticus str. YJ06167B
EU854917.1 gg_id:305927 Vibrio sp. 6G12
DQ664544.1 gg_id:170529 Vibrio alginolyticus str. RH2
AY911396.1 gg_id:112486 Vibrio harveyi str. SW-3
GQ391944.1 gg_id:517522 Vibrio sp. str. PaH1.39

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| AM778463.1 | 235347 | 8381.7 | 6421.6 | 7306.3 | 6423.7 | 4422.8 | 3605.4 |
| DQ068938.1 | 128050 | 11751.3 | 12100.3 | 10511.4 | 10110.0 | 13915.4 | 11927.9 |
| EF584019.1 | 233630 | 2650.1 | 1938.8 | 3347.2 | 2751.6 | 3074.8 | 3478.9 |
| FJ457542.1 | 540493 | 179.8 | 190.3 | 215.2 | 161.2 | 486.4 | 655.9 |
| AY373027.1 | 94344 | 4784.4 | 6454.6 | 5877.7 | 6293.3 | 10482.8 | 9155.8 |
| NZ_ACFN01000056.1 | 589213 | 4363.6 | 4992.6 | 5271.1 | 5031.7 | 6746.9 | 6098.3 |
| X56580.1 | 9213 | 356.9 | 459.6 | 229.6 | 353.1 | 1427.9 | 400.8 |
| EU854949.1 | 327660 | 654.4 | 584.3 | 1139.5 | 480.4 | 845.8 | 669.5 |
| NZ_ACFN01000122.1 | 585208 | 464.3 | 920.6 | 1056.3 | 1013.5 | 891.5 | 934.0 |
| FJ457344.1 | 543817 | 1119.7 | 1128.5 | 1316.6 | 1036.0 | 1748.4 | 1826.9 |
| AJ874352.1 | 110401 | 2037.4 | 1874.7 | 2769.3 | 1986.6 | 4318.0 | 2366.1 |
| AJ560649.1 | 102693 | 262.3 | 220.8 | 100.3 | 427.6 | 131.6 | 1240.3 |
| EU660313.1 | 295179 | 2195.6 | 2322.6 | 2763.4 | 2577.8 | 3332.7 | 3372.5 |
| EU022572.1 | 249726 | 199.0 | 459.6 | 1300.5 | 348.5 | 629.4 | 914.7 |
| EU854919.1 | 325753 | 513.1 | 597.7 | 1404.6 | 239.0 | 625.6 | 509.1 |
| AY770723.1 | 109758 | 963.8 | 628.2 | 745.2 | 77.0 | 76.0 | 108.1 |
| FJ465010.1 | 553472 | 902.5 | 698.0 | 1584.4 | 1062.3 | 72.5 | 270.4 |
| FM204864.1 | 362393 | 213.5 | 301.0 | 366.7 | 216.8 | 638.2 | 102.2 |
| EU931113.1 | 317447 | 1855.3 | 1022.8 | 1627.9 | 3141.1 | 1923.3 | 3401.7 |
| AJ874353.1 | 110903 | 1872.6 | 1115.3 | 2501.1 | 1486.8 | 2011.6 | 895.4 |
| FJ952771.1 | 409574 | 494.1 | 465.8 | 849.2 | 495.3 | 1216.4 | 273.4 |
| GQ180184.1 | 585556 | 7923.9 | 13070.9 | 6932.0 | 6049.4 | 8438.9 | 6064.6 |
| EF467290.1 | 218679 | 271.8 | 333.2 | 403.5 | 342.1 | 183.0 | 222.7 |
| AM159568.1 | 184396 | 2975.6 | 2255.4 | 3315.4 | 2426.2 | 3411.6 | 2434.6 |
| DQ814117.1 | 165805 | 6424.2 | 6817.7 | 7256.7 | 6421.3 | 7467.0 | 6026.0 |
| EU884928.1 | 325564 | 3677.4 | 3044.4 | 3623.4 | 3171.9 | 5367.6 | 5550.7 |
| DQ079634.1 | 128193 | 3780.0 | 2776.1 | 4255.2 | 3176.7 | 3482.3 | 3105.3 |
| EU854921.1 | 331930 | 10336.9 | 8716.8 | 6695.4 | 6251.2 | 9957.5 | 7929.3 |
| AY264922.1 | 105294 | 1397.8 | 1320.7 | 1623.2 | 1113.7 | 2017.8 | 1966.0 |
| EU333880.1 | 274586 | 1467.7 | 1442.4 | 1325.0 | 1318.0 | 2439.7 | 1159.7 |
| EF199917.1 | 202707 | 5980.5 | 8565.6 | 6212.2 | 7845.3 | 7625.1 | 7104.3 |
| EU854922.1 | 315723 | 991.6 | 1112.1 | 1326.4 | 748.0 | 1370.7 | 989.7 |
| DQ304558.1 | 143830 | 556.1 | 572.5 | 1264.3 | 293.4 | 187.6 | 690.1 |
| AB257333.2 | 178521 | 3579.8 | 2309.6 | 3477.0 | 3127.9 | 3801.6 | 3531.6 |
| EF542800.1 | 218383 | 840.9 | 765.2 | 894.4 | 580.1 | 201.9 | 267.6 |
| EU854917.1 | 305927 | 962.8 | 1034.3 | 2105.9 | 275.5 | 1058.7 | 1161.8 |
| DQ664544.1 | 170529 | 2305.8 | 2220.4 | 2924.3 | 2580.8 | 3297.7 | 3491.7 |
| AY911396.1 | 112486 | 3079.3 | 4527.4 | 6138.3 | 5846.6 | 3939.6 | 3864.9 |
| GQ391944.1 | 517522 | 62.9 | 313.4 | 778.4 | 145.1 | 163.5 | 134.6 |

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FJ227114.1 gg_id:554540 Vibrio harveyi EHP8
FJ200649.1 gg_id:345203 Vibrio lentus str. I 80
EU188117.1 gg_id:318402 Uncultivated oceanic unicellular N2-fixing cyanobacteria are picoplankton unusual 7(
AJ316169.1 gg_id:73534 Vibrio sp. str. LMG 19270
EU854927.1 gg_id:309342 Vibrio sp. 6H6
FJ952824.1 gg_id:402184 Vibrio sp. str. 2tc2
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AJ440009.1 gg_id:100541 Vibrio gallicus str. LMG 21330
EU854823.1 gg_id:344632 Vibrio sp. 1A1
EU854827.1 gg_id:308115 Vibrio sp. 3B6
EU372926.1 gg_id:271355 Vibrio sp. str. S4
GQ906772.1 gg_id:575876 Pseudomonas fluorescens str. MR-6
EU854833.1 gg_id:305431 Vibrio sp. 1E7
DQ922916.1 gg_id:226196 Vibrio comitatus str. GHG24
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FJ171336.1 gg_id:346087 Vibrio natriegens str. WT01
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FJ594056.1 gg_id:552960 Vibrio parahaemolyticus str. ASKB-081039
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DQ235159.1 gg_id:144816 Vibrio sp. str. O2
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EU854918.1 gg_id:306600 Vibrio sp. 6E4
EU854945.1 gg_id:327451 Vibrio sp. 7A11(2008)
AJ421444.1 gg_id:68895 Vibrio penaeicida str. DSM 14398T
FJ457312.1 gg_id:559091 Vibrio sp. str. S278
FM162398.1 gg_id:297192 Vibrio harveyi str. a91
AAWP01000248.1 gg_id:256913 Vibrio harveyi str. HY01

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| EU188117.1 | 318402 | 7218.6 | 9479.0 | 8677.3 | 7373.5 | 9903.1 | 7961.0 |
| AJ316169.1 | 73534 | 836.0 | 723.0 | 1357.0 | 984.1 | 1143.6 | 423.7 |
| EU854927.1 | 309342 | 4172.1 | 4280.4 | 5731.3 | 7399.6 | 7528.3 | 4390.6 |
| FJ952824.1 | 402184 | 481.3 | 352.2 | 800.9 | 475.4 | 1115.7 | 201.9 |
| EU854890.1 | 313041 | 515.1 | 419.6 | 1060.8 | 194.2 | 523.6 | 444.1 |
| NZ_AAWP01000159.1 | 246627 | 510.4 | 551.2 | 1529.1 | 470.0 | 820.0 | 1067.3 |
| AJ874359.1 | 109806 | 1149.8 | 606.8 | 1114.8 | 1121.9 | 919.9 | 2006.4 |
| EU660364.1 | 297368 | 182.6 | 452.3 | 450.7 | 179.4 | 558.9 | 329.1 |
| FJ176466.1 | 564291 | 525.2 | 226.9 | 254.4 | 784.5 | 71.9 | 962.3 |
| NC_009783.1 | 471499 | 256.5 | 303.1 | 954.2 | 427.2 | 178.7 | 272.2 |
| EU517637.1 | 268839 | 2700.7 | 1892.4 | 2210.8 | 1099.1 | 1923.1 | 1603.4 |
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| FM204869.1 | 367865 | 1112.5 | 1351.4 | 2722.1 | 957.8 | 383.6 | 735.4 |
| DQ005876.1 | 131549 | 2635.8 | 2576.9 | 4075.1 | 1728.1 | 3505.6 | 3018.9 |
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| AJ316193.1 | 71896 | 546.4 | 307.4 | 238.8 | 578.4 | 78.4 | 284.3 |
| AJ440009.1 | 100541 | 221.5 | 614.1 | 1406.5 | 365.2 | 910.4 | 1489.7 |
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| GQ906772.1 | 575876 | 1833.5 | 1311.1 | 1964.5 | 1608.9 | 1607.6 | 1847.7 |
| EU854833.1 | 305431 | 406.4 | 473.7 | 1044.7 | 148.2 | 200.6 | 475.8 |
| DQ922916.1 | 226196 | 375.3 | 337.4 | 673.4 | 374.7 | 660.8 | 658.6 |
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| AJ414132.1 | 74395 | 7981.0 | 8558.8 | 7309.9 | 8710.0 | 10745.1 | 9165.4 |
| FJ594056.1 | 552960 | 1443.2 | 1693.1 | 2705.7 | 2661.3 | 2020.9 | 1992.0 |
| EF584045.1 | 233383 | 101.1 | 335.9 | 1729.2 | 211.7 | 353.8 | 431.2 |
| DQ235159.1 | 144816 | 371.0 | 255.5 | 697.4 | 408.9 | 300.7 | 1247.0 |
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EF584085.1 gg_id:232685 Vibrio sp. str. TUN8
EU517645.1 gg_id:263861 Vibrio sp. str. 5D9
AM921804.1 gg_id:253912 Vibrio alginolyticus
EF645832.1 gg_id:247677 Vibrio parahaemolyticus str. H040823-1
EU517643.1 gg_id:258894 Vibrio sp. str. 4C3
EU854911.1 gg_id:312073 Vibrio sp. 6D1
EU043382.1 gg_id:254129 Vibrio sinaloensis str. CAIM 636; LMG 21563
EU419926.1 gg_id:259946 Vibrio fortis str. RW39
GQ391945.1 gg_id:524646 Vibrio sp. str. PaH2.01a1
EU517638.1 gg_id:274062 Vibrio sp. str. 4H2
FJ176453.1 gg_id:552887 Vibrio pacinii str. S-M2-14-B1
DQ079633.1 gg_id:131667 Vibrio coralliilyticus str. NA0301
FJ605240.1 gg_id:561761 Vibrio harveyi str. HS08001
DQ097524.1 gg_id:132459 Vibrio litoralis str. mano22p
EU854895.1 gg_id:346295 Vibrio sp. 6B2
FJ227110.1 gg_id:559045 Vibrio harveyi UCP9
AF218244.1 gg_id:19456 Vibrio sp
DQ269211.1 gg_id:141139 Vibrio alginolyticus str. SR1
GQ281380.1 gg_id:579117 Vibrio sp. str. KTW-12
AY562192.1 gg_id:113713 Vibrio parahaemolyticus str. Sh06
FM204856.1 gg_id:367994 Vibrio campbellii str. R1311
AB457058.1 gg_id:319566 Vibrio sp. str. SB-I1
FJ024709.1 gg_id:346035 Copper affects reduction and genetic enriched sulfate reducing coastal sediments exp
EU833997.1 gg_id:568897 Vibrio alginolyticus str. UST981101-032
EU854908.1 gg_id:314683 Vibrio sp. 6E2
EF219054.1 gg_id:214480 Vibrio alginolyticus str. H050815-1
EU854929.1 gg_id:344477 Vibrio sp. 6G11
FJ172044.1 gg_id:512369 Vibrio parahaemolyticus str. RW1
FJ457435.1 gg_id:511250 Vibrio sp. str. S2321
AY928014.1 gg_id:112649 Vibrio harveyi
GQ260161.1 gg_id:584728 Vibrio tapetis str. C11.25
EU854894.1 gg_id:324980 Vibrio sp. 6B1
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X97988.1 gg_id:9232 Vibrio sp str. VI966/26
FJ176451.1 gg_id:563362 Vibrio natriegens str. J-C2-40
AY264921.1 gg_id:105131 Vibrio harveyi str. 47666-1
EU854951.1 gg_id:340143 Vibrio sp. 7B4

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| AB457055.1 | 340467 | 8663.8 | 7022.3 | 7986.6 | 8902.2 | 11949.9 | 9284.8 |
| AB457057.1 | 342157 | 11701.1 | 13666.4 | 6809.2 | 11486.5 | 11387.8 | 9629.0 |
| EU043380.1 | 257742 | 600.9 | 685.6 | 1640.1 | 1230.5 | 355.0 | 976.5 |
| EU854901.1 | 328904 | 411.4 | 467.8 | 635.9 | 327.4 | 1315.3 | 472.8 |
| EF584085.1 | 232685 | 31.8 | 83.8 | 217.4 | 108.6 | 106.9 | 34.3 |
| EU517645.1 | 263861 | 9991.2 | 8053.3 | 7861.7 | 6578.4 | 10976.3 | 8312.0 |
| AM921804.1 | 253912 | 2280.8 | 1771.5 | 3654.1 | 1792.0 | 1781.6 | 2071.0 |
| EF645832.1 | 247677 | 1736.0 | 2315.0 | 2628.6 | 1050.9 | 2850.9 | 2640.4 |
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| EU854911.1 | 312073 | 3202.7 | 4655.7 | 3491.5 | 4267.1 | 4444.5 | 4724.1 |
| EU043382.1 | 254129 | 378.0 | 382.0 | 697.3 | 334.8 | 214.6 | 523.7 |
| EU419926.1 | 259946 | 1020.2 | 664.6 | 1160.4 | 1302.7 | 100.3 | 419.3 |
| GQ391945.1 | 524646 | 449.0 | 638.1 | 1084.9 | 369.8 | 1378.7 | 551.0 |
| EU517638.1 | 274062 | 1907.6 | 2019.8 | 1441.0 | 519.3 | 2964.0 | 1724.6 |
| FJ176453.1 | 552887 | 6000.8 | 3296.5 | 6387.0 | 5089.4 | 2824.6 | 3524.5 |
| DQ079633.1 | 131667 | 686.6 | 745.8 | 859.1 | 1461.8 | 1507.9 | 2982.5 |
| FJ605240.1 | 561761 | 95.7 | 258.2 | 268.7 | 412.3 | 196.0 | 388.5 |
| DQ097524.1 | 132459 | 111.5 | 291.6 | 725.4 | 148.5 | 112.0 | 412.8 |
| EU854895.1 | 346295 | 1532.1 | 1670.7 | 588.9 | 448.5 | 2121.6 | 1116.4 |
| FJ227110.1 | 559045 | 1928.8 | 2234.5 | 1945.9 | 1608.8 | 1922.6 | 2340.8 |
| AF218244.1 | 19456 | 6774.6 | 5976.0 | 3853.9 | 7240.6 | 10104.1 | 7779.7 |
| DQ269211.1 | 141139 | 1375.2 | 1222.4 | 1984.8 | 1332.3 | 665.7 | 1062.7 |
| GQ281380.1 | 579117 | 75.7 | 159.8 | 880.5 | 206.3 | 63.0 | 221.4 |
| AY562192.1 | 113713 | 209.2 | 420.1 | 372.1 | 259.3 | 87.2 | 232.7 |
| FM204856.1 | 367994 | 3152.0 | 3575.5 | 3149.6 | 1510.5 | 3328.7 | 3275.2 |
| AB457058.1 | 319566 | 12066.0 | 14312.2 | 9915.9 | 11169.3 | 17955.5 | 11637.3 |
| FJ024709.1 | 346035 | 1728.3 | 1157.3 | 1211.0 | 569.4 | 509.9 | 355.2 |
| EU833997.1 | 568897 | 2014.4 | 1667.4 | 3711.5 | 488.4 | 518.2 | 830.1 |
| EU854908.1 | 314683 | 907.3 | 1132.6 | 745.7 | 553.6 | 1308.4 | 878.6 |
| EF219054.1 | 214480 | 521.1 | 662.9 | 1033.2 | 255.1 | 569.8 | 531.1 |
| EU854929.1 | 344477 | 809.5 | 981.3 | 1458.4 | 411.3 | 1138.0 | 1029.9 |
| FJ172044.1 | 512369 | 1936.2 | 2286.4 | 2732.6 | 2256.7 | 3254.3 | 3349.8 |
| FJ457435.1 | 511250 | 3394.1 | 3187.2 | 2887.1 | 1988.2 | 2308.5 | 3255.8 |
| AY928014.1 | 112649 | 6473.5 | 5132.8 | 2159.5 | 6495.7 | 5242.0 | 5516.1 |
| GQ260161.1 | 584728 | 1304.9 | 915.3 | 1661.0 | 1131.5 | 560.1 | 587.0 |
| EU854894.1 | 324980 | 1065.4 | 953.3 | 703.8 | 454.4 | 954.8 | 568.7 |
| FJ176462.1 | 508766 | 3317.3 | 3947.8 | 3353.5 | 1956.2 | 2701.0 | 3405.6 |
| X97988.1 | 9232 | 2794.0 | 3782.0 | 2908.5 | 3636.0 | 3709.1 | 3945.1 |
| FJ176451.1 | 563362 | 1334.5 | 1136.3 | 2666.3 | 641.7 | 524.1 | 872.6 |
| AY264921.1 | 105131 | 326.2 | 865.3 | 1129.4 | 290.0 | 489.9 | 450.9 |
| EU854951.1 | 340143 | 140.6 | 454.1 | 778.3 | 203.1 | 410.3 | 179.7 |

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FJ176459.1 gg_id:557146 Vibrio sp. str. J-S2-26
EU660319.1 gg_id:299937 Vibrio parahaemolyticus str. CM2
X97989.1 gg_id:9241 Vibrio sp str. VI1067/44
EU579452.1 gg_id:273618 Vibrio pomeroyi str. 929
EU073023.1 gg_id:237745 Vibrio penaeicida HC051105-6
GQ203114.1 gg_id:544229 Vibrio alginolyticus str. 23-6PIN
EU517646.1 gg_id:263182 Vibrio sp. str. 5E9
AB038029.1 gg_id:17434 Vibrio sp. str. OM02
NC_009783.1 gg_id:471497 Vibrio harveyi BAA-1116 str. ATCC BAA-1116; BB120
U57919.1 gg_id:9278 Vibrio cyclitrophicus str. 2P44
EU082035.1 gg_id:252648 Vibrio sp. str. cn83
AY654760.1 gg_id:99936 Oculina mucus isolate 11
AJ316194.1 gg_id:70306 Vibrio pacinii str. LMG 19999
FJ202493.1 gg_id:320634 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k
EU170469.1 gg_id:242658 Vibrio parahaemolyticus str. 070925
EF488080.1 gg_id:224355 Vibrio porteresiae str. MSSRF31
EU854924.1 gg_id:356007 Vibrio sp. 6E9
EU854902.1 gg_id:348515 Vibrio sp. 6B5
AM422800.1 gg_id:238361 Vibrio harveyi str. 04101
EF203212.1 gg_id:214385 Vibrio parahaemolyticus str. R22
EF584041.1 gg_id:231968 Vibrio sp. str. DS7
DQ856554.1 gg_id:245610 intestinal microflora Chinese mitten crab (Eriocheir sinensis) clone C3S
FJ203285.1 gg_id:339560 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c
NC_009783.1 gg_id:471502 Vibrio harveyi BAA-1116 str. ATCC BAA-1116; BB120
DQ173157.1 gg_id:139193 Vibrio alginolyticus str. zouA
AB038030.1 gg_id:47694 Vibrio splendidus str. ATCC33789
EU854912.1 gg_id:353304 Vibrio sp. 6D10
EF584056.1 gg_id:232714 Vibrio sp. str. HE3
EU854944.1 gg_id:308043 Vibrio sp. 7A10(2008)
GU194174.1 gg_id:524536 Vibrio cyclitrophicus str. Col 15
EU636230.1 gg_id:286820 Vibrio natriegens str. V6
GU064378.1 gg_id:544893 Vibrio parahaemolyticus str. 489
X74701.1 gg_id:9315 Vibrio diazotrophicus str. ATCC 33466T
FJ866782.1 gg_id:557937 Rhodobacter capsulatus str. PSB-03
NZ_ACFN01000147.1 gg_id:580234 Vibrio parahaemolyticus str. AQ4037
EU373091.1 gg_id:268687 Vibrio harveyi str. BB170
EU854946.1 gg_id:351124 Vibrio sp. 7A12(2008)
NC_009783.1 gg_id:471498 Vibrio harveyi BAA-1116 str. ATCC BAA-1116; BB120
FJ202872.1 gg_id:308237 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k
AJ874360.1 gg_id:111259 Vibrio splendidus str. 01/104
EU517633.1 gg_id:262574 Vibrio sp. str. 4D5

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| X97989.1 | 9241 | 762.3 | 996.4 | 1051.3 | 574.7 | 1500.8 | 804.5 |
| EU579452.1 | 273618 | 99.6 | 217.8 | 1166.0 | 180.3 | 733.5 | 755.3 |
| EU073023.1 | 237745 | 415.2 | 1404.3 | 1111.7 | 363.8 | 687.6 | 933.7 |
| GQ203114.1 | 544229 | 1211.4 | 859.0 | 3065.1 | 276.6 | 71.9 | 613.1 |
| EU517646.1 | 263182 | 3671.9 | 4225.8 | 4737.4 | 3914.5 | 6537.8 | 4789.1 |
| AB038029.1 | 17434 | 868.6 | 312.5 | 433.1 | 620.8 | 455.1 | 600.6 |
| NC_009783.1 | 471497 | 1876.7 | 1450.0 | 2173.1 | 1397.0 | 2172.8 | 2631.3 |
| U57919.1 | 9278 | 7849.9 | 10467.6 | 6161.7 | 8998.1 | 9672.2 | 10322.5 |
| EU082035.1 | 252648 | 504.8 | 440.0 | 1600.3 | 743.9 | 470.5 | 405.4 |
| AY654760.1 | 99936 | 301.5 | 585.4 | 1235.0 | 353.3 | 1502.9 | 942.7 |
| AJ316194.1 | 70306 | 3200.2 | 1143.7 | 2240.2 | 1845.2 | 481.7 | 981.1 |
| FJ202493.1 | 320634 | 7696.4 | 8890.5 | 8257.3 | 9650.1 | 9102.8 | 7799.1 |
| EU170469.1 | 242658 | 2495.6 | 1828.3 | 3781.4 | 702.3 | 608.6 | 793.2 |
| EF488080.1 | 224355 | 50.1 | 50.3 | 252.1 | 98.8 | 90.9 | 107.2 |
| EU854924.1 | 356007 | 950.3 | 886.1 | 2430.9 | 284.4 | 582.1 | 970.3 |
| EU854902.1 | 348515 | 374.8 | 427.8 | 605.4 | 303.5 | 1130.8 | 407.3 |
| AM422800.1 | 238361 | 648.6 | 480.8 | 1397.2 | 464.7 | 598.0 | 1216.2 |
| EF203212.1 | 214385 | 2456.2 | 2370.8 | 2691.4 | 2574.6 | 3278.4 | 3708.4 |
| EF584041.1 | 231968 | 37.4 | 33.4 | 44.0 | 58.4 | 112.1 | 74.9 |
| DQ856554.1 | 245610 | 1264.6 | 2055.4 | 2173.4 | 1416.0 | 2874.4 | 3139.8 |
| FJ203285.1 | 339560 | 3294.8 | 2784.5 | 4962.3 | 3744.2 | 3179.7 | 2381.3 |
| NC_009783.1 | 471502 | 592.6 | 286.5 | 824.5 | 542.8 | 484.3 | 863.4 |
| DQ173157.1 | 139193 | 1949.6 | 1519.1 | 2048.2 | 653.4 | 916.4 | 1146.5 |
| AB038030.1 | 47694 | 312.1 | 254.9 | 249.7 | 152.7 | 64.8 | 448.4 |
| EU854912.1 | 353304 | 2999.3 | 2429.0 | 2883.3 | 2710.9 | 2815.5 | 2962.4 |
| EF584056.1 | 232714 | 2244.3 | 2239.0 | 2875.8 | 3221.1 | 4914.0 | 3260.1 |
| EU854944.1 | 308043 | 5811.3 | 4990.8 | 3889.9 | 6567.4 | 7631.9 | 5639.6 |
| GU194174.1 | 524536 | 837.2 | 748.2 | 604.5 | 1146.4 | 1807.5 | 1528.4 |
| EU636230.1 | 286820 | 1404.1 | 1395.0 | 1726.4 | 1235.7 | 1542.8 | 1456.3 |
| GU064378.1 | 544893 | 93.8 | 211.3 | 354.3 | 195.1 | 323.4 | 592.3 |
| X74701.1 | 9315 | 55.0 | 158.5 | 348.8 | 72.1 | 207.2 | 142.9 |
| FJ866782.1 | 557937 | 2195.4 | 2268.3 | 3034.5 | 1911.8 | 2828.2 | 3519.0 |
| NZ_ACFN01000147.1 | 580234 | 6247.6 | 7385.1 | 5552.5 | 6323.0 | 7600.6 | 6024.8 |
| EU373091.1 | 268687 | 1656.8 | 1212.4 | 1774.9 | 1388.9 | 2430.5 | 2295.5 |
| EU854946.1 | 351124 | 3544.0 | 3908.5 | 2259.8 | 4227.2 | 6866.1 | 5515.7 |
| NC_009783.1 | 471498 | 685.5 | 807.3 | 1077.6 | 562.8 | 868.5 | 983.1 |
| FJ202872.1 | 308237 | 146.3 | 170.1 | 620.1 | 131.1 | 157.2 | 156.7 |
| AJ874360.1 | 111259 | 2119.9 | 898.3 | 2120.8 | 1764.3 | 2267.4 | 1115.2 |
| EU517633.1 | 262574 | 6129.7 | 11327.7 | 4816.5 | 5271.4 | 10996.1 | 10690.2 |

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EU854947.1 gg_id:316417 Vibrio sp. 7A1
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AY911394.1 gg_id:112657 Vibrio parahaemolyticus str. SW-1
FJ202676.1 gg_id:344716 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k
AB470933.1 gg_id:556034 Vibrio sp. str. r27
AM941185.1 gg_id:286468 Microbes enriched seawater after addition coral mucus and reef waters mixture1-8
EU854897.1 gg_id:306077 Vibrio sp. 6B3
NZ_ACFO01000050.1 gg_id:577439 Vibrio parahaemolyticus str. -5034
AY863432.1 gg_id:113088 Vibrio qinhuangdaora
AF513447.1 gg_id:55336 Vibrio alginolyticus str. LA6
DQ146990.1 gg_id:149211 Vibrio sp. str. V759
AY785255.1 gg_id:108413 microbial fuel cell anode clone 19
EU636231.1 gg_id:284716 Vibrio parahaemolyticus str. V7
FJ952769.1 gg_id:410605 Vibrio sp. str. 1ta5
EU854825.1 gg_id:307164 Vibrio sp. 1B10(2008)
EF584054.1 gg_id:230635 Vibrio sp. str. HE1
EU246793.1 gg_id:243190 polyphasic description Pocillopora meandrina Palmyra Atoll Calcinus obscurus abdon
FJ154796.1 gg_id:311946 Vibrio harveyi str. WG1702
NC_009783.1 gg_id:471500 Vibrio harveyi BAA-1116 str. ATCC BAA-1116; BB120
EU854926.1 gg_id:322675 Vibrio sp. 6G9
AY426982.1 gg_id:101603 Vibrio ezurae str. HDV1-1
EU517647.1 gg_id:274949 Vibrio sp. str. 4G11
X97990.1 gg_id:9224 Vibrio sp str. VI1964/75
FM995173.1 gg_id:568021 digestive gland QX infected and naive Sydney rock oysters Saccostrea glomerata Vib
AY967727.1 gg_id:115357 Vibrio alginolyticus IS3
AY785254.1 gg_id:108410 microbial fuel cell anode clone 17
EU854824.1 gg_id:318618 Vibrio sp. 1G1

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| FJ025780.1 | 343704 | 1219.1 | 1198.1 | 2160.2 | 1306.5 | 622.0 | 572.5 |
| EU419940.1 | 273151 | 2000.2 | 1476.5 | 2281.0 | 860.2 | 942.0 | 1289.2 |
| AY940169.1 | 114484 | 899.9 | 765.2 | 941.3 | 579.4 | 203.9 | 267.6 |
| EU372922.1 | 272836 | 121.0 | 267.9 | 215.9 | 176.0 | 635.3 | 115.8 |
| EU854947.1 | 316417 | 629.8 | 1124.0 | 1561.1 | 375.4 | 429.1 | 430.5 |
| AF493803.1 | 93679 | 485.0 | 488.7 | 639.6 | 151.1 | 409.4 | 933.7 |
| EU854829.1 | 332034 | 118.1 | 313.5 | 442.2 | 145.9 | 294.3 | 80.4 |
| AJ316167.1 | 73319 | 2890.9 | 2906.8 | 5072.4 | 3518.6 | 6812.3 | 4644.3 |
| AF513465.1 | 60374 | 1595.3 | 763.6 | 1470.0 | 1636.9 | 1779.1 | 1027.1 |
| X74720.1 | 9240 | 729.9 | 1332.7 | 2021.4 | 1359.8 | 847.6 | 1110.0 |
| Z31657.1 | 9268 | 7354.3 | 8735.9 | 5502.5 | 10042.7 | 10671.5 | 9961.3 |
| EU699809.1 | 335968 | 8404.4 | 9700.3 | 10707.1 | 8719.0 | 13464.9 | 12013.7 |
| AY332566.1 | 91317 | 160.1 | 290.1 | 560.9 | 215.0 | 114.5 | 252.4 |
| EU854930.1 | 323930 | 720.4 | 716.0 | 1443.1 | 481.6 | 820.1 | 611.3 |
| AAWP01000045.1 | 256024 | 741.9 | 863.2 | 1071.0 | 560.2 | 863.8 | 983.2 |
| X74698.1 | 9313 | 164.3 | 233.1 | 546.7 | 145.9 | 2049.2 | 601.1 |
| AY911394.1 | 112657 | 1714.5 | 1311.1 | 1920.0 | 1613.3 | 1609.6 | 1978.6 |
| FJ202676.1 | 344716 | 1174.2 | 903.2 | 457.3 | 627.1 | 1409.7 | 746.4 |
| AB470933.1 | 556034 | 1126.9 | 623.5 | 132.6 | 1120.9 | 428.0 | 380.7 |
| AM941185.1 | 286468 | 683.5 | 905.9 | 2275.7 | 1514.4 | 2000.6 | 1921.5 |
| EU854897.1 | 306077 | 654.3 | 792.7 | 1278.9 | 257.9 | 1049.9 | 1059.3 |
| NZ_ACFO01000050.1 | 577439 | 286.9 | 388.3 | 456.9 | 390.3 | 393.5 | 558.4 |
| AY863432.1 | 113088 | 2004.6 | 1520.1 | 1440.0 | 750.4 | 165.1 | 1530.1 |
| AF513447.1 | 55336 | 2305.8 | 2217.2 | 2761.4 | 2576.6 | 3280.0 | 3712.1 |
| DQ146990.1 | 149211 | 2218.4 | 1452.9 | 2151.2 | 2271.4 | 1658.8 | 1479.3 |
| AY785255.1 | 108413 | 2334.7 | 1711.3 | 2434.5 | 3543.9 | 1658.5 | 1290.3 |
| EU636231.1 | 284716 | 1062.7 | 1236.9 | 1903.3 | 1203.7 | 703.8 | 675.4 |
| FJ952769.1 | 410605 | 754.4 | 588.0 | 1489.5 | 990.3 | 1487.3 | 568.8 |
| EU854825.1 | 307164 | 1542.6 | 1307.0 | 1402.1 | 484.2 | 2502.8 | 1441.9 |
| EF584054.1 | 230635 | 45.4 | 75.1 | 219.5 | 149.5 | 85.6 | 94.4 |
| EU246793.1 | 243190 | 4002.0 | 4344.5 | 3742.9 | 4528.2 | 7144.8 | 7497.7 |
| FJ154796.1 | 311946 | 168.7 | 189.0 | 271.5 | 191.0 | 105.9 | 359.1 |
| NC_009783.1 | 471500 | 1656.5 | 2246.2 | 2152.6 | 1376.2 | 2301.5 | 2153.8 |
| EU854926.1 | 322675 | 4287.5 | 3488.1 | 5008.0 | 5509.5 | 7623.4 | 4345.8 |
| AY426982.1 | 101603 | 632.6 | 372.8 | 832.1 | 584.3 | 254.9 | 862.0 |
| EU517647.1 | 274949 | 450.6 | 368.5 | 1089.2 | 149.9 | 275.2 | 453.6 |
| X97990.1 | 9224 | 2416.9 | 3210.9 | 3262.5 | 2038.3 | 5879.7 | 2951.9 |
| FM995173.1 | 568021 | 9459.2 | 9392.7 | 5861.6 | 7247.7 | 9055.1 | 7707.7 |
| AY967727.1 | 115357 | 2558.2 | 2171.4 | 4251.1 | 2944.9 | 3027.2 | 2972.8 |
| AY785254.1 | 108410 | 66.9 | 90.9 | 104.9 | 368.6 | 116.3 | 745.0 |
| EU854824.1 | 318618 | 474.5 | 554.9 | 587.3 | 262.2 | 1366.7 | 638.9 |

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DQ026024.1 gg_id:160559 Vibrio parahaemolyticus 2
NR_029222.1 gg_id:585239 Vibrio campbellii str. 40; ATCC 25920
NC_004460.1 gg_id:235488 Vibrio vulnificus str. CMCP6
DQ304557.1 gg_id:144132 Vibrio harveyi str. FA-1
EF584063.1 gg_id:233712 Vibrio sp. str. HE12
EU077545.1 gg_id:245149 Vibrio parahaemolyticus str. HN12
AY911392.1 gg_id:112501 Vibrio shilonii str. MP-3
AY264926.1 gg_id:105905 Vibrio harveyi str. OVL 99-52331-
AY372930.1 gg_id:143887 marine sponge Rhabdastrella globostellata symbiont
Z19003.1 gg_id:9249 Kryptophanaron alfredi symbiont
GQ375456.1 gg_id:583549 Vibrio splendidus str. GHrC13
AY332401.1 gg_id:224717 Vibrio harveyi str. EHR1
GQ205448.1 gg_id:434247 Vibrio parahaemolyticus str. JGB080708-1
EF100710.1 gg_id:191629 Vibrio sp. str. V134
AB239476.1 gg_id:154281 Vibrio campbellii str. LC1-257
EU043379.1 gg_id:246983 Vibrio sinaloensis str. CAIM 798
AB470937.1 gg_id:566097 Vibrio harveyi str. r44
AB297941.1 gg_id:212446 Vibrio nigripulchritudo str. FPC1062
EU541605.1 gg_id:276875 Vibrio sp. str. CECT 7244
AY245190.1 gg_id:86266 Vibrio parahaemolyticus 21
X74714.1 gg_id:9230 Vibrio natriegens str. ATCC 14048T
AM778456.1 gg_id:252007 Vibrio sp. Y310
EU854864.1 gg_id:332457 Vibrio sp. 2F3
DQ995519.1 gg_id:175212 Vibrio alginolyticus str. A3G-2
EF584039.1 gg_id:233082 Vibrio sp. str. DS5
AY911391.1 gg_id:112498 Vibrio parahaemolyticus str. MP-2
X74690.1 gg_id:9234 Vibrio alginolyticus str. ATCC 17749T
Z19085.1 gg_id:9245 Photoblepharon palpebratus symbiont
GQ406675.1 gg_id:531375 Vibrio sp. str. PaD3.34b
EU854950.1 gg_id:319651 Vibrio sp. 7B2
EU660311.1 gg_id:295546 Vibrio parahaemolyticus str. V1
EU854896.1 gg_id:319020 Vibrio sp. 6B10
EU854928.1 gg_id:339400 Vibrio sp. 6H1
EF584020.1 gg_id:229796 Vibrio sp. str. BISLTS1
EF584044.1 gg_id:237322 Vibrio sp. str. DS12
AM778459.1 gg_id:246260 Vibrio sp. Y332
AY785252.1 gg_id:108408 microbial fuel cell anode clone 12
AY876051.1 gg_id:128096 Vibrio sp. HB-8
DQ497399.1 gg_id:159333 Vibrio alginolyticus str. GCSL 29
DQ497398.1 gg_id:159058 Vibrio parahaemolyticus str. 93A-5807
EU854826.1 gg_id:320027 Vibrio sp. 1E8

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| NR_029222.1 | 585239 | 2447.1 | 3712.5 | 2468.8 | 1207.1 | 5970.1 | 3467.1 |
| NC_004460.1 | 235488 | 7267.0 | 10009.2 | 2469.4 | 5326.1 | 10053.0 | 10577.1 |
| DQ304557.1 | 144132 | 11701.6 | 9733.8 | 4745.6 | 10561.9 | 12589.2 | 10517.5 |
| EF584063.1 | 233712 | 8630.4 | 7418.7 | 7237.8 | 7502.5 | 9022.7 | 9110.3 |
| EU077545.1 | 245149 | 470.2 | 1028.4 | 1133.9 | 1215.0 | 818.8 | 387.4 |
| AY911392.1 | 112501 | 500.6 | 428.9 | 657.0 | 530.9 | 210.2 | 1178.6 |
| AY264926.1 | 105905 | 64.0 | 150.7 | 1146.7 | 155.7 | 268.6 | 356.4 |
| AY372930.1 | 143887 | 751.2 | 845.9 | 996.4 | 861.3 | 2111.2 | 2190.4 |
| Z19003.1 | 9249 | 45.5 | 96.6 | 53.9 | 97.9 | 134.0 | 82.1 |
| GQ375456.1 | 583549 | 7524.5 | 6587.1 | 4774.4 | 6356.7 | 7470.8 | 7662.0 |
| AY332401.1 | 224717 | 920.5 | 927.8 | 395.8 | 689.1 | 1190.3 | 1102.4 |
| GQ205448.1 | 434247 | 948.7 | 697.1 | 1007.0 | 662.9 | 525.4 | 1601.6 |
| EF100710.1 | 191629 | 1174.4 | 1209.1 | 853.0 | 349.2 | 82.7 | 218.3 |
| AB239476.1 | 154281 | 983.6 | 724.9 | 2547.6 | 396.5 | 140.3 | 668.4 |
| EU043379.1 | 246983 | 205.5 | 252.5 | 265.9 | 188.1 | 486.0 | 707.2 |
| AB470937.1 | 566097 | 1229.4 | 605.0 | 2145.0 | 1363.6 | 679.1 | 1804.1 |
| AB297941.1 | 212446 | 554.3 | 400.7 | 1526.5 | 319.7 | 73.3 | 495.3 |
| EU541605.1 | 276875 | 409.4 | 249.9 | 647.4 | 211.0 | 1442.2 | 430.5 |
| AY245190.1 | 86266 | 10376.8 | 10972.0 | 13535.6 | 8095.6 | 10132.7 | 8852.8 |
| X74714.1 | 9230 | 1016.0 | 672.5 | 849.2 | 417.5 | 146.3 | 344.6 |
| AM778456.1 | 252007 | 472.2 | 288.9 | 376.4 | 324.0 | 1009.5 | 333.6 |
| EU854864.1 | 332457 | 3609.4 | 4357.0 | 5083.0 | 4856.1 | 11735.9 | 10379.3 |
| DQ995519.1 | 175212 | 102.4 | 220.5 | 316.3 | 172.9 | 420.7 | 195.4 |
| EF584039.1 | 233082 | 61.3 | 160.6 | 781.1 | 146.0 | 282.8 | 420.6 |
| AY911391.1 | 112498 | 222.4 | 494.0 | 643.3 | 797.1 | 330.7 | 234.6 |
| X74690.1 | 9234 | 1097.8 | 1371.3 | 2062.8 | 1654.6 | 629.8 | 930.9 |
| Z19085.1 | 9245 | 136.3 | 186.8 | 266.6 | 261.2 | 519.9 | 508.3 |
| GQ406675.1 | 531375 | 471.3 | 311.4 | 344.4 | 429.6 | 1104.6 | 175.4 |
| EU854950.1 | 319651 | 8951.2 | 8448.2 | 3594.7 | 7590.6 | 7688.4 | 6654.7 |
| EU660311.1 | 295546 | 1838.8 | 1444.8 | 3266.9 | 1265.1 | 1847.1 | 1742.4 |
| EU854896.1 | 319020 | 1413.1 | 1654.6 | 1311.4 | 451.9 | 3039.4 | 1310.2 |
| EU854928.1 | 339400 | 7893.2 | 7781.1 | 4123.0 | 6293.1 | 10097.8 | 8772.2 |
| EF584020.1 | 229796 | 8054.0 | 7357.4 | 4959.0 | 5035.7 | 9016.5 | 7157.8 |
| EF584044.1 | 237322 | 3029.4 | 3100.4 | 2228.9 | 3126.9 | 3284.4 | 2931.1 |
| AM778459.1 | 246260 | 1115.6 | 1095.1 | 1959.6 | 962.6 | 333.3 | 1703.5 |
| AY785252.1 | 108408 | 14786.7 | 14934.7 | 14444.8 | 12133.1 | 14649.1 | 12592.2 |
| AY876051.1 | 128096 | 207.3 | 609.6 | 598.0 | 225.8 | 235.5 | 440.7 |
| DQ497399.1 | 159333 | 4996.7 | 5529.0 | 4211.6 | 4197.5 | 5326.8 | 5017.4 |
| DQ497398.1 | 159058 | 228.4 | 239.1 | 433.4 | 197.3 | 354.4 | 353.1 |
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EU854923.1 gg_id:351053 Vibrio sp. 6F8
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EU404191.2 gg_id:334804 Vibrio harveyi str. MCCB 111
DQ530290.1 gg_id:230076 Vibrio fischeri str. EHR3
EF199915.1 gg_id:200870 Vibrio sp. str. DH98
AY530930.1 gg_id:103088 Vibrio ordalii str. 2003/09/511-2063
GQ372983.1 gg_id:580669 Vibrio aestuarianus str. TS1
EF091705.1 gg_id:177990 Listonella anguillarum str. MHK9
EF579965.1 gg_id:230360 Listonella anguillarum str. MN
DQ068759.1 gg_id:128185 Listonella anguillarum str. HF010522-1
AM162655.1 gg_id:142807 Listonella anguillarum str. 610
AM423154.1 gg_id:208406 marine str. MH-160
AJ310647.1 gg_id:32562 Vibrio agarivorans str. 289T CECT 5085T
DQ146937.1 gg_id:139192 Vibrio harveyi str. LB13
AY035896.1 gg_id:31661 Vibrio campbellii str. L61
DQ005911.1 gg_id:133997 Vibrio harveyi str. 642
AY264924.1 gg_id:105604 Vibrio harveyi str. UQM 2849
CP001485.1 gg_id:526736 Vibrio cholerae str. MJ-1236
EF684900.1 gg_id:278039 Vibrio cholerae RC466
AY494842.1 gg_id:100088 Vibrio cholerae str. SIO
AY426981.1 gg_id:101436 Vibrio ezurae str. HDS1-2
NR_025575.1 gg_id:568332 Vibrio fortis str. CAIM 629; LMG 21557
DQ985231.1 gg_id:177824 Vibrio aestuarianus str. Man2
AJ514917.1 gg_id:104831 Vibrio fortis str. LMG 21566
AJ293802.1 gg_id:46271 Listonella pelagia str. CECT 4202T
AB180389.1 gg_id:109221 Vibrio sp. str. No. 58
AJ514915.1 gg_id:104527 Vibrio fortis str. LMG 21562
AY257971.1 gg_id:84052 Vibrio gallicus str. CIP 107864; HT 1-3
AB000390.2 gg_id:9208 Vibrio halioticoli str. IAM14596T
AY245186.1 gg_id:84838 Vibrio parahaemolyticus 17
FJ457478.1 gg_id:552397 Vibrio sp. str. S2757
EU624428.1 gg_id:281266 Vibrio parahaemolyticus str. S6-06
DQ068936.1 gg_id:128101 Vibrio harveyi str. ATCC 33843
FM204841.1 gg_id:364286 Vibrio harveyi str. LPD 1-1-10
AB512467.1 gg_id:540512 Vibrio harveyi str. AM6
EF635306.1 gg_id:254619 Vibrio harveyi HQ050227-1
AB497061.1 gg_id:564525 Vibrio harveyi str. 7-1
EU031646.1 gg_id:235697 Vibrio harveyi str. AK1

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| AB512471.1 | 554579 | 1254.1 | 1103.7 | 1826.0 | 114.4 | 51.2 | 997.4 |
| EU854923.1 | 351053 | 45.3 | 134.9 | 787.7 | 145.5 | 237.0 | 181.5 |
| NZ_AAWP01000198.1 | 237998 | 112.6 | 207.8 | 648.4 | 212.2 | 126.7 | 231.0 |
| EU404191.2 | 334804 | 5842.8 | 5176.4 | 7020.9 | 8633.3 | 6849.9 | 6185.1 |
| DQ530290.1 | 230076 | 617.8 | 1227.0 | 2052.4 | 1345.3 | 1498.7 | 780.5 |
| EF199915.1 | 200870 | 8253.7 | 8770.1 | 9017.4 | 7068.3 | 10438.4 | 10033.8 |
| AY530930.1 | 103088 | 1435.9 | 1354.8 | 2479.4 | 2399.0 | 2639.1 | 2042.2 |
| GQ372983.1 | 580669 | 1474.3 | 881.4 | 1714.5 | 1398.2 | 112.2 | 921.6 |
| EF091705.1 | 177990 | 980.2 | 787.6 | 890.5 | 1117.0 | 565.6 | 660.7 |
| EF579965.1 | 230360 | 968.8 | 522.4 | 1142.7 | 950.5 | 88.3 | 592.2 |
| DQ068759.1 | 128185 | 12391.6 | 11906.5 | 7953.7 | 9282.1 | 11111.2 | 10863.2 |
| AM162655.1 | 142807 | 618.5 | 408.0 | 1004.7 | 554.8 | 1492.8 | 925.8 |
| AM423154.1 | 208406 | 1387.0 | 1050.3 | 2145.3 | 798.9 | 1688.6 | 839.5 |
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| DQ146937.1 | 139192 | 3563.5 | 2218.4 | 3925.2 | 3134.5 | 3704.3 | 4080.8 |
| AY035896.1 | 31661 | 551.1 | 851.2 | 1304.6 | 416.5 | 475.6 | 795.3 |
| DQ005911.1 | 133997 | 3008.5 | 2069.2 | 2388.1 | 2502.6 | 2980.6 | 3332.8 |
| AY264924.1 | 105604 | 260.3 | 529.9 | 586.3 | 257.0 | 1876.1 | 658.7 |
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| EF684900.1 | 278039 | 264.4 | 333.9 | 819.4 | 337.2 | 722.7 | 716.6 |
| AY494842.1 | 100088 | 9956.4 | 11709.0 | 10462.9 | 8144.8 | 14705.0 | 12778.5 |
| AY426981.1 | 101436 | 641.4 | 274.0 | 403.9 | 706.1 | 233.7 | 1192.0 |
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| DQ985231.1 | 177824 | 629.7 | 574.2 | 688.3 | 524.5 | 1666.2 | 903.7 |
| AJ514917.1 | 104831 | 364.4 | 234.4 | 723.2 | 309.4 | 775.3 | 385.7 |
| AJ293802.1 | 46271 | 7347.2 | 7466.0 | 4598.7 | 5744.6 | 3872.6 | 5386.2 |
| AB180389.1 | 109221 | 273.7 | 347.6 | 300.2 | 285.0 | 890.5 | 963.2 |
| AJ514915.1 | 104527 | 486.2 | 588.6 | 1517.1 | 686.2 | 355.9 | 607.5 |
| AY257971.1 | 84052 | 328.3 | 181.5 | 125.2 | 391.0 | 78.5 | 255.4 |
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| EU624428.1 | 281266 | 7447.8 | 5877.6 | 5940.4 | 5788.1 | 5653.4 | 4877.2 |
| DQ068936.1 | 128101 | 320.5 | 641.7 | 1333.8 | 163.1 | 214.0 | 242.1 |
| FM204841.1 | 364286 | 375.5 | 452.5 | 876.2 | 449.1 | 234.6 | 545.4 |
| AB512467.1 | 540512 | 561.9 | 492.5 | 1110.6 | 504.8 | 593.7 | 735.5 |
| EF635306.1 | 254619 | 312.2 | 580.3 | 1770.5 | 338.4 | 656.4 | 900.3 |
| AB497061.1 | 564525 | 380.7 | 631.9 | 1527.6 | 680.7 | 710.0 | 796.3 |
| EU031646.1 | 235697 | 517.4 | 691.0 | 1278.1 | 291.9 | 201.8 | 693.0 |

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U46579.1 gg_id:9286 Vibrio scophthalmi str. CECT 4638; A089
AB257339.2 gg_id:196408 Vibrio kanaloae str. Do-155
AB257330.2 gg_id:175599 Vibrio kanaloae str. Do-40
DQ068937.1 gg_id:128196 Vibrio metschnikovii str. ATCC 7708
AY837747.1 gg_id:141151 Vibrio metschnikovii str. CCUG 49718 E2.5
X97987.1 gg_id:9174 Vibrio sp str. VI737/19
X74719.1 gg_id:9170 Vibrio orientalis str. ATCC 33934T
DQ978991.1 gg_id:198609 Vibrio sp. S-10
DQ978993.1 gg_id:196541 Vibrio sp. S-12
GQ406597.1 gg_id:528119 Vibrio sp. str. PaD1.29
GQ406593.1 gg_id:517204 Vibrio sp. str. PaD1.21b
NR_029344.1 gg_id:559028 Vibrio pectenicida str. Ifremer A365; CIP 105190
AJ514914.1 gg_id:104376 Vibrio fortis str. LMG 21559
AF124055.3 gg_id:202555 Vibrio aerogenes str. FG1; CCRC 17041; ATCC 700797
FJ176463.1 gg_id:553847 Vibrio sp. str. J-S2-8
AF462458.1 gg_id:47306 Vibrio ruber str. VR1; JCM 11486; CCRC 17186
EU854910.1 gg_id:342299 Vibrio sp. 6C7
FJ952776.1 gg_id:421759 Vibrio sp. str. 2ta10
AJ345063.1 gg_id:94006 Vibrio hepatarius str. LMG 20362
GQ889354.1 gg_id:548764 Vibrio sp. str. Mj2
AB470936.1 gg_id:548949 Vibrio sp. str. r11
X99762.2 gg_id:9228 Vibrio diabolicus str. HE800
DQ273663.1 gg_id:141489 Vibrio mangrovensis str. MSSRF10
DQ847123.1 gg_id:161711 Vibrio rhizosphaerae str. MSSRF3

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| AB512477.1 | 533825 | 375.9 | 423.4 | 977.3 | 451.7 | 240.4 | 546.5 |
| FN554612.2 | 555037 | 7972.0 | 12896.7 | 6805.7 | 5603.2 | 7958.3 | 5702.4 |
| AY332564.1 | 91201 | 144.0 | 379.9 | 947.8 | 124.2 | 192.2 | 162.4 |
| DQ995520.1 | 178502 | 2596.5 | 1592.1 | 1663.2 | 1949.1 | 1736.4 | 2183.9 |
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| GQ327950.1 | 544280 | 517.9 | 635.1 | 1386.4 | 294.8 | 208.5 | 694.1 |
| AB512473.1 | 573785 | 774.9 | 683.2 | 1474.1 | 1002.6 | 739.4 | 1184.5 |
| FJ937908.1 | 556363 | 29.4 | 57.4 | 206.5 | 81.1 | 55.5 | 59.5 |
| X74693.1 | 9214 | 432.4 | 516.0 | 788.4 | 494.7 | 238.3 | 654.0 |
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| GQ406758.1 | 524766 | 11345.9 | 12490.5 | 8124.7 | 9100.2 | 14101.9 | 9585.8 |
| AY254041.1 | 82765 | 2426.4 | 1434.5 | 2503.4 | 2618.0 | 1699.1 | 2732.0 |
| U46579.1 | 9286 | 1202.4 | 1080.5 | 1774.7 | 680.1 | 823.2 | 1216.6 |
| AB257339.2 | 196408 | 3311.1 | 1840.2 | 3936.7 | 4512.2 | 2468.2 | 1812.9 |
| AB257330.2 | 175599 | 2558.8 | 1447.9 | 3303.1 | 3295.9 | 1398.2 | 1791.8 |
| DQ068937.1 | 128196 | 2145.6 | 1456.9 | 3362.3 | 3999.3 | 4334.6 | 3505.3 |
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| X74719.1 | 9170 | 217.6 | 428.4 | 574.2 | 575.8 | 1071.9 | 643.1 |
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| DQ978993.1 | 196541 | 325.4 | 538.6 | 939.1 | 309.5 | 96.2 | 1455.5 |
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| X99762.2 | 9228 | 41.3 | 102.9 | 92.5 | 109.2 | 106.5 | 312.9 |
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| o__Vibrionales | f__Vibrionaceae |
| o__Xanthomonadales | f__Sinobacteraceae |
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g__Vibrio
g__Vibrio
g__Vibrio
g__Vibrio
g__Vibrio
g__Vibrio
g__Hydrocarboniphaga
g__Hydrocarboniphaga
g__Nevskia
g__Nevskia
g__Nevskia
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified

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| s__Vibrio orientalis | 7514 |
| s__Vibrio orientalis | 7534 |
| s__Vibrio ponticus | 6605 |
| s__Vibrio ponticus | 7171 |
| s__Vibrio ponticus | 7573 |
| s__Vibrio proteolyticus | 6580 |
| s__Vibrio proteolyticus | 6826 |
| s__Vibrio proteolyticus | 7468 |
| s__Vibrio rotiferianus | 6524 |
| s__Vibrio rotiferianus | 7278 |
| s__Vibrio rotiferianus | 7507 |
| s__Vibrio rumoiensis | 6592 |
| s__Vibrio rumoiensis | 6995 |
| s__Vibrio rumoiensis | 7452 |
| s__Vibrio shilonii | 6265 |
| s__Vibrio shilonii | 7509 |
| s__Vibrio sp. AND4 | 7193 |
| s__Vibrio sp. Ex25 | 7325 |
| s__Vibrio tapetis | 6277 |
| s__Vibrio tapetis | 6645 |
| s__Vibrio tapetis | 6702 |
| s__Vibrio tapetis | 6934 |
| s__Vibrio vulnificus | 6301 |
| s__Vibrio vulnificus | 6715 |
| s__Vibrio vulnificus | 7228 |
| s__Vibrionales bacterium SWAT-3 | 6550 |
| s__Vibrionales bacterium SWAT-3 | 6663 |
| s__Vibrionales bacterium SWAT-3 | 6933 |
| s__Vibrionales bacterium SWAT-3 | 7145 |
| s__Vibrionales bacterium SWAT-3 | 7147 |
| s__Hydrocarboniphaga effusa | 17330 |
| s__unclassified | 16660 |
| s__Nevskia ramosa | 16003 |
| s__unclassified | 16199 |
| s__unclassified | 17403 |
| s__unclassified | 16042 |
| s__unclassified | 16143 |
| s__unclassified | 16233 |
| s__unclassified | 16378 |
| s__unclassified | 16689 |
| s__unclassified | 16788 |

X99761.1 gg_id:9233 Vibrio mytili
AF199438.1 gg_id:9197 Vibrio sp. str. DS40M5
AY897206.2 gg_id:122102 Vibrio ponticus str. RP30
DQ005880.1 gg_id:128085 Vibrio sp. str. A358
AJ630102.1 gg_id:109158 Vibrio ponticus str. CECT 5870
AF513463.1 gg_id:60376 Vibrio proteolyticus str. PH8
NR_026128.1 gg_id:554644 Vibrio proteolyticus str. ATCC 15338
DQ995521.1 gg_id:190831 Vibrio proteolyticus str. A2G-5B
FM204861.1 gg_id:368147 Vibrio rotiferianus str. LPD 1-1-11
FM204862.1 gg_id:357874 Vibrio rotiferianus str. LPD 1-1-24
FM204858.1 gg_id:357595 Vibrio rotiferianus
AY332407.1 gg_id:227760 Vibrio rumoiensis str. UDP1
EU123937.1 gg_id:342373 Ulcerative enteritis Homarus americanus: case report and intestinal aerobic apparen
DQ530292.1 gg_id:234292 Vibrio rumoiensis str. LAR3
EF584027.1 gg_id:229162 Vibrio sp. str. BS11
AY911395.1 gg_id:112524 Vibrio shilonii str. SW-2
NZ_ABGR01000018.1 gg_id:238096 Vibrio campbellii str. AND4
FJ176450.1 gg_id:570249 Vibrio natriegens str. T-C2-11
AY800101.1 gg_id:255891 Vibrio tapetis str. HH6087
FN554604.2 gg_id:548927 Vibrio tapetis str. HJ4
AY800099.1 gg_id:255639 Vibrio tapetis str. UK6
AY129278.1 gg_id:78597 Vibrio tapetis str. LP2
EF546255.1 gg_id:277789 Polymorphisms Vibrio vulnificus clone 03_C01
EF546280.1 gg_id:279479 Polymorphisms Vibrio vulnificus clone 05_C08
GQ392008.1 gg_id:527025 Vibrio sp. str. PaD2.27
AJ515220.1 gg_id:69396 Vibrio splendidus str. LMG 10952
NR_025480.1 gg_id:547832 Vibrio chagasii str. R-3712; DSM 17138
AJ515219.1 gg_id:74459 Vibrio splendidus str. TNNIII7
AJ515218.1 gg_id:56555 Vibrio splendidus str. TNEMF6
FJ457370.1 gg_id:545463 Vibrio sp. str. S1132
AY363245.1 gg_id:94021 Hydrocarboniphaga effusa str. AP103; ATCC BAA-332
EU313812.1 gg_id:256598 Hydrocarboniphaga sp. str. B2-9
AY102326.1 gg_id:65459 heavy metal-contaminated soil clone a13128
GU205299.1 gg_id:516554 unusual Microbial Venezuelan Tepui (Orthoquartzite) Cave: Dominance Chloroflexal
FJ466262.1 gg_id:546919 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea
AB257720.1 gg_id:158622 Panacagrimonas perspica str. Gsoil 142
GQ389062.1 gg_id:536669 quality deterioration drinking system during serious red water outbreak clone S18
EU328045.1 gg_id:278173 dynamics during bioremediation crude oil contaminated moderate saline soil clone B
GQ389123.1 gg_id:575267 quality deterioration drinking system during serious red water outbreak clone S76
AJ867659.1 gg_id:109705 melted-ice water clone JFJ-ICE-Bact-31
GQ389067.1 gg_id:538784 quality deterioration drinking system during serious red water outbreak clone S22

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|---|---|---|---|---|---|---|---|
| X99761.1 | 9233 | 2164.8 | 2338.0 | 2577.2 | 2684.8 | 2013.0 | 1744.3 |
| AF199438.1 | 9197 | 147.9 | 230.0 | 521.0 | 290.1 | 797.8 | 1396.4 |
| AY897206.2 | 122102 | 768.0 | 915.0 | 648.8 | 688.9 | 365.3 | 446.4 |
| DQ005880.1 | 128085 | 14.9 | 18.4 | 27.8 | 54.6 | 53.6 | 17.4 |
| AJ630102.1 | 109158 | 817.7 | 1150.1 | 1103.8 | 772.2 | 2531.5 | 761.2 |
| AF513463.1 | 60376 | 69.5 | 92.5 | 76.0 | 93.0 | 68.8 | 271.7 |
| NR_026128.1 | 554644 | 1464.6 | 1705.7 | 2047.7 | 925.8 | 122.0 | 389.2 |
| DQ995521.1 | 190831 | 1607.9 | 1746.0 | 1514.0 | 2686.3 | 6218.7 | 5890.9 |
| FM204861.1 | 368147 | 832.3 | 768.6 | 2313.1 | 636.9 | 2026.1 | 1142.0 |
| FM204862.1 | 357874 | 169.8 | 352.1 | 1360.0 | 375.4 | 839.3 | 800.4 |
| FM204858.1 | 357595 | 506.7 | 365.0 | 1415.3 | 480.7 | 630.6 | 1214.8 |
| AY332407.1 | 227760 | 100.5 | 307.9 | 761.4 | 151.8 | 212.7 | 264.0 |
| EU123937.1 | 342373 | 1735.4 | 1542.0 | 2915.6 | 1521.1 | 1947.0 | 1591.3 |
| DQ530292.1 | 234292 | 302.7 | 743.3 | 2010.2 | 437.3 | 576.4 | 806.5 |
| EF584027.1 | 229162 | 2334.2 | 1584.2 | 1364.7 | 1241.5 | 152.2 | 446.8 |
| AY911395.1 | 112524 | 1337.4 | 971.3 | 1005.4 | 948.5 | 665.9 | 1414.0 |
| NZ_ABGR01000018.1 | 238096 | 869.2 | 659.6 | 1526.2 | 1370.4 | 90.9 | 545.2 |
| FJ176450.1 | 570249 | 1558.2 | 1811.1 | 2939.2 | 2993.4 | 1875.6 | 1474.6 |
| AY800101.1 | 255891 | 9492.4 | 11131.8 | 7071.6 | 8682.1 | 7943.8 | 7813.7 |
| FN554604.2 | 548927 | 6914.4 | 7155.6 | 3361.8 | 7808.3 | 7898.4 | 5801.8 |
| AY800099.1 | 255639 | 13767.0 | 18160.1 | 6679.7 | 9288.7 | 10218.2 | 9460.3 |
| AY129278.1 | 78597 | 978.2 | 895.4 | 1588.4 | 879.5 | 236.1 | 492.6 |
| EF546255.1 | 277789 | 3292.6 | 4584.2 | 4150.8 | 2320.9 | 8650.9 | 5882.7 |
| EF546280.1 | 279479 | 577.2 | 755.8 | 518.5 | 1442.3 | 339.2 | 1352.7 |
| GQ392008.1 | 527025 | 1756.1 | 1826.9 | 3309.5 | 2466.0 | 4531.7 | 2162.7 |
| AJ515220.1 | 69396 | 1594.5 | 968.8 | 2014.0 | 1303.2 | 2271.7 | 667.2 |
| NR_025480.1 | 547832 | 1203.0 | 812.6 | 2002.6 | 1276.2 | 2092.3 | 653.9 |
| AJ515219.1 | 74459 | 5164.1 | 6653.4 | 5047.2 | 4092.4 | 8014.2 | 6917.9 |
| AJ515218.1 | 56555 | 982.5 | 678.8 | 694.4 | 1847.2 | 526.5 | 807.8 |
| FJ457370.1 | 545463 | 713.9 | 513.3 | 1405.3 | 502.0 | 862.6 | 497.2 |
| AY363245.1 | 94021 | 35.4 | 48.6 | 76.1 | 65.6 | 72.4 | 51.9 |
| EU313812.1 | 256598 | 6868.7 | 7286.5 | 4179.6 | 4377.8 | 7841.5 | 6138.9 |
| AY102326.1 | 65459 | 10018.1 | 8690.3 | 9364.0 | 9971.2 | 9252.9 | 7987.7 |
| GU205299.1 | 516554 | 5274.3 | 5832.3 | 6477.3 | 5986.5 | 6569.0 | 7805.3 |
| FJ466262.1 | 546919 | 4065.5 | 4278.5 | 5863.1 | 3556.7 | 5215.0 | 7030.7 |
| AB257720.1 | 158622 | 107.8 | 213.3 | 188.4 | 96.1 | 101.3 | 205.3 |
| GQ389062.1 | 536669 | 4136.3 | 4809.3 | 2946.1 | 5726.7 | 7484.3 | 5903.2 |
| EU328045.1 | 278173 | 2821.7 | 4253.9 | 4670.7 | 3903.6 | 5447.4 | 4019.5 |
| GQ389123.1 | 575267 | 1764.8 | 2828.0 | 6273.0 | 2386.8 | 2393.0 | 2748.0 |
| AJ867659.1 | 109705 | 4668.2 | 5933.3 | 2256.2 | 3298.6 | 3462.3 | 4153.0 |
| GQ389067.1 | 538784 | 600.8 | 2147.0 | 2925.4 | 965.7 | 799.9 | 2054.2 |

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|---|---|---|---|
| k__Bacteria | k__Bacteria | p__Proteobacteria | c__Gammaproteobacteria |
| k__Bacteria | k__Bacteria | p__Proteobacteria | c__Gammaproteobacteria |
| k__Bacteria | k__Bacteria | p__Proteobacteria | c__Gammaproteobacteria |
| k__Bacteria | k__Bacteria | p__Proteobacteria | c__Gammaproteobacteria |
| k__Bacteria | k__Bacteria | p__Proteobacteria | c__Gammaproteobacteria |
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| k__Bacteria | k__Bacteria | p__Proteobacteria | c__Gammaproteobacteria |
| k__Bacteria | k__Bacteria | p__Proteobacteria | c__Gammaproteobacteria |
| k__Bacteria | k__Bacteria | p__Proteobacteria | c__Gammaproteobacteria |
| k__Bacteria | k__Bacteria | p__Proteobacteria | c__Gammaproteobacteria |
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| k__Bacteria | k__Bacteria | p__Proteobacteria | c__Gammaproteobacteria |
| k__Bacteria | k__Bacteria | p__Proteobacteria | c__Gammaproteobacteria |
| k__Bacteria | k__Bacteria | p__Proteobacteria | c__Gammaproteobacteria |
| k__Bacteria | k__Bacteria | p__Proteobacteria | c__Gammaproteobacteria |
| k__Bacteria | k__Bacteria | p__Proteobacteria | c__Gammaproteobacteria |
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| k__Bacteria | k__Bacteria | p__Proteobacteria | c__Gammaproteobacteria |
| k__Bacteria | k__Bacteria | p__Proteobacteria | c__Gammaproteobacteria |
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| o__Xanthomonadales | f__Solimonaceae |
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| o__Xanthomonadales | f__Xanthomonadaceae |

g__Solimonas
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g__Solimonas
g__Solimonas
g__Aquimonas
g__Arenimonas
g__Arenimonas
g__Arenimonas
g__Dokdonella
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g__Dokdonella
g__Dokdonella
g__Dokdonella
g__Dokdonella
g__Dokdonella
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g__Dyella
g__Frateuria
g__Frateuria
g__Frateuria
g__Frateuria
g__Frateuria
g__Frateuria
g__Frateuria
g__Frateuria
g__Ignatzschineria
g__Ignatzschineria
g__Ignatzschineria
g__Ignatzschineria
g__Luteibacter

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|---|---|
| s__Solimonas soli | 15913 |
| s__unclassified | 15934 |
| s__unclassified | 16067 |
| s__unclassified | 16158 |
| s__unclassified | 16413 |
| s__unclassified | 16968 |
| s__unclassified | 17110 |
| s__unclassified | 17271 |
| s__unclassified | 15938 |
| s__unclassified | 16487 |
| s__unclassified | 16786 |
| s__unclassified | 17010 |
| s__Dokdonella koreensis | 16704 |
| s__unclassified | 16040 |
| s__unclassified | 16192 |
| s__unclassified | 16255 |
| s__unclassified | 16281 |
| s__unclassified | 16513 |
| s__unclassified | 16667 |
| s__unclassified | 16860 |
| s__unclassified | 17175 |
| s__unclassified | 17392 |
| s__Dyella ginsengisoli | 17021 |
| s__Dyella ginsengisoli | 17397 |
| s__Dyella japonica | 17167 |
| s__unclassified | 16382 |
| s__unclassified | 17015 |
| s__unclassified | 17332 |
| s__Frateuria aurantia | 16282 |
| s__Frateuria aurantia | 16403 |
| s__Frateuria aurantia | 16835 |
| s__Frateuria aurantia | 17262 |
| s__unclassified | 16226 |
| s__unclassified | 16453 |
| s__unclassified | 16832 |
| s__unclassified | 17350 |
| s__Ignatzschineria larvae | 3670 |
| s__unclassified | 3546 |
| s__unclassified | 3815 |
| s__unclassified | 3883 |
| s__Luteibacter rhizovicinus | 16393 |

EF067861.1 gg_id:197220 Solimonas soli str. DCY12
AB074648.1 gg_id:78370 pea aphid symbiont clone APe2_11
GQ009435.1 gg_id:500228 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw77
EU542470.1 gg_id:269231 Effects chemical structure concentration on pathways microbial during dechlorinatio
GQ009794.1 gg_id:499871 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw77
AJ318170.1 gg_id:37497 waste-gas biofilter clone BIrii5
AM935172.1 gg_id:541995 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
GQ009827.1 gg_id:499839 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw77
AY544768.1 gg_id:101731 Aquamonas vora str. BPTSA20
AF445723.1 gg_id:33015 travertine hot spring clone SM2D10
AF445726.1 gg_id:18696 travertine hot spring clone SM2E10
DQ239766.1 gg_id:143429 Rhodanobacter sp. str. CC-JY-1
EF589679.1 gg_id:233714 Dokdonella koreensis str. NML 01-0233
EU276578.1 gg_id:370138 -DGGE and Approaches Analyze Effect Agricultural Practices on Soil agricultural soil c
CU466843.1 gg_id:354759 Evry wastewater treatment plant anoxic basin clone
EF516860.1 gg_id:223206 grassland soil clone FCPS392
EF125947.1 gg_id:571774 Biofilm-reactor Based Enrichment Utilizing Oligotrophic Concentrations Acyl-homose
EU150285.1 gg_id:279341 acidobacteria and dry meadow soil Niwot Ridge LTER clone Ni_H08_DMDN
EU708508.1 gg_id:293748 and Situ Quantification Arsenite Oxidizing Denitrifying Enrichment anoxic arsenite ox
AM981201.1 gg_id:266974 Dokdonella sp. str. PYM5-11
FJ971728.1 gg_id:462787 microbial autrotrophic denitrification granular sludge clone R1-B4
AB245362.1 gg_id:149239 Dokdonella ginsengisoli str. Gsoil 191
AB245367.1 gg_id:146494 Dyella ginsengisoli str. Gsoil 3046
EF191353.1 gg_id:199169 Dyella ginsengisoli str. LA-3
AB110496.1 gg_id:102417 Dyemonas todaii str. XD10
DQ451515.1 gg_id:156994 forest soil clone FAC76
EU682683.1 gg_id:329236 Frateuria sp. str. VA24
DQ378209.1 gg_id:154251 oil-polluted soil clone F47_Pitesti
AB091195.1 gg_id:105821 Frateuria aurantia str. IFO3247
AB091196.1 gg_id:105973 Frateuria aurantia str. IFO3249
AB091198.1 gg_id:106286 Frateuria aurantia str. IFO13329
AB091194.1 gg_id:105669 Frateuria aurantia str. IFO3245
AY792283.1 gg_id:120471 Humic Lake clone CrystalBog571C8
GU458291.1 gg_id:522526 Dyella sp. str. ST6D
AY913255.1 gg_id:114384 forest soil clone DUNssu037 (-2A) (OTU#012)
AY884571.1 gg_id:112345 Dyella soli str. BB4
AJ252143.1 gg_id:47724 Schineria larvae str. L1/68
EU008091.1 gg_id:370121 Ignatzschineria sp. str. C2H18
DQ337535.1 gg_id:148917 Schineria sp. CHNDP40
AM397063.1 gg_id:170943 Schineria sp. str. S5
AJ580498.1 gg_id:99030 Luteibactor rhizovicina str. LJ96

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| EF067861.1 | 197220 | 6739.1 | 6774.5 | 3054.7 | 4191.8 | 3359.5 | 4907.2 |
| AB074648.1 | 78370 | 5530.8 | 5285.2 | 6946.1 | 5191.7 | 5452.2 | 5940.7 |
| GQ009435.1 | 500228 | 13946.5 | 13397.5 | 8159.7 | 11531.1 | 11908.6 | 11360.2 |
| EU542470.1 | 269231 | 5220.8 | 5824.4 | 2953.9 | 3532.5 | 2522.2 | 3421.3 |
| GQ009794.1 | 499871 | 7310.4 | 9048.3 | 2576.7 | 4179.1 | 5302.0 | 6262.5 |
| AJ318170.1 | 37497 | 2322.4 | 3021.5 | 4546.4 | 1111.2 | 2185.6 | 1571.9 |
| AM935172.1 | 541995 | 3997.7 | 6706.1 | 4543.4 | 4226.5 | 6974.3 | 7019.5 |
| GQ009827.1 | 499839 | 20097.8 | 19854.5 | 17052.9 | 14244.9 | 20514.7 | 18532.8 |
| AY544768.1 | 101731 | 145.7 | 129.6 | 456.4 | 116.7 | 192.5 | 416.0 |
| AF445723.1 | 33015 | 3189.4 | 4439.3 | 3989.3 | 4826.0 | 3609.6 | 6481.2 |
| AF445726.1 | 18696 | 6201.1 | 7918.9 | 6449.0 | 3349.3 | 5044.6 | 10277.0 |
| DQ239766.1 | 143429 | 3908.4 | 4350.8 | 3062.8 | 2308.1 | 3638.1 | 7033.4 |
| EF589679.1 | 233714 | 1523.2 | 1245.3 | 1931.9 | 1266.0 | 555.1 | 2058.0 |
| EU276578.1 | 370138 | 912.8 | 987.3 | 1037.7 | 1760.6 | 2228.5 | 2203.5 |
| CU466843.1 | 354759 | 1807.8 | 2539.4 | 368.2 | 65.1 | 454.9 | 1517.1 |
| EF516860.1 | 223206 | 944.0 | 1632.6 | 857.6 | 109.0 | 266.3 | 1707.4 |
| EF125947.1 | 571774 | 88.2 | 92.2 | 89.2 | 148.9 | 115.3 | 131.6 |
| EU150285.1 | 279341 | 4178.2 | 5695.2 | 7113.2 | 4631.6 | 3748.8 | 5114.4 |
| EU708508.1 | 293748 | 6063.8 | 6036.2 | 1353.8 | 4548.4 | 5877.8 | 6206.0 |
| AM981201.1 | 266974 | 3480.0 | 3807.6 | 2727.4 | 891.1 | 1940.1 | 2289.9 |
| FJ971728.1 | 462787 | 1389.4 | 2453.8 | 2477.9 | 1650.9 | 2059.4 | 2935.1 |
| AB245362.1 | 149239 | 1845.3 | 2959.2 | 2017.3 | 951.0 | 2564.6 | 3538.1 |
| AB245367.1 | 146494 | 4797.7 | 4254.7 | 8908.1 | 4020.3 | 5972.6 | 4334.8 |
| EF191353.1 | 199169 | 10280.9 | 10586.1 | 10255.7 | 7772.6 | 11692.9 | 8321.7 |
| AB110496.1 | 102417 | 1869.6 | 1170.1 | 4859.7 | 1509.4 | 1050.3 | 2741.3 |
| DQ451515.1 | 156994 | 665.5 | 1797.1 | 5177.2 | 589.2 | 1633.8 | 1949.8 |
| EU682683.1 | 329236 | 7317.8 | 8160.6 | 9183.5 | 4755.7 | 7498.9 | 7036.8 |
| DQ378209.1 | 154251 | 13221.2 | 10883.1 | 9017.2 | 7763.9 | 9292.3 | 8663.9 |
| AB091195.1 | 105821 | 18465.8 | 18612.5 | 18975.1 | 16828.0 | 19190.7 | 17998.9 |
| AB091196.1 | 105973 | 4100.3 | 3080.4 | 7081.7 | 7402.5 | 3832.2 | 4632.8 |
| AB091198.1 | 106286 | 7796.0 | 5330.4 | 5169.5 | 9480.4 | 5480.3 | 4534.1 |
| AB091194.1 | 105669 | 14228.8 | 12831.0 | 10672.6 | 14761.5 | 14252.8 | 12329.2 |
| AY792283.1 | 120471 | 7346.2 | 7426.8 | 10074.5 | 4938.0 | 4467.6 | 6051.6 |
| GU458291.1 | 522526 | 213.9 | 942.6 | 5436.9 | 470.0 | 164.3 | 897.7 |
| AY913255.1 | 114384 | 8008.2 | 7748.5 | 9883.9 | 8375.3 | 8893.3 | 9223.3 |
| AY884571.1 | 112345 | 6572.7 | 5905.4 | 8961.3 | 9841.5 | 2202.9 | 4839.3 |
| AJ252143.1 | 47724 | 4792.3 | 2848.5 | 1715.6 | 1497.9 | 1818.5 | 1722.1 |
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| AM397063.1 | 170943 | 13768.5 | 14464.6 | 15003.8 | 12255.9 | 16966.6 | 13750.3 |
| AJ580498.1 | 99030 | 7646.1 | 5935.6 | 6062.1 | 5133.9 | 7353.7 | 6238.1 |

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| s__Lysobacter taiwanensis | 17157 |
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DQ984591.1 gg_id:242890 Mt. Nan-Jen litterfall clone IYF125
DQ986460.1 gg_id:192082 Luteibacter sp. str. MDA0897
DQ532183.1 gg_id:165763 Geographical Variation Microbial Burden and Spacecraft Assembly Johnson Space Ce
AB433628.1 gg_id:275651 Luteimonas mephitis
DQ337599.1 gg_id:146003 Luteimonas sp. CHNTR51
AJ012228.1 gg_id:7793 Luteimonas mephitis str. B1953/27.1
AB246805.2 gg_id:150537 Luteimonas sp. str. Q-1
AY500144.1 gg_id:104583 Luteimonas sp. H10 str. H10; AS 1.3529
FJ750462.1 gg_id:510835 Luteimonas sp. str. EM0590
DQ323663.1 gg_id:146080 Lysobacter taiwanensis str. DD-1133
AB299978.2 gg_id:258113 Lysobacter spongicola str. KMM 329
AY599704.1 gg_id:101000 fungal ascocarp clone Cl-11-TB4-II
GQ003601.1 gg_id:506057 Topographical and Temporal Human Skin Microbiome skin alar crease clone nbu54h
GU361114.1 gg_id:524518 Lysobacter enzymogenes str. T226
EU440727.1 gg_id:557970 Soil are Changed Agricultural Practices agricultural soil clone Plot17-C01
AY642571.1 gg_id:151984 and carbonate precipitation giant microbialites ly alkaline Lake Van Turkey microbiali
EF173350.1 gg_id:199667 Options situ remediation contaminated mixture chlorinated hydrocarbons hydrocarb
EU244029.1 gg_id:359969 16SrRNA probes river Leine sediment clone sls1316
DQ191178.1 gg_id:140061 Lysobacter sp. str. GH 1-9
DQ532277.1 gg_id:163869 Geographical Variation Microbial Burden and Spacecraft Assembly Johnson Space Ce
AM930380.1 gg_id:245194 Lysobacter enzymogenes str. 3.1T8
AY557615.1 gg_id:101503 Silanimonas lenta str. 25-4
EU908051.1 gg_id:326693 Lysobacter sp. str. ZLD-17
FJ674447.1 gg_id:520058 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
EU236311.1 gg_id:296150 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg1bA3
DQ129253.1 gg_id:138668 microarray level air two cities Texas urban aerosol clone AKIW751
EU800949.1 gg_id:353183 It's all ranking aquatic Delaware Bay NJ clone 2C229208
AY599709.1 gg_id:101824 fungal ascocarp clone Cl-106-TB4-II
EU881196.1 gg_id:333628 Karst region natural restoration land soil clone KNR200711-002
AJ534675.1 gg_id:75877 ground water deep-well injection disposal site radioactive wastes Tomsk-7 clone S15A
AM111012.1 gg_id:140927 Lysobacter sp. str. 3070
AJ582198.1 gg_id:93932 soil near uranium mill tailings clone Gitt-GS-126
AB166878.1 gg_id:100144 Lysobacter sp. str. Dae16
EU662609.1 gg_id:567662 Productivity- Chemolithoautotrophically Based Sulfidic Karst Systems floating microb
FN357197.1 gg_id:541979 Lysobacter capsici str. 10.4.5
AB008507.1 gg_id:7875 Pseudoxanthomonas japonensis str. 12-3
GQ480839.1 gg_id:537693 Pseudoxanthomonas mexicana str. L2
AF273082.1 gg_id:41720 Pseudoxanthomonas mexicana str. AMX 26B
AM932276.1 gg_id:276970 Pseudoxanthomonas taiwanensis str. S22-49
AF427039.2 gg_id:72795 Pseudoxanthomonas taiwanensis str. CB-226
GQ263885.1 gg_id:572981 Structure Simulated Level Waste Site simulated level waste site clone WC2_134

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| DQ984591.1 | 242890 | 1346.8 | 2105.2 | 2075.9 | 1595.1 | 3259.4 | 3441.4 |
| DQ986460.1 | 192082 | 5174.2 | 5148.1 | 5572.4 | 3098.3 | 2650.2 | 4114.4 |
| DQ532183.1 | 165763 | 3661.7 | 3154.4 | 4620.7 | 4251.8 | 4063.8 | 5116.6 |
| AB433628.1 | 275651 | 5347.4 | 4665.5 | 2715.1 | 5630.6 | 6628.9 | 6797.5 |
| DQ337599.1 | 146003 | 5854.6 | 6116.7 | 6639.3 | 5405.2 | 6874.5 | 8325.3 |
| AJ012228.1 | 7793 | 1350.4 | 2356.0 | 3058.1 | 259.8 | 1985.4 | 2140.5 |
| AB246805.2 | 150537 | 977.2 | 1874.1 | 2859.6 | 637.6 | 3449.3 | 2853.5 |
| AY500144.1 | 104583 | 791.3 | 1307.0 | 4463.5 | 203.2 | 955.5 | 893.8 |
| FJ750462.1 | 510835 | 1955.3 | 3083.6 | 7014.2 | 895.5 | 1624.8 | 1286.8 |
| DQ323663.1 | 146080 | 1061.4 | 1644.5 | 168.7 | 66.3 | 134.6 | 65.5 |
| AB299978.2 | 258113 | 3729.8 | 3726.8 | 5252.6 | 1675.2 | 3034.2 | 3851.5 |
| AY599704.1 | 101000 | 885.3 | 748.7 | 2099.2 | 806.6 | 2640.1 | 1323.4 |
| GQ003601.1 | 506057 | 2018.7 | 3091.9 | 2594.7 | 1365.3 | 2503.2 | 2121.9 |
| GU361114.1 | 524518 | 2638.9 | 3855.8 | 6363.5 | 1885.7 | 2746.4 | 2399.4 |
| EU440727.1 | 557970 | 1011.4 | 2483.9 | 2232.9 | 458.3 | 732.2 | 1853.1 |
| AY642571.1 | 151984 | 219.3 | 544.7 | 433.7 | 236.1 | 186.5 | 528.1 |
| EF173350.1 | 199667 | 579.0 | 763.8 | 1989.6 | 747.2 | 4692.1 | 2619.9 |
| EU244029.1 | 359969 | 565.8 | 964.2 | 2247.1 | 524.1 | 641.2 | 859.1 |
| DQ191178.1 | 140061 | 1756.7 | 2220.2 | 5974.0 | 3484.9 | 6134.8 | 2339.2 |
| DQ532277.1 | 163869 | 4865.7 | 4859.1 | 4753.8 | 1862.7 | 2368.5 | 3831.5 |
| AM930380.1 | 245194 | 17447.7 | 17372.4 | 15828.2 | 11596.1 | 12921.2 | 13227.4 |
| AY557615.1 | 101503 | 6673.9 | 8847.0 | 6567.0 | 3840.1 | 6963.6 | 8509.4 |
| EU908051.1 | 326693 | 2229.9 | 2616.9 | 5007.9 | 1978.1 | 4422.4 | 2017.3 |
| FJ674447.1 | 520058 | 1869.1 | 2736.3 | 2752.0 | 2217.5 | 1455.1 | 2517.2 |
| EU236311.1 | 296150 | 1568.1 | 2624.9 | 2979.1 | 1827.8 | 1991.1 | 3411.2 |
| DQ129253.1 | 138668 | 3058.8 | 4833.2 | 4118.1 | 3565.7 | 1902.0 | 3992.0 |
| EU800949.1 | 353183 | 2707.2 | 1722.8 | 2339.5 | 1936.3 | 2356.5 | 2454.5 |
| AY599709.1 | 101824 | 3399.5 | 3749.8 | 6120.1 | 5011.4 | 7462.9 | 4479.6 |
| EU881196.1 | 333628 | 4146.0 | 3979.4 | 2321.9 | 2080.6 | 2934.8 | 2127.9 |
| AJ534675.1 | 75877 | 10097.1 | 8867.7 | 6487.8 | 6715.2 | 9085.3 | 9007.9 |
| AM111012.1 | 140927 | 1140.2 | 2480.8 | 2630.5 | 1562.9 | 8521.9 | 3192.0 |
| AJ582198.1 | 93932 | 1358.8 | 2181.6 | 3308.1 | 842.3 | 3118.0 | 2237.7 |
| AB166878.1 | 100144 | 870.0 | 1788.5 | 1797.0 | 955.7 | 333.9 | 3194.6 |
| EU662609.1 | 567662 | 5619.2 | 4755.1 | 4320.9 | 3906.6 | 5353.6 | 7374.2 |
| FN357197.1 | 541979 | 418.0 | 1258.0 | 1313.5 | 302.3 | 194.0 | 267.9 |
| AB008507.1 | 7875 | 8950.8 | 11019.1 | 13373.3 | 9730.3 | 14099.6 | 12832.5 |
| GQ480839.1 | 537693 | 949.3 | 1730.2 | 728.1 | 624.9 | 1547.2 | 822.5 |
| AF273082.1 | 41720 | 1929.2 | 3324.7 | 1773.6 | 849.4 | 828.4 | 1619.8 |
| AM932276.1 | 276970 | 2079.3 | 1567.8 | 2625.6 | 2224.5 | 2386.1 | 4126.1 |
| AF427039.2 | 72795 | 187.2 | 411.0 | 112.9 | 61.2 | 92.4 | 265.2 |
| GQ263885.1 | 572981 | 5670.5 | 3877.7 | 3543.6 | 7148.0 | 6074.1 | 5541.9 |

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DQ984597.1 gg_id:246060 Mt. Nan-Jen litterfall clone IYF77
GQ263865.1 gg_id:554529 Structure Simulated Level Waste Site simulated level waste site clone WC2_11
GQ263804.1 gg_id:561211 Structure Simulated Level Waste Site simulated level waste site clone WC1_b45
GQ263736.1 gg_id:539166 Structure Simulated Level Waste Site simulated level waste site clone WC1_a52
AY686710.1 gg_id:99791 Pseudoxanthomonas johnstonii str. JA40
AB271140.1 gg_id:165390 Pseudoxanthomonas suwonensis str. MX8-2
GQ264214.1 gg_id:532909 Structure Simulated Level Waste Site simulated level waste site clone WW1_a91
EU589254.1 gg_id:276619 China Ningxia rice paddy field soil clone 1_A10
AM418384.1 gg_id:191835 Pseudoxanthomonas spadix str. IMMIB AFH-5
AB245360.1 gg_id:149042 Pseudoxanthomonas ginsengisoli str. Gsoil 175
AJ581600.1 gg_id:93887 soil near uranium mill tailings clone KCM-B-65
DQ419968.1 gg_id:155699 Frateuria sp. DM-HM
DQ370020.1 gg_id:154977 Rhodanobacter lindaniclasticus str. czh-131
AY495959.1 gg_id:101644 Frateuria sp. str. WJ69
AF312216.1 gg_id:28808 South Africa: KwaZulu-Natal Province Pietermaritzburg clone Y14-2 bacterium
AY081991.1 gg_id:68655 atrazine-catabolizing microbial absence methanol clone KRA30-20
GQ047745.1 gg_id:430929 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor
EU818793.1 gg_id:354823 Rhodanobacter sp. str. LQ-2
DQ837296.1 gg_id:256803 Archaeal and pristine National Park Spain Donana coastal aquifer clone 49S1_1B_51
EF166075.1 gg_id:196704 Rhodanobacter ginsengisoli str. GR17-7
FJ167498.1 gg_id:305737 microbiology granular sludge under autotrophic mixotrophic and heterotrophic denit
GQ250431.2 gg_id:593647 Rhodanobacter sp. str. MJ01
AY218756.1 gg_id:81132 penguin droppings sediments clone KD6-20
GU134907.1 gg_id:582647 Acid-tolerant microaerophilic oxdizing enhance Fe(III) accumulation Fe(II) oxidizing e
AY218745.1 gg_id:81880 penguin droppings sediments clone KD6-1
AY218667.1 gg_id:81461 penguin droppings sediments clone KD9-36
AY188308.1 gg_id:79780 marine? clone KD3-82
AB286179.1 gg_id:182472 Rhodanobacter thiooxidans str. LCS2
AB100608.1 gg_id:79383 Swingsiella fulva str. Jip2
DQ125745.1 gg_id:133703 uranium contaminated soil clone AKAU3857
EF166076.1 gg_id:192094 Rhodanobacter terrae str. GP18-1
EU332829.1 gg_id:256674 Rhodanobacter sp. str. LnR5-47
DQ125806.1 gg_id:133317 uranium contaminated soil clone AKAU3949
AY218740.1 gg_id:82238 penguin droppings sediments clone KD5-73
FJ538158.1 gg_id:560044 metagenomics study rice treated milk vetch and no-tillage paddy field soil clone MBM
FJ405366.1 gg_id:359626 Rhodanobacter terrae str. SPg
AY188317.1 gg_id:79298 penguin droppings sediment clone KD5-51
FJ466329.1 gg_id:511559 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea
AY218719.1 gg_id:81363 penguin droppings sediments clone KD7-89
EU196307.1 gg_id:253030 Rhodanobacter sp. NP47
AY218723.1 gg_id:81676 penguin droppings sediments clone KD5-100

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| DQ984597.1 | 246060 | 2031.1 | 2818.6 | 2719.3 | 1573.2 | 3487.3 | 1458.0 |
| GQ263865.1 | 554529 | 2166.5 | 2515.4 | 1755.8 | 1539.8 | 4000.9 | 3812.9 |
| GQ263804.1 | 561211 | 6790.4 | 7789.7 | 7000.2 | 7273.6 | 9494.7 | 6160.3 |
| GQ263736.1 | 539166 | 1563.5 | 1967.0 | 2049.7 | 2277.7 | 3082.6 | 2483.2 |
| AY686710.1 | 99791 | 1001.0 | 1917.2 | 1458.6 | 1940.8 | 1007.0 | 400.6 |
| AB271140.1 | 165390 | 5175.3 | 5300.5 | 7692.4 | 6016.6 | 9451.8 | 5112.0 |
| GQ264214.1 | 532909 | 3506.2 | 3107.2 | 2596.5 | 2936.3 | 3973.9 | 2500.2 |
| EU589254.1 | 276619 | 5375.7 | 6070.0 | 4657.8 | 5813.8 | 6574.0 | 3462.9 |
| AM418384.1 | 191835 | 3999.1 | 5103.5 | 5934.0 | 4766.4 | 4559.1 | 3126.3 |
| AB245360.1 | 149042 | 4755.1 | 5703.6 | 5557.8 | 2719.7 | 6076.3 | 3395.1 |
| AJ581600.1 | 93887 | 5512.9 | 6687.2 | 4129.7 | 4974.0 | 6042.0 | 4323.5 |
| DQ419968.1 | 155699 | 630.2 | 1043.1 | 4327.7 | 428.8 | 1954.6 | 4764.2 |
| DQ370020.1 | 154977 | 2128.8 | 1651.8 | 4105.8 | 3224.9 | 2161.4 | 1659.6 |
| AY495959.1 | 101644 | 3981.5 | 3173.6 | 6405.5 | 4994.4 | 6563.1 | 6124.5 |
| AF312216.1 | 28808 | 58.8 | 118.5 | 455.3 | 154.1 | 103.7 | 458.9 |
| AY081991.1 | 68655 | 16895.8 | 16976.5 | 11560.1 | 15072.3 | 17852.3 | 16094.1 |
| GQ047745.1 | 430929 | 4308.0 | 4377.9 | 7810.6 | 3658.7 | 3598.5 | 3918.1 |
| EU818793.1 | 354823 | 1105.7 | 2160.4 | 4276.5 | 1492.7 | 1246.9 | 3884.4 |
| DQ837296.1 | 256803 | 3176.8 | 5426.1 | 5129.5 | 2498.2 | 2215.5 | 3587.2 |
| EF166075.1 | 196704 | 3149.8 | 3338.5 | 3535.8 | 3435.8 | 2115.2 | 2887.0 |
| FJ167498.1 | 305737 | 2213.9 | 2968.4 | 5275.4 | 3934.5 | 6329.2 | 2913.0 |
| GQ250431.2 | 593647 | 977.0 | 881.4 | 3367.3 | 432.2 | 342.0 | 1782.7 |
| AY218756.1 | 81132 | 8365.8 | 8018.2 | 2537.9 | 3967.3 | 4392.9 | 4907.9 |
| GU134907.1 | 582647 | 290.7 | 1263.1 | 4013.7 | 581.9 | 367.7 | 1661.6 |
| AY218745.1 | 81880 | 2729.2 | 2297.7 | 747.2 | 1588.6 | 1000.7 | 2766.4 |
| AY218667.1 | 81461 | 1968.7 | 3009.9 | 6594.3 | 2469.0 | 3976.2 | 6169.9 |
| AY188308.1 | 79780 | 3332.0 | 3540.5 | 3876.3 | 2911.8 | 7760.5 | 5545.3 |
| AB286179.1 | 182472 | 38.8 | 73.4 | 781.1 | 69.5 | 81.0 | 2846.3 |
| AB100608.1 | 79383 | 4881.5 | 2555.6 | 4844.8 | 4857.7 | 3642.6 | 5079.2 |
| DQ125745.1 | 133703 | 1306.3 | 1796.8 | 2016.7 | 1286.7 | 1551.2 | 1842.4 |
| EF166076.1 | 192094 | 3405.4 | 2712.2 | 4388.3 | 3033.9 | 5692.5 | 5423.3 |
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| DQ125806.1 | 133317 | 7445.3 | 7913.0 | 6670.7 | 4747.8 | 14387.5 | 6132.0 |
| AY218740.1 | 82238 | 3139.1 | 3582.1 | 4389.1 | 4676.6 | 6417.1 | 2369.1 |
| FJ538158.1 | 560044 | 835.5 | 1536.3 | 5605.6 | 1430.7 | 3757.4 | 1774.6 |
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| AY188317.1 | 79298 | 39.4 | 69.5 | 181.6 | 73.3 | 266.4 | 173.6 |
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| EU196307.1 | 253030 | 5680.4 | 5542.3 | 5522.8 | 6645.1 | 6288.0 | 7062.2 |
| AY218723.1 | 81676 | 1308.6 | 1476.4 | 2369.8 | 578.3 | 1111.8 | 1145.6 |

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| s__Pseudomonas geniculata | 16520 |
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| s__Pseudomonas geniculata | 16868 |
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| s__Stenotrophomonas nitritireducens | 17063 |
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| s__unclassified | 16016 |
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| s__unclassified | 16046 |

AF376025.1 gg_id:50262 Frateuria sp. str. NO-16
AY218606.1 gg_id:82101 penguin droppings sediments clone KD3-139
DQ230920.1 gg_id:143831 Stenotrophomonas maltophilia str. KB2
DQ912806.1 gg_id:242976 Stenotrophomonas maltophilia str. ZX-PKU-003
FM213382.2 gg_id:332451 Stenotrophomonas maltophilia str. MN6
AY641540.1 gg_id:100214 Stenotrophomonas maltophilia str. BK
AY738260.1 gg_id:106659 Stenotrophomonas maltophilia str. TKW1
AB194323.1 gg_id:138821 Stenotrophomonas maltophilia str. BL-12
DQ192172.1 gg_id:139973 Stenotrophomonas maltophilia str. flds
AB299977.1 gg_id:224930 Stenotrophomonas maltophilia str. 26-3 (= KMM 3045)
EU857419.1 gg_id:344187 Stenotrophomonas maltophilia str. BF-S6
EU239471.1 gg_id:239046 Pseudomonas geniculata str. XJUHX-9
EF102868.1 gg_id:245040 Stenotrophomonas maltophilia str. G-5-5-1
DQ077704.1 gg_id:132159 Stenotrophomonas maltophilia FLX
DQ327729.1 gg_id:146179 Stenotrophomonas maltophilia str. DHHJ
EU239465.1 gg_id:243036 Pseudomonas geniculata str. XJUHX-2
EU239476.1 gg_id:257977 Pseudomonas geniculata str. XJUHX-18
FM213378.2 gg_id:314300 Stenotrophomonas maltophilia str. KJPB14
FJ976090.1 gg_id:426140 Stenotrophomonas maltophilia str. ATCC 53510
GU265557.1 gg_id:577388 Stenotrophomonas acidaminiphila str. BTY
DQ864512.1 gg_id:170684 Stenotrophomonas maltophilia
EF174242.1 gg_id:192384 direct activated 1st maturation stage sludge clone B17-814
DQ824702.1 gg_id:174317 human fecal clone RL185_aaj72a04
DQ824618.1 gg_id:185994 human fecal clone RL185_aaj70e05
FJ268981.1 gg_id:366073 unculturable rhizospheric soil Phragmites cummunis growing wetland ecosystem dist
EU434427.1 gg_id:276010 Stenotrophomonas koreensis str. a197
DQ824602.1 gg_id:175201 human fecal clone RL185_aaj70c07
DQ824541.1 gg_id:179102 human fecal clone RL185_aaj69d09
AJ012229.1 gg_id:7812 Stenotrophomonas nitritireducens str. L2
FJ950643.1 gg_id:396619 Stenotrophomonas maltophilia str. c199
FJ405360.1 gg_id:360816 Stenotrophomonas maltophilia str. SPa
DQ469587.1 gg_id:158226 Stenotrophomonas maltophilia Sm777
FM178869.1 gg_id:310433 Acetobacter pasteurianus str. CCM 3606
AJ131782.1 gg_id:7817 Stenotrophomonas maltophilia str. LMG 10873
GQ268318.1 gg_id:589026 Stenotrophomonas maltophilia str. Y1
AF511522.1 gg_id:65384 Stenotrophomonas maltophilia SaO5lg
AJ293466.1 gg_id:39173 Stenotrophomonas maltophilia str. e-p20
AJ293469.1 gg_id:50487 Stenotrophomonas maltophilia str. c20
FJ347998.1 gg_id:334679 Stenotrophomonas sp. str. GGC-D7A
EU239472.1 gg_id:253725 Pseudomonas geniculata str. XJUHX-10
EU779483.1 gg_id:349163 Hartmann's Mountain Zebra feces clone AFZEB_aaj71b07

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| AF376025.1 | 50262 | 3909.5 | 4481.2 | 4916.5 | 4313.6 | 6838.4 | 6434.3 |
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| DQ230920.1 | 143831 | 5513.2 | 5037.4 | 7777.2 | 9156.1 | 8565.2 | 5025.9 |
| DQ912806.1 | 242976 | 8655.1 | 9199.2 | 5564.0 | 10720.1 | 8772.9 | 5423.8 |
| FM213382.2 | 332451 | 3546.8 | 5229.3 | 8531.6 | 7052.1 | 10258.9 | 7192.7 |
| AY641540.1 | 100214 | 73.0 | 264.8 | 326.4 | 587.3 | 953.3 | 241.5 |
| AY738260.1 | 106659 | 3294.0 | 3716.2 | 4478.6 | 5347.0 | 6133.1 | 2957.5 |
| AB194323.1 | 138821 | 1451.7 | 1618.3 | 2592.0 | 3248.8 | 3335.1 | 1954.1 |
| DQ192172.1 | 139973 | 411.2 | 532.2 | 668.6 | 467.2 | 1219.3 | 350.5 |
| AB299977.1 | 224930 | 749.9 | 1109.6 | 1116.9 | 239.2 | 913.5 | 500.7 |
| EU857419.1 | 344187 | 1340.2 | 1585.9 | 1519.3 | 1696.0 | 3034.4 | 1298.5 |
| EU239471.1 | 239046 | 807.5 | 1502.2 | 1092.3 | 310.0 | 2622.5 | 2955.3 |
| EF102868.1 | 245040 | 609.7 | 1384.8 | 1425.6 | 312.7 | 3393.9 | 2546.4 |
| DQ077704.1 | 132159 | 2366.6 | 2645.6 | 1583.2 | 692.2 | 3600.4 | 1579.9 |
| DQ327729.1 | 146179 | 7416.8 | 7093.0 | 4981.6 | 5322.7 | 8275.1 | 6017.6 |
| EU239465.1 | 243036 | 604.5 | 993.2 | 1589.2 | 904.9 | 3171.4 | 2131.3 |
| EU239476.1 | 257977 | 758.5 | 1316.7 | 2126.3 | 1600.3 | 3506.0 | 2442.4 |
| FM213378.2 | 314300 | 2027.6 | 2294.8 | 2313.0 | 3493.5 | 4417.7 | 2123.8 |
| FJ976090.1 | 426140 | 3332.3 | 4790.7 | 4411.2 | 3138.0 | 4612.5 | 3878.1 |
| GU265557.1 | 577388 | 680.9 | 1475.4 | 1687.5 | 1308.5 | 1566.2 | 789.8 |
| DQ864512.1 | 170684 | 3353.0 | 1475.1 | 9076.4 | 6679.7 | 3081.2 | 4759.2 |
| EF174242.1 | 192384 | 3496.5 | 2702.2 | 6663.0 | 3262.8 | 7883.8 | 4392.4 |
| DQ824702.1 | 174317 | 8266.0 | 6918.2 | 4139.3 | 6729.5 | 7033.1 | 8139.5 |
| DQ824618.1 | 185994 | 401.7 | 2734.8 | 925.8 | 208.1 | 336.3 | 5239.8 |
| FJ268981.1 | 366073 | 8994.3 | 9477.8 | 3244.0 | 9097.3 | 8916.9 | 7283.4 |
| EU434427.1 | 276010 | 8409.6 | 7867.3 | 3894.2 | 5431.2 | 4444.7 | 4102.9 |
| DQ824602.1 | 175201 | 6024.3 | 6415.5 | 5331.6 | 4192.1 | 6486.0 | 5298.4 |
| DQ824541.1 | 179102 | 1913.3 | 2635.3 | 2174.5 | 1083.6 | 2184.3 | 1785.8 |
| AJ012229.1 | 7812 | 7459.1 | 6992.2 | 9634.9 | 8799.5 | 9246.2 | 5759.9 |
| FJ950643.1 | 396619 | 3577.5 | 3994.7 | 3162.4 | 3268.6 | 2185.0 | 3964.8 |
| FJ405360.1 | 360816 | 11.8 | 20.2 | 21.9 | 49.0 | 51.6 | 17.6 |
| DQ469587.1 | 158226 | 34.5 | 148.7 | 103.1 | 71.0 | 211.9 | 134.4 |
| FM178869.1 | 310433 | 2385.6 | 3577.2 | 1953.9 | 2745.9 | 3018.6 | 3108.6 |
| AJ131782.1 | 7817 | 3686.0 | 4446.4 | 6045.6 | 5175.6 | 5020.8 | 4252.0 |
| GQ268318.1 | 589026 | 1102.9 | 1583.2 | 2069.1 | 3500.0 | 6500.4 | 1315.6 |
| AF511522.1 | 65384 | 998.7 | 1244.9 | 888.2 | 245.2 | 3295.4 | 1937.0 |
| AJ293466.1 | 39173 | 1769.0 | 2331.9 | 1711.8 | 1824.8 | 2482.0 | 1615.6 |
| AJ293469.1 | 50487 | 10587.2 | 10195.4 | 11885.5 | 11654.1 | 13302.0 | 11554.5 |
| FJ347998.1 | 334679 | 1309.7 | 2214.9 | 2138.9 | 965.2 | 1281.1 | 1833.4 |
| EU239472.1 | 253725 | 672.9 | 1154.3 | 1594.5 | 1588.8 | 3530.7 | 2382.0 |
| EU779483.1 | 349163 | 1138.6 | 1636.3 | 1683.0 | 475.5 | 330.0 | 409.7 |

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EU434498.1 gg_id:263531 Stenotrophomonas maltophilia str. b314
FJ554664.1 gg_id:550358 Pseudomonas hibiscicola str. PB2
EF620464.1 gg_id:246737 Stenotrophomonas maltophilia str. ISSDS-774
AY484506.1 gg_id:106950 Stenotrophomonas maltophilia
DQ424865.1 gg_id:213325 Stenotrophomonas maltophilia str. KNUC163
AF390081.1 gg_id:53734 Stenotrophomonas maltophilia str. Sea-11
EU564819.1 gg_id:271361 Stenotrophomonas maltophilia str. HB
AB547226.1 gg_id:514890 Stenotrophomonas maltophilia str. NCCP-45
EU934076.1 gg_id:344292 Stenotrophomonas maltophilia str. FR2_1con
AY738614.1 gg_id:105623 Stenotrophomonas maltophilia str. nj1
AB299975.1 gg_id:219684 Stenotrophomonas maltophilia str. KMM 339
FJ493060.1 gg_id:586234 Stenotrophomonas chelatiphaga str. G-7
EU263112.1 gg_id:257886 Stenotrophomonas maltophilia str. TPID9
EF221779.1 gg_id:200228 Stenotrophomonas sp. str. tap-11
EU442189.1 gg_id:300964 Stenotrophomonas maltophilia str. IdR
AF100731.1 gg_id:25594 Stenotrophomonas maltophilia VUN10001
X95924.1 gg_id:7814 Stenotrophomonas maltophilia str. LMG 11087
AB547227.1 gg_id:519787 Stenotrophomonas maltophilia str. NCCP-47
AB294557.1 gg_id:206457 Stenotrophomonas maltophilia str. NCB0306-284
AJ560626.1 gg_id:100999 Achromobacter xylosoxidans wp22
Y13836.1 gg_id:7806 Stenotrophomonas sp
AJ293464.1 gg_id:43807 Stenotrophomonas maltophilia str. e-p3
FJ859699.1 gg_id:575987 Stenotrophomonas maltophilia str. BIHB 357
AB194708.1 gg_id:138533 Stenotrophomonas maltophilia str. S-1
EU927145.1 gg_id:350559 Stenotrophomonas maltophilia str. G2
AF100733.1 gg_id:70857 Stenotrophomonas maltophilia VUN10003
AJ293474.1 gg_id:23220 Stenotrophomonas maltophilia str. e-a22
EU239466.1 gg_id:247577 Pseudomonas geniculata str. XJUHX-3
EF221775.1 gg_id:202238 Stenotrophomonas sp. str. tap-7
EF221776.1 gg_id:201486 Stenotrophomonas sp. str. tap-8
X95925.1 gg_id:7815 Stenotrophomonas maltophilia str. LMG 11114
AJ293471.1 gg_id:52247 Stenotrophomonas maltophilia str. e-a1
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EF620466.1 gg_id:248993 Stenotrophomonas maltophilia str. ISSDS-782
FJ527557.1 gg_id:555593 Stenotrophomonas maltophilia str. YMG-3
DQ424870.2 gg_id:209104 Stenotrophomonas maltophilia str. KNUC171
EF620444.1 gg_id:242386 Stenotrophomonas maltophilia str. ISSDS-424
AJ131903.1 gg_id:7819 Stenotrophomonas maltophilia str. LMG 10879

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| EU434498.1 | 263531 | 1806.9 | 1600.2 | 1665.1 | 700.6 | 1444.3 | 1610.1 |
| FJ554664.1 | 550358 | 1793.3 | 2547.2 | 2594.0 | 1702.5 | 1518.7 | 1973.2 |
| EF620464.1 | 246737 | 2196.6 | 2307.5 | 4946.0 | 4008.3 | 3606.8 | 2551.2 |
| AY484506.1 | 106950 | 512.7 | 880.6 | 1141.3 | 869.0 | 2874.7 | 1315.6 |
| DQ424865.1 | 213325 | 5127.9 | 4741.5 | 5992.6 | 8312.2 | 5414.0 | 4636.1 |
| AF390081.1 | 53734 | 1043.9 | 876.6 | 1812.6 | 3189.4 | 1944.5 | 1063.3 |
| EU564819.1 | 271361 | 429.5 | 474.1 | 1174.1 | 852.7 | 1885.5 | 1272.0 |
| AB547226.1 | 514890 | 1679.4 | 1668.0 | 1624.2 | 751.8 | 1437.2 | 1615.9 |
| EU934076.1 | 344292 | 3434.7 | 3683.1 | 4354.1 | 3501.4 | 2792.9 | 3362.2 |
| AY738614.1 | 105623 | 16411.0 | 12439.3 | 10600.0 | 15299.7 | 15311.7 | 12901.4 |
| AB299975.1 | 219684 | 75.4 | 275.3 | 148.5 | 68.0 | 87.6 | 98.6 |
| FJ493060.1 | 586234 | 326.6 | 892.9 | 313.1 | 672.7 | 894.5 | 306.3 |
| EU263112.1 | 257886 | 2523.9 | 3646.3 | 4068.9 | 1804.0 | 2255.0 | 3248.7 |
| EF221779.1 | 200228 | 8896.6 | 9222.5 | 8958.6 | 7386.2 | 10561.5 | 9187.3 |
| EU442189.1 | 300964 | 579.2 | 1956.6 | 404.8 | 616.9 | 1676.3 | 1453.1 |
| AF100731.1 | 25594 | 1748.6 | 2351.1 | 1913.6 | 840.1 | 1879.8 | 1771.4 |
| X95924.1 | 7814 | 1108.8 | 1803.9 | 1502.6 | 741.7 | 1767.4 | 1678.2 |
| AB547227.1 | 519787 | 2855.7 | 3168.7 | 3033.5 | 2607.3 | 3293.5 | 2914.9 |
| AB294557.1 | 206457 | 1685.9 | 1770.6 | 2576.3 | 3243.3 | 2358.0 | 1499.5 |
| AJ560626.1 | 100999 | 4948.4 | 5115.9 | 4891.6 | 3228.6 | 4397.2 | 4202.3 |
| Y13836.1 | 7806 | 2052.5 | 2249.7 | 2955.5 | 1948.3 | 2034.5 | 3065.0 |
| AJ293464.1 | 43807 | 633.4 | 1039.7 | 1263.1 | 452.8 | 874.5 | 878.2 |
| FJ859699.1 | 575987 | 4027.5 | 3900.3 | 5403.1 | 7018.9 | 6445.3 | 3077.6 |
| AB194708.1 | 138533 | 1706.6 | 1928.5 | 3068.1 | 3680.9 | 3710.8 | 1998.2 |
| EU927145.1 | 350559 | 3914.1 | 3870.9 | 4731.6 | 5977.2 | 7110.3 | 2917.6 |
| AF100733.1 | 70857 | 2932.2 | 3669.4 | 2941.5 | 1867.8 | 1695.6 | 3016.5 |
| AJ293474.1 | 23220 | 4361.3 | 4019.2 | 5960.9 | 6783.5 | 5152.9 | 4307.7 |
| EU239466.1 | 247577 | 726.7 | 1377.4 | 1156.6 | 304.0 | 3303.5 | 3139.2 |
| EF221775.1 | 202238 | 2322.0 | 2538.5 | 1742.7 | 1909.4 | 2386.9 | 1452.3 |
| EF221776.1 | 201486 | 1939.2 | 1921.2 | 2331.1 | 1707.7 | 965.2 | 1933.9 |
| X95925.1 | 7815 | 2065.8 | 2443.2 | 3062.3 | 1994.2 | 2077.4 | 2276.1 |
| AJ293471.1 | 52247 | 1027.3 | 1651.2 | 1436.9 | 1067.0 | 6762.6 | 2438.5 |
| GU549434.1 | 518084 | 3415.5 | 2706.3 | 4278.0 | 5197.2 | 6763.5 | 3177.4 |
| DQ141193.1 | 138419 | 1712.0 | 2018.7 | 2497.9 | 2519.3 | 3164.2 | 1821.5 |
| AY277550.1 | 88987 | 4533.4 | 5586.8 | 6469.9 | 2626.5 | 4924.3 | 7450.8 |
| EF620455.1 | 249332 | 11863.0 | 12292.3 | 4535.4 | 6824.2 | 6103.4 | 5942.3 |
| EF620466.1 | 248993 | 1415.1 | 1439.8 | 648.4 | 364.7 | 251.2 | 1311.3 |
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| EF620444.1 | 242386 | 6975.3 | 7180.8 | 2905.2 | 4733.6 | 6148.0 | 4362.3 |
| AJ131903.1 | 7819 | 1153.8 | 1338.5 | 793.5 | 575.4 | 673.3 | 1158.1 |

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GU186115.1 gg_id:552717 Stenotrophomonas maltophilia str. IHB B 1365
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| AB294554.1 | 210322 | 2988.0 | 3269.1 | 1110.7 | 314.2 | 503.7 | 1668.4 |
| AM159126.2 | 144942 | 711.7 | 1001.3 | 295.2 | 89.7 | 490.2 | 740.3 |
| AJ293472.1 | 46966 | 2901.9 | 4344.9 | 5959.5 | 7984.3 | 6074.7 | 4142.8 |
| AJ293470.1 | 20877 | 3242.6 | 3728.9 | 4506.0 | 4302.0 | 5630.8 | 2799.3 |
| GQ267816.1 | 540690 | 5228.6 | 6073.1 | 4979.7 | 5036.2 | 3768.5 | 3569.5 |
| AJ306833.1 | 71314 | 1852.4 | 2887.9 | 3326.6 | 2794.6 | 5822.9 | 3391.6 |
| EU627172.1 | 278738 | 12454.9 | 12892.0 | 12253.6 | 18630.3 | 20743.6 | 15119.4 |
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| EF102866.1 | 247514 | 4753.1 | 5067.1 | 5913.1 | 4612.1 | 4702.9 | 5601.9 |
| FN395263.1 | 392327 | 4529.2 | 5423.6 | 6766.0 | 6465.3 | 5500.4 | 6227.8 |
| FJ184334.1 | 316000 | 261.0 | 417.2 | 626.0 | 1389.7 | 1145.0 | 670.5 |
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| FJ950659.1 | 388170 | 3800.7 | 4606.8 | 3975.3 | 2117.5 | 3123.0 | 3365.9 |
| AJ973277.1 | 129907 | 7684.6 | 6345.2 | 6995.2 | 7670.4 | 8762.3 | 6567.1 |
| EU708603.1 | 331219 | 1306.1 | 2188.6 | 2249.2 | 2537.4 | 6230.1 | 5494.0 |
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| FJ418173.1 | 357672 | 726.5 | 875.0 | 1042.7 | 885.7 | 2275.4 | 628.1 |
| EU834246.1 | 347257 | 1521.2 | 1822.1 | 3143.2 | 2064.2 | 3260.1 | 2172.5 |
| DQ777866.1 | 162978 | 2520.2 | 2661.3 | 4219.3 | 4486.9 | 6110.6 | 2940.5 |
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| AJ131909.1 | 7832 | 4105.2 | 4621.8 | 7027.1 | 6223.7 | 4822.4 | 5324.4 |
| DQ530084.1 | 160828 | 1161.3 | 985.7 | 1800.7 | 2944.3 | 1710.6 | 1163.7 |
| AY512625.1 | 103604 | 2838.2 | 4395.0 | 4301.9 | 1792.2 | 3007.5 | 3745.0 |
| FN395260.1 | 401337 | 3142.4 | 2936.6 | 4528.6 | 4911.8 | 7097.7 | 2927.2 |
| FJ950567.1 | 418822 | 978.9 | 1732.0 | 1458.7 | 674.0 | 1304.4 | 1521.5 |
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| GU186115.1 | 552717 | 2226.6 | 2685.2 | 2610.8 | 1320.5 | 1644.6 | 2517.0 |
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| AJ131115.1 | 7808 | 3289.4 | 3891.4 | 5547.8 | 6594.6 | 6202.7 | 3349.3 |
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| s__Xanthomonas retroflexus | 16361 |
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| s__Thermomonas fusca | 16156 |
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AY748889.1 gg_id:100468 Stenotrophomonas maltophilia N6.8
AY970826.1 gg_id:115298 Stenotrophomonas maltophilia str. CCF00024
AY943389.2 gg_id:132966 Stenotrophomonas maltophilia str. c6
DQ466570.1 gg_id:156954 Stenotrophomonas maltophilia str. B8R
EU056836.1 gg_id:255845 Stenotrophomonas maltophilia str. NK-ST
DQ067559.1 gg_id:136180 Stenotrophomonas maltophilia str. Cgmcc 1.1788
AF390080.1 gg_id:17139 Stenotrophomonas maltophilia str. Sea-8
GQ889255.1 gg_id:573375 Stenotrophomonas maltophilia str. S17
FJ481929.1 gg_id:572456 Stenotrophomonas maltophilia str. AF-222
AJ131116.1 gg_id:7809 Stenotrophomonas maltophilia str. LMG 981
AY880273.1 gg_id:111725 Stenotrophomonas maltophilia str. M5-2
EU834257.1 gg_id:343623 Stenotrophomonas maltophilia str. DS34
GQ861456.1 gg_id:581534 Stenotrophomonas maltophilia str. LZC3
AY748888.1 gg_id:100312 Stenotrophomonas maltophilia N5.18
EU373409.1 gg_id:266618 Stenotrophomonas maltophilia str. YRL04
AJ293467.1 gg_id:43218 Stenotrophomonas maltophilia str. c5
GU202014.1 gg_id:593848 Stenotrophomonas sp. str. JSG1
EF102867.1 gg_id:244364 Stenotrophomonas maltophilia str. P-5-22
DQ337602.1 gg_id:149673 Xanthomonas retroflexus BBTR24
EU429452.1 gg_id:258517 Stenotrophomonas maltophilia Algi-7
AM495257.1 gg_id:240513 Xanthomonas retroflexus str. INBB4
AB294555.1 gg_id:214045 Stenotrophomonas maltophilia str. IAM 1566
AJ519987.1 gg_id:76350 Thermomonas fusca str. LMG 21738
AJ519985.1 gg_id:75052 Thermomonas fusca str. LMG 21736
AB101446.1 gg_id:79280 Xanthomonas axonopodis str. S54
AJ786786.1 gg_id:108063 Xanthomonas sp. R-20819
AF508111.1 gg_id:66233 Thermomonas haemolytica TJ7
AF508105.1 gg_id:66237 Thermomonas haemolytica N22
EU665168.1 gg_id:562931 Soil are Changed Agricultural Practices agricultural soil clone Plot22-2B06
EU834276.1 gg_id:316695 Thermomonas brevis str. DS60
AJ576411.1 gg_id:101026 midgut homogenate Pachnoda ephippiata larva clone PeM51
NR_025265.1 gg_id:572324 Thermomonas hydrothermalis str. SGM-6; DSM 14834
EF219023.1 gg_id:261814 structure and significance Rhizobiales biofouling biofilms on reverse osmosis membra
CU919621.1 gg_id:555897 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
AY218573.1 gg_id:81039 penguin droppings sediments clone KD2-14
EU104238.1 gg_id:341846 Evidence Comamonadaceae determinants settling performance activated sludge clo
EU202907.1 gg_id:342175 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo
EU202899.1 gg_id:345071 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo
AB355702.1 gg_id:245102 Thermomonas brevis str. S47
EU662613.1 gg_id:539739 Productivity- Chemolithoautotrophically Based Sulfidic Karst Systems floating microb
EF633616.1 gg_id:250370 Thermomonas sp. str. lyso-lm521

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| AY748889.1 | 100468 | 2890.1 | 2379.6 | 2048.7 | 3181.3 | 1860.6 | 1922.1 |
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| DQ466570.1 | 156954 | 1684.0 | 1502.7 | 3334.2 | 3802.1 | 2171.3 | 1688.2 |
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| GQ889255.1 | 573375 | 4051.2 | 4713.0 | 6489.1 | 5687.5 | 5099.3 | 4989.3 |
| FJ481929.1 | 572456 | 12352.6 | 11343.8 | 5716.6 | 9264.4 | 6839.5 | 6922.6 |
| AJ131116.1 | 7809 | 12484.2 | 13968.6 | 9220.4 | 11157.6 | 13008.1 | 11697.7 |
| AY880273.1 | 111725 | 4894.5 | 5441.9 | 2715.1 | 3334.1 | 5152.2 | 4607.0 |
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| AJ293467.1 | 43218 | 2143.2 | 2136.9 | 4682.6 | 3645.0 | 6733.5 | 5548.5 |
| GU202014.1 | 593848 | 2965.6 | 3226.9 | 5102.9 | 4992.3 | 3332.8 | 2945.0 |
| EF102867.1 | 244364 | 48.0 | 284.7 | 430.9 | 86.2 | 432.1 | 280.8 |
| DQ337602.1 | 149673 | 2273.9 | 2392.8 | 2521.9 | 2968.7 | 2905.6 | 2491.1 |
| EU429452.1 | 258517 | 11624.5 | 11433.5 | 9632.1 | 12744.3 | 15249.2 | 11628.7 |
| AM495257.1 | 240513 | 1396.5 | 1600.7 | 1079.5 | 188.2 | 369.9 | 1195.8 |
| AB294555.1 | 214045 | 1221.9 | 1501.0 | 1104.1 | 344.4 | 339.2 | 1187.9 |
| AJ519987.1 | 76350 | 748.6 | 852.0 | 697.9 | 380.2 | 317.2 | 1367.2 |
| AJ519985.1 | 75052 | 4404.9 | 5337.2 | 3440.6 | 2691.5 | 4423.6 | 3971.6 |
| AB101446.1 | 79280 | 781.1 | 1268.2 | 2073.1 | 754.8 | 1088.9 | 1652.9 |
| AJ786786.1 | 108063 | 790.1 | 1811.5 | 2464.9 | 776.2 | 910.2 | 2134.3 |
| AF508111.1 | 66233 | 819.5 | 1278.4 | 1827.7 | 732.8 | 2116.2 | 914.9 |
| AF508105.1 | 66237 | 6890.1 | 8346.3 | 8334.5 | 8445.9 | 11980.5 | 11392.9 |
| EU665168.1 | 562931 | 1286.9 | 1947.6 | 3338.5 | 495.2 | 1683.5 | 2003.0 |
| EU834276.1 | 316695 | 4434.0 | 4377.0 | 3948.3 | 2841.7 | 3811.0 | 5936.7 |
| AJ576411.1 | 101026 | 5176.3 | 7976.9 | 6327.2 | 4623.5 | 8456.7 | 7875.5 |
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AJ863416.1 gg_id:124055 poplar tree microcosm rhizosphere flooded clone 17RHF39
AJ519989.1 gg_id:76525 Thermomonas brevis str. LMG 21746
EF682964.1 gg_id:244345 Eastern Mediterranean atmosphere clone F15_3C_FL
DQ659212.1 gg_id:218635 acid mine drainage clone DBS-Clone37
DQ833483.1 gg_id:172808 detected analyses depth sediment Guanting Reservoir clone 35-10
GQ181039.1 gg_id:569287 Dyella marensis str. LNP9
AJ536871.1 gg_id:150596 s wastes primer pairs uranium mining waste pile soil clone JG30a-KF-75
GQ016481.1 gg_id:493186 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
FJ675586.1 gg_id:529819 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
CU926385.1 gg_id:556012 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
EU151438.1 gg_id:265662 oligonucleotide prokaryotic acidophile microarray: validation its use monitor seasona
FJ670842.1 gg_id:521246 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
AY546512.1 gg_id:105121 soda lake sediment clone 5H_90
EU340183.1 gg_id:238503 on Aquatic Macrophytes Geothermally Active Area Sedge Bay Yellowstone Lake WY
AB240487.1 gg_id:145000 microbial structure rhizosphere biofilm Sapporo root-tip (0 40 mm) Phragmites Sosei
AM934875.1 gg_id:541193 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
EF018572.1 gg_id:203659 aspen rhizosphere clone Amb_16S_839
FM873350.1 gg_id:357693 occupant source house floor dust clone FD02B06
CU926903.1 gg_id:562146 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
AM400231.1 gg_id:170471 Stenotrophomonas sp. str. KC-5
AM697474.1 gg_id:226122 sequencing libraries indoor dust clone BF0001D089
DQ984619.1 gg_id:254845 YK oil-contaminated soil clone YK_20
EF688352.1 gg_id:239403 soil clone F4-100
EU665174.1 gg_id:538171 Soil are Changed Agricultural Practices agricultural soil clone Plot22-G05
GQ062403.1 gg_id:450601 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
EU735671.1 gg_id:324704 archaeal structures oil contaminated and soils China pristine soil Jidong Oilfield clone
EU250249.1 gg_id:252154 acid mine drainage clone GXDC-35
AM934797.1 gg_id:544247 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
AM934946.1 gg_id:563489 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
AY218736.1 gg_id:81928 penguin droppings sediments clone KD5-27
EU104136.1 gg_id:340602 Evidence Comamonadaceae determinants settling performance activated sludge clo
AM936180.1 gg_id:537205 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
DQ450791.1 gg_id:160992 Microbial Alpine Tundra Wet Meadow Soil: Chloroflexi Cold Water-Saturated saturat
DQ984639.1 gg_id:236708 YK oil-contaminated soil clone YK_159
AF139997.1 gg_id:7792 Xanthomonas sp. str. ML-122
EU131040.1 gg_id:237966 alkaline China coal mine soil clone SIP CM35
CU466816.1 gg_id:339285 Evry wastewater treatment plant anoxic basin clone
GU332843.1 gg_id:593908 Arenimonas sp. str. NA-09
AJ619045.1 gg_id:102209 Brewery bottling plant clone MTAC25
EU449635.1 gg_id:535385 Soil are Changed Agricultural Practices agricultural soil clone Plot4-2E09
GU180157.1 gg_id:579953 Impact coplanar PCBs on microbial activity anaerobic estuarine sediments sediment

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| AJ863416.1 | 124055 | 855.4 | 1659.7 | 2028.0 | 3130.0 | 925.0 | 2706.6 |
| AJ519989.1 | 76525 | 587.9 | 1532.1 | 2361.4 | 273.5 | 728.9 | 1008.4 |
| EF682964.1 | 244345 | 6670.4 | 7148.5 | 7677.6 | 6225.8 | 5331.0 | 6539.4 |
| DQ659212.1 | 218635 | 8285.9 | 7103.2 | 8188.0 | 8376.3 | 11195.6 | 8969.8 |
| DQ833483.1 | 172808 | 73.5 | 192.8 | 66.3 | 45.3 | 83.9 | 48.5 |
| GQ181039.1 | 569287 | 1531.6 | 1998.5 | 3513.9 | 4074.5 | 297.8 | 2202.0 |
| AJ536871.1 | 150596 | 2826.2 | 3437.2 | 4142.0 | 3068.5 | 5856.6 | 7311.7 |
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| FJ675586.1 | 529819 | 3632.3 | 4122.9 | 2486.5 | 3969.8 | 4211.5 | 4552.7 |
| CU926385.1 | 556012 | 9598.3 | 10650.3 | 13998.5 | 9863.3 | 12430.1 | 13412.6 |
| EU151438.1 | 265662 | 16931.5 | 18097.3 | 18402.4 | 14204.7 | 19192.4 | 17395.9 |
| FJ670842.1 | 521246 | 136.4 | 240.9 | 618.9 | 109.9 | 261.4 | 208.5 |
| AY546512.1 | 105121 | 1117.6 | 1624.8 | 701.1 | 1087.3 | 2887.2 | 1939.4 |
| EU340183.1 | 238503 | 4504.2 | 5824.1 | 5640.0 | 4640.2 | 6210.6 | 6037.8 |
| AB240487.1 | 145000 | 414.8 | 476.9 | 75.9 | 77.5 | 80.3 | 36.5 |
| AM934875.1 | 541193 | 9287.4 | 8791.8 | 5376.2 | 8667.7 | 7810.5 | 8900.0 |
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| FM873350.1 | 357693 | 4198.4 | 3393.1 | 6634.6 | 3476.0 | 2433.0 | 4743.9 |
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| AM400231.1 | 170471 | 969.6 | 1344.5 | 2960.9 | 351.9 | 708.2 | 3371.9 |
| AM697474.1 | 226122 | 3973.8 | 4934.1 | 2228.2 | 1258.0 | 1259.9 | 2537.3 |
| DQ984619.1 | 254845 | 4134.0 | 4432.8 | 7965.7 | 2667.3 | 3977.5 | 4517.6 |
| EF688352.1 | 239403 | 7472.3 | 7709.8 | 3516.7 | 7378.5 | 8927.6 | 7522.5 |
| EU665174.1 | 538171 | 4404.0 | 3426.8 | 5225.2 | 4650.0 | 1502.4 | 4551.0 |
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EU662620.1 gg_id:580798 Productivity- Chemolithoautotrophically Based Sulfidic Karst Systems floating microb
AF140004.1 gg_id:50378 Xanthomonas sp. str. ML-168b
DQ984626.1 gg_id:251179 YK oil-contaminated soil clone YK_62
AB240283.1 gg_id:143176 microbial structure Phragmites rhizosphere biofilm reed bed reactor laboratory clone
GQ354936.1 gg_id:566599 structure between two geochemically distinct springs Alum Rock Park spring clone M
AY922114.1 gg_id:113915 farm soil clone AKYH1464
DQ856527.1 gg_id:240149 intestinal microflora Chinese mitten crab (Eriocheir sinensis) clone C2G
FJ538122.1 gg_id:555549 metagenomics study rice treated milk vetch and no-tillage paddy field soil clone MBT
AY218741.1 gg_id:82032 penguin droppings sediments clone KD5-86
AM932272.1 gg_id:275388 Luteimonas sp. str. S22-40
FJ671430.1 gg_id:524537 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
DQ846687.1 gg_id:168681 Cibimonas vasta str. CC-YY255
AM939778.1 gg_id:263341 Dyella marensis str. CS5-B2
DQ125662.1 gg_id:130301 uranium contaminated soil clone AKAU3728
AM229325.1 gg_id:151541 Xanthomonas sp. str. T7-07
AF159581.1 gg_id:7897 Xanthomonas pv. campestris str. L2
EF018705.1 gg_id:209670 aspen rhizosphere clone Amb_16S_1156
AY328765.1 gg_id:88178 drinking water system simulator clone DSSD67
AM936392.1 gg_id:563988 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
AM935846.1 gg_id:566333 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
AB240508.1 gg_id:141461 microbial structure rhizosphere biofilm Sapporo root-base (80 160 mm) Phragmites S
EU202908.1 gg_id:331342 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo
AB161360.1 gg_id:99159 Lysobacter brunescens str. KCTC 12130
GU250851.1 gg_id:571730 Anaerobic biodegradation branched hydrocarbon biomarker analog pristane waste
GQ039397.1 gg_id:430138 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbu
EU276577.1 gg_id:362681 -DGGE and Approaches Analyze Effect Agricultural Practices on Soil agricultural soil c
AM934790.1 gg_id:572655 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
AM980880.1 gg_id:272797 Aspromonas sp. UK-29
FJ612198.1 gg_id:550784 and Biogeochemistry Dongping Lake Ecosystems lake water clone DP3.5.36
GQ264123.1 gg_id:585780 Structure Simulated Level Waste Site simulated level waste site clone WC3_60
EF174287.1 gg_id:177737 direct activated sludge last compost maturation stage clone J56-814
EU015100.1 gg_id:244451 Investigation estrogen-degrading bioreactors membrane bioreactor suspension and
EF540404.1 gg_id:222135 oil-shale semi-coke solid waste clone 3_16MK
EU421886.1 gg_id:260668 Un-culturable Indian Himalayas soil under glacier Lahaul-Spiti Valley clone KC-84
AB008508.1 gg_id:7884 ultramicrobacterium str. DY01
AY963358.1 gg_id:156208 structures and correlated ecological factors soils two evergreen broad-leaved forests
EF660758.1 gg_id:256944 Luteimonas aestuarii str. B9
DQ984608.1 gg_id:253110 LY oil-contaminated soil clone LYC172
AY218631.1 gg_id:203227 Penguin Droppings Sediments Ardley Island Antarctica clone KD4-32
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AJ604540.1 gg_id:102773 Collembola-associated clone za04

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| GQ354936.1 | 566599 | 3696.4 | 3335.7 | 2303.7 | 3403.8 | 1650.4 | 3035.1 |
| AY922114.1 | 113915 | 3370.3 | 4532.7 | 3232.2 | 888.9 | 2703.9 | 4741.5 |
| DQ856527.1 | 240149 | 2956.6 | 4242.8 | 3193.1 | 2824.4 | 1829.4 | 3114.4 |
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| AM932272.1 | 275388 | 401.9 | 1256.8 | 201.5 | 129.3 | 155.6 | 240.2 |
| FJ671430.1 | 524537 | 9133.8 | 9312.3 | 3574.2 | 4604.8 | 9363.6 | 5933.7 |
| DQ846687.1 | 168681 | 2321.2 | 3003.2 | 2209.5 | 2010.5 | 2956.6 | 3709.4 |
| AM939778.1 | 263341 | 5860.9 | 5311.8 | 10510.6 | 8401.1 | 5853.8 | 5250.6 |
| DQ125662.1 | 130301 | 3100.3 | 5412.8 | 7018.2 | 5616.0 | 9096.7 | 7420.2 |
| AM229325.1 | 151541 | 3313.4 | 4566.9 | 3677.7 | 1758.2 | 2014.7 | 7093.8 |
| AF159581.1 | 7897 | 2012.5 | 3717.4 | 912.7 | 2963.3 | 8196.0 | 6248.7 |
| EF018705.1 | 209670 | 180.6 | 247.9 | 112.7 | 217.7 | 199.7 | 904.6 |
| AY328765.1 | 88178 | 3916.8 | 3513.2 | 3443.9 | 4871.5 | 5564.9 | 6564.2 |
| AM936392.1 | 563988 | 2008.0 | 3073.7 | 2451.6 | 1844.2 | 2256.5 | 7277.8 |
| AM935846.1 | 566333 | 3010.3 | 3434.9 | 3541.2 | 4243.0 | 2704.6 | 4955.2 |
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| EU202908.1 | 331342 | 5638.7 | 4153.9 | 4823.9 | 9073.4 | 8781.5 | 8329.1 |
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| AM980880.1 | 272797 | 706.4 | 1818.3 | 3198.0 | 944.7 | 2056.1 | 5258.8 |
| FJ612198.1 | 550784 | 2811.1 | 2786.7 | 2197.1 | 999.5 | 747.6 | 1418.8 |
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| EF174287.1 | 177737 | 44.0 | 92.5 | 85.6 | 70.9 | 119.2 | 65.0 |
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AJ318204.1 gg_id:74443 Waste-gas biofilter clone BIyi3
AY294012.1 gg_id:136003 activated sludge enriched nonylphenol ethoxylates clone S3A1
FJ380131.1 gg_id:369488 ornithogenic Ross Sea region Antarctica AB1 soil clone 1/2/2D
AY372931.1 gg_id:142723 marine sponge Pseudoceratina clavata symbiont
GQ396926.1 gg_id:592861 Functional unvegetated perhumid recently-deglaciated soils do not correlate shifts s
AB274846.1 gg_id:163937 Variation predominant microbial consortium N.22 d on medium containg aromatic ai
FN563156.1 gg_id:590307 Impact changing HRT OLR on prokaryotes involved biomethanizitaion and fuzzy logic
FJ380132.1 gg_id:367350 ornithogenic Ross Sea region Antarctica AB1 soil clone 1/2/4D
EU236277.1 gg_id:297307 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone HgCo4
GU208439.1 gg_id:559226 Study on Sediment Dongping Lake sediment clone Fr3-6
GU444064.1 gg_id:514899 Effects amendments on fertility and microbial structure cucumber Cucumis sativus L
AM490086.1 gg_id:202402 Xanthomonas sp. str. P2-12-1
GQ009333.1 gg_id:500330 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
DQ228359.1 gg_id:142243 microbial compositions two subglacial possible role microbes chemical weathering p
AJ311653.1 gg_id:71415 Fulvimonas soli str. LMG 19981T
X95919.1 gg_id:7871 Xanthomonas axonopodis str. LMG 538-T
AM991237.1 gg_id:279266 Microbial groundwater and their potential use biomonitoring karst spring water clo
AF523890.1 gg_id:63325 forested wetland clone RCP1-10
GU250856.1 gg_id:580658 Anaerobic biodegradation branched hydrocarbon biomarker analog pristane waste
EU237492.1 gg_id:241713 Lysobacter sp. str. XM415
GQ250435.1 gg_id:585059 Xanthomonas sp. str. MJ09
EU662625.1 gg_id:583425 Productivity- Chemolithoautotrophically Based Sulfidic Karst Systems floating microb
EU134744.1 gg_id:253642 tallgrass prarie soil clone FFCH13468
DQ458014.1 gg_id:158419 acid mine drainage clone DX17
AB288902.1 gg_id:202916 termite gut homogenate clone BOf5-13
DQ001634.1 gg_id:157598 Microbial seeps asphalt seep clone E91-46
DQ660840.1 gg_id:238846 DongChuan copper pyrites PRC determined acid mine drainage (AMD) clone DCN-I-1
AM934799.1 gg_id:539344 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
AB245363.1 gg_id:147794 Lysobacter ginsengisoli str. Gsoil 357
EU104170.1 gg_id:351052 Evidence Comamonadaceae determinants settling performance activated sludge clo
FJ674765.1 gg_id:516410 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
EU834776.1 gg_id:513843 methods extraction nucleic acid activated lab scale EBPR-activated sludge clone L68
EU449638.1 gg_id:575082 Soil are Changed Agricultural Practices agricultural soil clone Plot4-2H07
AJ307936.1 gg_id:50142 derived microbial 'pearl'- community clone sipK9
EF157085.1 gg_id:237178 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon
EF492981.1 gg_id:235704 Iron-manganese Nodule and Its Surrounding Soil soil around iron-manganese nodule
GU208447.1 gg_id:580506 Study on Sediment Dongping Lake sediment clone Fr2-6
GU208400.1 gg_id:539242 Study on Sediment Dongping Lake sediment clone Fh2-4
EF648150.1 gg_id:257386 dynamics during produced water treatment aerobic activated sludge clone XJ100
EU134776.1 gg_id:244985 tallgrass prarie soil clone FFCH9956
GU169062.1 gg_id:584355 Biofilms formed on substances: response f conditions and carbon concentrations syr

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| AY294012.1 | 136003 | 1526.8 | 2447.5 | 1266.4 | 167.6 | 646.1 | 371.4 |
| FJ380131.1 | 369488 | 169.4 | 346.7 | 256.3 | 90.6 | 101.3 | 66.5 |
| AY372931.1 | 142723 | 2315.2 | 2760.0 | 3516.4 | 157.1 | 1216.8 | 5179.1 |
| GQ396926.1 | 592861 | 5561.3 | 6963.2 | 11789.5 | 6257.0 | 9658.8 | 8688.1 |
| AB274846.1 | 163937 | 102.2 | 175.3 | 90.7 | 118.0 | 90.2 | 100.0 |
| FN563156.1 | 590307 | 4026.9 | 3674.1 | 2578.0 | 999.8 | 2790.9 | 3823.4 |
| FJ380132.1 | 367350 | 27.9 | 48.7 | 1362.4 | 56.5 | 166.7 | 1518.2 |
| EU236277.1 | 297307 | 1817.8 | 3274.9 | 3753.8 | 1816.6 | 956.2 | 1589.0 |
| GU208439.1 | 559226 | 3801.0 | 5115.1 | 4856.8 | 4335.5 | 4077.8 | 5241.8 |
| GU444064.1 | 514899 | 3656.4 | 4166.2 | 6032.6 | 3170.6 | 3036.5 | 5016.5 |
| AM490086.1 | 202402 | 3339.5 | 4106.3 | 2363.1 | 895.8 | 2636.1 | 2578.1 |
| GQ009333.1 | 500330 | 6230.9 | 8367.8 | 5454.0 | 2925.6 | 8639.3 | 7962.5 |
| DQ228359.1 | 142243 | 92.6 | 131.5 | 377.7 | 189.8 | 179.0 | 243.0 |
| AJ311653.1 | 71415 | 1238.5 | 2275.6 | 3815.3 | 1414.8 | 7972.7 | 3743.2 |
| X95919.1 | 7871 | 2389.3 | 2176.7 | 1136.0 | 2229.5 | 781.6 | 2021.6 |
| AM991237.1 | 279266 | 6462.3 | 5700.6 | 7737.9 | 5181.4 | 7556.4 | 6193.4 |
| AF523890.1 | 63325 | 468.5 | 788.9 | 772.0 | 193.1 | 336.1 | 664.9 |
| GU250856.1 | 580658 | 1180.4 | 550.3 | 2369.9 | 513.4 | 425.5 | 1300.0 |
| EU237492.1 | 241713 | 4137.1 | 4428.8 | 5828.0 | 4975.4 | 4899.3 | 3682.0 |
| GQ250435.1 | 585059 | 1407.0 | 3059.2 | 1007.4 | 324.1 | 645.2 | 1499.9 |
| EU662625.1 | 583425 | 1164.5 | 987.1 | 3250.2 | 652.4 | 1053.2 | 1316.6 |
| EU134744.1 | 253642 | 7126.8 | 7710.5 | 11645.6 | 10369.0 | 9823.0 | 11246.2 |
| DQ458014.1 | 158419 | 7220.1 | 7658.7 | 7437.8 | 7512.5 | 3882.3 | 4880.6 |
| AB288902.1 | 202916 | 11190.8 | 12104.1 | 6364.5 | 8965.1 | 13433.4 | 10801.4 |
| DQ001634.1 | 157598 | 11.6 | 32.4 | 23.7 | 34.0 | 71.2 | 43.6 |
| DQ660840.1 | 238846 | 871.0 | 1370.2 | 1998.0 | 1621.9 | 2758.1 | 1962.4 |
| AM934799.1 | 539344 | 8937.7 | 5291.4 | 6926.3 | 6812.5 | 8829.8 | 8149.4 |
| AB245363.1 | 147794 | 1370.3 | 1927.1 | 4139.3 | 1372.2 | 1224.2 | 2495.0 |
| EU104170.1 | 351052 | 5787.9 | 6999.3 | 7625.0 | 6059.8 | 5575.8 | 6186.8 |
| FJ674765.1 | 516410 | 4879.4 | 4486.1 | 2779.7 | 4861.9 | 4744.8 | 3796.8 |
| EU834776.1 | 513843 | 2486.5 | 4222.0 | 3778.1 | 1828.2 | 3253.7 | 4467.1 |
| EU449638.1 | 575082 | 8175.4 | 9072.3 | 10150.7 | 5915.7 | 13440.1 | 9329.5 |
| AJ307936.1 | 50142 | 162.2 | 201.4 | 127.9 | 230.8 | 485.5 | 174.2 |
| EF157085.1 | 237178 | 3182.5 | 4424.7 | 4394.1 | 1961.6 | 1583.2 | 4801.5 |
| EF492981.1 | 235704 | 4243.9 | 4060.2 | 5959.3 | 5303.4 | 5528.1 | 6260.5 |
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| EU134776.1 | 244985 | 7278.3 | 8382.5 | 5658.6 | 2376.5 | 3840.6 | 7292.1 |
| GU169062.1 | 584355 | 3977.4 | 4222.1 | 2376.7 | 3366.0 | 2984.5 | 2969.3 |

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EU775768.1 gg_id:323292 Horse feces clone horsem_aai94g01
AY102313.1 gg_id:65469 clone a13106
EU134748.1 gg_id:249305 tallgrass prarie soil clone FFCH14140
GQ129910.1 gg_id:457990 Genetic inventory 'JPL-SAF' during MSL mission spacecraft assembly clean room floc
GQ396811.1 gg_id:511988 Functional unvegetated perhumid recently-deglaciated soils do not correlate shifts s
FJ598363.1 gg_id:512980 Study Prokaryotic Some Selected Niches Western Ghats India water clone BCWCWP1
AB118236.1 gg_id:100967 Halothiobacillus sp. str. SO07
FJ947035.1 gg_id:542102 Study Prokaryotic Some Selected Niches Western Ghats India sediment clone BCWCS
GU144259.1 gg_id:542178 Xanthomonas arboricola pv. poinsettiicola str. LMG 8675
Y10754.1 gg_id:7889 Xanthomonas hyacinthi str. LMG 739 T
AY247064.1 gg_id:83056 Xanthomonas translucens pv. graminis
AF000946.1 gg_id:7876 Xanthomonas pv. campestris str. Xc17
Y10766.1 gg_id:7862 Xanthomonas sacchari str. LMG 471 T
Y10756.1 gg_id:7878 Xanthomonas melonis str. LMG 8670 T
NR_029332.1 gg_id:587741 Xanthomonas theicola str. TC1; LMG 8684
EF101975.1 gg_id:186642 Xanthomonas campestris str. EUS14
X99298.1 gg_id:7880 Xanthomonas campestris str. LMG 726
GU086451.1 gg_id:544600 Xanthomonas campestris str. N5
AY253329.1 gg_id:85823 Xanthomonas translucens pv. poae
AF290420.1 gg_id:73182 Xanthomonas campestris 19316a
NZ_ACHS01000481.1 gg_id:531786 Xanthomonas campestris pv. vasculorum str. NCPPB702
AY994101.1 gg_id:156291 Xanthomonas translucens str. P25
NR_026387.1 gg_id:572380 Xanthomonas cucurbitae str. LMG 690
AY572961.1 gg_id:99262 Xanthomonas translucens pv. poae str. ATCC 33804
EU723184.1 gg_id:344976 Xanthomonas sp. str. kmd_489
GU373652.1 gg_id:527773 Xanthomonas pv. campestris str. XCC10
X95918.1 gg_id:7894 Xanthomonas albilineans str. LMG 494-T
FJ606765.1 gg_id:539828 Xanthomonas arboricola pv. pruni str. LMG852
Y10761.1 gg_id:7857 Xanthomonas vesicatoria str. LMG 911 T
Y10764.1 gg_id:7856 Xanthomonas bromi str. LMG 947 T
X95922.1 gg_id:7861 Xanthomonas populi str. LMG 5743-T
NC_007705.1 gg_id:152746 Xanthomonas pv. oryzae str. MAFF 311018
EU364838.1 gg_id:564962 Xanthomonas pv. campestris Xcc-H9
EU741037.1 gg_id:338929 Xanthomonas sp. str. FeL06
AY576651.1 gg_id:105820 Xanthomonas axonopodis pv. syngonii str. X191
AY576639.1 gg_id:105873 Xanthomonas axonopodis pv. dieffenbachiae str. LMG8664
AY576652.1 gg_id:105970 Xanthomonas axonopodis pv. syngonii str. LMG9055
AF442744.1 gg_id:68801 Xanthomonas axonopodis pv. citri str. Lw
EF101979.1 gg_id:191402 Xanthomonas axonopodis str. MSF
Y10765.1 gg_id:7883 Xanthomonas codiaei str. LMG 8678 T
AF442739.1 gg_id:68804 Xanthomonas axonopodis pv. aurantifolii str. X84 pv.

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| EU775768.1 | 323292 | 3302.7 | 5856.4 | 6518.5 | 4280.5 | 2537.5 | 3169.6 |
| AY102313.1 | 65469 | 46.9 | 49.8 | 42.2 | 62.4 | 69.1 | 36.0 |
| EU134748.1 | 249305 | 10328.7 | 9021.6 | 7042.2 | 8391.3 | 4775.4 | 7808.0 |
| GQ129910.1 | 457990 | 94.5 | 237.3 | 647.8 | 168.8 | 162.0 | 131.5 |
| GQ396811.1 | 511988 | 7016.1 | 9206.6 | 6486.5 | 5149.6 | 3763.0 | 4220.8 |
| FJ598363.1 | 512980 | 1494.5 | 1661.6 | 2941.0 | 1135.2 | 706.8 | 1841.2 |
| AB118236.1 | 100967 | 3989.1 | 3087.9 | 3689.2 | 3241.7 | 994.4 | 2061.4 |
| FJ947035.1 | 542102 | 6503.4 | 5944.0 | 4924.5 | 6979.7 | 6998.7 | 8157.2 |
| GU144259.1 | 542178 | 979.2 | 1497.0 | 1582.6 | 1292.5 | 985.7 | 1592.2 |
| Y10754.1 | 7889 | 1715.0 | 3068.5 | 2224.6 | 1095.1 | 4031.8 | 4123.4 |
| AY247064.1 | 83056 | 3794.6 | 4051.1 | 5326.5 | 3462.5 | 4412.2 | 6599.2 |
| AF000946.1 | 7876 | 1613.0 | 2244.0 | 2407.8 | 1254.0 | 1307.2 | 3024.2 |
| Y10766.1 | 7862 | 2334.8 | 3737.7 | 3145.6 | 1421.5 | 2084.0 | 3730.4 |
| Y10756.1 | 7878 | 1273.2 | 2141.7 | 2437.2 | 1333.8 | 926.4 | 1841.0 |
| NR_029332.1 | 587741 | 2851.3 | 3321.3 | 1137.3 | 3668.7 | 1802.0 | 1050.1 |
| EF101975.1 | 186642 | 7498.8 | 8777.4 | 6303.7 | 8270.0 | 11636.9 | 7876.2 |
| X99298.1 | 7880 | 4224.5 | 6383.1 | 7015.5 | 3413.9 | 6526.8 | 8967.7 |
| GU086451.1 | 544600 | 1741.9 | 2208.2 | 2487.2 | 1259.7 | 1328.0 | 3035.5 |
| AY253329.1 | 85823 | 2107.5 | 3957.0 | 3704.2 | 1453.5 | 2711.2 | 6605.8 |
| AF290420.1 | 73182 | 8220.8 | 8603.1 | 7354.7 | 8071.7 | 13076.0 | 11393.2 |
| NZ_ACHS01000481.1 | 531786 | 507.4 | 975.9 | 1005.8 | 869.8 | 222.7 | 713.9 |
| AY994101.1 | 156291 | 3002.5 | 4745.7 | 4493.4 | 1940.0 | 3690.8 | 7949.5 |
| NR_026387.1 | 572380 | 3665.8 | 4500.1 | 3479.4 | 2571.2 | 2074.3 | 4062.9 |
| AY572961.1 | 99262 | 2592.2 | 4401.1 | 4347.0 | 2112.9 | 2820.0 | 6714.6 |
| EU723184.1 | 344976 | 3599.8 | 4885.6 | 2864.9 | 1890.5 | 2698.7 | 6044.5 |
| GU373652.1 | 527773 | 12655.6 | 11245.7 | 5757.6 | 8081.4 | 10200.2 | 8966.7 |
| X95918.1 | 7894 | 1771.5 | 2924.4 | 3998.4 | 1522.5 | 1422.1 | 4095.2 |
| FJ606765.1 | 539828 | 1114.5 | 1464.5 | 1464.3 | 846.2 | 787.2 | 1514.0 |
| Y10761.1 | 7857 | 1680.4 | 2704.3 | 3312.0 | 1505.8 | 2348.6 | 3037.4 |
| Y10764.1 | 7856 | 457.7 | 790.9 | 1097.9 | 561.0 | 428.6 | 766.9 |
| X95922.1 | 7861 | 3755.8 | 4179.5 | 4090.3 | 3008.0 | 3195.3 | 4678.3 |
| NC_007705.1 | 152746 | 509.9 | 983.8 | 754.0 | 1113.3 | 1156.1 | 501.5 |
| EU364838.1 | 564962 | 11040.6 | 10985.7 | 6378.9 | 7896.5 | 9646.5 | 8700.1 |
| EU741037.1 | 338929 | 3903.1 | 5693.4 | 4704.4 | 2480.9 | 5008.4 | 6306.6 |
| AY576651.1 | 105820 | 714.1 | 1255.3 | 1289.9 | 894.7 | 1289.0 | 885.6 |
| AY576639.1 | 105873 | 859.4 | 1689.9 | 2005.0 | 1248.3 | 1701.9 | 817.0 |
| AY576652.1 | 105970 | 4179.6 | 4346.0 | 3166.0 | 3929.6 | 5373.7 | 5319.0 |
| AF442744.1 | 68801 | 830.9 | 1758.3 | 1931.8 | 1063.7 | 1084.7 | 798.4 |
| EF101979.1 | 191402 | 15966.9 | 16634.4 | 14954.7 | 12435.5 | 17265.9 | 15478.2 |
| Y10765.1 | 7883 | 895.7 | 1641.8 | 1920.2 | 852.6 | 1083.6 | 771.7 |
| AF442739.1 | 68804 | 1784.8 | 3297.5 | 3899.6 | 2940.9 | 3889.8 | 2396.0 |

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| s__Xanthomonas axonopodis | 16163 |
| s__Xanthomonas axonopodis | 16425 |
| s__Xanthomonas axonopodis | 16429 |
| s__Xanthomonas axonopodis | 16501 |
| s__Xanthomonas axonopodis | 16894 |
| s__Xanthomonas axonopodis | 16916 |
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| s__Xanthomonas oryzae | 15986 |
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| s__Pseudomonas boreopolis | 15998 |
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AY576650.1 gg_id:105665 Xanthomonas axonopodis pv. syngonii str. X430
X99297.1 gg_id:7901 Xanthomonas campestris str. LMG 682
AY576648.1 gg_id:101916 Xanthomonas axonopodis pv. dieffenbachiae str. X195
EF989734.1 gg_id:258137 Xanthomonas axonopodis pv. spondiae str. CFBP 2547
EF101977.1 gg_id:174832 Xanthomonas axonopodis str. IP1-36
AY576642.1 gg_id:100921 Xanthomonas axonopodis pv. dieffenbachiae str. ATCC 23379; LMG 7399
X95920.1 gg_id:7869 Xanthomonas fragariae str. LMG 708-T
AY576640.1 gg_id:100609 Xanthomonas axonopodis pv. dieffenbachiae str. LMG7400
GU144258.1 gg_id:578397 Xanthomonas axonopodis pv. poinsettiicola str. LMG 849
AY576645.1 gg_id:101405 Xanthomonas axonopodis pv. dieffenbachiae str. X1688
AF442743.1 gg_id:68800 Xanthomonas axonopodis pv. citri str. MA
AF442740.1 gg_id:68803 Xanthomonas axonopodis pv. aurantifolii str. X341
AY576641.1 gg_id:100760 Xanthomonas axonopodis pv. dieffenbachiae str. LMG695
GU112762.1 gg_id:572972 Xanthomonas campestris pv. mangiferaeindicae str. Xcm3
AF442742.1 gg_id:68799 Xanthomonas axonopodis pv. citri str. MI
AE013598.1 gg_id:112369 Xanthomonas pv. oryzae str. KACC10331
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AY855874.1 gg_id:154350 Xanthomonas translucens pv. graminis Xtg31
AY855844.1 gg_id:156167 Xanthomonas translucens pv. arrhenatheri str. LMG 727
AY855848.1 gg_id:153580 Xanthomonas translucens pv. graminis Xtg03
AY855846.1 gg_id:153182 Xanthomonas translucens pv. graminis Xtg01
AY855872.1 gg_id:152764 Xanthomonas translucens pv. graminis Xtg29
AY855857.1 gg_id:155672 Xanthomonas translucens pv. graminis Xtg12
AY855871.1 gg_id:151132 Xanthomonas translucens pv. graminis Xtg28
AY855869.1 gg_id:153002 Xanthomonas translucens pv. graminis Xtg25
AY855862.1 gg_id:151559 Xanthomonas translucens pv. graminis Xtg18
AB246809.1 gg_id:149852 Pseudomonas boreopolis str. Q-5
AJ864722.1 gg_id:199736 Pseudomonas boreopolis str. S2-s-PMWA-6
AF203388.1 gg_id:21170 Xylella fastidiosa str. PL.788; ATCC35871
AF203392.1 gg_id:25098 Xylella fastidiosa str. PE.PLS
EU526732.1 gg_id:259129 Xylella fastidiosa str. EO
AF159572.1 gg_id:7844 Xylella fastidiosa str. PCE-FG; ATCC35881
EF433940.1 gg_id:214495 Xylella fastidiosa CaVc3
EF433931.1 gg_id:208471 Xylella fastidiosa VvIIc2
DQ991191.1 gg_id:197140 Xylella fastidiosa str. 4BD7
AF159576.1 gg_id:7848 Xylella fastidiosa str. Mul-2
EF157080.1 gg_id:243037 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon
EF095437.1 gg_id:579168 Application and DGGE fingerprinting detection microbial Malaysian sweet crude oil cl
EF095417.1 gg_id:581718 Application and DGGE fingerprinting detection microbial Malaysian sweet crude oil cl
EF095420.1 gg_id:571046 Application and DGGE fingerprinting detection microbial Malaysian sweet crude oil cl
AY770703.1 gg_id:111106 sea urchin Paracentrotus lividus clone PlS55

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|---|---|---|---|---|---|---|---|
| AY576650.1 | 105665 | 1154.2 | 1822.4 | 2243.9 | 810.2 | 1465.0 | 1485.7 |
| X99297.1 | 7901 | 1709.3 | 3293.0 | 3711.8 | 2489.6 | 2524.0 | 2803.6 |
| AY576648.1 | 101916 | 1902.3 | 3649.9 | 4335.2 | 1192.9 | 2093.7 | 2794.8 |
| EF989734.1 | 258137 | 7427.3 | 9545.3 | 3598.2 | 6703.4 | 8259.4 | 7312.5 |
| EF101977.1 | 174832 | 14108.4 | 13906.6 | 13401.4 | 11898.7 | 14184.9 | 12196.6 |
| AY576642.1 | 100921 | 1603.4 | 3056.5 | 4030.8 | 1742.7 | 3195.4 | 2652.8 |
| X95920.1 | 7869 | 2875.5 | 4597.6 | 1647.9 | 3450.8 | 1946.2 | 4208.9 |
| AY576640.1 | 100609 | 9868.7 | 11970.6 | 8476.6 | 8043.6 | 10726.2 | 9980.1 |
| GU144258.1 | 578397 | 2504.1 | 4416.1 | 3834.6 | 2704.7 | 2777.3 | 2724.6 |
| AY576645.1 | 101405 | 1398.4 | 1808.5 | 1791.9 | 997.8 | 4651.4 | 2775.0 |
| AF442743.1 | 68800 | 825.1 | 1770.2 | 1936.8 | 1058.9 | 1072.7 | 817.4 |
| AF442740.1 | 68803 | 6678.0 | 8381.8 | 3068.1 | 4853.3 | 8900.6 | 8027.0 |
| AY576641.1 | 100760 | 1257.7 | 2520.0 | 3086.1 | 1725.0 | 3028.7 | 1948.8 |
| GU112762.1 | 572972 | 1407.4 | 2549.4 | 2113.5 | 1523.5 | 1144.9 | 1442.7 |
| AF442742.1 | 68799 | 1516.1 | 3194.2 | 3278.5 | 2244.9 | 2401.4 | 2080.3 |
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AY829009.1 gg_id:131064 Methylothermus thermalis str. MYHT
AATS01000005.1 gg_id:164411 Mariprofundus ferrooxydans str. PV-1
FJ205309.1 gg_id:536608 Prokaryotic deep-sea region East Lau Spreading Centre active hydrothermal field sedi
FJ905694.1 gg_id:556057 s Tonga-Kermadec iron oxide sediments Volcano 1 Tonga Arc clone V1F7b
FJ497659.1 gg_id:594030 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun
FJ905704.1 gg_id:569688 s Tonga-Kermadec iron oxide sediments Volcano 1 Tonga Arc clone V1F25b
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FJ535254.1 gg_id:510570 within iron-containing flocculent mats submarine volcanoes along Kermadec Arc iron
FJ905673.1 gg_id:544778 s Tonga-Kermadec iron oxide chimney-like structure on Volcano 19 Tonga Arc clone V
AY458631.1 gg_id:101443 marine waters clone EBAC750-03B02
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EF645961.1 gg_id:253216 Potential interactions particle- anammox and archaeal partners namibian Namibian u
GQ337084.1 gg_id:554277 Hydrography shapes biogeography deep Arctic Ocean water depth 1191m clone NB1
AF355047.1 gg_id:35861 marine clone Arctic96B-7
GQ346885.1 gg_id:549072 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
EU035866.2 gg_id:343475 Insight microbial structure Norwegian deep-water water deep-sea coral reef off Nor
EF572490.1 gg_id:232479 Coco's Island site 23 marine clone S23_589
EF573580.1 gg_id:228552 Coco's Island site 23 marine clone S23_1679
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DQ009458.1 gg_id:121667 bacterioplankton clone SPOTSMAY03_500m4
EF645950.1 gg_id:240496 Potential interactions particle- anammox and archaeal partners namibian Namibian u
AY033318.1 gg_id:68979 marine bacterioplankton clone MB13C05
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EF571979.1 gg_id:230588 Coco's Island site 23 marine clone S23_78
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AB292141.1 gg_id:200579 Microbial Subseafloor Suiyo Seamount hydrothermal fluid clone SSmAB08-64
AF406544.1 gg_id:60631 bacterioplankton clone AEGEAN_225
GQ348843.1 gg_id:583337 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
GQ347305.1 gg_id:592130 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
GQ347277.1 gg_id:538806 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
GQ350783.1 gg_id:584685 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
GQ350921.1 gg_id:566050 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
GQ347000.1 gg_id:583074 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
EU491156.1 gg_id:272826 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak
GQ337151.1 gg_id:542779 Hydrography shapes biogeography deep Arctic Ocean water depth 1000m clone CB:
GQ375269.1 gg_id:527667 Hydrography shapes biogeography deep Arctic Ocean water depth 1000 m clone CB
AY907734.1 gg_id:137390 identification picoplankton contrasting waters Arabian Sea water clone A313015
FJ745056.1 gg_id:557852 Transporter genes expressed coastal response dissolved organic carbon surface wate
AY907788.1 gg_id:137418 identification picoplankton contrasting waters Arabian Sea water clone A713003
AY907769.1 gg_id:137410 identification picoplankton contrasting waters Arabian Sea water clone A712021
FJ264782.1 gg_id:347223 Manganese and Iron Dependent Anaerobic Oxidation Methane methane seep sedime
DQ351751.1 gg_id:146140 Microbial Adherent Sediment Particles Heavy Metal Contaminated North Sea Surfac
GQ259264.1 gg_id:576577 Microbial activities coastal marine sediments and water column Svalbard deep sedir
FJ716273.1 gg_id:568134 Chlorobi dominate shal chemocline Bahamas Sawmill Sink column 10.3 m water dept
AY344400.1 gg_id:91672 Lake Kauhako 30 m clone K2-30-7
AB193918.1 gg_id:108876 deep-sea vent clone Sc-NB04
GQ350808.1 gg_id:562101 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
GQ349373.1 gg_id:546851 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
GQ350951.1 gg_id:590939 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
GQ349359.1 gg_id:573931 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
GQ347432.1 gg_id:550150 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
GQ349016.1 gg_id:568455 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
AF275926.2 gg_id:102419 anaerobic digester clone AB16
EU592362.1 gg_id:590482 Seasonal changes Salton Sea hypersaline water clone SSW63Au
EU385747.1 gg_id:259814 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S
EU385761.1 gg_id:276241 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S
FJ746183.1 gg_id:563570 Microbial oligotrophic marine sediments: South Pacific Gyre ocean sediment 5306 m
EU181491.1 gg_id:255266 Prokaryotic enhanced organic matter remineralization continental margin marine se
DQ513074.1 gg_id:161026 Microbial life fluids ridge flank crustal fluid clone FS266-18B-03
DQ513039.1 gg_id:159771 Microbial life fluids ridge flank crustal fluid clone FS142-62B-02
AY907781.1 gg_id:137211 identification picoplankton contrasting waters Arabian Sea water clone A712049
GQ351198.1 gg_id:579754 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Eastern
DQ009452.1 gg_id:127630 bacterioplankton clone SPOTSMAY03_150m11
AF406551.1 gg_id:103827 complex marine community d at depth 200 m North Aegean Sea (Station 3) clone AE
GQ337246.1 gg_id:568401 Hydrography shapes biogeography deep Arctic Ocean water depth 1000m clone CB:
GQ375271.1 gg_id:515331 Hydrography shapes biogeography deep Arctic Ocean water depth 1000 m clone CB

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| DQ513039.1 | 159771 | 13707.9 | 14467.2 | 5688.0 | 10893.8 | 12444.6 | 11510.4 |
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AB193937.1 gg_id:108899 deep-sea vent clone Sd-NB05
GQ337265.1 gg_id:590436 Hydrography shapes biogeography deep Arctic Ocean water depth 428m clone CB18
AB187008.1 gg_id:106295 Suiyo seamount hydrothermal vent water 0.2micro-m filterable fraction clone SSM-N
AB187006.1 gg_id:105980 Suiyo seamount hydrothermal vent water 0.2micro-m filterable fraction clone SSM-N
FJ746090.1 gg_id:567620 Microbial oligotrophic marine sediments: South Pacific Gyre ocean sediment 5306 m
EF573230.1 gg_id:231910 Coco's Island site 23 marine clone S23_1329
DQ889875.1 gg_id:171291 natural product producing octocoral Erythropodium caribaeorum clone EC214
EU491524.1 gg_id:270326 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR4C
EF018452.1 gg_id:206024 aspen rhizosphere clone Amb_16S_1077
EF494370.1 gg_id:222885 Nunnock River granitic landscape clone NR.1.116
AM997686.1 gg_id:571356 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A
FJ205353.1 gg_id:510135 Prokaryotic deep-sea hydrothermal region East Lau Spreading Centre deep marine se
EU374029.1 gg_id:263284 southern Cretan margin (eastern Mediterranean Sea) canyon and slope sediment clc
EU048632.1 gg_id:245214 Microbial surface marine sediment Xisha Trough South China Sea clone MD2902-B28
EU491675.1 gg_id:260885 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39
AB530197.1 gg_id:537501 Monitoring Suez and Tokyo bays based on analyses marine sediment clone Suez..Bac
EU491531.1 gg_id:267736 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR4C
DQ988317.1 gg_id:189693 Microbial lab-scale A1-A2-O fixed biofilm system coking wastewater treatment with
AM935293.1 gg_id:564786 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
EU491632.1 gg_id:272860 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39
AM935547.1 gg_id:545441 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
DQ395515.1 gg_id:151247 deep-sea octacoral clone ctg_CGOCA20
EU135311.1 gg_id:246322 tallgrass prarie soil clone FFCH7260
GU454958.1 gg_id:530796 Understanding short-chain fatty acids accumulation enhanced alkaline digestion: kir
AY218601.1 gg_id:81510 penguin droppings sediments clone KD3-113
AJ863240.1 gg_id:120514 poplar tree microcosm bulk soil flooded clone 26BSF3
DQ248296.1 gg_id:143458 carbon tetrachloride contaminated soil clone TF2
GQ116329.1 gg_id:384169 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw691e06
GQ002367.1 gg_id:507292 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu176f02
FJ455888.1 gg_id:512694 Variations archaeal and sulfate-methane transition zone continental margin sediment
EU048664.1 gg_id:246357 and archaeal surface marine sediment Slope South China Sea clone MD2896-B3
AF254404.1 gg_id:41280 4MB-degrading consortium clone UASB_TL26
EU344940.1 gg_id:262115 Hepialus gonggaensis guts equalized library larval gut clone Hg5-30
DQ990931.2 gg_id:184899 Microbial Rock Varnish Yungay Atacama Desert Chile rock varnish clone AYRV1-033
EF516747.1 gg_id:225432 grassland soil clone FCPS434
EF018189.1 gg_id:206828 aspen rhizosphere clone Amb_16S_532
EF018382.1 gg_id:205209 aspen rhizosphere clone Amb_16S_760
AB179676.1 gg_id:200752 Clones Deep-Groundwater Microorganisms That Pass through 0.2-Micrometer-Pore-
EU246293.1 gg_id:250492 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-P6-E01
EF018234.1 gg_id:213599 aspen rhizosphere clone Amb_16S_585
EU335431.1 gg_id:250861 Changes microbial metabolic and along hydrogeochemically variable profile unsatura

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AJ519639.1 gg_id:77042 uranium tailings soil clone Sh765B-AG-45
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AM991193.1 gg_id:279508 Microbial groundwater and their potential use biomonitoring karst spring water clo
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EU881156.1 gg_id:306708 Karst region primary forest soil clone KPF200711-139
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GU444065.1 gg_id:525151 Effects amendments on fertility and microbial structure cucumber Cucumis sativus L
AB487162.1 gg_id:592058 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNIR0
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EU135321.1 gg_id:249043 tallgrass prarie soil clone FFCH6980
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AB093305.1 gg_id:84017 Brachyspira innocens D3D/6/15
AB093307.1 gg_id:83843 Brachyspira innocens D7D/6/15
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AY514024.1 gg_id:100496 Brachyspira pilosicoli Br1622
AY312492.1 gg_id:88867 Brachyspira murdochii str. 56-150
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U14933.1 gg_id:3783 Brachyspira innocens str. 983-90 (group II)
DQ922565.1 gg_id:171642 Brachyspira hyodysenteriae str. 91507-8x/01 (T21)
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EF164966.1 gg_id:254733 Brachyspira intermedia AN3536/03
AB093323.1 gg_id:84667 Brachyspira innocens D1A/11/9
AB093308.1 gg_id:82681 Brachyspira innocens D9D/6/15
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AB093304.1 gg_id:84263 Brachyspira innocens D2A/6/15

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| EU881156.1 | 306708 | 996.1 | 2919.4 | 5167.9 | 688.2 | 743.5 | 1444.3 |
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| AB120010.1 | 100441 | 7202.2 | 6973.5 | 7166.2 | 8571.4 | 9672.2 | 9217.9 |
| FM178385.1 | 350706 | 7474.9 | 7450.7 | 7272.6 | 8307.1 | 11113.9 | 10350.2 |
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| EU819059.1 | 369616 | 8899.9 | 9457.1 | 9074.3 | 10385.5 | 11972.3 | 11151.2 |
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| AY514024.1 | 100496 | 20113.8 | 20532.0 | 14991.2 | 18725.3 | 17537.6 | 17689.2 |
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| k__Bacteria | k__Bacteria | p__Spirochaetes | c__Leptospirae |
| k__Bacteria | k__Bacteria | p__Spirochaetes | c__Leptospirae |
| k__Bacteria | k__Bacteria | p__Spirochaetes | c__Leptospirae |
| k__Bacteria | k__Bacteria | p__Spirochaetes | c__Leptospirae |

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| o__Brachyspirales | f__Brachyspiraceae |
| o__Brachyspirales | f__Brachyspiraceae |
| o__Brachyspirales | f__Brachyspiraceae |
| o__Brachyspirales | f__Brachyspiraceae |
| o__Brachyspirales | f__Brachyspiraceae |
| o__Brachyspirales | f__Brachyspiraceae |
| o__IF025 | f__unclassified |
| o__IF025 | f__unclassified |
| o__IF025 | f__unclassified |
| o__IF025 | f__unclassified |
| o__IF025 | f__unclassified |
| o__unclassified | f__unclassified |
| o__Leptospirales | f__Leptospiraceae |
| o__Leptospirales | f__Leptospiraceae |
| o__Leptospirales | f__Leptospiraceae |
| o__Leptospirales | f__Leptospiraceae |
| o__Leptospirales | f__Leptospiraceae |
| o__Leptospirales | f__Leptospiraceae |
| o__Leptospirales | f__Leptospiraceae |
| o__Leptospirales | f__Leptospiraceae |
| o__Leptospirales | f__Leptospiraceae |
| o__Leptospirales | f__Leptospiraceae |
| o__Leptospirales | f__Leptospiraceae |
| o__Leptospirales | f__Leptospiraceae |
| o__Leptospirales | f__Leptospiraceae |
| o__Leptospirales | f__Leptospiraceae |
| o__Leptospirales | f__Leptospiraceae |
| o__Leptospirales | f__Leptospiraceae |
| o__Leptospirales | f__Leptospiraceae |
| o__Leptospirales | f__Leptospiraceae |
| o__Leptospirales | f__Leptospiraceae |
| o__Leptospirales | f__Leptospiraceae |
| o__Leptospirales | f__Leptospiraceae |
| o__Leptospirales | f__Leptospiraceae |
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| o__Leptospirales | f__Leptospiraceae |
| o__Leptospirales | f__Leptospiraceae |
| o__Leptospirales | f__Leptospiraceae |
| o__Leptospirales | f__Leptospiraceae |
| o__Leptospirales | f__Leptospiraceae |
| o__Leptospirales | f__Leptospiraceae |

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g__sfB
g__sfA
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g__Leptospira
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g__Leptospira

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| s__unclassified | 76798 |
| s__unclassified | 76968 |
| s__unclassified | 77008 |
| s__unclassified | 77029 |
| s__unclassified | 76295 |
| s__unclassified | 76289 |
| s__unclassified | 76655 |
| s__unclassified | 76779 |
| s__unclassified | 77087 |
| s__unclassified | 76082 |
| s__unclassified | 76848 |
| s__Leptonema illini | 76617 |
| s__Leptospira alexanderi | 76297 |
| s__Leptospira biflexa | 76467 |
| s__Leptospira biflexa | 76602 |
| s__Leptospira biflexa | 77020 |
| s__Leptospira borgpetersenii | 76904 |
| s__Leptospira borgpetersenii | 77063 |
| s__Leptospira borgpetersenii | 77126 |
| s__Leptospira inadai | 77107 |
| s__Leptospira interrogans | 76236 |
| s__Leptospira kirschneri | 75973 |
| s__Leptospira kirschneri | 76243 |
| s__Leptospira kirschneri | 76403 |
| s__Leptospira kirschneri | 76724 |
| s__Leptospira licerasiae | 76569 |
| s__Leptospira licerasiae | 76716 |
| s__Leptospira noguchii | 76018 |
| s__Leptospira santarosai | 76164 |
| s__Leptospira weilii | 76785 |
| s__unclassified | 76034 |
| s__unclassified | 76146 |
| s__unclassified | 76203 |
| s__unclassified | 76227 |
| s__unclassified | 76340 |
| s__unclassified | 76404 |
| s__unclassified | 76469 |
| s__unclassified | 76500 |
| s__unclassified | 76502 |
| s__unclassified | 76509 |

AB093320.1 gg_id:85067 Brachyspira innocens D6B/10/25
U14920.1 gg_id:3770 Brachyspira innocens str. B256 (group III)
EF164976.1 gg_id:240387 Brachyspira innocens AN4113/03
AB079583.1 gg_id:77935 Brachyspira ibaraki str. HIS24/11/99
EF164969.1 gg_id:257537 Brachyspira intermedia AN5112/03
FJ461892.1 gg_id:569032 Microbial ecology industrial digestor mesophilic anaerobic reactor fed effluent chemi
EU245543.1 gg_id:249265 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M2-H0
AY605147.1 gg_id:104927 microbial mat clone IF004
AY605151.1 gg_id:100106 microbial mat clone IF025
AY605148.1 gg_id:105069 microbial mat clone IF007
EU245476.1 gg_id:250068 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M2-A0
DQ329632.1 gg_id:159296 Guerrero Negro hypersaline microbial mat clone 05D2Z42
Z21632.1 gg_id:4396 Leptonema illini str. 3055
DQ991481.1 gg_id:186857 Leptospira alexanderi serovar Mengla str. A85
NC_010842.1 gg_id:304981 Leptospira biflexa serovar strain 'Patoc (Ames)' str. Patoc 1 (Ames)
Z12821.1 gg_id:4383 Leptospira biflexa serovar str. patoc Patoc 1
Z21638.1 gg_id:4384 Leptospira wolbachii str. BIFLEXA CDC
EF537007.1 gg_id:229607 Leptospira borgpetersenii serovar Javanica 969
FJ154592.1 gg_id:343791 Leptospira borgpetersenii serovar Mini str. Sari
Z21630.1 gg_id:4348 Leptospira borgpetersenii str. JAVANICA VELDRAT BATAVIA 46
AY631891.1 gg_id:107131 Leptospira inadai serovar Aguarana str. MW-4
AM050566.1 gg_id:138386 Leptospira interrogans serovar Canicola str. Utrecht V
FJ154562.1 gg_id:343537 Leptospira kirschneri serovar str. Kambale
FJ154560.2 gg_id:330258 Leptospira kirschneri serovar Erinaceiauriti str. Erinaceus Auritus 670
EF596782.1 gg_id:231150 Leptospira interrogans L1207
FJ154570.1 gg_id:350766 Leptospira kirschneri serovar Grippotyphosa str. Mandemarkers
EF612285.1 gg_id:233710 Leptospira licerasiae serovar Varillal str. CEH010
EF612287.1 gg_id:233288 Leptospira licerasiae serovar Varillal str. MMD835
Z21635.1 gg_id:4347 Leptospira noguchii str. PANAMA CZ 214
DQ991493.1 gg_id:195575 Leptospira santarosai serovar str. Alice
U12673.1 gg_id:4307 Leptospira weilii str. serogroup Icterohaemorrhagiae s WB46
Z21631.1 gg_id:4382 Leptospira biflexa serovar Canela str. CANELA
EF025496.1 gg_id:190457 Leptospira wolffi str. Korat-H2
U12670.2 gg_id:4306 Leptospira borgpetersenii str. serovar hardjo strain Hardjo bo BD50
EF205465.1 gg_id:211824 among geographically regions central Tibet geothermal spring mat clone YCB65
FJ660552.1 gg_id:562022 Correlation functional stability and dynamics full-scale wastewater treatment plant a
AY631880.1 gg_id:101978 Leptospira alexanderi serovar Manhao 3 str. L 60
Z21633.1 gg_id:4381 Leptospira biflexa serovar Jequitaia str. JEQUITAIA
Z26969.1 gg_id:4372 Leptospira biflexa str. tororo TORORO MUTANT STRAIN PARENT
DQ066980.1 gg_id:134767 Lake Washington sediment clone pLW-94
Z21649.1 gg_id:4305 Leptospira santarosai str. SHERMANI 1342 K

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| AB093320.1 | 85067 | 5266.3 | 5374.3 | 5231.2 | 5619.9 | 6258.4 | 4953.2 |
| U14920.1 | 3770 | 11467.7 | 11691.3 | 12069.8 | 11517.6 | 13760.8 | 12029.4 |
| EF164976.1 | 240387 | 8411.7 | 9111.6 | 7626.9 | 10009.6 | 10943.9 | 10826.1 |
| AB079583.1 | 77935 | 5738.7 | 5566.7 | 7117.2 | 7714.7 | 3813.2 | 5187.7 |
| EF164969.1 | 257537 | 7636.9 | 7108.1 | 5431.0 | 8836.8 | 13866.3 | 11527.9 |
| FJ461892.1 | 569032 | 79.4 | 76.6 | 190.5 | 145.4 | 79.4 | 75.1 |
| EU245543.1 | 249265 | 4787.0 | 5646.6 | 7398.5 | 8365.1 | 6765.9 | 7005.8 |
| AY605147.1 | 104927 | 159.3 | 199.6 | 73.5 | 380.1 | 632.6 | 376.1 |
| AY605151.1 | 100106 | 51.3 | 41.6 | 82.6 | 88.8 | 76.6 | 28.4 |
| AY605148.1 | 105069 | 419.1 | 1809.9 | 1469.1 | 1983.5 | 493.0 | 1278.5 |
| EU245476.1 | 250068 | 261.7 | 315.9 | 1379.5 | 1371.4 | 144.6 | 175.7 |
| DQ329632.1 | 159296 | 3581.6 | 4878.5 | 1087.1 | 1780.2 | 1007.9 | 329.4 |
| Z21632.1 | 4396 | 29.9 | 49.9 | 71.8 | 72.3 | 63.9 | 68.0 |
| DQ991481.1 | 186857 | 16770.0 | 16303.4 | 10362.6 | 15282.8 | 14607.6 | 14066.7 |
| NC_010842.1 | 304981 | 2226.2 | 1880.1 | 2637.2 | 3084.8 | 775.2 | 1852.4 |
| Z12821.1 | 4383 | 692.3 | 564.0 | 780.0 | 916.3 | 215.1 | 249.7 |
| Z21638.1 | 4384 | 1574.8 | 1151.8 | 1741.6 | 2045.7 | 319.4 | 626.5 |
| EF537007.1 | 229607 | 4291.9 | 5099.8 | 4608.9 | 4684.5 | 5510.9 | 4838.3 |
| FJ154592.1 | 343791 | 4901.8 | 5809.9 | 4692.0 | 5916.4 | 4673.0 | 7034.8 |
| Z21630.1 | 4348 | 4284.4 | 5076.7 | 4341.4 | 4574.3 | 5507.5 | 5152.7 |
| AY631891.1 | 107131 | 2429.5 | 3630.6 | 4681.6 | 3799.7 | 2353.0 | 3567.8 |
| AM050566.1 | 138386 | 2818.0 | 4075.4 | 5453.4 | 2817.5 | 4773.8 | 4874.6 |
| FJ154562.1 | 343537 | 2034.9 | 3752.9 | 4002.4 | 2430.7 | 2500.8 | 3626.8 |
| FJ154560.2 | 330258 | 1440.7 | 1863.3 | 2619.2 | 1739.3 | 1822.7 | 2418.0 |
| EF596782.1 | 231150 | 2106.9 | 3188.5 | 4322.1 | 2049.5 | 4430.8 | 4212.4 |
| FJ154570.1 | 350766 | 1768.0 | 2288.5 | 3139.1 | 1836.5 | 2703.3 | 2844.6 |
| EF612285.1 | 233710 | 2418.8 | 2382.2 | 4774.9 | 2409.6 | 1996.9 | 2573.2 |
| EF612287.1 | 233288 | 7899.2 | 8596.5 | 13304.5 | 9106.9 | 9934.0 | 9187.1 |
| Z21635.1 | 4347 | 3595.8 | 4298.5 | 6147.1 | 5348.4 | 6220.7 | 5891.8 |
| DQ991493.1 | 195575 | 3627.2 | 4740.3 | 3536.4 | 5962.2 | 1993.1 | 5087.6 |
| U12673.1 | 4307 | 2249.6 | 3001.2 | 2314.3 | 2977.7 | 2487.1 | 4846.0 |
| Z21631.1 | 4382 | 2250.3 | 1656.8 | 2040.4 | 2489.8 | 660.9 | 908.3 |
| EF025496.1 | 190457 | 6917.5 | 6743.1 | 3299.9 | 7062.6 | 1501.1 | 1664.8 |
| U12670.2 | 4306 | 3320.3 | 4165.9 | 3183.0 | 3128.8 | 3901.0 | 5209.8 |
| EF205465.1 | 211824 | 482.6 | 785.0 | 450.5 | 404.9 | 280.2 | 287.3 |
| FJ660552.1 | 562022 | 309.2 | 1806.0 | 1236.5 | 522.8 | 643.4 | 344.4 |
| AY631880.1 | 101978 | 5745.0 | 7223.1 | 5650.9 | 7510.8 | 5553.2 | 7448.6 |
| Z21633.1 | 4381 | 9401.0 | 11144.6 | 5542.3 | 7662.4 | 6071.3 | 7880.1 |
| Z26969.1 | 4372 | 15632.7 | 14144.6 | 11417.2 | 13495.7 | 12335.9 | 13190.3 |
| DQ066980.1 | 134767 | 12977.2 | 15363.0 | 8696.6 | 7366.9 | 8774.2 | 9731.3 |
| Z21649.1 | 4305 | 6631.5 | 8335.5 | 8388.9 | 7453.8 | 10061.7 | 8931.5 |

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|---|---|---|---|
| k__Bacteria | k__Bacteria | p__Spirochaetes | c__Leptospirae |
| k__Bacteria | k__Bacteria | p__Spirochaetes | c__Leptospirae |
| k__Bacteria | k__Bacteria | p__Spirochaetes | c__Leptospirae |
| k__Bacteria | k__Bacteria | p__Spirochaetes | c__Leptospirae |
| k__Bacteria | k__Bacteria | p__Spirochaetes | c__Leptospirae |
| k__Bacteria | k__Bacteria | p__Spirochaetes | c__Leptospirae |
| k__Bacteria | k__Bacteria | p__Spirochaetes | c__Leptospirae |
| k__Bacteria | k__Bacteria | p__Spirochaetes | c__Leptospirae |
| k__Bacteria | k__Bacteria | p__Spirochaetes | c__Leptospirae |
| k__Bacteria | k__Bacteria | p__Spirochaetes | c__Leptospirae |
| k__Bacteria | k__Bacteria | p__Spirochaetes | c__Leptospirae |
| k__Bacteria | k__Bacteria | p__Spirochaetes | c__Leptospirae |
| k__Bacteria | k__Bacteria | p__Spirochaetes | c__Leptospirae |
| k__Bacteria | k__Bacteria | p__Spirochaetes | c__Leptospirae |
| k__Bacteria | k__Bacteria | p__Spirochaetes | c__Leptospirae |
| k__Bacteria | k__Bacteria | p__Spirochaetes | c__Leptospirae |
| k__Bacteria | k__Bacteria | p__Spirochaetes | c__Leptospirae |
| k__Bacteria | k__Bacteria | p__Spirochaetes | c__M1NP2-04 |
| k__Bacteria | k__Bacteria | p__Spirochaetes | c__M1NP2-04 |
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| k__Bacteria | k__Bacteria | p__Spirochaetes | c__Spirochaetes |
| k__Bacteria | k__Bacteria | p__Spirochaetes | c__Spirochaetes |
| k__Bacteria | k__Bacteria | p__Spirochaetes | c__Spirochaetes |
| k__Bacteria | k__Bacteria | p__Spirochaetes | c__Spirochaetes |
| k__Bacteria | k__Bacteria | p__Spirochaetes | c__Spirochaetes |
| k__Bacteria | k__Bacteria | p__Spirochaetes | c__Spirochaetes |
| k__Bacteria | k__Bacteria | p__Spirochaetes | c__Spirochaetes |
| k__Bacteria | k__Bacteria | p__Spirochaetes | c__Spirochaetes |
| k__Bacteria | k__Bacteria | p__Spirochaetes | c__Spirochaetes |
| k__Bacteria | k__Bacteria | p__Spirochaetes | c__Spirochaetes |
| k__Bacteria | k__Bacteria | p__Spirochaetes | c__Spirochaetes |
| k__Bacteria | k__Bacteria | p__Spirochaetes | c__Spirochaetes |
| k__Bacteria | k__Bacteria | p__Spirochaetes | c__Spirochaetes |
| k__Bacteria | k__Bacteria | p__Spirochaetes | c__Spirochaetes |
| k__Bacteria | k__Bacteria | p__Spirochaetes | c__Spirochaetes |
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| k__Bacteria | k__Bacteria | p__Spirochaetes | c__Spirochaetes |
| k__Bacteria | k__Bacteria | p__Spirochaetes | c__Spirochaetes |

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| o__Leptospirales | f__Leptospiraceae |
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| o__Leptospirales | f__Leptospiraceae |
| o__Leptospirales | f__Leptospiraceae |
| o__unclassified | f__unclassified |
| o__unclassified | f__unclassified |
| o__unclassified | f__unclassified |
| o__Sphaerochaetales | f__Sphaerochaetaceae |
| o__Sphaerochaetales | f__Sphaerochaetaceae |
| o__Sphaerochaetales | f__Sphaerochaetaceae |
| o__Sphaerochaetales | f__Sphaerochaetaceae |
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| o__Spirochaetales | f__Spirochaetaceae |

g__Leptospira
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| s__unclassified | 76587 |
| s__unclassified | 76651 |
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| s__unclassified | 76846 |
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| s__unclassified | 76679 |
| s__unclassified | 76736 |
| s__unclassified | 76802 |
| s__unclassified | 76874 |
| s__Borrelia afzelii | 76040 |
| s__Borrelia burgdorferi | 76339 |
| s__Borrelia carolinensis | 76524 |
| s__Borrelia coriaceae | 76160 |
| s__Borrelia garinii | 76027 |
| s__Borrelia garinii | 76982 |
| s__Borrelia hermsii | 76475 |
| s__Borrelia japonica | 77067 |
| s__Borrelia lonestari | 76875 |
| s__Borrelia lonestari | 77142 |
| s__Borrelia sinica | 77077 |
| s__Borrelia turdi | 76098 |
| s__unclassified | 75941 |
| s__unclassified | 75978 |

FJ154588.1 gg_id:311421 Leptospira noguchii serovar Orleans str. LSU 2580
CP000348.1 gg_id:176749 Leptospira borgpetersenii serovar Hardjo-bovis str. L550
Z21634.1 gg_id:4346 Leptospira inadai str. LYME
Z21629.1 gg_id:4370 Leptospira biflexa serovar Ancona str. ANCONA PORTO
AY631885.1 gg_id:102755 Leptospira fainei serovar Hurstbridge str. BUT 6
AB279549.1 gg_id:181283 Leptospira kmetyi serovar Malaysia str. Bejo-Iso9
U60594.1 gg_id:4349 Leptospira fainei str. Hurstbridge
X17547.1 gg_id:4333 Leptospira interrogans str. serovar canicola strain Moulton
GQ441345.1 gg_id:584418 and dynamic mat present vs. active nitrogen-fixing microorganisms marine microbia
AE016823.1 gg_id:149405 Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130
EU358706.1 gg_id:334061 structure archaeal denaturing gel electrophoresis and sequencing mesophilic biogas
EU887797.1 gg_id:317015 and RFLP anaerobes Nisargruna biogas plant anaerobic digester clone 48IVSN
AB447738.1 gg_id:550451 Microbial Structure and Dynamics Granules Expanded Granular Sludge Bed (EGSB) R
AB089124.1 gg_id:77837 termite gut homogenate clone Rs-H88
AB244313.1 gg_id:143845 Microbial mesophilic chemostat cultivation long-chain fatty acids-degrading methan
AB191983.1 gg_id:143791 termite gut homogenate clone M1PT4-10
AY293856.1 gg_id:88155 Leptospira parva str. H; NCTC 11395
AB191844.1 gg_id:141715 termite gut homogenate clone M1NP2-04
EF454943.2 gg_id:217661 termite hindgut clone 290cost002-P3L-731
AB191843.1 gg_id:141819 termite gut homogenate clone M2PT2-76
EF586003.1 gg_id:243633 Methanol-assimilating anaerobic solid waste digester fed methanol clone M35_D8_L
EU358680.1 gg_id:352774 structure archaeal denaturing gel electrophoresis and sequencing mesophilic biogas
EU462396.1 gg_id:288748 Sumatran orangutan feces clone orang1_aai53g01
AF357916.2 gg_id:28706 Spirochaeta sp. str. Buddy
AJ698092.1 gg_id:105838 Spirochaeta sp. str. SPN1
AM982634.1 gg_id:277877 microbial and slurry pig saw dust spent bedding clone PISD-AJA01
DQ833400.1 gg_id:172254 Sphaerochaeta sp. str. TQ1
X85194.1 gg_id:4173 Borrelia afzelii str. DK4
NZ_ABGJ01000002.1 gg_id:270217 Borrelia burgdorferi str. 72a
EU085407.1 gg_id:560956 Borrelia carolinensis SCW-22
AF210136.1 gg_id:38090 Borrelia coriaceae CA435
AY342029.1 gg_id:99035 Borrelia garinii str. SIKA1
AY342031.1 gg_id:102963 Borrelia garinii str. PD89
U42292.1 gg_id:4241 Borrelia hermsii
L40598.1 gg_id:4269 Borrelia japonica str. IKA2
AY166715.1 gg_id:76818 Borrelia lonestari
U23211.1 gg_id:4172 Borrelia lonestari str. Texas 20
AB022101.2 gg_id:4288 Borrelia sinica str. CMN3
D67024.1 gg_id:4215 Borrelia turdi str. Ac502
AB113315.1 gg_id:104671 Borrelia duttonii VS4
X85189.1 gg_id:4157 Borrelia burgdorferi str. 272

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| AB447738.1 | 550451 | 4070.6 | 3256.7 | 5924.5 | 6168.6 | 3345.4 | 3690.6 |
| AB089124.1 | 77837 | 3245.2 | 3436.3 | 4868.2 | 3051.5 | 1823.0 | 1404.8 |
| AB244313.1 | 143845 | 165.7 | 178.1 | 1041.7 | 403.6 | 66.7 | 99.6 |
| AB191983.1 | 143791 | 5994.8 | 8782.8 | 3058.5 | 2418.3 | 2852.9 | 2861.6 |
| AY293856.1 | 88155 | 5500.9 | 6023.7 | 6950.1 | 5007.3 | 7950.9 | 5598.0 |
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| EF586003.1 | 243633 | 5904.2 | 6532.0 | 6036.3 | 4901.0 | 2519.3 | 6958.3 |
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| U42292.1 | 4241 | 2209.2 | 2269.3 | 2593.1 | 2666.5 | 830.7 | 1173.9 |
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| U23211.1 | 4172 | 4730.8 | 5218.2 | 4301.7 | 4259.7 | 4178.7 | 5177.0 |
| AB022101.2 | 4288 | 8358.4 | 8896.3 | 7940.1 | 9303.3 | 8281.9 | 8169.9 |
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| AB113315.1 | 104671 | 1451.4 | 1672.1 | 1770.8 | 1412.2 | 783.0 | 1060.5 |
| X85189.1 | 4157 | 7103.5 | 7888.2 | 7259.9 | 8230.2 | 7033.0 | 6671.8 |

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FM242277.1 gg_id:320359 sequences sediment clone 6bis T0h-oil
DQ154805.1 gg_id:138982 Diel Migration Restructures Hypersaline Microbial Mat hypersaline microbial mat cl
AY605171.1 gg_id:101310 microbial mat clone LH042
FJ202296.1 gg_id:326880 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k
AF104475.1 gg_id:3806 Olavius loisae endosymbiont 4
AM493256.1 gg_id:348409 Multiple symbionts two species co-occurring gutless oligochaete worms Mediterrar
AJ431239.1 gg_id:79373 Cytophaga sp. str. BHI80-86
AB186802.1 gg_id:100628 polychlorinated dioxin dechlorinating microcosm clone TSBW25
EF515721.1 gg_id:219079 Electricigen Enrichment MFC full-scale anaerobic bioreactor sludge treating brewery
AB244312.1 gg_id:143685 Microbial mesophilic chemostat cultivation long-chain fatty acids-degrading methan
EU073764.1 gg_id:256394 Microbial subsurface beds and methanogenic s coal enrichment clone ObedB-2A
AF050549.1 gg_id:3966 contaminated aquifer clone WCHB1-40
AY426468.1 gg_id:107508 full-scale anaerobic UASB bioreactor treating paper mill wastewater clone E3
EF515259.1 gg_id:219657 Electricigen Enrichment MFC upf microbial fuel cell anode clone 22a12
CU922644.1 gg_id:559340 Towards definition core microorganisms involved digestion mesophilic anaerobic dig

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| EF570073.1 | 279638 | 5218.0 | 5297.3 | 4577.3 | 5812.9 | 5110.6 | 4743.3 |
| L40596.1 | 4283 | 9011.0 | 9105.2 | 6830.6 | 8392.7 | 6445.4 | 6405.5 |
| EU081286.1 | 508944 | 6622.4 | 6600.3 | 4570.2 | 6711.7 | 6083.8 | 5407.1 |
| X85201.1 | 4280 | 9389.5 | 9819.1 | 8387.6 | 10000.3 | 8468.1 | 8512.8 |
| U28503.1 | 4205 | 5780.6 | 7253.1 | 6734.0 | 7173.3 | 5880.6 | 9303.1 |
| AY626138.1 | 99408 | 11276.8 | 10921.2 | 9205.6 | 11698.4 | 9302.7 | 8507.9 |
| U42284.1 | 4182 | 8025.8 | 7179.6 | 5578.3 | 8791.3 | 3920.8 | 5488.6 |
| EU135596.1 | 318700 | 5857.4 | 6399.8 | 5668.3 | 6699.4 | 6176.7 | 6352.6 |
| DQ103657.1 | 132946 | 184.5 | 233.5 | 525.4 | 162.7 | 138.2 | 122.5 |
| DQ154846.1 | 139275 | 218.4 | 1815.8 | 58.5 | 224.0 | 66.2 | 34.6 |
| DQ329736.1 | 159199 | 1306.8 | 2858.3 | 5897.7 | 2413.4 | 3200.2 | 3445.7 |
| DQ103658.1 | 134251 | 18.5 | 26.9 | 26.3 | 39.9 | 59.9 | 17.1 |
| GU118739.1 | 594444 | 332.3 | 747.7 | 1379.2 | 406.3 | 494.6 | 685.8 |
| AY605135.1 | 99534 | 5229.1 | 6103.9 | 9281.9 | 6499.9 | 4049.2 | 4046.5 |
| EU246240.1 | 255595 | 4513.4 | 4026.9 | 4777.8 | 2855.5 | 3153.0 | 4178.5 |
| GU118767.1 | 545372 | 973.3 | 1388.3 | 1087.7 | 563.5 | 1013.3 | 796.6 |
| AY605154.1 | 100580 | 36.7 | 56.9 | 159.9 | 64.7 | 69.1 | 35.3 |
| EU246071.1 | 240820 | 4845.9 | 5441.6 | 5771.8 | 3779.4 | 5626.5 | 5101.9 |
| AY605174.1 | 101818 | 27.4 | 32.4 | 30.2 | 41.9 | 67.8 | 26.6 |
| FM242277.1 | 320359 | 160.6 | 337.5 | 983.9 | 123.0 | 65.6 | 164.1 |
| DQ154805.1 | 138982 | 44.8 | 53.8 | 142.6 | 72.9 | 72.1 | 25.5 |
| AY605171.1 | 101310 | 300.1 | 90.6 | 189.8 | 162.8 | 76.0 | 43.5 |
| FJ202296.1 | 326880 | 440.5 | 597.7 | 1726.1 | 340.8 | 336.1 | 516.3 |
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| AJ431239.1 | 79373 | 19.8 | 26.4 | 25.3 | 54.7 | 53.9 | 20.6 |
| AB186802.1 | 100628 | 2359.5 | 3473.6 | 6052.8 | 1881.8 | 4977.3 | 4024.5 |
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| AF050549.1 | 3966 | 1643.3 | 2136.2 | 4442.9 | 1152.0 | 2041.6 | 2031.2 |
| AY426468.1 | 107508 | 281.3 | 75.8 | 606.8 | 62.3 | 54.9 | 28.8 |
| EF515259.1 | 219657 | 80.9 | 54.6 | 96.2 | 59.2 | 64.9 | 53.1 |
| CU922644.1 | 559340 | 2483.2 | 3677.6 | 2258.1 | 3290.1 | 5726.9 | 4410.7 |

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| s__Spirochaeta thermophila | 76235 |
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| s__Spirochaeta thermophila | 76441 |
| s__Spirochaeta thermophila | 76511 |
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| s__unclassified | 76169 |

CU918048.1 gg_id:572172 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
AB240336.1 gg_id:141219 microbial structure Phragmites rhizosphere biofilm reed bed reactor laboratory clone
AY605178.1 gg_id:102429 microbial mat clone LL026
EU246179.1 gg_id:237552 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-P4-G12
EU245523.1 gg_id:249436 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M2-F05
AY605126.1 gg_id:103618 microbial mat clone IE015
EU245802.1 gg_id:256467 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M6-E12
AY605169.1 gg_id:106409 microbial mat clone LH032
AJ431240.1 gg_id:79117 Spirochaeta sp. str. BHI80-158
DQ154820.1 gg_id:139224 Diel Migration Restructures Hypersaline Microbial Mat hypersaline microbial mat clo
GU118646.1 gg_id:570244 Threatened Corals Provide Microbial Habitats clone Mfav_L02
AB121100.1 gg_id:99658 cold seep sediment clone JS624-4
EU245482.1 gg_id:255522 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M2-B03
AB177323.1 gg_id:128374 seafloor methane hydrate clone ODP1251B20.23
FJ516894.1 gg_id:548153 semiarid 'Tablas de Daimiel National Park' wetland (Central Spain) unravelled upper s
AY605142.1 gg_id:104169 microbial mat clone IE071
NR_027585.1 gg_id:560417 Spirochaeta smaragdinae str. SEBR 4228; DSM 11293
FJ203346.1 gg_id:320773 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h
AB088873.1 gg_id:77729 termite gut homogenate clone Rs-D16 sp.
EU245577.1 gg_id:237886 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M3-C06
EU245839.1 gg_id:242567 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M7-A11
AY605137.1 gg_id:99854 microbial mat clone IE046
AY605176.1 gg_id:102131 microbial mat clone LH079
AY605141.1 gg_id:104007 microbial mat clone IE070
GU117988.1 gg_id:577654 Threatened Corals Provide Microbial Habitats clone Acer_D05
FM242378.1 gg_id:306448 sequences sediment clone 78 T9d+oil
EU245233.1 gg_id:251576 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-H4-E05
AM236337.1 gg_id:168305 Evidence chemoautotrophic symbiosis Mediterranean cold seep clam (Bivalvia: Luci
DQ329738.1 gg_id:159150 Guerrero Negro hypersaline microbial mat clone 05D2Z88
AF507855.1 gg_id:62701 Mono Lake at depth 23 m station 6 July 2000 clone ML623J-23 bacterium
FJ462030.1 gg_id:570445 Microbial ecology industrial digestor mesophilic anaerobic reactor fed effluent chemi
EF031095.1 gg_id:182638 Prokaryotic Tirez La Macha Spain endorheic hypersaline atalasohaline lake clone SalB
AY605165.1 gg_id:105791 microbial mat clone LG016
EU245551.1 gg_id:244538 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M3-A01
AY922180.1 gg_id:112885 whalefall clone 131573
FJ203063.1 gg_id:347941 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c
AY605131.1 gg_id:98915 microbial mat clone IE024
X97096.1 gg_id:3801 peat bog clone TM3
EU385698.1 gg_id:262150 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S
EF203193.1 gg_id:212910 phylotypes sediments Lake Kastoria Greece sediment clone Kas148B
EU488038.1 gg_id:540607 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and

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|---|---|---|---|---|---|---|---|
| CU918048.1 | 572172 | 457.7 | 904.2 | 2060.3 | 500.9 | 475.4 | 674.9 |
| AB240336.1 | 141219 | 49.0 | 1057.5 | 4161.3 | 811.7 | 421.3 | 458.1 |
| AY605178.1 | 102429 | 63.8 | 56.1 | 50.3 | 63.4 | 68.8 | 36.6 |
| EU246179.1 | 237552 | 47.1 | 85.2 | 48.5 | 68.0 | 73.8 | 40.0 |
| EU245523.1 | 249436 | 5404.6 | 5985.5 | 7382.4 | 6468.3 | 7826.5 | 7087.1 |
| AY605126.1 | 103618 | 151.1 | 328.9 | 299.9 | 136.9 | 115.4 | 89.9 |
| EU245802.1 | 256467 | 2388.7 | 3207.3 | 4185.0 | 3074.9 | 2646.0 | 2895.9 |
| AY605169.1 | 106409 | 33.4 | 24.5 | 18.0 | 48.2 | 71.7 | 25.2 |
| AJ431240.1 | 79117 | 1785.6 | 1789.9 | 3092.9 | 2467.2 | 1880.5 | 2550.1 |
| DQ154820.1 | 139224 | 6877.9 | 9909.6 | 3757.3 | 7958.3 | 11049.8 | 10504.9 |
| GU118646.1 | 570244 | 10158.8 | 11197.0 | 10308.8 | 9800.3 | 6575.5 | 8023.5 |
| AB121100.1 | 99658 | 87.7 | 139.9 | 104.3 | 103.6 | 92.8 | 52.4 |
| EU245482.1 | 255522 | 490.9 | 843.2 | 2219.5 | 379.7 | 225.3 | 778.0 |
| AB177323.1 | 128374 | 3597.5 | 6507.9 | 4313.7 | 4468.3 | 4770.5 | 4822.7 |
| FJ516894.1 | 548153 | 2045.2 | 2401.5 | 3559.4 | 1458.8 | 1161.4 | 1736.0 |
| AY605142.1 | 104169 | 341.1 | 343.4 | 250.2 | 217.9 | 267.0 | 195.0 |
| NR_027585.1 | 560417 | 14.6 | 24.2 | 25.1 | 46.4 | 45.8 | 16.2 |
| FJ203346.1 | 320773 | 11381.5 | 13426.6 | 10129.9 | 12066.7 | 10621.7 | 10530.6 |
| AB088873.1 | 77729 | 1304.0 | 2951.1 | 3100.2 | 1506.3 | 3247.0 | 4505.8 |
| EU245577.1 | 237886 | 1570.9 | 1935.6 | 1526.8 | 240.5 | 165.6 | 193.8 |
| EU245839.1 | 242567 | 8462.8 | 9430.2 | 8615.8 | 7709.9 | 4056.2 | 5346.6 |
| AY605137.1 | 99854 | 11426.3 | 18579.0 | 13456.6 | 8668.1 | 12193.8 | 11809.6 |
| AY605176.1 | 102131 | 49.4 | 49.5 | 120.6 | 60.0 | 66.8 | 33.7 |
| AY605141.1 | 104007 | 3431.5 | 3593.0 | 6058.2 | 2471.3 | 4286.1 | 3860.6 |
| GU117988.1 | 577654 | 13920.9 | 14891.9 | 10408.4 | 14518.4 | 16205.4 | 15225.9 |
| FM242378.1 | 306448 | 39.7 | 62.9 | 41.0 | 78.2 | 73.6 | 38.2 |
| EU245233.1 | 251576 | 7207.3 | 8847.3 | 5809.8 | 5508.3 | 2823.2 | 5625.5 |
| AM236337.1 | 168305 | 61.2 | 69.2 | 119.9 | 97.2 | 58.2 | 52.8 |
| DQ329738.1 | 159150 | 178.0 | 366.2 | 204.9 | 122.6 | 96.1 | 110.4 |
| AF507855.1 | 62701 | 15.5 | 29.7 | 26.8 | 45.8 | 61.0 | 20.8 |
| FJ462030.1 | 570445 | 202.8 | 607.7 | 718.2 | 357.3 | 519.4 | 960.9 |
| EF031095.1 | 182638 | 21.8 | 28.5 | 23.8 | 43.8 | 58.1 | 28.7 |
| AY605165.1 | 105791 | 62.0 | 78.6 | 50.3 | 101.9 | 91.2 | 40.7 |
| EU245551.1 | 244538 | 1104.0 | 1493.2 | 1536.3 | 623.7 | 3012.5 | 2586.7 |
| AY922180.1 | 112885 | 28.5 | 33.8 | 69.4 | 51.6 | 69.8 | 34.7 |
| FJ203063.1 | 347941 | 15419.3 | 16739.7 | 14895.0 | 14952.2 | 13771.3 | 14312.1 |
| AY605131.1 | 98915 | 226.5 | 301.4 | 569.6 | 230.5 | 237.0 | 358.8 |
| X97096.1 | 3801 | 52.6 | 113.3 | 488.0 | 103.2 | 85.3 | 67.1 |
| EU385698.1 | 262150 | 3323.7 | 3989.9 | 8927.2 | 4169.2 | 2588.5 | 4081.7 |
| EF203193.1 | 212910 | 2146.0 | 3245.2 | 3790.9 | 3186.6 | 1669.7 | 1612.4 |
| EU488038.1 | 540607 | 2395.4 | 3631.5 | 4436.9 | 3665.3 | 1907.6 | 2745.6 |

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| s__Treponema amylovorum | 77125 |
| s__Treponema azotonutricium | 76026 |
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| s__Treponema azotonutricium | 77007 |
| s__Treponema denticola | 76611 |
| s__Treponema lecithinolyticum | 76120 |
| s__Treponema medium | 75971 |
| s__Treponema pallidum | 76410 |
| s__Treponema parvum | 76332 |
| s__Treponema pedis | 76586 |
| s__Treponema phagedenis | 76024 |
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DQ676428.1 gg_id:221514 Archaeal and plankton freshwater pond suboxic freshwater-pond sediment clone M
EU734981.1 gg_id:347105 assemblages sediment station DBSE Northern Bering Sea clone 075B7
EU048676.1 gg_id:250799 and archaeal surface marine sediment Slope South China Sea clone MD2896-B17
AY605145.1 gg_id:104643 microbial mat clone IE094
DQ329747.1 gg_id:159087 Guerrero Negro hypersaline microbial mat clone 072DZ15
FJ748821.1 gg_id:582122 Vertical and sulfate-reducing prokaryotes estuarine Southern China Pearl River Estuar
X89050.1 gg_id:4043 termite hindgut clone mpsp2
AJ458944.1 gg_id:83652 Mixotricha paradoxa is flagellate hindgut Mastotermes darwiniensis clone mp1 of
AJ458945.1 gg_id:83413 Mixotricha paradoxa is flagellate hindgut Mastotermes darwiniensis clone mp3 of
X89052.1 gg_id:4082 termite hindgut clone mpsp16
X89044.1 gg_id:4038 termite hindgut clone sp5_18
GU432215.1 gg_id:573932 Human Oral Microbiome oral cavity
FJ976389.1 gg_id:573319 Interindividual healthy human oral microbiota mouth clone 24B016
GU408851.1 gg_id:574066 Human Oral Microbiome oral cavity
AF385536.1 gg_id:29328 swab advanced noma lesion clone BZ013
NR_025141.1 gg_id:570521 Treponema azotonutricium str. ZAS-9; DSM 13862
AB088874.1 gg_id:77582 termite gut homogenate clone Rs-D40 sp.
AB088888.1 gg_id:77749 termite gut homogenate clone Rs-E64 sp.
D85438.1 gg_id:3915 Treponema denticola str. ATCC33520
X87139.1 gg_id:63015 Treponema lecithinolyticum periodontitis patient PFB4G
FJ204241.1 gg_id:317194 Treponema medium subsp. bovis str. T52B
M88726.1 gg_id:3964 Treponema pallidum
AF302938.1 gg_id:30574 Treponema parvum str. OMZ842
EF061267.1 gg_id:199343 Treponema pedis str. T354A
EF061263.1 gg_id:197926 Treponema bovis str. T323C
AB088896.1 gg_id:78075 termite gut homogenate clone Rs-B05 sp.
AY571472.1 gg_id:114451 termite gut clone RsaP136
AB231032.1 gg_id:147653 termite gut wall clone HsW01-016
AB231029.1 gg_id:146387 termite gut wall clone HsW01-003
AF068334.1 gg_id:4047 termite gut homogenate clone RFS11
AF068420.1 gg_id:4099 termite gut homogenate clone RFS7
AF093251.1 gg_id:4009 Treponema primitia str. ZAS-1
AB088916.1 gg_id:78032 termite gut homogenate clone Rs-Q68
DQ009704.2 gg_id:141895 termite gut homogenate clone R38A5
AB015889.1 gg_id:3841 Treponema subsp. socranskii 128B
AB191946.1 gg_id:143013 termite gut homogenate clone M2PT2-10
AB085159.1 gg_id:72109 termite gut clone NkS-Dev14
EF454259.2 gg_id:222608 termite hindgut clone 290cost002-P3L-1859
X79548.1 gg_id:4015 Spirochaeta species
AJ458946.1 gg_id:86557 Mixotricha paradoxa is flagellate hindgut Mastotermes darwiniensis clone mp4 of
EU773678.1 gg_id:342601 Capybara feces clone CAP_aai00b06

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| DQ676428.1 | 221514 | 39.4 | 71.6 | 80.9 | 68.7 | 105.4 | 56.2 |
| EU734981.1 | 347105 | 7465.5 | 8486.1 | 5427.2 | 6687.8 | 6415.1 | 5639.0 |
| EU048676.1 | 250799 | 10342.6 | 10550.5 | 4647.7 | 6136.2 | 6926.2 | 5132.0 |
| AY605145.1 | 104643 | 24.2 | 33.8 | 49.3 | 47.2 | 56.7 | 16.1 |
| DQ329747.1 | 159087 | 171.4 | 238.7 | 373.7 | 153.2 | 141.1 | 384.6 |
| FJ748821.1 | 582122 | 12352.9 | 13468.1 | 15103.8 | 13242.7 | 12575.2 | 11401.9 |
| X89050.1 | 4043 | 37.3 | 54.9 | 33.1 | 84.6 | 88.8 | 34.0 |
| AJ458944.1 | 83652 | 649.7 | 648.0 | 416.8 | 520.7 | 795.3 | 696.0 |
| AJ458945.1 | 83413 | 57.1 | 84.8 | 68.0 | 111.0 | 89.7 | 51.7 |
| X89052.1 | 4082 | 64.2 | 147.7 | 142.9 | 136.9 | 117.1 | 81.1 |
| X89044.1 | 4038 | 41.5 | 58.0 | 55.9 | 94.8 | 76.3 | 37.2 |
| GU432215.1 | 573932 | 8414.2 | 7943.8 | 4799.8 | 10246.5 | 9863.9 | 10258.4 |
| FJ976389.1 | 573319 | 206.5 | 358.0 | 726.6 | 242.4 | 545.8 | 390.4 |
| GU408851.1 | 574066 | 714.3 | 574.8 | 699.4 | 1332.7 | 447.7 | 531.9 |
| AF385536.1 | 29328 | 37.3 | 72.0 | 60.1 | 66.8 | 71.5 | 39.5 |
| NR_025141.1 | 570521 | 282.3 | 416.5 | 399.2 | 865.6 | 117.5 | 100.6 |
| AB088874.1 | 77582 | 41.6 | 59.1 | 284.0 | 89.1 | 71.2 | 33.6 |
| AB088888.1 | 77749 | 1827.9 | 1742.6 | 2384.4 | 1959.1 | 2019.4 | 1970.5 |
| D85438.1 | 3915 | 217.9 | 226.9 | 2259.9 | 246.8 | 84.6 | 206.5 |
| X87139.1 | 63015 | 46.6 | 56.7 | 49.9 | 165.9 | 188.2 | 98.6 |
| FJ204241.1 | 317194 | 332.7 | 418.3 | 1245.4 | 412.0 | 661.7 | 410.6 |
| M88726.1 | 3964 | 103.3 | 137.3 | 231.4 | 114.6 | 91.8 | 91.8 |
| AF302938.1 | 30574 | 22.2 | 27.7 | 27.9 | 51.3 | 70.4 | 19.3 |
| EF061267.1 | 199343 | 130.3 | 179.2 | 244.0 | 151.6 | 75.1 | 44.4 |
| EF061263.1 | 197926 | 33.5 | 51.8 | 61.1 | 154.5 | 76.8 | 36.6 |
| AB088896.1 | 78075 | 86.2 | 280.7 | 181.3 | 121.6 | 169.1 | 109.7 |
| AY571472.1 | 114451 | 70.4 | 61.7 | 128.9 | 104.1 | 60.3 | 68.7 |
| AB231032.1 | 147653 | 361.9 | 586.4 | 581.8 | 1256.9 | 2416.7 | 1010.8 |
| AB231029.1 | 146387 | 509.2 | 980.9 | 1304.3 | 442.6 | 793.5 | 894.0 |
| AF068334.1 | 4047 | 180.9 | 241.6 | 348.8 | 790.1 | 146.8 | 262.9 |
| AF068420.1 | 4099 | 2565.4 | 2584.0 | 904.7 | 2666.3 | 2616.2 | 2167.9 |
| AF093251.1 | 4009 | 1776.7 | 1668.3 | 4007.6 | 772.8 | 1803.7 | 2606.7 |
| AB088916.1 | 78032 | 10.3 | 15.7 | 12.6 | 30.9 | 44.4 | 10.3 |
| DQ009704.2 | 141895 | 1998.7 | 5463.1 | 1517.0 | 3444.1 | 3099.5 | 3060.6 |
| AB015889.1 | 3841 | 1410.7 | 2424.5 | 974.0 | 2491.5 | 1786.6 | 2053.6 |
| AB191946.1 | 143013 | 29.6 | 57.7 | 47.5 | 46.2 | 43.9 | 28.6 |
| AB085159.1 | 72109 | 7195.1 | 6522.8 | 1834.4 | 4298.8 | 4420.7 | 4493.3 |
| EF454259.2 | 222608 | 5400.4 | 6184.2 | 6444.9 | 6674.1 | 5519.9 | 6886.9 |
| X79548.1 | 4015 | 25.0 | 108.0 | 67.7 | 44.9 | 70.8 | 27.0 |
| AJ458946.1 | 86557 | 19.0 | 23.9 | 25.9 | 51.1 | 64.9 | 27.9 |
| EU773678.1 | 342601 | 2990.5 | 5354.6 | 2161.0 | 2609.1 | 1838.7 | 1753.8 |

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EU464086.1 gg_id:289662 reticulated giraffe feces clone gir_aah93c07
AB088884.1 gg_id:78359 termite gut homogenate clone Rs-J14 sp.
AF061347.1 gg_id:3931 Treponema sp. I:Q:AT20 str. AT20
AB088881.1 gg_id:78047 termite gut homogenate clone Rs-D57 sp.
GQ502611.1 gg_id:582361 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf7-
AF068405.1 gg_id:4094 termite gut homogenate clone ZAS89
EF454213.1 gg_id:220388 termite hindgut clone 290cost002-P3L-1803
EF453852.2 gg_id:218658 termite hindgut clone 290cost002-P3L-1216
AF023029.1 gg_id:3906 Treponema sp. str. III:13:D94
AB234361.1 gg_id:150211 termite gut homogenate clone MgMjD-028
AB192147.1 gg_id:141512 termite gut homogenate clone RsTz-89
AB192141.1 gg_id:142334 termite gut homogenate clone RsTz-84
AB231057.1 gg_id:146440 termite gut wall clone NkW01-009
EF453913.2 gg_id:218561 termite hindgut clone 290cost002-P3L-1301
GQ502615.1 gg_id:536096 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf7-
EF454897.2 gg_id:226681 termite hindgut clone 290cost002-P3L-619
EF454832.1 gg_id:217886 termite hindgut clone 290cost002-P3L-484
AJ419816.1 gg_id:22449 Spirochaeta sp
AB191964.1 gg_id:141888 termite gut homogenate clone M1NP2-77
AB088905.1 gg_id:77877 termite gut homogenate clone Rs-A09 sp.
AB231063.1 gg_id:147373 termite gut wall clone NkW01-044
AB084952.1 gg_id:69074 termite gut clone NkS1
EU794266.1 gg_id:346741 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_P10
AB062832.1 gg_id:31994 termite gut homogenate clone BCf6-15
AB360375.1 gg_id:265198 Identification endosymbiotic methanogen and ectosymbiotic spirochetes protists ter
AF068341.1 gg_id:4087 termite gut homogenate clone RFS41
AB088901.1 gg_id:78179 termite gut homogenate clone Rs-C91 sp.
AM942448.1 gg_id:302412 Evidence multiple Treponema phylotypes involved bovine shown 16rDNA and fluore
EU771469.1 gg_id:354983 Hamadryas Baboon feces clone AFBAB_aai04f02
AY571478.1 gg_id:114784 termite gut clone RsaHf303
AB088882.2 gg_id:77600 termite gut homogenate clone Rs-P25 sp.
AF023063.1 gg_id:3947 Treponema sp. str. I:N:D47
AF068345.1 gg_id:4049 termite gut homogenate clone CFS6
AF371928.1 gg_id:68837 swine intestine clone p-2159-s959-3
AB192251.1 gg_id:143974 termite gut homogenate clone RPK-14
EF454122.2 gg_id:220481 termite hindgut clone 290cost002-P3L-1667
EF454300.2 gg_id:223993 termite hindgut clone 290cost002-P3L-1914
EF454181.2 gg_id:222160 termite hindgut clone 290cost002-P3L-1759
AY212749.1 gg_id:105320 equine manure clone wet198
EU794214.1 gg_id:316624 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_S39
EF562545.1 gg_id:251512 stable microbial consortia capable degrading complex organic matter paper pulp colu

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|---|---|---|---|---|---|---|---|
| EU464086.1 | 289662 | 7417.8 | 9855.1 | 7596.7 | 8546.8 | 14011.7 | 10841.3 |
| AB088884.1 | 78359 | 189.3 | 1086.2 | 581.4 | 1050.1 | 585.6 | 1055.7 |
| AF061347.1 | 3931 | 889.3 | 838.9 | 1122.9 | 991.5 | 557.8 | 889.6 |
| AB088881.1 | 78047 | 64.6 | 72.1 | 136.3 | 86.5 | 68.5 | 46.1 |
| GQ502611.1 | 582361 | 3376.9 | 3335.8 | 3785.9 | 4697.7 | 4894.5 | 4969.7 |
| AF068405.1 | 4094 | 65.1 | 106.1 | 72.5 | 164.7 | 513.2 | 123.9 |
| EF454213.1 | 220388 | 3774.8 | 4234.7 | 4741.7 | 3846.3 | 3278.1 | 3631.8 |
| EF453852.2 | 218658 | 3787.6 | 4191.0 | 6555.1 | 4239.5 | 5192.0 | 4760.8 |
| AF023029.1 | 3906 | 701.6 | 1124.9 | 3677.7 | 635.0 | 910.7 | 845.7 |
| AB234361.1 | 150211 | 47.6 | 138.1 | 721.7 | 107.9 | 145.8 | 150.8 |
| AB192147.1 | 141512 | 700.0 | 922.9 | 1046.4 | 513.5 | 2547.3 | 1537.9 |
| AB192141.1 | 142334 | 76.5 | 135.8 | 419.4 | 58.3 | 87.4 | 74.4 |
| AB231057.1 | 146440 | 43.2 | 44.5 | 64.3 | 58.0 | 67.9 | 27.0 |
| EF453913.2 | 218561 | 35.3 | 58.7 | 48.9 | 67.7 | 64.6 | 48.5 |
| GQ502615.1 | 536096 | 2496.6 | 1809.7 | 1980.7 | 2627.5 | 1619.0 | 2132.1 |
| EF454897.2 | 226681 | 2550.1 | 3236.0 | 2891.2 | 3132.8 | 1558.6 | 2670.5 |
| EF454832.1 | 217886 | 11164.7 | 11540.0 | 8632.0 | 10061.2 | 10067.7 | 9439.9 |
| AJ419816.1 | 22449 | 46.0 | 44.0 | 36.9 | 62.0 | 57.1 | 31.7 |
| AB191964.1 | 141888 | 1044.6 | 1346.9 | 2109.2 | 499.2 | 518.8 | 1024.8 |
| AB088905.1 | 77877 | 50.5 | 64.2 | 153.8 | 85.2 | 81.8 | 39.5 |
| AB231063.1 | 147373 | 31.0 | 51.5 | 34.7 | 67.5 | 64.0 | 40.2 |
| AB084952.1 | 69074 | 37.5 | 79.8 | 45.0 | 70.4 | 66.3 | 32.2 |
| EU794266.1 | 346741 | 30.6 | 49.3 | 22.1 | 63.5 | 65.2 | 23.0 |
| AB062832.1 | 31994 | 124.9 | 261.9 | 109.1 | 109.3 | 252.1 | 86.6 |
| AB360375.1 | 265198 | 30.7 | 39.7 | 16.2 | 95.1 | 64.6 | 59.5 |
| AF068341.1 | 4087 | 33.6 | 85.7 | 41.4 | 46.1 | 59.4 | 23.4 |
| AB088901.1 | 78179 | 290.1 | 76.5 | 490.4 | 100.2 | 78.8 | 56.0 |
| AM942448.1 | 302412 | 8823.8 | 7583.7 | 8236.0 | 9825.1 | 6739.3 | 5553.1 |
| EU771469.1 | 354983 | 3034.3 | 3291.2 | 4873.1 | 2471.8 | 3509.5 | 4045.2 |
| AY571478.1 | 114784 | 1340.9 | 1887.5 | 615.2 | 189.4 | 134.4 | 347.0 |
| AB088882.2 | 77600 | 1898.2 | 2994.1 | 3359.0 | 2445.5 | 3736.2 | 4385.5 |
| AF023063.1 | 3947 | 333.0 | 540.4 | 1820.7 | 524.6 | 161.2 | 245.2 |
| AF068345.1 | 4049 | 39.5 | 57.7 | 127.7 | 90.8 | 76.9 | 41.9 |
| AF371928.1 | 68837 | 20.6 | 39.4 | 24.7 | 50.4 | 48.9 | 23.4 |
| AB192251.1 | 143974 | 1380.4 | 2490.5 | 4211.8 | 1417.9 | 2669.3 | 2093.9 |
| EF454122.2 | 220481 | 8550.3 | 6881.8 | 4953.0 | 8654.2 | 8491.8 | 7784.6 |
| EF454300.2 | 223993 | 2131.3 | 2661.6 | 3399.6 | 4367.2 | 1354.3 | 2063.8 |
| EF454181.2 | 222160 | 10727.8 | 11574.7 | 10199.1 | 9233.9 | 9882.7 | 10269.4 |
| AY212749.1 | 105320 | 155.2 | 246.8 | 754.6 | 148.3 | 95.9 | 56.2 |
| EU794214.1 | 316624 | 35.1 | 19.0 | 65.4 | 63.7 | 74.0 | 30.8 |
| EF562545.1 | 251512 | 3513.5 | 4479.5 | 7628.2 | 4224.8 | 5413.9 | 5068.5 |

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AB192254.1 gg_id:141999 termite gut homogenate clone RPK-37
AB191821.1 gg_id:144329 termite gut homogenate clone M1NP1-80
AB084965.1 gg_id:74426 termite gut clone NkS50
GU408735.1 gg_id:557008 Human Oral Microbiome oral cavity
AF023052.1 gg_id:3939 Treponema sp. str. I:G:C1
AF023053.1 gg_id:3940 Treponema sp. str. I:F:D13
AF023031.1 gg_id:3908 Treponema sp. str. II:C:T1
GQ502617.1 gg_id:545719 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf7-
EF454600.2 gg_id:219918 termite hindgut clone 290cost002-P3L-2386
AB192144.1 gg_id:142525 termite gut homogenate clone RsTz-02
AM182455.1 gg_id:146784 Treponema sp. str. SPIT5
AB360374.1 gg_id:276247 Identification endosymbiotic methanogen and ectosymbiotic spirochetes protists ter
AB062823.1 gg_id:48891 termite gut homogenate clone BCf4-14
EU358687.1 gg_id:313606 structure archaeal denaturing gel electrophoresis and sequencing mesophilic biogas
AY735103.1 gg_id:102578 Spirochaeta taiwanensis str. K1LY
AB192255.1 gg_id:143026 termite gut homogenate clone RPK-39
GQ068618.1 gg_id:417534 Topographical and Temporal Human Skin Microbiome skin nare clone nbw152g06c1
GU408631.1 gg_id:564057 Human Oral Microbiome oral cavity
AB088908.1 gg_id:78092 termite gut homogenate clone Rs-D13 sp.
AB191856.1 gg_id:144192 termite gut homogenate clone M1NP1-86
AB191941.1 gg_id:143947 termite gut homogenate clone M2PT2-47
AB255896.1 gg_id:165815 Localization Cell Morphologies Members Candidate TG3 and Subphylum Phylum Fibr
EF454002.2 gg_id:220062 termite hindgut clone 290cost002-P3L-1429
AB084960.1 gg_id:69104 termite gut clone NkS21
EF453804.1 gg_id:223738 termite hindgut clone 290cost002-P3L-1157
AM980448.1 gg_id:301091 Treponema sp. PT9 PT8
AF068347.1 gg_id:4118 termite gut homogenate clone CFS121
AB062834.1 gg_id:46398 termite gut homogenate clone BCf6-24
AF068342.1 gg_id:3984 termite gut homogenate clone RFS6
AB189699.1 gg_id:112977 termite gut homogenate clone Tc-69
EU472054.1 gg_id:294974 francois langur feces clone FL_1aaa01h05
GQ039064.1 gg_id:441410 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbu41
AB191917.1 gg_id:141191 termite gut homogenate clone M2PB4-42
AB198448.1 gg_id:135888 termite gut wall fraction clone RsW01-008
AB192242.1 gg_id:141806 termite gut homogenate clone RPK-17
AB084968.1 gg_id:69543 termite gut clone NkS83
GQ502646.1 gg_id:555083 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf7-
GQ502659.1 gg_id:565920 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf7-
EU471602.1 gg_id:295386 Asiatic elephant feces clone AE1_aaa04f01
EF454215.2 gg_id:226149 termite hindgut clone 290cost002-P3L-1805
AB088900.1 gg_id:77591 termite gut homogenate clone Rs-Q78 sp.

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| AB192254.1 | 141999 | 121.6 | 239.2 | 548.1 | 154.8 | 361.9 | 367.3 |
| AB191821.1 | 144329 | 50.7 | 89.1 | 175.6 | 87.1 | 82.8 | 177.0 |
| AB084965.1 | 74426 | 13.2 | 20.2 | 35.5 | 33.8 | 46.1 | 12.0 |
| GU408735.1 | 557008 | 921.6 | 666.2 | 350.4 | 1249.5 | 723.7 | 710.6 |
| AF023052.1 | 3939 | 409.6 | 777.3 | 2428.1 | 637.3 | 1424.5 | 747.9 |
| AF023053.1 | 3940 | 176.0 | 157.6 | 776.2 | 263.3 | 80.9 | 305.7 |
| AF023031.1 | 3908 | 31.7 | 35.3 | 48.7 | 54.3 | 57.1 | 26.6 |
| GQ502617.1 | 545719 | 1011.5 | 881.8 | 1103.9 | 440.2 | 1077.3 | 1443.9 |
| EF454600.2 | 219918 | 3959.8 | 5248.9 | 4295.9 | 5239.1 | 3088.7 | 3620.5 |
| AB192144.1 | 142525 | 36.9 | 60.1 | 71.4 | 56.9 | 67.4 | 48.3 |
| AM182455.1 | 146784 | 26.0 | 31.6 | 28.8 | 57.5 | 59.2 | 34.5 |
| AB360374.1 | 276247 | 235.6 | 225.4 | 798.3 | 720.0 | 102.8 | 173.8 |
| AB062823.1 | 48891 | 408.1 | 633.8 | 210.2 | 942.8 | 841.0 | 1606.9 |
| EU358687.1 | 313606 | 1776.6 | 2265.2 | 5948.7 | 2798.3 | 2100.5 | 1492.7 |
| AY735103.1 | 102578 | 154.6 | 186.6 | 297.9 | 156.4 | 229.5 | 235.4 |
| AB192255.1 | 143026 | 92.5 | 323.3 | 309.6 | 104.7 | 113.3 | 150.2 |
| GQ068618.1 | 417534 | 1064.1 | 2479.2 | 4239.6 | 2313.4 | 3191.1 | 2392.3 |
| GU408631.1 | 564057 | 779.8 | 2100.0 | 2912.4 | 2675.5 | 2569.0 | 2269.8 |
| AB088908.1 | 78092 | 75.2 | 213.5 | 685.6 | 200.9 | 243.3 | 293.4 |
| AB191856.1 | 144192 | 36.0 | 44.0 | 32.2 | 67.1 | 79.3 | 49.5 |
| AB191941.1 | 143947 | 23.3 | 18.9 | 18.0 | 45.7 | 60.7 | 40.2 |
| AB255896.1 | 165815 | 58.3 | 89.7 | 158.0 | 103.9 | 93.0 | 92.2 |
| EF454002.2 | 220062 | 2197.8 | 2149.7 | 2969.3 | 2795.0 | 951.9 | 2114.2 |
| AB084960.1 | 69104 | 74.4 | 61.6 | 99.7 | 82.3 | 75.7 | 65.1 |
| EF453804.1 | 223738 | 4849.4 | 3918.5 | 2196.7 | 4093.6 | 2998.4 | 3300.8 |
| AM980448.1 | 301091 | 460.0 | 1890.4 | 2894.8 | 1819.4 | 2717.6 | 2001.7 |
| AF068347.1 | 4118 | 52.4 | 52.8 | 34.8 | 68.3 | 89.8 | 81.6 |
| AB062834.1 | 46398 | 23.7 | 20.8 | 37.6 | 44.7 | 80.5 | 61.5 |
| AF068342.1 | 3984 | 18.9 | 17.3 | 59.4 | 62.5 | 77.3 | 15.9 |
| AB189699.1 | 112977 | 82.1 | 147.6 | 154.7 | 89.7 | 97.5 | 97.9 |
| EU472054.1 | 294974 | 418.6 | 366.5 | 1514.3 | 2927.9 | 933.0 | 788.7 |
| GQ039064.1 | 441410 | 306.2 | 479.9 | 2182.6 | 607.3 | 289.5 | 468.6 |
| AB191917.1 | 141191 | 64.9 | 76.3 | 191.6 | 88.6 | 82.6 | 68.9 |
| AB198448.1 | 135888 | 87.3 | 154.7 | 606.9 | 139.6 | 158.9 | 67.4 |
| AB192242.1 | 141806 | 63.6 | 93.5 | 99.4 | 91.1 | 69.9 | 65.6 |
| AB084968.1 | 69543 | 39.5 | 72.3 | 174.8 | 74.8 | 65.7 | 39.4 |
| GQ502646.1 | 555083 | 3144.3 | 4132.3 | 2122.2 | 3715.7 | 5149.3 | 4724.7 |
| GQ502659.1 | 565920 | 749.8 | 1155.1 | 1100.2 | 284.3 | 214.5 | 512.3 |
| EU471602.1 | 295386 | 7071.0 | 5812.5 | 7888.1 | 10369.4 | 3659.7 | 6250.7 |
| EF454215.2 | 226149 | 1237.5 | 2127.5 | 758.9 | 1051.5 | 2226.9 | 1556.2 |
| AB088900.1 | 77591 | 26.0 | 35.8 | 62.6 | 56.6 | 55.2 | 19.8 |

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

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| AB299520.1 | 241126 | 1340.4 | 1541.8 | 1581.6 | 1205.3 | 915.6 | 880.4 |
| AB231059.1 | 145031 | 63.4 | 85.4 | 56.2 | 91.3 | 127.3 | 67.7 |
| EF454250.2 | 217773 | 5830.2 | 6306.0 | 2099.1 | 6142.2 | 8286.0 | 7801.8 |
| AF068416.1 | 4098 | 26.1 | 37.9 | 27.5 | 48.6 | 68.0 | 31.0 |
| AB088894.1 | 78213 | 329.1 | 554.9 | 1093.9 | 322.1 | 392.9 | 367.8 |
| AB231025.1 | 146570 | 5019.4 | 7544.1 | 5222.9 | 5460.9 | 4307.2 | 6208.4 |
| AB088891.1 | 77621 | 45.2 | 28.9 | 44.7 | 66.8 | 72.4 | 20.4 |
| AB192151.1 | 143612 | 47.5 | 61.1 | 94.1 | 88.4 | 62.2 | 39.5 |
| NR_029348.1 | 572161 | 1775.1 | 2623.0 | 957.5 | 1309.7 | 799.1 | 235.7 |
| EU464306.1 | 295712 | 827.8 | 659.7 | 2752.9 | 1358.7 | 681.0 | 710.9 |
| DQ003618.1 | 124523 | 714.3 | 1216.2 | 2986.2 | 2374.5 | 1518.6 | 1551.9 |
| EF454942.2 | 225337 | 9175.5 | 8719.7 | 9833.9 | 8744.3 | 9137.5 | 8100.8 |
| EF453933.2 | 221957 | 8290.7 | 7176.5 | 5411.8 | 5560.4 | 7767.8 | 10115.9 |
| AB191865.1 | 142763 | 65.3 | 105.2 | 609.4 | 107.0 | 85.1 | 89.5 |
| GU408605.1 | 562976 | 543.5 | 767.5 | 1512.8 | 433.9 | 314.0 | 541.5 |
| EF454221.1 | 223424 | 4854.4 | 4193.7 | 3624.4 | 6446.3 | 4148.1 | 4231.7 |
| AB032009.1 | 25824 | 40.1 | 481.4 | 57.2 | 767.4 | 700.0 | 83.0 |
| AB231031.1 | 145132 | 70.4 | 125.3 | 157.9 | 94.0 | 77.0 | 56.7 |
| AM420109.1 | 248721 | 52.0 | 57.7 | 130.8 | 84.7 | 79.8 | 52.2 |
| GQ502650.1 | 573443 | 894.1 | 1384.7 | 1119.2 | 618.7 | 804.1 | 1564.2 |
| AJ419821.1 | 40667 | 31.3 | 49.4 | 49.7 | 64.8 | 67.7 | 26.0 |
| EF454883.2 | 218947 | 3201.5 | 3350.7 | 859.9 | 3803.3 | 5726.3 | 4865.9 |
| AB088911.1 | 78206 | 252.5 | 485.8 | 459.0 | 329.7 | 397.1 | 282.4 |
| EF453968.2 | 225557 | 25.5 | 30.7 | 13.9 | 50.0 | 56.5 | 23.3 |
| AB231058.1 | 148743 | 309.0 | 411.8 | 846.5 | 294.7 | 217.8 | 430.9 |
| AB191854.1 | 143614 | 30.8 | 45.1 | 229.1 | 64.2 | 63.0 | 26.5 |
| AY341822.1 | 93141 | 248.2 | 353.1 | 1083.0 | 351.1 | 505.0 | 326.6 |
| AF068426.1 | 4127 | 71.1 | 95.3 | 85.8 | 109.9 | 84.2 | 46.7 |
| AB299519.1 | 252938 | 4249.2 | 4373.4 | 2697.6 | 4112.0 | 6042.4 | 4483.1 |
| EF453971.2 | 222007 | 2285.0 | 2457.2 | 3966.9 | 4503.2 | 2652.5 | 2828.5 |
| AB084956.1 | 73924 | 21.4 | 25.0 | 28.2 | 45.9 | 52.9 | 18.3 |
| AF068346.1 | 4117 | 3367.0 | 3446.4 | 2098.0 | 2832.4 | 5738.5 | 4631.9 |
| EU748341.1 | 339907 | 2755.0 | 1942.1 | 2110.1 | 2667.6 | 2292.7 | 2665.7 |
| AB255898.1 | 171504 | 38.9 | 91.1 | 156.3 | 87.3 | 203.8 | 162.4 |
| EF454202.2 | 227383 | 247.6 | 55.7 | 235.7 | 98.0 | 82.0 | 55.3 |
| AM420288.1 | 239628 | 987.2 | 1185.7 | 1448.9 | 460.9 | 280.9 | 496.5 |
| AB541984.1 | 585733 | 1332.2 | 1441.0 | 2343.4 | 973.1 | 621.3 | 1208.2 |
| AF023051.1 | 3938 | 432.1 | 575.9 | 2215.7 | 760.8 | 228.3 | 301.4 |
| AB191908.1 | 142284 | 2243.9 | 2504.3 | 2098.2 | 3349.7 | 3674.4 | 3580.8 |
| DQ065758.1 | 134428 | 42.8 | 41.8 | 33.8 | 74.7 | 97.0 | 42.1 |
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FJ976395.1 gg_id:571435 Interindividual healthy human oral microbiota mouth clone 24B241
AB191817.1 gg_id:141230 termite gut homogenate clone M1PT4-88
AB231061.1 gg_id:149915 termite gut wall clone NkW01-037
AY518274.1 gg_id:104346 Treponema sp. str. 14V28
AY178844.1 gg_id:104881 Treponema sp. str. Sy24
GQ502618.1 gg_id:536459 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf7-
AB192139.1 gg_id:142969 termite gut homogenate clone RsTz-33
EF453877.2 gg_id:227094 termite hindgut clone 290cost002-P3L-1254
AB062839.1 gg_id:27323 termite gut homogenate clone BCf7-24
AY369252.1 gg_id:94775 Treponema vincentii str. OMZ 861
AF182831.1 gg_id:3955 Treponema sp. str. I:V:AU076
AB062840.1 gg_id:38586 termite gut homogenate clone BCf8-03
EU473593.1 gg_id:299900 Somali wild ass feces clone WA_aaa02d10
EF454129.2 gg_id:226390 termite hindgut clone 290cost002-P3L-1681
AB198654.1 gg_id:135860 termite gut fluid and protists fraction clone RsC01-085
AM980447.1 gg_id:299619 Treponema sp. PT8
AY369247.1 gg_id:95168 Treponema sp. str. OMZ 839
EF453952.2 gg_id:220850 termite hindgut clone 290cost002-P3L-1363
EF454455.2 gg_id:227278 termite hindgut clone 290cost002-P3L-2160
GQ502643.1 gg_id:534577 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf7-
GQ502639.1 gg_id:536207 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf7-
AB255894.1 gg_id:162987 Localization Cell Morphologies Members Candidate TG3 and Subphylum Phylum Fibr
FJ976308.1 gg_id:558616 Interindividual healthy human oral microbiota mouth clone 10B549
GQ502652.1 gg_id:591066 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf7-
AY571470.1 gg_id:114589 termite gut clone RsaHf241
AB085158.1 gg_id:72963 termite gut clone NkS-Dev1
AB243262.1 gg_id:149532 acetone-preserved termite gut clone M2PB4a-025
DQ307690.1 gg_id:144644 termite intestinal tract clone MTG-91
GU304073.1 gg_id:541314 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c
EF454406.2 gg_id:222609 termite hindgut clone 290cost002-P3L-2077
EF453999.2 gg_id:226973 termite hindgut clone 290cost002-P3L-1424
EF454271.2 gg_id:225517 termite hindgut clone 290cost002-P3L-1873
AB084973.1 gg_id:73490 termite gut clone NkS97
AB191834.1 gg_id:141753 termite gut homogenate clone M1PT4-49
AB191848.1 gg_id:142623 termite gut homogenate clone M1NP1-75
AB088915.1 gg_id:78017 termite gut homogenate clone Rs-Q13 sp.
AF068423.1 gg_id:4053 termite gut homogenate clone RFS94
AB085166.1 gg_id:69238 termite gut clone NkS-Oxy25
GQ502657.1 gg_id:589527 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf7-
DQ003625.1 gg_id:121373 human mouth clone MB4_G11
AF357565.1 gg_id:71422 mpn-isolate group 17

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| AB191817.1 | 141230 | 2200.5 | 1422.3 | 398.8 | 2184.6 | 3912.6 | 3559.8 |
| AB231061.1 | 149915 | 71.4 | 118.7 | 108.1 | 93.4 | 179.4 | 122.3 |
| AY518274.1 | 104346 | 544.8 | 769.1 | 288.6 | 740.1 | 543.8 | 545.6 |
| AY178844.1 | 104881 | 16.7 | 33.0 | 23.2 | 49.3 | 60.6 | 25.7 |
| GQ502618.1 | 536459 | 638.2 | 748.4 | 487.9 | 317.7 | 195.9 | 423.4 |
| AB192139.1 | 142969 | 21.6 | 81.5 | 24.9 | 62.0 | 65.2 | 29.0 |
| EF453877.2 | 227094 | 4678.9 | 4648.0 | 2479.0 | 3166.2 | 3312.5 | 3856.3 |
| AB062839.1 | 27323 | 49.0 | 89.2 | 95.8 | 74.6 | 74.5 | 46.4 |
| AY369252.1 | 94775 | 151.3 | 263.7 | 836.2 | 297.6 | 178.2 | 138.7 |
| AF182831.1 | 3955 | 207.4 | 251.9 | 973.2 | 437.5 | 139.6 | 286.9 |
| AB062840.1 | 38586 | 211.7 | 248.8 | 613.0 | 147.4 | 634.7 | 480.8 |
| EU473593.1 | 299900 | 1851.6 | 5711.5 | 5152.2 | 5082.9 | 6203.7 | 6505.4 |
| EF454129.2 | 226390 | 7603.0 | 9234.9 | 10264.3 | 7533.1 | 5986.5 | 6641.3 |
| AB198654.1 | 135860 | 35.0 | 34.4 | 23.5 | 67.4 | 80.2 | 23.4 |
| AM980447.1 | 299619 | 558.2 | 694.8 | 1838.6 | 787.6 | 137.9 | 113.9 |
| AY369247.1 | 95168 | 274.1 | 309.4 | 175.4 | 654.6 | 1001.0 | 610.4 |
| EF453952.2 | 220850 | 281.8 | 447.6 | 292.5 | 489.3 | 938.6 | 233.7 |
| EF454455.2 | 227278 | 618.3 | 1809.6 | 1826.4 | 1499.6 | 584.7 | 593.0 |
| GQ502643.1 | 534577 | 2265.7 | 2525.7 | 1950.4 | 2647.7 | 5407.5 | 3728.1 |
| GQ502639.1 | 536207 | 255.7 | 519.2 | 818.9 | 319.3 | 380.9 | 606.9 |
| AB255894.1 | 162987 | 2058.3 | 3302.1 | 6542.7 | 5343.2 | 2553.2 | 2751.0 |
| FJ976308.1 | 558616 | 8073.9 | 9055.0 | 5782.5 | 5489.9 | 9311.3 | 8489.9 |
| GQ502652.1 | 591066 | 1189.7 | 1658.3 | 1573.5 | 1676.4 | 2536.9 | 1731.7 |
| AY571470.1 | 114589 | 2380.1 | 2401.1 | 803.5 | 4344.4 | 5517.7 | 5535.7 |
| AB085158.1 | 72963 | 20.6 | 34.5 | 52.4 | 31.0 | 48.3 | 29.5 |
| AB243262.1 | 149532 | 6275.5 | 8175.3 | 3613.9 | 7397.3 | 6568.1 | 7979.3 |
| DQ307690.1 | 144644 | 357.3 | 724.3 | 1121.7 | 259.1 | 296.0 | 352.1 |
| GU304073.1 | 541314 | 40.6 | 51.1 | 44.7 | 60.3 | 62.9 | 31.1 |
| EF454406.2 | 222609 | 12979.6 | 13215.3 | 13155.4 | 11095.0 | 16432.2 | 13557.7 |
| EF453999.2 | 226973 | 3278.4 | 3630.6 | 4741.8 | 4650.3 | 4810.3 | 5586.3 |
| EF454271.2 | 225517 | 9070.6 | 9506.3 | 4029.5 | 5933.3 | 5991.8 | 6542.2 |
| AB084973.1 | 73490 | 26.3 | 63.6 | 87.8 | 86.5 | 60.7 | 20.9 |
| AB191834.1 | 141753 | 235.9 | 387.6 | 933.9 | 394.1 | 424.5 | 465.9 |
| AB191848.1 | 142623 | 54.8 | 76.6 | 52.5 | 58.1 | 270.6 | 80.2 |
| AB088915.1 | 78017 | 25.1 | 35.7 | 90.2 | 65.7 | 72.0 | 26.9 |
| AF068423.1 | 4053 | 183.8 | 428.4 | 657.4 | 438.1 | 1176.6 | 1103.9 |
| AB085166.1 | 69238 | 22.3 | 22.9 | 35.7 | 45.5 | 49.9 | 20.8 |
| GQ502657.1 | 589527 | 192.0 | 291.6 | 483.6 | 217.0 | 137.3 | 45.3 |
| DQ003625.1 | 121373 | 10823.5 | 10492.0 | 10412.6 | 11622.6 | 11535.3 | 10786.9 |
| AF357565.1 | 71422 | 170.8 | 220.3 | 85.2 | 294.9 | 221.0 | 203.1 |

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

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| AB182309.1 | 105400 | 36.2 | 61.3 | 93.5 | 89.2 | 80.5 | 40.6 |
| AB191824.1 | 143359 | 115.5 | 310.4 | 1524.2 | 328.0 | 94.8 | 84.8 |
| AB192253.1 | 143938 | 395.3 | 415.7 | 864.7 | 2120.7 | 692.1 | 770.6 |
| GQ502658.1 | 590884 | 3130.3 | 3741.9 | 2296.6 | 4905.9 | 4863.0 | 4232.5 |
| GQ422733.1 | 565720 | 4702.2 | 4269.6 | 2356.9 | 5645.2 | 6155.4 | 4726.1 |
| AY005081.1 | 45933 | 127.7 | 157.5 | 635.8 | 176.9 | 154.9 | 143.5 |
| AB191928.1 | 144853 | 81.5 | 112.8 | 194.8 | 77.5 | 110.4 | 73.9 |
| EU464271.1 | 302795 | 7214.2 | 7170.1 | 6416.7 | 6140.3 | 8797.5 | 9895.0 |
| EU794206.1 | 324511 | 2912.5 | 2860.4 | 6338.2 | 3693.3 | 3434.9 | 2990.6 |
| AB088903.1 | 77948 | 57.9 | 85.4 | 101.0 | 111.8 | 66.5 | 46.6 |
| GQ039162.1 | 400332 | 996.6 | 1082.5 | 2254.7 | 768.7 | 1754.9 | 1042.3 |
| AB191968.1 | 141054 | 784.3 | 1220.9 | 1789.9 | 2117.3 | 679.0 | 955.7 |
| EU471558.1 | 291957 | 6833.0 | 6401.2 | 6487.9 | 7713.5 | 4225.6 | 5247.2 |
| AF068336.1 | 4116 | 36.2 | 46.5 | 73.2 | 50.3 | 63.0 | 47.7 |
| GQ502644.1 | 543504 | 36.4 | 49.4 | 134.0 | 66.5 | 79.1 | 69.3 |
| GQ502653.1 | 547244 | 1350.8 | 1309.7 | 814.2 | 1311.7 | 756.1 | 1119.1 |
| AM420275.1 | 240104 | 5746.3 | 5927.7 | 5208.6 | 5295.7 | 8055.2 | 7982.5 |
| AY134898.1 | 59569 | 704.8 | 423.2 | 1549.7 | 865.1 | 120.3 | 156.2 |
| AB062768.1 | 21434 | 34.8 | 66.8 | 72.5 | 77.9 | 74.5 | 39.6 |
| AF182836.1 | 3922 | 21.1 | 17.5 | 85.6 | 55.9 | 68.1 | 23.0 |
| GU408692.1 | 546393 | 123.7 | 281.9 | 759.9 | 570.0 | 156.2 | 256.8 |
| AB088889.1 | 78084 | 169.9 | 237.3 | 150.5 | 367.9 | 422.2 | 358.6 |
| GU428680.1 | 538832 | 22.7 | 39.9 | 27.5 | 56.2 | 76.7 | 29.5 |
| AB084969.1 | 70817 | 33.5 | 56.1 | 91.9 | 84.9 | 71.7 | 36.2 |
| AB234367.1 | 146849 | 161.2 | 320.5 | 935.7 | 145.6 | 439.3 | 483.8 |
| AB191868.1 | 144495 | 64.5 | 64.0 | 130.0 | 88.3 | 117.9 | 46.1 |
| AB032000.1 | 36987 | 12028.1 | 13003.0 | 11470.9 | 11931.3 | 12997.2 | 9758.7 |
| EF454895.2 | 226214 | 11857.4 | 12056.9 | 13525.8 | 10684.0 | 12865.7 | 14089.4 |
| AB234372.1 | 148779 | 64.4 | 58.5 | 61.5 | 104.7 | 56.1 | 37.0 |
| AB085163.1 | 70117 | 84.4 | 57.7 | 60.4 | 74.7 | 93.2 | 49.8 |
| AB084955.1 | 69510 | 174.4 | 73.7 | 64.6 | 81.4 | 83.2 | 32.5 |
| GQ502640.1 | 539398 | 155.3 | 241.1 | 511.1 | 666.3 | 237.6 | 303.9 |
| AB192247.1 | 143443 | 102.7 | 555.1 | 1135.1 | 345.7 | 218.2 | 275.8 |
| AB084954.1 | 74331 | 48.0 | 44.2 | 30.3 | 74.0 | 81.5 | 42.5 |
| EF559163.1 | 220887 | 56.4 | 59.9 | 94.6 | 59.4 | 72.6 | 42.1 |
| GQ502642.1 | 584558 | 832.2 | 988.7 | 1030.1 | 404.6 | 2026.1 | 1082.0 |
| GQ426550.1 | 552289 | 11022.3 | 11103.0 | 9398.8 | 11987.0 | 13337.3 | 13100.0 |
| AF275918.1 | 46681 | 29.1 | 38.3 | 51.9 | 53.3 | 55.5 | 30.0 |
| AB191836.1 | 143094 | 121.2 | 553.2 | 203.7 | 200.4 | 116.8 | 89.1 |
| AB088880.1 | 77953 | 114.2 | 162.1 | 389.5 | 366.0 | 255.0 | 1107.0 |
| AY337320.1 | 106877 | 40.6 | 80.2 | 42.1 | 53.3 | 116.2 | 92.4 |

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| k__Bacteria | k__Bacteria | p__Spirochaetes | c__WWE1 |

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EU245777.1 gg_id:244285 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M6-B1
FJ380060.1 gg_id:586280 Spirochaeta sp. str. SR
X93928.1 gg_id:3802 Spirochaeta africana
AY605180.1 gg_id:106187 microbial mat clone LL026
AY337319.1 gg_id:103241 Spirochaeta sp. str. M6
X93926.1 gg_id:3807 Spirochaeta asiatica str. Z-7591
AF166259.1 gg_id:37803 Spironema culicis str. BR91
EU448140.1 gg_id:266509 Spirochaeta sp. str. SIP1
EU245914.1 gg_id:251213 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M8-B0
AB192150.1 gg_id:142321 termite gut homogenate clone RsTz-71
GQ406200.1 gg_id:583561 Benthic submerged sinkhole ecosystems sediment clone -45-14
AB088897.1 gg_id:77774 termite gut homogenate clone Rs-B68 sp.
EU385774.1 gg_id:273317 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S
EU245152.1 gg_id:240123 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-H3-B03
GU139329.1 gg_id:593443 lactate formate propionate hydrogen donors reductive dehalogenation trichloroeth
GU139313.1 gg_id:542335 lactate formate propionate hydrogen donors reductive dehalogenation trichloroeth
EF602483.1 gg_id:233469 metabolic phylum Planctomycetes anaerobic sulfide and sulfur-rich spring (Zodletone
AJ278165.1 gg_id:65483 anaerobic bioreactor clone SHA-116
AF286040.1 gg_id:51888 saltmarsh clone LCP-5
CU918232.1 gg_id:568533 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
AB248650.1 gg_id:146622 mesophilic anaerobic butyrate-degrading reactor clone BHB21
CU918313.1 gg_id:562644 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
CU918359.1 gg_id:540776 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
EU887773.1 gg_id:336104 and RFLP anaerobes Nisargruna biogas plant anaerobic digester clone 8SN
FJ825527.1 gg_id:561904 Microbial during start-up mesophilic biogas plant clone 42B_BS1_4
EF515598.1 gg_id:222084 Electricigen Enrichment MFC full-scale anaerobic bioreactor sludge treating brewery
CU917471.1 gg_id:560582 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
EU639140.1 gg_id:356001 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n
CT574476.1 gg_id:154406 major candidate division within anaerobic sludge digester Evry municipal wastewate
CR933095.1 gg_id:110532 municipal wastewater treatment plant clone 029C09_P_DI_P15
CT574479.1 gg_id:150885 major candidate division within anaerobic sludge digester Evry municipal wastewate
CT574480.1 gg_id:153806 major candidate division within anaerobic sludge digester Evry municipal wastewate
EU638532.1 gg_id:348562 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n
CT574516.1 gg_id:154664 major candidate division within anaerobic sludge digester Evry municipal wastewate
CT574541.1 gg_id:151349 major candidate division within anaerobic sludge digester Evry municipal wastewate
CT574543.1 gg_id:151105 major candidate division within anaerobic sludge digester Evry municipal wastewate
CT574501.1 gg_id:154819 major candidate division within anaerobic sludge digester Evry municipal wastewate
CU918874.1 gg_id:540010 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
CU918574.1 gg_id:551980 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
EU639264.1 gg_id:339506 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n
GQ461620.1 gg_id:567190 Coupling -ITS Clone Libraries and Automated Intergenic Spacer Microbial TCE Bioren

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| EU245777.1 | 244285 | 395.0 | 528.4 | 1107.1 | 305.0 | 161.2 | 165.0 |
| FJ380060.1 | 586280 | 3853.1 | 6198.2 | 5915.7 | 3456.9 | 2735.6 | 3254.9 |
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| AY605180.1 | 106187 | 285.6 | 167.2 | 76.3 | 197.2 | 155.7 | 74.4 |
| AY337319.1 | 103241 | 108.4 | 86.8 | 240.8 | 87.7 | 138.3 | 101.7 |
| X93926.1 | 3807 | 58.7 | 28.3 | 446.7 | 98.9 | 89.5 | 179.3 |
| AF166259.1 | 37803 | 76.2 | 86.3 | 93.8 | 119.3 | 125.1 | 145.0 |
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| EU245914.1 | 251213 | 43.7 | 40.1 | 37.5 | 61.1 | 60.6 | 34.2 |
| AB192150.1 | 142321 | 48.5 | 140.6 | 54.9 | 83.0 | 99.2 | 55.8 |
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| AB088897.1 | 77774 | 54.1 | 95.5 | 178.5 | 90.2 | 296.3 | 92.6 |
| EU385774.1 | 273317 | 5656.3 | 6347.3 | 3984.3 | 3218.4 | 5439.5 | 5325.3 |
| EU245152.1 | 240123 | 1632.2 | 1207.3 | 141.2 | 918.9 | 1055.1 | 1054.7 |
| GU139329.1 | 593443 | 4129.5 | 5087.9 | 6191.4 | 6430.6 | 7518.5 | 7659.7 |
| GU139313.1 | 542335 | 4167.9 | 4888.4 | 5732.4 | 3540.9 | 6445.2 | 6677.6 |
| EF602483.1 | 233469 | 790.6 | 960.8 | 2456.3 | 717.9 | 2082.7 | 2422.3 |
| AJ278165.1 | 65483 | 53.7 | 133.9 | 40.9 | 70.2 | 87.3 | 46.0 |
| AF286040.1 | 51888 | 48.1 | 133.8 | 89.2 | 156.1 | 90.7 | 42.3 |
| CU918232.1 | 568533 | 12395.4 | 13559.9 | 6067.8 | 9798.7 | 13141.4 | 12302.6 |
| AB248650.1 | 146622 | 53.1 | 149.5 | 54.6 | 102.4 | 124.9 | 110.2 |
| CU918313.1 | 562644 | 7809.0 | 9006.5 | 8587.4 | 6764.1 | 9093.3 | 6765.0 |
| CU918359.1 | 540776 | 1271.9 | 1029.7 | 1290.3 | 1375.3 | 1506.9 | 1428.3 |
| EU887773.1 | 336104 | 3984.6 | 4362.6 | 8830.0 | 5573.3 | 1497.3 | 2914.6 |
| FJ825527.1 | 561904 | 1239.6 | 1140.9 | 1819.0 | 2026.5 | 711.3 | 1498.1 |
| EF515598.1 | 222084 | 20.3 | 31.9 | 71.5 | 57.2 | 74.7 | 13.3 |
| CU917471.1 | 560582 | 9073.0 | 9849.9 | 7905.8 | 6269.0 | 8895.2 | 7737.2 |
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| CT574476.1 | 154406 | 4465.6 | 5225.0 | 3519.0 | 3460.0 | 5932.9 | 5483.6 |
| CR933095.1 | 110532 | 1945.5 | 2838.1 | 3209.9 | 1843.6 | 4108.5 | 3600.1 |
| CT574479.1 | 150885 | 5933.1 | 4750.9 | 2197.1 | 5237.9 | 2706.5 | 3276.5 |
| CT574480.1 | 153806 | 12074.6 | 12405.7 | 8054.4 | 8670.2 | 10587.4 | 8676.7 |
| EU638532.1 | 348562 | 1674.9 | 1821.7 | 1780.8 | 2464.5 | 3847.0 | 4094.7 |
| CT574516.1 | 154664 | 16096.4 | 14224.4 | 14303.0 | 12202.2 | 14623.8 | 13220.6 |
| CT574541.1 | 151349 | 6146.6 | 6672.4 | 7229.2 | 4356.5 | 5501.7 | 6233.5 |
| CT574543.1 | 151105 | 4248.2 | 5762.2 | 2655.4 | 3040.4 | 1621.3 | 1855.2 |
| CT574501.1 | 154819 | 1569.1 | 2664.4 | 4118.5 | 927.3 | 607.2 | 1451.2 |
| CU918874.1 | 540010 | 12215.3 | 7858.4 | 12958.8 | 8520.7 | 13146.2 | 12265.1 |
| CU918574.1 | 551980 | 9658.7 | 9135.9 | 5071.4 | 6971.8 | 9612.7 | 7737.7 |
| EU639264.1 | 339506 | 5940.3 | 5354.7 | 3436.8 | 4347.5 | 6225.5 | 5868.5 |
| GQ461620.1 | 567190 | 69.0 | 116.5 | 251.6 | 142.3 | 90.4 | 93.5 |

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| k__Bacteria | k__Bacteria | p__Synergistetes | c__Synergistia |

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| o__PBS-18 | f__SHA-4 |
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| o__PBS-18 | f__SHA-4 |
| o__PBS-18 | f__SHA-4 |
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| o__unclassified | f__unclassified |
| o__unclassified | f__unclassified |
| o__unclassified | f__unclassified |
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| o__Synergistales | f__Anaerobaculaceae |
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| o__Synergistales | f__Dethiosulfovibrionaceae |
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g__W22
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g__Pyramidobacter

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| s__unclassified | 51221 |
| s__unclassified | 51409 |
| s__unclassified | 54948 |
| s__unclassified | 54990 |
| s__unclassified | 55427 |
| s__Anaerobaculum hydrogeniformans | 55350 |
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| s__unclassified | 55254 |
| s__unclassified | 55555 |
| s__unclassified | 55683 |
| s__unclassified | 56015 |
| s__unclassified | 56046 |
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| s__unclassified | 55479 |
| s__unclassified | 56343 |
| s__unclassified | 54955 |
| s__unclassified | 55194 |
| s__unclassified | 55855 |
| s__Jonquetella anthropi | 55629 |
| s__unclassified | 55601 |
| s__Pyramidobacter piscolens | 55733 |

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

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|---|---|---|---|---|---|---|---|
| DQ988271.1 | 203045 | 1408.3 | 1334.8 | 2775.3 | 1174.0 | 665.7 | 941.9 |
| CU927274.1 | 539547 | 211.2 | 380.0 | 656.8 | 194.6 | 437.8 | 194.0 |
| AB175393.1 | 99923 | 330.4 | 1342.4 | 931.3 | 582.0 | 545.1 | 643.0 |
| EU864445.1 | 335847 | 5147.0 | 5585.1 | 9272.4 | 8241.3 | 7799.0 | 11540.5 |
| CU923797.1 | 567700 | 4071.4 | 7732.2 | 9717.2 | 4853.8 | 4163.0 | 5067.7 |
| AB513440.1 | 566297 | 29.1 | 20.0 | 14.0 | 57.0 | 52.3 | 17.7 |
| AJ306785.1 | 66916 | 130.8 | 110.8 | 359.7 | 245.2 | 163.4 | 132.5 |
| AY426469.1 | 107649 | 68.8 | 119.8 | 79.9 | 57.5 | 68.6 | 39.7 |
| EF602475.1 | 256047 | 6073.5 | 7595.3 | 9296.9 | 7918.7 | 784.8 | 1354.3 |
| EF602476.1 | 227609 | 900.7 | 1270.1 | 1625.4 | 494.1 | 2131.9 | 1888.9 |
| EU381859.1 | 271582 | 18568.5 | 20083.1 | 20181.1 | 16719.4 | 16564.7 | 16026.2 |
| EU474681.1 | 290320 | 7626.1 | 9390.4 | 9502.2 | 6477.2 | 5395.1 | 6017.0 |
| AB231045.1 | 203507 | 2956.4 | 3394.5 | 3033.5 | 5883.5 | 2521.7 | 4196.9 |
| EU283584.1 | 278222 | 2327.0 | 2037.4 | 7528.1 | 3189.0 | 1722.3 | 3795.7 |
| EU101271.1 | 242859 | 14782.3 | 15601.3 | 9460.5 | 12398.7 | 14273.4 | 13974.6 |
| EU681994.1 | 287458 | 13424.5 | 15340.1 | 14700.0 | 10196.7 | 12037.9 | 11060.6 |
| AF255601.1 | 74652 | 191.8 | 1427.8 | 1506.9 | 1647.7 | 1793.1 | 1581.3 |
| EU635940.1 | 278855 | 3610.7 | 2883.2 | 3535.4 | 2398.6 | 402.9 | 764.7 |
| CU926426.1 | 573323 | 425.5 | 932.4 | 1390.4 | 1019.9 | 2045.6 | 2722.4 |
| CU926777.1 | 558738 | 39.1 | 49.6 | 47.9 | 74.8 | 83.9 | 45.4 |
| AF129869.1 | 1641 | 900.7 | 1675.6 | 1068.1 | 281.1 | 1019.9 | 787.0 |
| NZ_ACJX02000009.1 | 484357 | 9796.1 | 6524.7 | 14879.8 | 10007.0 | 7080.0 | 8560.4 |
| EU878334.1 | 565884 | 9644.9 | 9018.1 | 10521.3 | 8547.9 | 9559.0 | 9473.7 |
| NR_028903.1 | 591885 | 5248.6 | 7499.9 | 9167.4 | 5897.2 | 6986.5 | 8131.8 |
| U50711.1 | 1634 | 6342.1 | 5216.5 | 9196.3 | 6493.9 | 6165.7 | 5738.6 |
| EU639374.1 | 343828 | 1896.1 | 1884.6 | 2684.3 | 1829.5 | 2611.0 | 2577.1 |
| EU276415.1 | 290298 | 4787.7 | 4018.9 | 7678.4 | 4792.5 | 5338.8 | 5067.6 |
| CU919006.1 | 533770 | 1017.5 | 1393.5 | 2730.2 | 945.1 | 2412.1 | 2902.3 |
| GU357466.1 | 574739 | 176.5 | 221.4 | 430.6 | 185.4 | 311.7 | 325.3 |
| AB175377.1 | 99359 | 59.7 | 35.1 | 34.8 | 86.9 | 75.6 | 34.1 |
| EU234248.1 | 249038 | 106.5 | 115.4 | 165.1 | 127.8 | 138.7 | 227.3 |
| AF069287.1 | 1649 | 408.5 | 512.6 | 1121.7 | 2134.6 | 4323.9 | 5182.7 |
| EF559198.1 | 218020 | 9966.1 | 6064.1 | 4559.9 | 9420.3 | 6040.4 | 5578.0 |
| AF234542.1 | 71455 | 146.2 | 394.3 | 95.4 | 124.5 | 178.3 | 98.9 |
| AY005466.1 | 72749 | 6612.1 | 6166.0 | 5147.6 | 6022.8 | 880.7 | 5631.4 |
| CU917598.1 | 543835 | 6548.7 | 8092.1 | 8708.7 | 5109.2 | 4402.2 | 7155.6 |
| AY953224.1 | 114635 | 7088.2 | 5280.2 | 5258.7 | 3334.3 | 2146.5 | 3390.3 |
| CU925573.1 | 553988 | 10054.8 | 9479.6 | 9825.8 | 7286.8 | 5733.8 | 8893.2 |
| EF436500.1 | 204216 | 206.0 | 798.9 | 1024.0 | 229.5 | 127.8 | 150.3 |
| CU920428.1 | 539058 | 38.4 | 30.7 | 21.9 | 52.9 | 69.0 | 47.5 |
| EU462629.1 | 302106 | 3426.7 | 3687.6 | 2564.2 | 2064.8 | 1534.8 | 1392.0 |

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| k__Bacteria | k__Bacteria | p__Synergistetes | c__Synergistia |
| k__Bacteria | k__Bacteria | p__Synergistetes | c__Synergistia |
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| k__Bacteria | k__Bacteria | p__Synergistetes | c__Synergistia |

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|---|---|
| o__Synergistales | f__Dethiosulfovibrionaceae |
| o__Synergistales | f__Dethiosulfovibrionaceae |
| o__Synergistales | f__Dethiosulfovibrionaceae |
| o__Synergistales | f__Dethiosulfovibrionaceae |
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| o__Synergistales | f__Synergistaceae |

g__Pyramidobacter
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g__TG5
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g__Thermanaerovibrio
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| s__Pyramidobacter piscolens | 55782 |
| s__unclassified | 55483 |
| s__unclassified | 55003 |
| s__unclassified | 55359 |
| s__unclassified | 55404 |
| s__unclassified | 55405 |
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| s__unclassified | 56056 |
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| s__unclassified | 55044 |
| s__unclassified | 55131 |
| s__unclassified | 55512 |
| s__Thermanaerovibrio acidaminovorans | 55567 |
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| s__unclassified | 55224 |
| s__unclassified | 55242 |
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| s__unclassified | 55967 |
| s__unclassified | 56013 |

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

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|---|---|---|---|---|---|---|---|
| DQ308572.1 | 149439 | 24.0 | 19.8 | 24.7 | 52.3 | 66.7 | 18.6 |
| GU303160.1 | 585815 | 5643.5 | 4870.7 | 3665.0 | 5519.0 | 1946.0 | 1526.6 |
| AB288913.1 | 199975 | 8626.0 | 8826.6 | 7331.6 | 5506.2 | 6196.7 | 7754.6 |
| DQ085087.1 | 132438 | 45.7 | 85.6 | 217.8 | 69.7 | 54.9 | 65.4 |
| AF125200.1 | 1643 | 4260.0 | 5523.9 | 8723.2 | 3473.8 | 3698.9 | 4054.9 |
| AF125199.2 | 1642 | 9732.1 | 9818.4 | 10771.1 | 9565.2 | 11059.5 | 12685.0 |
| GU410680.1 | 540821 | 19391.2 | 18971.9 | 11773.1 | 16338.8 | 18232.7 | 19116.0 |
| AB062819.1 | 19846 | 7911.8 | 7237.3 | 7409.9 | 6284.3 | 5844.1 | 8442.3 |
| AB062836.1 | 38526 | 40.4 | 53.3 | 22.3 | 60.0 | 56.7 | 25.1 |
| AB192113.1 | 142452 | 543.8 | 516.9 | 573.6 | 980.7 | 583.7 | 422.4 |
| AB192116.1 | 143824 | 1724.5 | 2198.6 | 4028.3 | 2262.4 | 360.1 | 927.1 |
| AB234551.1 | 149454 | 211.9 | 919.9 | 185.4 | 151.3 | 184.6 | 278.0 |
| DQ307691.1 | 144040 | 42.0 | 62.4 | 73.6 | 68.5 | 80.3 | 59.8 |
| AB299560.1 | 254669 | 18468.0 | 18607.5 | 9355.1 | 11430.4 | 12263.8 | 12088.2 |
| AB192115.1 | 144260 | 25.6 | 66.6 | 117.8 | 68.4 | 65.2 | 41.1 |
| AB231081.1 | 146679 | 541.3 | 834.3 | 1657.7 | 325.2 | 452.6 | 543.7 |
| AB189694.1 | 113993 | 22.9 | 32.0 | 27.4 | 62.8 | 73.3 | 34.0 |
| AB299558.1 | 237398 | 1613.6 | 2178.4 | 3313.6 | 2212.9 | 2476.5 | 2413.8 |
| CU463952.1 | 276742 | 2867.4 | 3109.7 | 5190.8 | 3160.1 | 2191.4 | 4474.6 |
| EF551160.1 | 230271 | 4933.9 | 4922.6 | 5897.3 | 4047.7 | 3258.5 | 4636.6 |
| DQ412721.1 | 162959 | 3636.6 | 4611.0 | 5877.4 | 3171.6 | 4292.4 | 4600.0 |
| CP001818.1 | 523250 | 2469.3 | 2927.2 | 3167.8 | 2907.6 | 1488.4 | 1423.3 |
| CU927653.1 | 568704 | 4712.2 | 5478.1 | 4504.0 | 4627.1 | 2144.4 | 3038.1 |
| CU924623.1 | 558424 | 8434.0 | 8471.2 | 4870.5 | 9057.3 | 6848.8 | 5791.9 |
| EU234149.1 | 247916 | 133.9 | 109.9 | 327.0 | 280.6 | 214.6 | 199.4 |
| CU919451.1 | 575488 | 14215.8 | 12177.4 | 13223.1 | 13401.5 | 12619.2 | 13568.4 |
| EU471574.1 | 296843 | 5599.8 | 6119.7 | 7118.2 | 4065.8 | 1853.6 | 4140.1 |
| CU920720.1 | 536647 | 6857.2 | 6610.7 | 6281.5 | 6969.0 | 4817.7 | 5189.7 |
| EU471563.1 | 290654 | 13872.6 | 14314.9 | 12439.1 | 11739.2 | 15941.2 | 13318.2 |
| CU920536.1 | 552202 | 3960.9 | 4577.9 | 4119.1 | 3471.8 | 1697.2 | 1932.8 |
| CU923733.1 | 575163 | 2102.6 | 2401.5 | 1801.0 | 2936.8 | 2219.0 | 2824.1 |
| CT573946.1 | 156047 | 24.3 | 31.3 | 45.3 | 60.4 | 65.4 | 27.3 |
| CU926881.1 | 542837 | 3568.9 | 3525.9 | 6466.8 | 5227.4 | 2572.1 | 5462.3 |
| CU925055.1 | 568648 | 4268.0 | 4347.0 | 6641.6 | 5625.8 | 5934.8 | 10022.9 |
| FJ189547.1 | 354649 | 2457.6 | 2608.8 | 4825.6 | 5881.5 | 3183.8 | 4624.0 |
| CU927313.1 | 571181 | 6391.2 | 6390.9 | 2114.0 | 5987.4 | 4706.1 | 5207.4 |
| GQ377129.1 | 547330 | 157.6 | 218.2 | 52.4 | 170.4 | 62.8 | 25.0 |
| CU920532.1 | 559188 | 7986.5 | 6330.8 | 6440.4 | 9221.8 | 4284.8 | 5473.6 |
| CU924981.1 | 573012 | 1576.1 | 2264.0 | 2913.4 | 2831.7 | 969.6 | 2619.5 |
| CU919042.1 | 563832 | 3889.5 | 3458.4 | 2761.0 | 2212.3 | 1209.9 | 2432.2 |
| AM933660.1 | 276480 | 6816.4 | 4791.8 | 4034.1 | 5382.7 | 5728.8 | 4206.2 |

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| k__Bacteria | k__Bacteria | p__Synergistetes | c__Synergistia |
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| k__Bacteria | k__Bacteria | p__Synergistetes | c__Synergistia |
| k__Bacteria | k__Bacteria | p__Tenericutes | c__Erysipelotrichi |
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| k__Bacteria | k__Bacteria | p__Tenericutes | c__Erysipelotrichi |
| k__Bacteria | k__Bacteria | p__Tenericutes | c__Erysipelotrichi |
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| k__Bacteria | k__Bacteria | p__Tenericutes | c__Erysipelotrichi |
| k__Bacteria | k__Bacteria | p__Tenericutes | c__Erysipelotrichi |

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| o__Synergistales | f__Synergistaceae |
| o__Synergistales | f__Thermovirgaceae |
| o__Synergistales | f__Thermovirgaceae |
| o__Synergistales | f__Thermovirgaceae |
| o__Synergistales | f__Thermovirgaceae |
| o__Synergistales | f__TTA_B6 |
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| o__Erysipelotrichales | f__Erysipelotrichaceae |
| o__Erysipelotrichales | f__Erysipelotrichaceae |
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g__Thermovirga
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| s__Allobaculum sp ID4 | 71302 |
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| s__Allobaculum sp ID4 | 71311 |
| s__Allobaculum sp ID4 | 71314 |
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GQ377130.1 gg_id:544607 structure two reactive PCE degrading enrichment s stimulated OU Duck Pond Norma
CU925946.1 gg_id:571391 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
DQ071273.1 gg_id:143575 Thermovirga lienii str. Cas60314
EU721809.1 gg_id:568879 microbial production water Alaskan mesothermic petroleum reservoir two methods
AB195868.1 gg_id:109151 Anaerobic sludge clone N42
CU918985.1 gg_id:552219 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
EF515514.1 gg_id:223171 Electricigen Enrichment MFC full-scale anaerobic bioreactor sludge treating brewery
FN563362.1 gg_id:539330 Impact changing HRT OLR on prokaryotes involved biomethanizitaion and fuzzy logic
AY553945.1 gg_id:114315 Baltimore Harbor sediment clone FA12
AB175356.1 gg_id:107021 mesophilic anaerobic BSA digester clone BSA1B-02
EU887988.1 gg_id:329262 Microbial structure hydrolytic stage two-stage anaerobic digestion grass silage leach
EU507776.1 gg_id:266082 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_aaa04f03
EU508945.1 gg_id:270089 cecal contents Mus musculus strain C57BL/6J; MD6 clone MD6_aap39h10
EU511474.1 gg_id:266450 cecal contents Mus musculus strain C57BL/6J; WD9 clone WD9_aak05b04
EU507857.1 gg_id:266027 cecal contents Mus musculus strain C57BL/6J; MD24 clone MD24_aaa02a05
EU508930.1 gg_id:258976 cecal contents Mus musculus strain C57BL/6J; MD6 clone MD6_aap39b10
EU504430.1 gg_id:259965 cecal contents Mus musculus strain C57BL/6J; CRWD6 clone CRWD6_aaa04c01
EU505286.1 gg_id:264866 cecal contents Mus musculus strain C57BL/6J; myd4 clone myd4_aaa01h06
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EU511346.1 gg_id:264641 cecal contents Mus musculus strain C57BL/6J; WD8 clone WD8_aak18g03
EU511034.1 gg_id:277428 cecal contents Mus musculus strain C57BL/6J; WD7 clone WD7_aal01f09
EU511295.1 gg_id:259850 cecal contents Mus musculus strain C57BL/6J; WD8 clone WD8_aak17g10
EU511348.1 gg_id:260083 cecal contents Mus musculus strain C57BL/6J; WD8 clone WD8_aak18g05
EU508531.1 gg_id:275302 cecal contents Mus musculus strain C57BL/6J; MD2 clone MD2_aap35a03
EU510958.1 gg_id:262201 cecal contents Mus musculus strain C57BL/6J; WD6 clone WD6_aak52d06
EF098358.1 gg_id:175699 mouse cecum clone SWPT15_aaa01e02
EU508927.1 gg_id:262108 cecal contents Mus musculus strain C57BL/6J; MD6 clone MD6_aap39a10
EU505295.1 gg_id:258773 cecal contents Mus musculus strain C57BL/6J; myd4 clone myd4_aaa02a12
EU511414.1 gg_id:276848 cecal contents Mus musculus strain C57BL/6J; WD8 clone WD8_aak19h01
EU504622.1 gg_id:273734 cecal contents Mus musculus strain C57BL/6J; myd1 clone myd1_aaa03d01
EU507921.1 gg_id:274791 cecal contents Mus musculus strain C57BL/6J; MD24 clone MD24_aaa03e06
EU511464.1 gg_id:263051 cecal contents Mus musculus strain C57BL/6J; WD8 clone WD8_aak20h06
EF099656.1 gg_id:173979 mouse cecum clone SWPT4_aaa02e05
EU509698.1 gg_id:269257 cecal contents Mus musculus strain C57BL/6J; WD10 clone WD10_aak47c08
EU509742.1 gg_id:258735 cecal contents Mus musculus strain C57BL/6J; WD10 clone WD10_aak48b11
EU505645.1 gg_id:268331 cecal contents Mus musculus strain C57BL/6J; myd5 clone myd5_aaa04a03
EU507618.1 gg_id:262103 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_aaa02a08
EU508439.1 gg_id:258863 cecal contents Mus musculus strain C57BL/6J; MD2 clone MD2_aap33e07
EU508879.1 gg_id:271759 cecal contents Mus musculus strain C57BL/6J; MD6 clone MD6_aap37f07
EU506729.1 gg_id:263588 cecal contents Mus musculus strain C57BL/6J; MD20 clone MD20_aap55c05
EF099678.1 gg_id:174236 mouse cecum clone SWPT4_aaa02g10

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| GQ377130.1 | 544607 | 240.4 | 799.2 | 729.8 | 497.2 | 943.2 | 770.1 |
| CU925946.1 | 571391 | 2628.4 | 3328.2 | 4309.7 | 3393.6 | 2631.4 | 3971.9 |
| DQ071273.1 | 143575 | 111.7 | 183.4 | 245.1 | 127.1 | 116.2 | 116.9 |
| EU721809.1 | 568879 | 46.5 | 52.9 | 108.1 | 164.5 | 51.4 | 27.9 |
| AB195868.1 | 109151 | 86.1 | 124.8 | 121.4 | 110.8 | 127.9 | 80.9 |
| CU918985.1 | 552219 | 5992.9 | 6713.4 | 2432.1 | 3760.8 | 3416.7 | 2051.1 |
| EF515514.1 | 223171 | 3030.4 | 2928.8 | 3818.0 | 6095.0 | 2271.4 | 2564.1 |
| FN563362.1 | 539330 | 3121.8 | 3766.8 | 5068.8 | 3417.5 | 3848.2 | 4502.9 |
| AY553945.1 | 114315 | 123.1 | 315.8 | 288.3 | 127.2 | 236.7 | 140.9 |
| AB175356.1 | 107021 | 46.3 | 78.2 | 24.7 | 72.7 | 79.1 | 58.3 |
| EU887988.1 | 329262 | 14228.6 | 14355.9 | 11695.7 | 13544.2 | 11441.1 | 10373.7 |
| EU507776.1 | 266082 | 12149.2 | 13711.3 | 8168.0 | 9780.6 | 13387.3 | 10834.7 |
| EU508945.1 | 270089 | 5364.6 | 5065.1 | 2713.2 | 4442.5 | 6032.3 | 4657.7 |
| EU511474.1 | 266450 | 7450.5 | 8049.1 | 5171.4 | 4946.6 | 10502.6 | 8142.5 |
| EU507857.1 | 266027 | 7146.5 | 7038.6 | 4373.3 | 3295.7 | 4234.0 | 3993.1 |
| EU508930.1 | 258976 | 4285.0 | 5826.3 | 4815.6 | 6070.6 | 10662.6 | 9969.1 |
| EU504430.1 | 259965 | 176.7 | 731.9 | 192.7 | 1189.0 | 379.9 | 615.6 |
| EU505286.1 | 264866 | 11852.7 | 10682.0 | 5322.2 | 10110.3 | 11387.9 | 10229.2 |
| EU511554.1 | 273187 | 8040.8 | 7406.5 | 3798.3 | 4002.7 | 5947.4 | 3093.4 |
| EU511346.1 | 264641 | 2218.0 | 3027.1 | 3122.5 | 3400.0 | 4552.8 | 3224.6 |
| EU511034.1 | 277428 | 310.7 | 189.5 | 663.4 | 259.0 | 135.7 | 164.9 |
| EU511295.1 | 259850 | 3902.9 | 8012.1 | 3773.7 | 2356.6 | 9653.8 | 6726.2 |
| EU511348.1 | 260083 | 5754.1 | 7233.8 | 2279.4 | 5833.9 | 8078.1 | 6802.5 |
| EU508531.1 | 275302 | 5018.2 | 5980.6 | 3695.2 | 2550.2 | 1350.3 | 1267.8 |
| EU510958.1 | 262201 | 3866.1 | 3996.8 | 2616.0 | 2655.5 | 4117.5 | 3059.0 |
| EF098358.1 | 175699 | 884.3 | 1724.4 | 1268.8 | 1661.5 | 418.2 | 1471.2 |
| EU508927.1 | 262108 | 9371.4 | 8707.0 | 6093.8 | 7174.5 | 5474.9 | 6902.3 |
| EU505295.1 | 258773 | 2177.2 | 2112.7 | 1259.2 | 1280.6 | 2169.2 | 1330.0 |
| EU511414.1 | 276848 | 3143.0 | 3471.2 | 2493.7 | 2371.6 | 6273.2 | 4240.4 |
| EU504622.1 | 273734 | 66.6 | 103.5 | 69.2 | 79.3 | 340.1 | 248.9 |
| EU507921.1 | 274791 | 5808.9 | 6231.0 | 2541.5 | 2189.0 | 2973.9 | 1601.2 |
| EU511464.1 | 263051 | 13868.6 | 12414.4 | 7121.7 | 5235.7 | 4278.6 | 4578.1 |
| EF099656.1 | 173979 | 10532.2 | 8724.3 | 2040.3 | 3084.8 | 4618.7 | 3531.8 |
| EU509698.1 | 269257 | 6524.9 | 6947.8 | 7903.6 | 7169.1 | 13629.3 | 8676.7 |
| EU509742.1 | 258735 | 4049.5 | 5042.3 | 2790.5 | 1404.9 | 4148.6 | 1823.9 |
| EU505645.1 | 268331 | 3968.7 | 4374.0 | 2837.4 | 3342.9 | 9860.8 | 6688.2 |
| EU507618.1 | 262103 | 802.9 | 1312.2 | 765.6 | 913.9 | 240.7 | 286.2 |
| EU508439.1 | 258863 | 3933.2 | 3834.5 | 2669.6 | 2497.7 | 6415.9 | 4010.9 |
| EU508879.1 | 271759 | 2269.7 | 3309.1 | 3562.8 | 3015.0 | 7503.2 | 5038.8 |
| EU506729.1 | 263588 | 6871.9 | 6815.4 | 4457.1 | 5889.0 | 7515.7 | 7033.2 |
| EF099678.1 | 174236 | 3805.9 | 3940.6 | 2893.7 | 3573.9 | 5748.1 | 3898.1 |

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|---|---|---|---|
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| k__Bacteria | k__Bacteria | p__Tenericutes | c__Erysipelotrichi |
| k__Bacteria | k__Bacteria | p__Tenericutes | c__Erysipelotrichi |
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|---|---|
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EU511038.1 gg_id:260292 cecal contents Mus musculus strain C57BL/6J; WD7 clone WD7_aal01g03
EU505346.1 gg_id:275252 cecal contents Mus musculus strain C57BL/6J; myd4 clone myd4_aaa02h09
EU508553.1 gg_id:259161 cecal contents Mus musculus strain C57BL/6J; MD2 clone MD2_aap35c08
EU508904.1 gg_id:262026 cecal contents Mus musculus strain C57BL/6J; MD6 clone MD6_aap38b10
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EU507820.1 gg_id:262850 cecal contents Mus musculus strain C57BL/6J; MD24 clone MD24_aaa01d08
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EU507144.1 gg_id:264111 cecal contents Mus musculus strain C57BL/6J; MD22 clone MD22_aaa02c04
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EU503726.1 gg_id:264512 cecal contents Mus musculus strain C57BL/6J; CRWD2 clone CRWD2_aaa03g04
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EU507690.1 gg_id:276757 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_aaa03c07
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EU505497.1 gg_id:264699 cecal contents Mus musculus strain C57BL/6J; myd5 clone myd5_aaa01e06
EU507351.1 gg_id:260179 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_2aaa02a09
EU511453.1 gg_id:270231 cecal contents Mus musculus strain C57BL/6J; WD8 clone WD8_aak20e11
EU507804.1 gg_id:262219 cecal contents Mus musculus strain C57BL/6J; MD24 clone MD24_aaa01b02
EU511437.1 gg_id:270460 cecal contents Mus musculus strain C57BL/6J; WD8 clone WD8_aak20c06
EU507851.1 gg_id:265433 cecal contents Mus musculus strain C57BL/6J; MD24 clone MD24_aaa01h07
EU505321.1 gg_id:274384 cecal contents Mus musculus strain C57BL/6J; myd4 clone myd4_aaa02e01

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| EU511038.1 | 260292 | 1348.2 | 2050.9 | 665.5 | 1380.4 | 1063.6 | 716.8 |
| EU505346.1 | 275252 | 3041.0 | 4311.1 | 4121.4 | 4307.2 | 10394.4 | 8876.4 |
| EU508553.1 | 259161 | 3271.1 | 4389.7 | 2143.1 | 5158.9 | 1409.3 | 1076.7 |
| EU508904.1 | 262026 | 3432.5 | 4172.1 | 1664.3 | 1243.2 | 749.5 | 476.7 |
| EU508454.1 | 270956 | 7582.3 | 8651.9 | 5037.5 | 5971.6 | 9312.5 | 7108.6 |
| EU507820.1 | 262850 | 2444.4 | 2638.5 | 1489.5 | 922.8 | 2544.4 | 1234.1 |
| EU507901.1 | 261338 | 9157.6 | 9426.4 | 8672.3 | 8708.9 | 7960.8 | 8815.9 |
| EU507144.1 | 264111 | 4010.8 | 6716.0 | 1675.3 | 1481.7 | 10221.6 | 5832.2 |
| AY960571.1 | 115098 | 12078.2 | 10745.8 | 13403.0 | 10689.9 | 12356.4 | 10088.3 |
| EU503726.1 | 264512 | 3230.6 | 2221.7 | 694.2 | 2231.1 | 3589.4 | 2963.0 |
| EU507352.1 | 262440 | 1913.9 | 3151.5 | 2766.4 | 2947.3 | 6896.5 | 4838.0 |
| EU507705.1 | 276487 | 9123.0 | 5817.3 | 6355.7 | 8402.5 | 9286.7 | 8623.4 |
| EU509693.1 | 266803 | 1714.2 | 2433.4 | 4846.1 | 3545.4 | 2312.6 | 2387.4 |
| EU509103.1 | 263498 | 794.3 | 1073.7 | 2075.8 | 2210.0 | 336.3 | 315.7 |
| EU511545.1 | 262139 | 3006.1 | 3935.7 | 4115.0 | 2392.5 | 3772.7 | 2229.5 |
| EU507105.1 | 263436 | 2223.5 | 4610.4 | 1800.3 | 2112.9 | 8050.8 | 3842.1 |
| EU511638.1 | 272358 | 2311.6 | 3197.3 | 3414.9 | 3001.5 | 5090.4 | 4010.8 |
| EU507110.1 | 268053 | 3161.1 | 4565.6 | 1110.2 | 2974.9 | 3250.5 | 1936.9 |
| EU506770.1 | 276156 | 820.7 | 1223.8 | 659.2 | 1132.7 | 452.9 | 318.9 |
| EU508273.1 | 258736 | 4658.0 | 6113.8 | 5232.6 | 2721.5 | 4383.1 | 3129.8 |
| EF099605.1 | 181334 | 7403.9 | 7651.7 | 6117.0 | 5852.6 | 11581.0 | 8413.7 |
| EU508420.1 | 260325 | 8591.7 | 7901.9 | 8948.4 | 7363.3 | 7847.5 | 6482.2 |
| EU507848.1 | 259647 | 920.0 | 1550.7 | 881.3 | 1148.4 | 228.9 | 437.7 |
| EU505410.1 | 264645 | 3325.0 | 4337.0 | 4026.4 | 4048.0 | 10886.6 | 7575.5 |
| EU510950.1 | 276638 | 4121.1 | 5613.5 | 1970.8 | 3296.7 | 1737.4 | 3613.6 |
| EU506817.1 | 261795 | 7506.4 | 10231.4 | 1873.2 | 5552.7 | 11196.6 | 9076.5 |
| EU508375.1 | 277042 | 4640.9 | 5301.1 | 6093.7 | 5962.5 | 8329.2 | 7120.7 |
| EU506604.1 | 261326 | 1648.5 | 2497.9 | 1080.8 | 1309.7 | 2772.8 | 1744.7 |
| EU508929.1 | 266817 | 14893.3 | 13823.5 | 5376.4 | 10756.1 | 13584.6 | 9873.5 |
| EU508441.1 | 273802 | 12290.3 | 13883.5 | 7349.7 | 12866.4 | 14937.8 | 14852.9 |
| EU506669.1 | 272190 | 9555.6 | 8773.8 | 2176.6 | 6878.6 | 10509.0 | 7221.9 |
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| EU511255.1 | 265361 | 5427.4 | 6174.4 | 3004.4 | 2241.2 | 3446.4 | 2101.3 |
| EU505497.1 | 264699 | 2790.5 | 3506.8 | 2721.0 | 1496.3 | 3366.9 | 2977.0 |
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| EU511453.1 | 270231 | 7211.8 | 8225.7 | 6578.0 | 6095.6 | 6968.3 | 6979.7 |
| EU507804.1 | 262219 | 1514.0 | 3125.7 | 796.5 | 1898.5 | 219.4 | 267.5 |
| EU511437.1 | 270460 | 8238.7 | 8770.1 | 4811.7 | 8070.3 | 9781.9 | 8837.7 |
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EU505326.1 gg_id:261861 cecal contents Mus musculus strain C57BL/6J; myd4 clone myd4_aaa02e07
EU510815.1 gg_id:275230 cecal contents Mus musculus strain C57BL/6J; WD6 clone WD6_aak49f10
EU510996.1 gg_id:277246 cecal contents Mus musculus strain C57BL/6J; WD7 clone WD7_aal01b02
EU507968.1 gg_id:267744 cecal contents Mus musculus strain C57BL/6J; MD24 clone MD24_aaa04h08
EU508609.1 gg_id:259298 cecal contents Mus musculus strain C57BL/6J; MD2 clone MD2_aap36c03
EU510924.1 gg_id:270518 cecal contents Mus musculus strain C57BL/6J; WD6 clone WD6_aak51f12
EU504465.1 gg_id:264394 cecal contents Mus musculus strain C57BL/6J; CRWD6 clone CRWD6_aaa04h06
EU508654.1 gg_id:274263 cecal contents Mus musculus strain C57BL/6J; MD2 clone MD2_aap36h05
EU509080.1 gg_id:264601 cecal contents Mus musculus strain C57BL/6J; MD7 clone MD7_aap43c06
EU508631.1 gg_id:271916 cecal contents Mus musculus strain C57BL/6J; MD2 clone MD2_aap36e08
EU509668.1 gg_id:276430 cecal contents Mus musculus strain C57BL/6J; WD10 clone WD10_aak46h06
EU510822.1 gg_id:274196 cecal contents Mus musculus strain C57BL/6J; WD6 clone WD6_aak49g07
EU507406.1 gg_id:262058 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_2aaa02g09
EU509057.1 gg_id:260836 cecal contents Mus musculus strain C57BL/6J; MD7 clone MD7_aap42g10
EU505389.1 gg_id:266572 cecal contents Mus musculus strain C57BL/6J; myd4 clone myd4_aaa03f10
EU505423.1 gg_id:273017 cecal contents Mus musculus strain C57BL/6J; myd4 clone myd4_aaa04c06
EU504523.1 gg_id:273270 cecal contents Mus musculus strain C57BL/6J; myd1 clone myd1_aaa01g09
EF099211.1 gg_id:197429 mouse cecum clone SWPT2_aaa04a05
EU507094.1 gg_id:275623 cecal contents Mus musculus strain C57BL/6J; MD22 clone MD22_aaa01c02
EU507091.1 gg_id:275882 cecal contents Mus musculus strain C57BL/6J; MD22 clone MD22_aaa01b03
EU507233.1 gg_id:258892 cecal contents Mus musculus strain C57BL/6J; MD22 clone MD22_aaa03h12
EU506791.1 gg_id:263684 cecal contents Mus musculus strain C57BL/6J; MD20 clone MD20_aap56d05
EU511078.1 gg_id:273953 cecal contents Mus musculus strain C57BL/6J; WD7 clone WD7_aal02d04
EU507701.1 gg_id:267813 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_aaa03d08

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|---|---|---|---|---|---|---|---|
| EU507151.1 | 259622 | 5564.8 | 6627.5 | 4713.0 | 2973.4 | 6761.7 | 5166.2 |
| EU506795.1 | 259351 | 7969.3 | 9031.7 | 11437.3 | 8878.9 | 14855.9 | 11095.9 |
| EU508639.1 | 271756 | 8402.3 | 9090.8 | 7374.5 | 6251.1 | 9154.1 | 8097.9 |
| EU506764.1 | 264481 | 14221.1 | 11272.3 | 5782.6 | 9283.5 | 12474.3 | 10303.0 |
| EU510765.1 | 266227 | 1766.8 | 2446.7 | 2711.9 | 1823.0 | 1467.2 | 2430.0 |
| EU511037.1 | 259314 | 5713.7 | 6510.2 | 5241.1 | 5409.0 | 5827.3 | 5180.3 |
| EU505265.1 | 260007 | 4804.5 | 5989.8 | 2038.2 | 2204.8 | 4398.6 | 3639.1 |
| EU507268.1 | 273137 | 10301.0 | 10081.8 | 5654.3 | 7602.2 | 6611.2 | 6320.9 |
| EU507889.1 | 259741 | 10481.1 | 9761.1 | 7275.2 | 11161.4 | 11574.0 | 8534.2 |
| EU511607.1 | 264282 | 2390.1 | 4587.8 | 1658.6 | 1056.0 | 1224.8 | 571.5 |
| EU505264.1 | 268970 | 6489.8 | 7369.0 | 3817.6 | 2859.6 | 4217.2 | 2997.6 |
| EU506704.1 | 258419 | 3455.7 | 3572.5 | 4077.3 | 3640.8 | 7236.9 | 4554.9 |
| EU508537.1 | 260583 | 819.1 | 1215.3 | 683.4 | 1180.8 | 842.2 | 667.6 |
| EU505385.1 | 276790 | 3049.2 | 3603.0 | 2591.3 | 1778.8 | 636.8 | 822.7 |
| EU508763.1 | 260625 | 3929.8 | 6336.8 | 2682.9 | 3075.8 | 7756.8 | 4977.6 |
| EU504373.1 | 276645 | 5646.7 | 7276.4 | 4333.2 | 5407.2 | 10668.7 | 7684.5 |
| EU507092.1 | 268381 | 5594.6 | 6678.5 | 3124.2 | 4911.3 | 7322.6 | 5400.8 |
| EU505326.1 | 261861 | 14057.8 | 13875.0 | 9810.7 | 12562.3 | 8270.6 | 8646.6 |
| EU510815.1 | 275230 | 5963.3 | 5198.8 | 4510.2 | 6000.8 | 8313.3 | 6517.1 |
| EU510996.1 | 277246 | 5789.4 | 7594.7 | 1986.1 | 1539.9 | 5584.5 | 2975.5 |
| EU507968.1 | 267744 | 2913.8 | 3677.6 | 1593.3 | 4261.0 | 3004.6 | 3818.2 |
| EU508609.1 | 259298 | 1605.9 | 2258.6 | 681.7 | 715.5 | 1534.8 | 892.0 |
| EU510924.1 | 270518 | 3763.3 | 5645.6 | 2274.0 | 1766.5 | 3904.9 | 2335.2 |
| EU504465.1 | 264394 | 11022.0 | 10411.1 | 10222.9 | 8873.1 | 9260.8 | 8118.0 |
| EU508654.1 | 274263 | 9730.9 | 7694.3 | 5172.1 | 7246.7 | 5961.3 | 5709.2 |
| EU509080.1 | 264601 | 3996.3 | 5393.7 | 3854.8 | 2691.5 | 572.4 | 1215.4 |
| EU508631.1 | 271916 | 6300.6 | 6997.2 | 6089.1 | 7846.9 | 13086.4 | 8755.9 |
| EU509668.1 | 276430 | 14310.5 | 14293.4 | 11121.9 | 12196.2 | 13959.5 | 12377.4 |
| EU510822.1 | 274196 | 9411.8 | 9470.7 | 9752.6 | 8121.3 | 8969.7 | 9646.4 |
| EU507406.1 | 262058 | 14265.3 | 14560.5 | 8109.4 | 10805.4 | 17326.5 | 12349.4 |
| EU509057.1 | 260836 | 1205.3 | 1822.5 | 410.4 | 956.2 | 1769.6 | 1066.5 |
| EU505389.1 | 266572 | 100.5 | 190.4 | 205.4 | 204.6 | 925.7 | 688.4 |
| EU505423.1 | 273017 | 119.9 | 314.8 | 81.4 | 238.0 | 203.9 | 200.3 |
| EU504523.1 | 273270 | 3254.8 | 2693.9 | 4177.4 | 4764.7 | 6570.5 | 4431.4 |
| EF099211.1 | 197429 | 5313.7 | 5605.4 | 3367.2 | 3241.7 | 3977.8 | 3783.7 |
| EU507094.1 | 275623 | 6416.4 | 6348.5 | 3420.7 | 3250.0 | 3398.3 | 2569.5 |
| EU507091.1 | 275882 | 13380.4 | 14707.1 | 9142.4 | 10684.9 | 14926.4 | 12067.8 |
| EU507233.1 | 258892 | 4959.1 | 6253.2 | 3067.5 | 2481.7 | 4864.5 | 2597.2 |
| EU506791.1 | 263684 | 11371.3 | 9805.7 | 9083.3 | 7975.4 | 11316.2 | 9002.5 |
| EU511078.1 | 273953 | 420.3 | 723.7 | 419.3 | 549.9 | 629.0 | 1112.4 |
| EU507701.1 | 267813 | 241.3 | 371.6 | 195.6 | 640.1 | 1613.3 | 1607.0 |

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| k__Bacteria | k__Bacteria | p__Tenericutes | c__Erysipelotrichi |
| k__Bacteria | k__Bacteria | p__Tenericutes | c__Erysipelotrichi |
| k__Bacteria | k__Bacteria | p__Tenericutes | c__Erysipelotrichi |
| k__Bacteria | k__Bacteria | p__Tenericutes | c__Erysipelotrichi |
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| k__Bacteria | k__Bacteria | p__Tenericutes | c__Erysipelotrichi |

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| o__Erysipelotrichales | f__Erysipelotrichaceae |
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| s__Allobaculum sp ID4 | 71726 |
| s__Allobaculum sp ID4 | 71728 |
| s__Allobaculum sp ID4 | 71734 |
| s__Allobaculum sp ID4 | 71738 |
| s__Allobaculum sp ID4 | 71739 |
| s__Allobaculum sp ID4 | 71744 |
| s__Allobaculum sp ID4 | 71751 |
| s__Allobaculum sp ID4 | 71753 |
| s__Allobaculum sp ID4 | 71756 |
| s__Allobaculum sp ID4 | 71760 |
| s__Allobaculum stercoricanis | 71600 |
| s__unclassified | 71433 |
| s__unclassified | 71467 |
| s__unclassified | 71480 |
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| s__unclassified | 71589 |
| s__unclassified | 71591 |
| s__unclassified | 71662 |
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| s__unclassified | 71693 |
| s__unclassified | 71749 |
| s__unclassified | 71750 |
| s__unclassified | 71755 |
| s__Eubacterium cylindroides | 71384 |
| s__Eubacterium cylindroides | 71666 |
| s__Eubacterium cylindroides | 71688 |
| s__Eubacterium biforme | 71312 |
| s__Eubacterium biforme | 71326 |
| s__Eubacterium biforme | 71347 |
| s__Eubacterium biforme | 71355 |
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| s__Eubacterium biforme | 71454 |
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| s__Eubacterium biforme | 71468 |
| s__Eubacterium biforme | 71474 |
| s__Eubacterium biforme | 71485 |
| s__Eubacterium biforme | 71505 |

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

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|---|---|---|---|---|---|---|---|
| EU509085.1 | 271704 | 1059.4 | 1608.1 | 1816.4 | 1479.2 | 708.9 | 725.2 |
| EU509052.1 | 258746 | 6205.9 | 6908.6 | 5687.5 | 6642.4 | 10417.6 | 9970.5 |
| EU509587.1 | 270157 | 5207.4 | 6408.1 | 2879.0 | 2317.4 | 2448.5 | 2485.2 |
| EU511456.1 | 274825 | 10908.6 | 10215.2 | 9162.6 | 9451.1 | 6744.8 | 5899.4 |
| EU507812.1 | 277029 | 1081.3 | 1356.4 | 1800.1 | 1773.2 | 457.1 | 598.9 |
| EU511344.1 | 276457 | 3252.5 | 5670.5 | 1700.6 | 1209.9 | 3235.4 | 1815.8 |
| EU508445.1 | 263759 | 8763.1 | 6529.9 | 3158.3 | 7521.4 | 1284.1 | 2082.6 |
| EU505392.1 | 259805 | 2447.5 | 2361.1 | 1380.3 | 461.4 | 531.2 | 327.5 |
| EU508551.1 | 261932 | 9251.4 | 9658.8 | 8798.1 | 6451.9 | 5851.7 | 5250.1 |
| EU505649.1 | 261890 | 734.3 | 1461.1 | 490.0 | 718.8 | 381.4 | 465.1 |
| EU511197.1 | 273662 | 4148.4 | 4926.2 | 3809.5 | 3877.2 | 6153.7 | 5244.0 |
| AJ417075.1 | 98789 | 1076.7 | 1337.0 | 827.0 | 1701.4 | 1152.5 | 1431.9 |
| FJ880109.1 | 404034 | 11250.3 | 11466.5 | 6079.1 | 7533.8 | 10112.2 | 8509.2 |
| FJ880453.1 | 385422 | 3211.3 | 4787.1 | 1876.4 | 2643.4 | 7107.2 | 3725.7 |
| FJ881278.1 | 371453 | 9186.5 | 9635.4 | 5618.0 | 5396.0 | 7858.2 | 7762.5 |
| FJ880804.1 | 438839 | 4086.6 | 4564.9 | 2627.1 | 2065.9 | 1981.7 | 2149.5 |
| FJ879085.1 | 454212 | 9477.6 | 9132.3 | 6774.8 | 7465.6 | 8232.1 | 7013.3 |
| FJ881066.1 | 443722 | 751.3 | 1347.6 | 926.8 | 680.6 | 1210.9 | 1139.5 |
| DQ113686.1 | 134101 | 267.1 | 685.8 | 555.1 | 148.2 | 239.8 | 243.2 |
| FJ881120.1 | 389961 | 7677.3 | 8519.1 | 6284.9 | 5685.6 | 7176.9 | 5076.4 |
| FJ879538.1 | 396494 | 46.2 | 54.8 | 162.4 | 60.9 | 62.2 | 120.9 |
| EU503550.1 | 260405 | 16.7 | 19.1 | 30.6 | 53.7 | 42.7 | 12.5 |
| FJ880589.1 | 393599 | 640.9 | 681.7 | 557.6 | 136.2 | 116.6 | 135.5 |
| FJ880248.1 | 409717 | 672.8 | 101.6 | 1519.9 | 405.8 | 2220.9 | 1017.7 |
| FJ879685.1 | 386583 | 97.1 | 138.2 | 212.8 | 96.3 | 80.3 | 131.9 |
| FJ881144.1 | 425371 | 5900.0 | 5595.5 | 3186.4 | 2808.0 | 5057.6 | 4666.1 |
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| FJ681704.1 | 529292 | 12186.6 | 12755.6 | 10960.6 | 9520.3 | 9302.1 | 9399.5 |
| FJ681342.1 | 528410 | 13414.6 | 12429.2 | 14820.3 | 11286.3 | 7110.7 | 8286.6 |
| DQ805198.1 | 193516 | 257.4 | 343.8 | 660.1 | 224.8 | 3410.0 | 1591.1 |
| EU467401.1 | 297126 | 580.7 | 431.5 | 149.5 | 1311.5 | 149.3 | 175.3 |
| FJ683962.1 | 528905 | 3457.9 | 3777.5 | 4021.2 | 3188.6 | 464.9 | 1420.1 |
| DQ796924.1 | 180379 | 1926.4 | 1787.3 | 1810.7 | 1231.6 | 783.0 | 1200.0 |
| DQ325889.1 | 150312 | 1081.0 | 1031.8 | 669.9 | 720.9 | 1959.9 | 2049.9 |
| DQ325904.1 | 148077 | 120.5 | 146.1 | 243.4 | 101.3 | 42.5 | 21.2 |
| DQ796045.1 | 190736 | 7130.3 | 7684.1 | 4086.9 | 7863.5 | 7127.5 | 7520.8 |
| DQ801091.1 | 194446 | 26.1 | 26.5 | 13.0 | 42.6 | 45.0 | 17.7 |
| DQ796640.1 | 195652 | 139.8 | 215.5 | 947.5 | 292.7 | 136.1 | 203.5 |
| DQ796955.1 | 184237 | 2495.6 | 2673.0 | 1726.7 | 3325.9 | 3214.3 | 2593.3 |
| FJ673811.1 | 526513 | 9828.6 | 12169.4 | 4067.4 | 6705.0 | 9756.0 | 9327.3 |
| FJ675938.1 | 521444 | 2143.1 | 3334.8 | 1105.7 | 1497.9 | 5317.6 | 3913.5 |

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g__Catenibacterium
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| s__Solobacterium moorei | 71382 |
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| s__Catenibacterium mitsuokai | 71329 |
| s__Catenibacterium mitsuokai | 71367 |
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| s__Catenibacterium mitsuokai | 71596 |

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

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| FJ683676.1 | 524279 | 11990.4 | 12423.2 | 9104.6 | 10316.3 | 12886.2 | 11785.1 |
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| AY977931.1 | 124370 | 954.6 | 1568.0 | 2217.2 | 1420.1 | 4748.4 | 2513.7 |
| DQ325818.1 | 150015 | 4318.2 | 5514.2 | 1750.5 | 1870.2 | 3775.2 | 3054.0 |
| DQ325686.1 | 147618 | 2662.2 | 3782.8 | 1738.2 | 422.6 | 6940.0 | 4935.3 |
| DQ796023.1 | 198115 | 1122.2 | 1249.2 | 243.6 | 251.9 | 226.1 | 194.5 |
| DQ810113.1 | 178347 | 395.6 | 629.5 | 564.9 | 409.0 | 54.0 | 74.3 |
| FJ677579.1 | 529596 | 8407.5 | 8524.8 | 5536.1 | 6000.4 | 4011.4 | 4771.7 |
| FJ672990.1 | 522129 | 1835.3 | 1659.0 | 1228.5 | 3641.2 | 265.3 | 542.4 |
| DQ796744.1 | 198851 | 2694.8 | 3458.5 | 2684.4 | 3205.3 | 2405.3 | 2844.3 |
| EU467482.1 | 292065 | 355.8 | 515.7 | 753.1 | 222.0 | 439.4 | 290.8 |
| DQ800165.1 | 184625 | 905.1 | 1316.2 | 1514.6 | 893.8 | 3465.7 | 3240.0 |
| DQ326393.1 | 150448 | 8357.0 | 10574.3 | 3806.8 | 5844.8 | 8818.6 | 8100.2 |
| DQ326047.1 | 148356 | 808.4 | 1069.8 | 696.6 | 1189.1 | 1333.2 | 779.2 |
| EU762827.1 | 342647 | 1063.8 | 1475.2 | 996.8 | 1760.7 | 4695.2 | 3626.6 |
| EU474482.1 | 296794 | 9550.7 | 9520.5 | 10613.6 | 7030.6 | 8968.2 | 12482.0 |
| NZ_ADFR01000011.1 | 532556 | 924.5 | 1328.7 | 2045.1 | 841.8 | 1685.5 | 1981.4 |
| Z36271.1 | 15722 | 9043.5 | 10299.0 | 4444.0 | 6850.7 | 5054.5 | 6225.2 |
| AF220064.1 | 31844 | 5385.7 | 5999.3 | 3875.7 | 4449.1 | 4411.0 | 6644.3 |
| FJ833972.1 | 542406 | 1342.6 | 2088.0 | 4116.8 | 2897.6 | 5066.7 | 6900.1 |
| EU776314.1 | 323045 | 2474.3 | 4346.6 | 6067.8 | 1683.1 | 2102.4 | 1936.5 |
| AB218311.1 | 146880 | 1646.8 | 2128.3 | 3390.1 | 2682.9 | 919.7 | 1196.1 |
| DQ325832.1 | 147485 | 11.3 | 16.8 | 16.7 | 42.2 | 39.7 | 6.4 |
| FJ832913.1 | 559793 | 5919.1 | 6263.0 | 7458.7 | 7219.8 | 4392.8 | 5997.2 |
| EU467125.1 | 302200 | 5187.1 | 6266.6 | 7398.7 | 6686.6 | 7717.8 | 7674.5 |
| FJ832594.1 | 584753 | 6995.8 | 8062.2 | 7126.8 | 8764.7 | 9384.8 | 8359.3 |
| FJ833018.1 | 576628 | 2848.0 | 3637.0 | 4311.0 | 3515.9 | 1870.1 | 3920.3 |
| EU462550.1 | 297719 | 3043.8 | 3670.8 | 4860.3 | 5015.2 | 4126.1 | 5746.5 |
| FJ832520.1 | 537476 | 5044.8 | 5437.2 | 7495.4 | 6557.9 | 3623.3 | 5582.4 |
| AB031056.1 | 21980 | 177.6 | 57.9 | 202.2 | 92.4 | 111.9 | 110.9 |
| EU774283.1 | 340869 | 6230.2 | 7408.8 | 5275.3 | 6616.3 | 9847.0 | 9280.7 |
| EU344272.1 | 275128 | 2307.7 | 3092.5 | 2597.1 | 2228.6 | 1683.4 | 2183.7 |
| EU344303.1 | 260783 | 2567.5 | 2050.9 | 4287.3 | 792.1 | 1152.5 | 1148.6 |
| FJ976219.1 | 582816 | 2072.0 | 4447.6 | 5427.4 | 4016.9 | 2917.0 | 4295.3 |
| AF371517.1 | 54730 | 1095.9 | 1039.1 | 1665.4 | 1328.4 | 1546.2 | 1664.3 |
| EU344300.1 | 259168 | 4615.0 | 4608.6 | 2554.6 | 1284.0 | 313.5 | 801.0 |
| DQ015346.1 | 132391 | 49.3 | 33.8 | 42.3 | 78.9 | 75.6 | 47.0 |
| AB030223.1 | 33198 | 9531.4 | 11693.3 | 7607.0 | 6648.4 | 10887.8 | 10479.6 |
| AB030222.1 | 27171 | 4805.0 | 4980.3 | 4994.6 | 2682.2 | 4831.6 | 4490.2 |
| AB030225.1 | 21138 | 12228.7 | 14662.3 | 8313.0 | 9595.1 | 13438.7 | 13473.7 |
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| s__Catenibacterium mitsuokai | 71692 |
| s__unclassified | 71325 |
| s__unclassified | 71327 |
| s__unclassified | 71349 |
| s__unclassified | 71396 |
| s__unclassified | 71399 |
| s__unclassified | 71412 |
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| s__unclassified | 71545 |
| s__unclassified | 71548 |
| s__unclassified | 71561 |
| s__unclassified | 71617 |
| s__unclassified | 71622 |
| s__unclassified | 71626 |
| s__unclassified | 71627 |
| s__unclassified | 71705 |
| s__unclassified | 71761 |
| s__Clostridium cocleatum | 71487 |
| s__Clostridium ramosum | 71308 |
| s__Clostridium spiroforme | 71452 |
| s__Clostridium spiroforme | 71535 |
| s__Clostridium spiroforme | 71553 |
| s__Clostridium spiroforme | 71580 |
| s__Clostridium spiroforme | 71615 |
| s__unclassified | 71299 |
| s__unclassified | 71303 |
| s__unclassified | 71317 |
| s__unclassified | 71336 |
| s__unclassified | 71343 |
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| s__unclassified | 71369 |
| s__unclassified | 71397 |
| s__unclassified | 71407 |
| s__unclassified | 71420 |
| s__unclassified | 71455 |
| s__unclassified | 71463 |
| s__unclassified | 71475 |
| s__unclassified | 71486 |
| s__unclassified | 71495 |
| s__unclassified | 71499 |

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

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| AB030226.1 | 40839 | 3882.7 | 3794.8 | 3947.1 | 2647.3 | 2187.8 | 2798.8 |
| DQ326116.1 | 145343 | 9734.1 | 11548.7 | 6437.0 | 6852.4 | 8659.3 | 9156.6 |
| DQ326286.1 | 145169 | 885.3 | 1156.4 | 2936.6 | 329.3 | 441.5 | 1037.6 |
| DQ325906.1 | 150498 | 2425.0 | 2589.9 | 1636.9 | 2898.5 | 1658.6 | 2456.3 |
| DQ325656.1 | 150173 | 19.9 | 221.2 | 156.3 | 72.7 | 65.2 | 49.4 |
| EU773418.1 | 309852 | 243.8 | 502.5 | 1362.0 | 506.5 | 2646.6 | 139.4 |
| EU461777.1 | 287510 | 1861.7 | 2556.8 | 2215.2 | 1963.3 | 753.1 | 1356.6 |
| DQ325879.1 | 146207 | 1402.9 | 1593.2 | 2918.6 | 1710.3 | 469.6 | 1066.3 |
| EU469507.1 | 289377 | 10485.3 | 9923.7 | 6457.8 | 8678.1 | 10744.7 | 9121.5 |
| EU459789.1 | 295705 | 5398.6 | 5853.3 | 4093.3 | 3615.3 | 4396.7 | 4332.6 |
| AY978040.1 | 122153 | 4309.0 | 6076.7 | 3981.3 | 2498.7 | 2908.6 | 2798.4 |
| EU530322.1 | 274970 | 1339.0 | 681.6 | 1352.3 | 299.6 | 225.6 | 501.3 |
| AY978152.1 | 125309 | 3043.1 | 8308.5 | 519.7 | 1497.3 | 1119.7 | 1986.5 |
| NZ_ACCK01000460.1 | 469918 | 2140.7 | 1264.3 | 1962.2 | 435.6 | 129.5 | 201.0 |
| EU469487.1 | 298026 | 11134.7 | 12561.7 | 10378.3 | 8423.4 | 18873.6 | 13593.3 |
| DQ325735.1 | 146738 | 10581.7 | 12551.0 | 3988.9 | 7485.9 | 9624.9 | 9367.2 |
| AY976273.1 | 124283 | 10300.2 | 23317.9 | 6031.0 | 5955.5 | 10874.8 | 9306.8 |
| DQ326095.1 | 145882 | 8311.7 | 10024.0 | 5301.6 | 5795.0 | 7459.9 | 7686.9 |
| NR_026495.1 | 550248 | 39.5 | 58.2 | 65.7 | 63.6 | 130.1 | 60.9 |
| NR_029247.1 | 590150 | 98.2 | 134.7 | 242.8 | 146.0 | 75.0 | 83.6 |
| EU462941.1 | 300521 | 1683.4 | 1738.8 | 4254.1 | 1387.6 | 857.3 | 1487.5 |
| NZ_ABIK02000003.1 | 259777 | 206.7 | 242.6 | 379.2 | 104.9 | 90.4 | 117.1 |
| ABIK02000013.1 | 270245 | 149.0 | 167.5 | 246.9 | 142.5 | 161.1 | 196.9 |
| X75908.1 | 15715 | 509.6 | 759.1 | 2998.0 | 528.7 | 1750.0 | 1679.2 |
| X73441.1 | 15716 | 2766.0 | 2590.6 | 5038.5 | 2679.1 | 1615.5 | 2688.9 |
| DQ825115.1 | 193907 | 7580.4 | 8553.3 | 1326.8 | 5576.2 | 12913.4 | 8797.7 |
| FJ673628.1 | 528507 | 12745.2 | 12754.2 | 4473.5 | 9053.0 | 9328.7 | 9883.7 |
| DQ100445.1 | 142563 | 43.8 | 36.3 | 47.3 | 85.3 | 82.9 | 33.5 |
| AJ576394.1 | 100232 | 490.4 | 733.5 | 897.6 | 367.2 | 1265.2 | 322.4 |
| GQ897372.1 | 571478 | 3467.7 | 3916.9 | 1978.8 | 2840.3 | 1002.4 | 1124.8 |
| EU542496.1 | 274239 | 7772.7 | 5364.9 | 5164.7 | 7618.1 | 4668.0 | 4092.3 |
| FJ364978.1 | 368625 | 1145.9 | 1344.8 | 4844.2 | 2630.0 | 993.3 | 1662.0 |
| DQ808012.1 | 199138 | 6058.1 | 7588.2 | 6052.5 | 5002.9 | 11018.3 | 7560.7 |
| AB288920.1 | 200664 | 359.8 | 790.0 | 1378.4 | 379.2 | 377.5 | 545.5 |
| DQ793967.1 | 187634 | 2207.5 | 1714.0 | 2200.6 | 2995.8 | 507.8 | 966.3 |
| FJ365022.1 | 368528 | 9266.2 | 9188.9 | 5175.2 | 7529.1 | 11524.9 | 9271.0 |
| DQ326867.1 | 149994 | 10653.4 | 10934.9 | 5470.6 | 7650.7 | 10650.9 | 9270.1 |
| FJ363684.1 | 357024 | 6699.3 | 7485.2 | 4086.4 | 3876.8 | 5180.4 | 5252.3 |
| FJ676587.1 | 516871 | 11783.0 | 12045.0 | 8683.6 | 8718.1 | 11927.6 | 9694.2 |
| EU134663.1 | 251385 | 55.4 | 91.3 | 503.4 | 134.0 | 83.2 | 55.6 |
| FJ678331.1 | 515661 | 2254.5 | 3359.8 | 1090.8 | 2390.6 | 5495.9 | 3928.4 |

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|---|---|---|---|
| k__Bacteria | k__Bacteria | p__Tenericutes | c__Erysipelotrichi |
| k__Bacteria | k__Bacteria | p__Tenericutes | c__Erysipelotrichi |
| k__Bacteria | k__Bacteria | p__Tenericutes | c__Erysipelotrichi |
| k__Bacteria | k__Bacteria | p__Tenericutes | c__Erysipelotrichi |
| k__Bacteria | k__Bacteria | p__Tenericutes | c__Erysipelotrichi |
| k__Bacteria | k__Bacteria | p__Tenericutes | c__Erysipelotrichi |
| k__Bacteria | k__Bacteria | p__Tenericutes | c__Erysipelotrichi |
| k__Bacteria | k__Bacteria | p__Tenericutes | c__Erysipelotrichi |
| k__Bacteria | k__Bacteria | p__Tenericutes | c__Erysipelotrichi |
| k__Bacteria | k__Bacteria | p__Tenericutes | c__Erysipelotrichi |
| k__Bacteria | k__Bacteria | p__Tenericutes | c__Erysipelotrichi |
| k__Bacteria | k__Bacteria | p__Tenericutes | c__Erysipelotrichi |
| k__Bacteria | k__Bacteria | p__Tenericutes | c__Erysipelotrichi |
| k__Bacteria | k__Bacteria | p__Tenericutes | c__Erysipelotrichi |
| k__Bacteria | k__Bacteria | p__Tenericutes | c__Erysipelotrichi |
| k__Bacteria | k__Bacteria | p__Tenericutes | c__Erysipelotrichi |
| k__Bacteria | k__Bacteria | p__Tenericutes | c__Erysipelotrichi |
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| k__Bacteria | k__Bacteria | p__Tenericutes | c__Erysipelotrichi |
| k__Bacteria | k__Bacteria | p__Tenericutes | c__Erysipelotrichi |
| k__Bacteria | k__Bacteria | p__Tenericutes | c__Erysipelotrichi |
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| k__Bacteria | k__Bacteria | p__Tenericutes | c__Erysipelotrichi |
| k__Bacteria | k__Bacteria | p__Tenericutes | c__Erysipelotrichi |
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| k__Bacteria | k__Bacteria | p__Tenericutes | c__Erysipelotrichi |

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| o__Erysipelotrichales | f__Erysipelotrichaceae |
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| o__Erysipelotrichales | f__Erysipelotrichaceae |

g__Clostridium
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g__CM970
g__CM970
g__Coprobacillus
g__Coprobacillus

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| s__unclassified | 71517 |
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| s__unclassified | 71523 |
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| s__unclassified | 71733 |
| s__unclassified | 71745 |
| s__unclassified | 71752 |
| s__unclassified | 71766 |
| s__Clostridium innocuum | 71373 |
| s__Clostridium innocuum | 71390 |
| s__Clostridium innocuum | 71496 |
| s__Clostridium innocuum | 71530 |
| s__Clostridium innocuum | 71642 |
| s__Coprobacillus cateniformis | 71640 |
| s__unclassified | 71330 |

FJ363710.1 gg_id:359315 feces adult twins and mothers; TS14 clone TS14_a02d04
DQ326852.1 gg_id:149140 Metagenomic gut microbiome healthy human stool clone E331
FJ370952.1 gg_id:358786 feces adult twins and mothers; TS5 clone TS5_a03b10
DQ794080.1 gg_id:183083 human fecal clone RL176_aan57g03
AY982801.1 gg_id:115534 human descending colon mucosal biopsy clone KZ46
FJ677018.1 gg_id:516022 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ441352.1 gg_id:191030 human intestinal biopsy clone CD101
DQ057480.1 gg_id:136526 str. ic1391
GQ492588.1 gg_id:580597 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
DQ798465.1 gg_id:181284 human fecal clone RL181_aan97a10
FJ679216.1 gg_id:521524 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ678731.1 gg_id:514684 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
GQ898739.1 gg_id:570735 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do
GQ491637.1 gg_id:588666 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
EF071177.1 gg_id:190872 library survey and quantitative measurement major mucosa- IBD human colonic muc
DQ798576.1 gg_id:178236 human fecal clone RL181_aan98e03
AY975735.1 gg_id:116787 human ascending colon mucosal biopsy clone Y182
DQ797930.1 gg_id:180338 human fecal clone RL302_aal93e08
FJ372126.1 gg_id:360238 feces adult twins and mothers; TS9 clone TS9_a02a08
FJ371039.1 gg_id:370335 feces adult twins and mothers; TS5 clone TS5_a04c01
AJ576387.1 gg_id:104610 midgut homogenate Pachnoda ephippiata larva clone PeM18
GQ046231.1 gg_id:427628 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw
FJ370907.1 gg_id:362830 feces adult twins and mothers; TS5 clone TS5_a02f06
DQ327268.1 gg_id:145872 Metagenomic gut microbiome healthy human stool clone E812
FJ370787.1 gg_id:363246 feces adult twins and mothers; TS5 clone TS5_a01c07
FJ370764.1 gg_id:362087 feces adult twins and mothers; TS5 clone TS5_a01a04
FJ369674.1 gg_id:360605 feces adult twins and mothers; TS51 clone TS51_a03e03
DQ797079.1 gg_id:194170 human fecal clone RL386_aao86g03
FJ368379.1 gg_id:359304 feces adult twins and mothers; TS3 clone TS3_a03f08
FJ368229.1 gg_id:358899 feces adult twins and mothers; TS3 clone TS3_a01g05
FJ678559.1 gg_id:516982 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ327312.1 gg_id:145134 Metagenomic gut microbiome healthy human stool clone E859
FJ366410.1 gg_id:359009 feces adult twins and mothers; TS26 clone TS26_a02g07
FJ370922.1 gg_id:358586 feces adult twins and mothers; TS5 clone TS5_a02h01
AM277455.2 gg_id:229069 fecal microbiota irritable bowel syndrome patients significantly that healthy subject
DQ804182.1 gg_id:198054 human fecal clone RL187_aah69h03
GQ492759.1 gg_id:587530 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
DQ440561.1 gg_id:156898 Clostridium innocuum str. Ulm 12
GQ492977.1 gg_id:586813 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
AB030220.1 gg_id:21822 Coprobacillus cateniformis str. JCM 10605
DQ803568.1 gg_id:177504 human fecal clone RL251_aaj87e08

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| FJ363710.1 | 359315 | 2563.8 | 2989.3 | 829.2 | 1385.6 | 3601.2 | 2455.5 |
| DQ326852.1 | 149140 | 567.3 | 1406.3 | 805.1 | 464.2 | 579.4 | 867.1 |
| FJ370952.1 | 358786 | 9143.9 | 9767.1 | 8424.0 | 7382.7 | 14466.9 | 12881.0 |
| DQ794080.1 | 183083 | 2660.9 | 3214.0 | 449.9 | 2470.9 | 236.2 | 1238.9 |
| AY982801.1 | 115534 | 4047.0 | 5327.9 | 4693.0 | 4732.1 | 6539.6 | 5355.7 |
| FJ677018.1 | 516022 | 1138.0 | 2103.5 | 2162.4 | 2043.5 | 4180.1 | 2130.8 |
| DQ441352.1 | 191030 | 1002.5 | 1342.5 | 1552.5 | 1107.4 | 1701.2 | 536.4 |
| DQ057480.1 | 136526 | 79.2 | 60.3 | 62.6 | 71.4 | 65.3 | 31.2 |
| GQ492588.1 | 580597 | 323.8 | 563.0 | 2331.1 | 380.7 | 749.7 | 939.6 |
| DQ798465.1 | 181284 | 1277.9 | 2381.3 | 1933.6 | 2102.5 | 1795.8 | 719.8 |
| FJ679216.1 | 521524 | 2364.6 | 1855.8 | 1332.3 | 3498.6 | 145.0 | 200.0 |
| FJ678731.1 | 514684 | 1191.6 | 2613.3 | 681.1 | 888.0 | 518.4 | 892.8 |
| GQ898739.1 | 570735 | 11233.9 | 9936.9 | 5355.0 | 9371.3 | 6692.1 | 7302.7 |
| GQ491637.1 | 588666 | 1554.3 | 1440.2 | 2966.4 | 1198.8 | 303.7 | 791.5 |
| EF071177.1 | 190872 | 481.3 | 231.3 | 976.7 | 492.1 | 62.1 | 123.4 |
| DQ798576.1 | 178236 | 11616.2 | 12057.9 | 5784.5 | 7544.6 | 8846.6 | 7928.0 |
| AY975735.1 | 116787 | 2664.5 | 2073.0 | 1341.4 | 3257.2 | 847.5 | 1114.8 |
| DQ797930.1 | 180338 | 287.8 | 586.7 | 669.2 | 251.9 | 248.8 | 663.9 |
| FJ372126.1 | 360238 | 285.9 | 224.6 | 424.7 | 178.5 | 1607.7 | 753.6 |
| FJ371039.1 | 370335 | 479.4 | 545.2 | 1177.8 | 276.5 | 201.8 | 522.1 |
| AJ576387.1 | 104610 | 515.6 | 1165.4 | 1809.2 | 621.4 | 1206.7 | 554.4 |
| GQ046231.1 | 427628 | 8790.3 | 9777.3 | 8676.7 | 7201.7 | 9324.5 | 8593.2 |
| FJ370907.1 | 362830 | 1549.2 | 1462.2 | 577.9 | 1158.3 | 329.6 | 433.4 |
| DQ327268.1 | 145872 | 537.1 | 745.4 | 914.6 | 320.7 | 347.8 | 360.0 |
| FJ370787.1 | 363246 | 2736.5 | 3401.7 | 573.7 | 2718.4 | 1997.5 | 1249.7 |
| FJ370764.1 | 362087 | 58.6 | 124.5 | 65.6 | 121.9 | 86.8 | 84.1 |
| FJ369674.1 | 360605 | 104.4 | 283.4 | 221.6 | 153.3 | 2209.8 | 1130.2 |
| DQ797079.1 | 194170 | 5541.7 | 5861.1 | 7202.5 | 5903.4 | 8717.2 | 5789.8 |
| FJ368379.1 | 359304 | 3709.1 | 3806.6 | 816.2 | 744.6 | 1669.6 | 2079.2 |
| FJ368229.1 | 358899 | 1961.2 | 2623.7 | 781.1 | 418.5 | 345.3 | 1354.9 |
| FJ678559.1 | 516982 | 4345.8 | 4014.4 | 401.9 | 3033.6 | 3044.6 | 1974.7 |
| DQ327312.1 | 145134 | 7698.8 | 6677.0 | 2635.1 | 4843.4 | 3408.5 | 1908.3 |
| FJ366410.1 | 359009 | 992.8 | 1269.6 | 249.4 | 192.5 | 235.4 | 421.2 |
| FJ370922.1 | 358586 | 12188.1 | 11433.1 | 8690.8 | 6035.8 | 8256.3 | 7341.9 |
| AM277455.2 | 229069 | 19.5 | 25.7 | 17.7 | 54.3 | 67.9 | 17.3 |
| DQ804182.1 | 198054 | 8263.0 | 9850.5 | 8918.2 | 6402.3 | 9852.7 | 9105.2 |
| GQ492759.1 | 587530 | 5735.5 | 6278.3 | 5308.1 | 6725.1 | 8972.0 | 9678.4 |
| DQ440561.1 | 156898 | 85.1 | 104.6 | 251.2 | 108.9 | 75.4 | 132.5 |
| GQ492977.1 | 586813 | 11980.7 | 12018.5 | 9442.0 | 10866.7 | 14873.9 | 14112.0 |
| AB030220.1 | 21822 | 51.3 | 70.8 | 55.5 | 72.6 | 91.2 | 33.1 |
| DQ803568.1 | 177504 | 1882.9 | 1567.3 | 630.9 | 1442.2 | 2872.3 | 1869.7 |

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| k__Bacteria | k__Bacteria | p__Tenericutes | c__Erysipelotrichi |

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| o__Erysipelotrichales | f__Erysipelotrichaceae |
| o__Erysipelotrichales | f__Erysipelotrichaceae |
| o__Erysipelotrichales | f__Erysipelotrichaceae |
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| o__Erysipelotrichales | f__Erysipelotrichaceae |

g__Coprobacillus
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| s__unclassified | 71656 |
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| s__EMP_E11 | 71441 |
| s__EMP_E11 | 71594 |
| s__EMP_E11 | 71727 |
| s__Erysipelothrix rhusiopathiae | 71515 |
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EU771920.1 gg_id:326369 Southern three-banded armadillo feces clone arma_aaj56h10
GQ448197.1 gg_id:585386 Microbiome neonatal calves: shedding microorganisms fecal clone calf32_6wks_grp
GQ175408.1 gg_id:509861 Chicken intestinal microbiota modulations various feed supplementations DGGE anc
AM275546.2 gg_id:231985 fecal microbiota irritable bowel syndrome patients significantly that healthy subject
FJ368343.1 gg_id:368662 feces adult twins and mothers; TS3 clone TS3_a03b11
AM275478.2 gg_id:233953 fecal microbiota irritable bowel syndrome patients significantly that healthy subject
DQ801017.1 gg_id:191700 human fecal clone RL387_aao91a01
EU507257.1 gg_id:276227 cecal contents Mus musculus strain C57BL/6J; MD22 clone MD22_aaa04e02
FJ676717.1 gg_id:510237 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
NZ_ABAW02000024.1 gg_id:470381 Eubacterium dolichum str. DSM 3991
FJ680914.1 gg_id:515268 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ681460.1 gg_id:519377 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ681610.1 gg_id:512366 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
M23728.1 gg_id:15730 Erysipelothrix rhusiopathiae
DQ462571.1 gg_id:157405 Erysipelothrix muris
AB055910.1 gg_id:78143 Erysipelothrix rhusiopathiae str. KG-BB2
AB540983.1 gg_id:581050 Erysipelothrix tonsillarum str. JCM 8533
AJ550617.1 gg_id:88075 Erysipelothrix inopinata str. 143-02
EU748014.1 gg_id:306059 neotropical folivorous flying bird adult hoatzin crop clone hoa12_36D05
Y11466.1 gg_id:15728 Holdemania filiformis str. ATCC 51649
FJ369019.1 gg_id:367215 feces adult twins and mothers; TS4 clone TS4_a03c12
EU761816.1 gg_id:341803 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1
FJ371255.1 gg_id:366464 feces adult twins and mothers; TS6 clone TS6_a02g10
EU461496.1 gg_id:296385 black rhinoceros feces clone RH_aaj91a04
FJ833665.1 gg_id:583224 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J1Q402_90B12
EU471859.1 gg_id:292053 Asiatic elephant feces clone AE3_aaa04h07
FJ364883.1 gg_id:356807 feces adult twins and mothers; TS19 clone TS19_a04c08
EU771726.1 gg_id:309403 African elephant feces clone AFYEL_aaj65d04
DQ353900.1 gg_id:149744 Fecal Wild Gorilla (Gorilla beringei) wild gorilla feces clone Z2
EU470295.1 gg_id:293994 Grevy's zebra feces clone GZ_aaa03h02
DQ353909.1 gg_id:149927 Fecal Wild Gorilla (Gorilla beringei) wild gorilla feces clone Z22
EU470473.1 gg_id:299480 Grevy's zebra feces clone GZ_aaa01g09
EU462969.1 gg_id:297568 southern three-banded armadillo feces clone arma_aaj55h06
EU467550.1 gg_id:294524 southern three-banded armadillo feces clone arma_h07
AJ629069.1 gg_id:188919 Eubacterium sp. Pei061
AY953174.1 gg_id:114580 anaerobic swine lagoon clone B-1F
EU981243.1 gg_id:332976 sulfate reducing living bench scale aquifer packed bed clone D7_FB
FJ382687.1 gg_id:562083 Potentially pathogenic and air stem cell transplant summer hospital shower water BM
EU104057.1 gg_id:355578 Evidence Comamonadaceae determinants settling performance activated sludge clo
FJ382255.1 gg_id:513876 Potentially pathogenic and air stem cell transplant summer hospital shower water BM
AY297808.1 gg_id:89878 waterlogged archaeological wood clone pACH93

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| EU771920.1 | 326369 | 80.1 | 204.5 | 54.9 | 70.4 | 54.0 | 35.6 |
| GQ448197.1 | 585386 | 3435.9 | 3047.0 | 3044.6 | 3049.3 | 1900.7 | 2766.6 |
| GQ175408.1 | 509861 | 166.6 | 124.2 | 95.7 | 118.4 | 110.7 | 117.6 |
| AM275546.2 | 231985 | 16.5 | 34.0 | 52.9 | 58.7 | 67.3 | 29.9 |
| FJ368343.1 | 368662 | 3127.4 | 3252.2 | 3561.0 | 4394.8 | 7800.2 | 8074.1 |
| AM275478.2 | 233953 | 132.2 | 228.9 | 379.1 | 129.6 | 264.3 | 140.6 |
| DQ801017.1 | 191700 | 76.4 | 188.9 | 134.8 | 114.1 | 1462.0 | 1198.7 |
| EU507257.1 | 276227 | 48.9 | 71.1 | 49.1 | 58.0 | 74.1 | 42.8 |
| FJ676717.1 | 510237 | 11449.0 | 9548.3 | 8746.1 | 9410.0 | 11110.5 | 10685.9 |
| NZ_ABAW02000024.1 | 470381 | 4719.9 | 5985.9 | 2472.0 | 4737.0 | 1143.8 | 1122.5 |
| FJ680914.1 | 515268 | 16706.1 | 17282.6 | 11459.7 | 16529.8 | 14276.3 | 12034.5 |
| FJ681460.1 | 519377 | 10243.6 | 7962.0 | 7863.3 | 10053.9 | 6898.0 | 7502.1 |
| FJ681610.1 | 512366 | 11562.7 | 11792.8 | 7069.8 | 11466.0 | 8856.5 | 7413.1 |
| M23728.1 | 15730 | 2364.1 | 2497.5 | 3136.7 | 3016.2 | 4963.4 | 3860.0 |
| DQ462571.1 | 157405 | 2188.9 | 2431.2 | 2789.7 | 3151.9 | 4160.8 | 3995.1 |
| AB055910.1 | 78143 | 2341.5 | 2370.8 | 2892.3 | 2394.1 | 3596.3 | 4044.0 |
| AB540983.1 | 581050 | 2232.4 | 2384.7 | 2732.7 | 3103.5 | 4038.9 | 4072.6 |
| AJ550617.1 | 88075 | 1557.3 | 1927.3 | 3351.1 | 1624.7 | 984.8 | 911.4 |
| EU748014.1 | 306059 | 4977.2 | 3592.7 | 4275.2 | 3599.6 | 691.2 | 2515.0 |
| Y11466.1 | 15728 | 2249.9 | 2339.8 | 4157.0 | 2032.4 | 734.3 | 1405.2 |
| FJ369019.1 | 367215 | 35.9 | 43.7 | 213.6 | 79.3 | 72.9 | 27.7 |
| EU761816.1 | 341803 | 2494.5 | 3271.8 | 4169.6 | 2737.1 | 1362.7 | 2036.9 |
| FJ371255.1 | 366464 | 760.7 | 540.7 | 1194.1 | 860.3 | 1068.3 | 437.8 |
| EU461496.1 | 296385 | 12862.7 | 13099.4 | 10577.8 | 11399.9 | 7831.4 | 9907.4 |
| FJ833665.1 | 583224 | 12189.4 | 10842.6 | 11338.8 | 8890.8 | 8497.8 | 8307.4 |
| EU471859.1 | 292053 | 12473.0 | 10412.8 | 5873.0 | 9578.1 | 3943.7 | 5855.6 |
| FJ364883.1 | 356807 | 29.8 | 35.8 | 52.8 | 69.5 | 66.2 | 33.2 |
| EU771726.1 | 309403 | 3616.5 | 4511.9 | 2329.2 | 3513.8 | 4383.8 | 5131.3 |
| DQ353900.1 | 149744 | 171.4 | 147.4 | 96.0 | 153.8 | 469.6 | 304.5 |
| EU470295.1 | 293994 | 1663.7 | 2777.9 | 2569.7 | 1994.6 | 2860.2 | 1751.2 |
| DQ353909.1 | 149927 | 1522.8 | 1901.5 | 3434.1 | 1236.2 | 1943.1 | 1339.9 |
| EU470473.1 | 299480 | 8722.9 | 9425.2 | 4559.1 | 2752.0 | 5237.1 | 4197.1 |
| EU462969.1 | 297568 | 8355.0 | 7591.1 | 4109.1 | 6443.4 | 3174.0 | 2588.2 |
| EU467550.1 | 294524 | 3600.1 | 4398.2 | 2936.3 | 4295.2 | 2105.4 | 2001.6 |
| AJ629069.1 | 188919 | 124.0 | 179.7 | 177.2 | 355.0 | 68.3 | 99.5 |
| AY953174.1 | 114580 | 2272.2 | 2320.5 | 3774.2 | 2456.6 | 2886.6 | 3400.7 |
| EU981243.1 | 332976 | 1324.0 | 1114.1 | 2643.2 | 1792.3 | 1056.7 | 1886.8 |
| FJ382687.1 | 562083 | 2834.0 | 3218.7 | 4246.8 | 3428.3 | 2123.0 | 3286.2 |
| EU104057.1 | 355578 | 2096.3 | 2718.2 | 3413.8 | 1983.7 | 3469.5 | 4113.3 |
| FJ382255.1 | 513876 | 11766.2 | 12141.1 | 5474.0 | 9775.4 | 11950.5 | 9707.4 |
| AY297808.1 | 89878 | 13596.7 | 16961.8 | 8028.8 | 11320.2 | 13851.4 | 11757.3 |

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

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| DQ266900.1 | 142208 | 2651.3 | 2671.6 | 3126.7 | 2715.8 | 2604.6 | 2510.8 |
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| AY953244.1 | 114755 | 4627.3 | 5565.6 | 6857.0 | 5699.8 | 8394.3 | 6750.2 |
| FM178530.1 | 350518 | 3972.5 | 6139.8 | 4405.6 | 2707.5 | 2257.4 | 2324.3 |
| AB210825.1 | 168842 | 24.4 | 42.2 | 36.9 | 50.9 | 65.7 | 29.6 |
| EU458708.1 | 300437 | 3860.5 | 4955.5 | 840.2 | 2207.2 | 3037.1 | 2845.8 |
| EU458757.1 | 289892 | 371.1 | 496.0 | 509.6 | 394.5 | 61.1 | 242.3 |
| EU458790.1 | 290793 | 2987.0 | 3009.7 | 3415.8 | 2756.5 | 1369.1 | 1567.1 |
| EU458745.1 | 295903 | 684.0 | 1096.8 | 879.2 | 960.5 | 1495.7 | 1587.6 |
| EU458772.1 | 295432 | 5525.4 | 6444.1 | 6129.1 | 4818.8 | 3210.6 | 3342.4 |
| EU458780.1 | 299091 | 5071.4 | 6337.5 | 6270.9 | 5630.8 | 6738.1 | 6231.0 |
| EU772354.1 | 328719 | 1227.7 | 1006.4 | 1849.6 | 2544.5 | 188.5 | 421.5 |
| EU773547.1 | 324232 | 479.5 | 423.8 | 832.0 | 215.5 | 48.9 | 78.9 |
| EU458750.1 | 297734 | 3337.0 | 1653.4 | 6466.2 | 3593.9 | 1591.7 | 2140.3 |
| EU772358.1 | 351169 | 804.9 | 1075.0 | 904.9 | 1997.8 | 374.7 | 704.0 |
| EU458715.1 | 287857 | 30.2 | 27.1 | 19.6 | 45.1 | 53.7 | 15.0 |
| AJ621549.1 | 129426 | 23.3 | 34.8 | 62.4 | 61.6 | 81.1 | 69.2 |
| AB192060.1 | 200153 | 3484.4 | 3569.1 | 5905.5 | 6081.6 | 6470.6 | 5213.7 |
| AB018186.1 | 49837 | 86.4 | 98.2 | 52.2 | 82.1 | 79.2 | 65.6 |
| FJ371145.1 | 360344 | 31.2 | 42.5 | 77.0 | 55.7 | 62.9 | 18.6 |
| DQ353903.1 | 148303 | 36.4 | 67.4 | 50.0 | 61.7 | 42.5 | 33.2 |
| GQ016276.1 | 493391 | 4626.9 | 4587.4 | 5298.9 | 3632.9 | 1310.9 | 2257.1 |
| AF371514.1 | 49369 | 57.7 | 61.6 | 73.8 | 61.8 | 62.0 | 27.6 |
| EU510761.1 | 276677 | 18.3 | 31.7 | 26.3 | 44.6 | 56.7 | 30.9 |
| AM405127.2 | 565289 | 535.9 | 1126.6 | 81.2 | 1717.3 | 439.1 | 78.6 |
| EU461077.1 | 288677 | 3051.6 | 3065.8 | 5820.3 | 4230.3 | 2948.7 | 4352.5 |
| EU458788.1 | 289655 | 629.0 | 760.0 | 300.1 | 918.9 | 1509.5 | 690.9 |
| GQ175443.1 | 539382 | 18.6 | 27.5 | 30.4 | 64.1 | 68.4 | 27.0 |
| EU504762.1 | 262375 | 6489.9 | 8102.6 | 6322.6 | 6065.4 | 7098.4 | 5213.3 |
| L34683.1 | 15729 | 6873.2 | 8067.4 | 7455.7 | 6296.7 | 4864.6 | 9833.5 |
| EF071180.1 | 195355 | 38.9 | 51.1 | 48.5 | 104.8 | 60.9 | 41.9 |
| EU850490.1 | 346727 | 3422.9 | 3279.7 | 3887.8 | 3186.3 | 2641.9 | 1990.4 |
| AB009222.1 | 15714 | 431.2 | 790.7 | 1168.6 | 972.1 | 1595.7 | 2150.0 |
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| EU459459.1 | 294991 | 5168.7 | 7618.0 | 6019.6 | 6277.1 | 3578.4 | 3870.1 |
| CU922014.1 | 541244 | 36.3 | 42.7 | 34.0 | 59.1 | 80.0 | 38.4 |
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| EU407216.1 | 259697 | 1681.1 | 2312.9 | 4395.7 | 2715.7 | 2349.0 | 2495.3 |
| EF445265.1 | 211927 | 26.4 | 34.5 | 53.2 | 57.2 | 66.3 | 29.5 |
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| s__Acholeplasma laidlawii | 73454 |
| s__Acholeplasma laidlawii | 73662 |
| s__Acholeplasma laidlawii | 73933 |
| s__Acholeplasma laidlawii | 74223 |
| s__Acholeplasma laidlawii | 74544 |
| s__Acholeplasma sp. DM-2009 | 74363 |
| s__unclassified | 73195 |
| s__unclassified | 73274 |

EU344443.1 gg_id:270947 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad
EU871420.1 gg_id:308656 Genetic Bovine (Bos taurus) Rumen Thailand clone CF413
EU463746.1 gg_id:301292 domesticated horse feces clone horsej_aai92a12
EU871344.1 gg_id:346271 Genetic Bovine (Bos taurus) Rumen Thailand clone CF16
FJ681865.1 gg_id:529472 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU842625.1 gg_id:352686 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi
EF515475.1 gg_id:221660 Electricigen Enrichment MFC upf microbial fuel cell anode clone 24h04
DQ456144.1 gg_id:158774 pre-adolescent turkey cecum clone CFT114H9
EU464340.1 gg_id:293385 hamadryas baboon feces clone AFBAB_aai03a08
FJ680789.1 gg_id:518054 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ205803.1 gg_id:335171 microbial integrating library sequences and metagenome data obtained 454-pyroseq
EU794282.1 gg_id:317703 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_K38
FJ684918.1 gg_id:530177 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU219944.1 gg_id:257268 study prokaryotic approach landfill soil 5.5 ft. depth clone C81B
FJ717180.1 gg_id:511931 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United King
EU050916.1 gg_id:236166 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_07_32
EU142042.1 gg_id:243175 Methyl sulfides intermediates anaerobic oxidation methane seep sediment clone SR
EU570894.1 gg_id:545311 transition and zone within near-shore anoxic basin: Nitinat Lake depth 13 m clone Ni
FJ366283.1 gg_id:360268 feces adult twins and mothers; TS25 clone TS25_a04h01
EF434374.1 gg_id:204256 human infant gastrointestinal tract microbiota stool mother babies 13 and 14 7 mont
FJ366026.1 gg_id:366738 feces adult twins and mothers; TS25 clone TS25_a01h02
CU924120.1 gg_id:551818 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
CU921361.1 gg_id:552601 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
AJ853619.1 gg_id:110120 landfill leachate clone GZKB127
FN436127.1 gg_id:559693 Molekularbiologische Charakterisierung der bakteriellen Populationsdynamik eines t
AY862794.2 gg_id:160460 prokaryotic genetic Salar de Atacama Northern Chile athalassohaline lake water clon
AF507895.1 gg_id:62666 Mono Lake at depth 2m station 6 July 2000 clone ML602J-25 G+C
EU778068.1 gg_id:313232 feces clone RL117_aae91b10
AM947541.1 gg_id:268726 Minor changes detected microbial structure and after three week thermophilic dige
AM947531.1 gg_id:265685 Minor changes detected microbial structure and after three week thermophilic dige
GU196243.1 gg_id:581038 Bioaugmentation improved recovery digesters after toxicant exposure lab-scale ana
GQ448397.1 gg_id:588815 Microbiome neonatal calves: shedding microorganisms fecal clone calf783_6wks_gr
AF412968.1 gg_id:21971 Acholeplasma axanthum str. S-743(T)
FJ226570.1 gg_id:355090 Acholeplasma laidlawii str. Haig 179L
AY257485.1 gg_id:83638 Mesoplasma pleciae str. ATCC 49582; PS-1
CP000896.1 gg_id:243946 Acholeplasma laidlawii str. PG-8A
U14905.1 gg_id:15691 Acholeplasma laidlawii str. PG8 ATCC 23206
AY785356.1 gg_id:108386 Acholeplasma sp. str. CODA 1G
FJ590762.1 gg_id:568272 Acholeplasma sp. DM-2009 str. Lorelei
EU517562.1 gg_id:274442 methanogenic microbial consortia mature oil sands tailings clone 12-7C
DQ337019.1 gg_id:145365 subsurface water clone EV818CFSSAHH219

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| EU344443.1 | 270947 | 11721.6 | 13296.8 | 13651.1 | 8421.1 | 10908.7 | 10000.1 |
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| EU463746.1 | 301292 | 4130.2 | 4512.5 | 4607.9 | 4716.0 | 3588.5 | 3450.2 |
| EU871344.1 | 346271 | 3241.4 | 4287.8 | 3910.7 | 1550.8 | 3915.0 | 3624.9 |
| FJ681865.1 | 529472 | 4834.9 | 5610.6 | 6079.9 | 5447.2 | 2104.1 | 3570.5 |
| EU842625.1 | 352686 | 5594.2 | 5932.4 | 4302.1 | 6489.5 | 3763.1 | 4693.9 |
| EF515475.1 | 221660 | 236.5 | 517.9 | 189.1 | 259.3 | 1736.8 | 972.4 |
| DQ456144.1 | 158774 | 42.4 | 85.9 | 42.5 | 68.1 | 63.8 | 40.1 |
| EU464340.1 | 293385 | 5563.8 | 5366.1 | 7055.7 | 4172.7 | 3576.4 | 2386.0 |
| FJ680789.1 | 518054 | 6376.3 | 8056.5 | 7555.1 | 7040.1 | 9096.5 | 6403.8 |
| FJ205803.1 | 335171 | 1528.3 | 1837.2 | 1310.1 | 1566.1 | 1266.2 | 1332.2 |
| EU794282.1 | 317703 | 4719.8 | 7022.7 | 7829.1 | 8206.2 | 4240.2 | 3865.5 |
| FJ684918.1 | 530177 | 3504.1 | 3882.0 | 3455.3 | 5451.5 | 2040.9 | 2116.0 |
| EU219944.1 | 257268 | 6005.5 | 8287.1 | 10190.0 | 8970.1 | 8856.7 | 8404.7 |
| FJ717180.1 | 511931 | 7984.5 | 10385.5 | 7545.1 | 7534.5 | 11250.3 | 9394.0 |
| EU050916.1 | 236166 | 4233.0 | 5041.3 | 5476.9 | 3754.0 | 10806.6 | 5146.9 |
| EU142042.1 | 243175 | 1439.7 | 1731.9 | 4156.2 | 1732.7 | 3726.7 | 2218.6 |
| EU570894.1 | 545311 | 7416.3 | 6550.4 | 9204.3 | 8248.8 | 6844.1 | 7484.1 |
| FJ366283.1 | 360268 | 11632.4 | 11150.4 | 9411.7 | 9025.2 | 10164.7 | 9856.9 |
| EF434374.1 | 204256 | 1755.5 | 1335.4 | 1199.0 | 1822.0 | 544.8 | 571.0 |
| FJ366026.1 | 366738 | 4814.7 | 5673.0 | 5571.6 | 4093.3 | 11094.2 | 11826.1 |
| CU924120.1 | 551818 | 74.8 | 83.2 | 102.6 | 86.7 | 82.1 | 50.6 |
| CU921361.1 | 552601 | 3152.6 | 4238.4 | 1722.6 | 2662.3 | 224.4 | 660.1 |
| AJ853619.1 | 110120 | 2949.9 | 3122.2 | 2164.6 | 2665.4 | 2008.2 | 4205.6 |
| FN436127.1 | 559693 | 5887.2 | 5784.2 | 4025.3 | 4903.9 | 5034.8 | 5577.6 |
| AY862794.2 | 160460 | 87.3 | 153.8 | 580.0 | 156.7 | 182.6 | 90.1 |
| AF507895.1 | 62666 | 162.1 | 193.2 | 169.6 | 848.5 | 144.0 | 86.5 |
| EU778068.1 | 313232 | 193.3 | 206.7 | 311.9 | 167.5 | 2131.6 | 475.1 |
| AM947541.1 | 268726 | 1361.5 | 2714.3 | 1385.6 | 2013.7 | 2262.1 | 1565.4 |
| AM947531.1 | 265685 | 8059.7 | 7119.6 | 7823.2 | 5776.7 | 7935.6 | 6924.4 |
| GU196243.1 | 581038 | 7717.2 | 8595.2 | 6151.6 | 7937.8 | 4887.3 | 5250.4 |
| GQ448397.1 | 588815 | 3435.6 | 3581.3 | 3064.9 | 5240.7 | 2390.3 | 3529.2 |
| AF412968.1 | 21971 | 3787.9 | 2533.1 | 6841.7 | 4898.9 | 3283.7 | 4225.4 |
| FJ226570.1 | 355090 | 4870.7 | 3654.7 | 718.8 | 253.4 | 290.5 | 266.5 |
| AY257485.1 | 83638 | 1937.2 | 1593.4 | 3116.5 | 1554.4 | 1456.1 | 2264.4 |
| CP000896.1 | 243946 | 290.9 | 252.4 | 510.7 | 507.8 | 371.3 | 240.9 |
| U14905.1 | 15691 | 204.1 | 230.4 | 537.1 | 180.8 | 708.8 | 358.0 |
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| EU517562.1 | 274442 | 22.4 | 15.5 | 21.7 | 39.7 | 56.4 | 16.3 |
| DQ337019.1 | 145365 | 1933.8 | 2135.6 | 1873.2 | 1256.5 | 525.6 | 996.8 |

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| s__unclassified | 74494 |
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| s__unclassified | 74574 |
| s__Artemisia witches-broom phytoplasma | 73654 |
| s__Artemisia witches-broom phytoplasma | 74444 |
| s__Aster yellows witches-broom phytoplasma | 73181 |
| s__Aster yellows witches-broom phytoplasma | 73377 |
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| s__Aster yellows witches-broom phytoplasma | 74097 |
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| s__Aster yellows witches-broom phytoplasma | 74579 |
| s__Cactus witches-broom phytoplasma | 73193 |
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| s__Candidatus Phytoplasma pini | 73934 |
| s__Candidatus Phytoplasma prunorum | 73777 |
| s__Candidatus Phytoplasma solani | 73731 |
| s__Cassava frogskin disease phytoplasma | 73310 |
| s__Cassava frogskin disease phytoplasma | 73414 |
| s__Cassava frogskin disease phytoplasma | 74305 |

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

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|---|---|---|---|---|---|---|---|
| AY538166.1 | 103660 | 234.3 | 315.8 | 839.9 | 459.4 | 1316.1 | 348.8 |
| AY538163.1 | 103238 | 24.6 | 21.7 | 23.3 | 48.3 | 66.2 | 30.4 |
| AM950255.1 | 540644 | 347.5 | 882.6 | 531.6 | 454.2 | 355.0 | 432.2 |
| L33734.1 | 15688 | 188.4 | 180.7 | 172.9 | 756.9 | 282.4 | 36.3 |
| AY538168.1 | 103956 | 62.3 | 53.3 | 38.0 | 66.6 | 108.2 | 91.8 |
| FJ876262.1 | 556175 | 526.8 | 599.5 | 1364.9 | 812.3 | 1303.9 | 730.3 |
| FJ825517.1 | 542107 | 2216.3 | 1956.3 | 2546.0 | 3058.3 | 2178.2 | 1432.8 |
| AM982581.2 | 278258 | 1590.0 | 1563.9 | 3160.4 | 2091.2 | 623.9 | 1024.8 |
| DQ337046.1 | 148755 | 8916.8 | 8867.3 | 4048.5 | 7446.1 | 10404.8 | 10735.4 |
| AY538170.1 | 107774 | 764.8 | 1007.2 | 1181.8 | 569.2 | 331.6 | 444.6 |
| EF586009.1 | 252219 | 5451.2 | 3695.0 | 7752.7 | 4675.5 | 4533.4 | 4802.1 |
| AB369182.1 | 235282 | 3866.9 | 4812.7 | 3510.6 | 3306.7 | 4091.9 | 3433.7 |
| AY538167.1 | 103806 | 9056.7 | 9164.2 | 8159.0 | 8281.4 | 5312.0 | 5921.1 |
| AY538164.1 | 103388 | 2404.3 | 4824.2 | 7600.1 | 4595.7 | 4827.3 | 4976.9 |
| DQ989179.1 | 235828 | 11765.1 | 11191.7 | 10873.0 | 10546.3 | 10682.2 | 9630.6 |
| AF411592.1 | 60512 | 9334.7 | 9267.0 | 9138.7 | 10878.7 | 10303.2 | 9571.6 |
| AY180931.1 | 100768 | 7018.6 | 7237.4 | 6949.0 | 6511.4 | 9450.7 | 6065.7 |
| AY180930.1 | 100615 | 4056.0 | 4394.5 | 4499.9 | 3614.1 | 6799.8 | 3671.3 |
| AY180925.1 | 105275 | 4705.9 | 5416.4 | 3259.1 | 3371.7 | 8500.0 | 6117.6 |
| AY265216.1 | 102638 | 8893.7 | 8282.1 | 4669.7 | 10665.0 | 15876.7 | 13360.3 |
| AY180941.1 | 105824 | 6989.5 | 7179.9 | 7277.4 | 6317.2 | 8120.6 | 6441.7 |
| AY180936.1 | 101585 | 5332.3 | 5557.9 | 5085.8 | 5194.0 | 6560.6 | 4015.0 |
| AY180933.1 | 101087 | 5089.0 | 5861.4 | 3496.9 | 4015.9 | 4002.0 | 3792.9 |
| AY180948.1 | 106919 | 7210.7 | 7239.9 | 5349.2 | 7000.9 | 11505.8 | 6128.5 |
| EU099556.1 | 275610 | 1800.2 | 1291.5 | 3392.8 | 2804.6 | 464.6 | 552.8 |
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| EU099555.1 | 275102 | 407.9 | 968.4 | 288.3 | 329.6 | 197.8 | 359.0 |
| EU099569.1 | 274000 | 486.3 | 1103.1 | 864.2 | 492.1 | 294.3 | 605.7 |
| EU099566.1 | 272756 | 7196.5 | 7365.8 | 4556.1 | 8635.3 | 9565.3 | 9617.1 |
| AY377868.1 | 106270 | 616.6 | 1142.3 | 1393.5 | 878.3 | 1601.4 | 983.0 |
| AB052872.1 | 106149 | 233.6 | 382.8 | 614.1 | 117.1 | 159.2 | 307.8 |
| X68339.1 | 15630 | 9211.3 | 8722.5 | 6304.5 | 9116.7 | 10187.8 | 9327.3 |
| NC_011047.1 | 345428 | 3368.7 | 4443.6 | 3972.1 | 2846.9 | 7677.1 | 4963.8 |
| AJ310849.2 | 53611 | 150.8 | 291.4 | 756.5 | 126.2 | 173.2 | 404.8 |
| X68374.1 | 15654 | 9513.7 | 9747.2 | 11485.5 | 11682.8 | 11826.7 | 9947.8 |
| GQ403235.1 | 561370 | 4250.2 | 4285.2 | 1477.9 | 6206.9 | 7098.3 | 6184.1 |
| FJ376625.1 | 582084 | 1102.3 | 1265.0 | 950.8 | 778.3 | 1481.1 | 1548.8 |
| AY731819.1 | 102742 | 2493.4 | 2978.3 | 1813.0 | 2540.9 | 3476.2 | 3700.6 |
| AY081817.1 | 58989 | 2926.9 | 3723.5 | 2462.3 | 3474.5 | 3501.2 | 3800.0 |

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| s__Cassava frogskin disease phytoplasma | 74424 |
| s__Chinaberry yellows phytoplasma | 73831 |
| s__Chinaberry yellows phytoplasma | 74434 |
| s__Clover phyllody phytoplasma | 73495 |
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| s__Clover phyllody phytoplasma | 74220 |
| s__Clover phyllody phytoplasma | 74526 |
| s__Clover phyllody phytoplasma | 74593 |
| s__Crotalaria witches-broom phytoplasma | 73334 |
| s__Crotalaria witches-broom phytoplasma | 73856 |
| s__Crotalaria witches-broom phytoplasma | 74238 |
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| s__Jujube witches-broom phytoplasma | 73175 |
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| s__Lethal yellowing phytoplasma | 73256 |
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| s__Loofah witches-broom phytoplasma | 73268 |
| s__Onion yellows phytoplasma | 74599 |

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

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| FJ376627.1 | 566603 | 4352.0 | 3723.6 | 5343.2 | 5431.1 | 10572.8 | 6071.7 |
| AF495882.1 | 67193 | 81.8 | 211.6 | 550.4 | 184.9 | 117.4 | 142.1 |
| DQ444264.1 | 201671 | 136.3 | 257.4 | 463.3 | 108.1 | 104.7 | 90.1 |
| AY787141.2 | 108981 | 4002.6 | 4379.4 | 4639.9 | 3623.0 | 6627.6 | 2823.7 |
| DQ640501.1 | 230702 | 4055.8 | 4441.5 | 3690.1 | 3723.7 | 6646.8 | 3711.6 |
| DQ640502.1 | 229957 | 5936.2 | 6301.1 | 5322.1 | 6039.6 | 7143.8 | 4489.4 |
| AY669063.1 | 137793 | 7017.3 | 7234.0 | 6947.1 | 6505.0 | 9443.0 | 6465.7 |
| AY265218.1 | 102937 | 6984.1 | 7182.1 | 6815.0 | 6425.3 | 8036.4 | 6448.1 |
| DQ452416.1 | 157195 | 7949.7 | 6627.4 | 3276.8 | 6816.9 | 9463.8 | 8462.8 |
| EF193357.1 | 202717 | 9759.6 | 8538.0 | 4494.2 | 8948.7 | 11023.9 | 11357.0 |
| EU513212.1 | 267241 | 1027.7 | 1206.1 | 1158.8 | 766.4 | 1331.9 | 988.8 |
| AB257290.1 | 183185 | 1023.3 | 1196.3 | 1050.0 | 752.4 | 1318.3 | 978.3 |
| EF990734.1 | 256711 | 981.0 | 1241.3 | 1217.6 | 836.4 | 1351.6 | 916.7 |
| GU184178.1 | 583290 | 5805.6 | 7142.4 | 5275.6 | 5453.6 | 6744.1 | 5899.9 |
| GU184173.1 | 561436 | 8073.5 | 8617.0 | 7258.5 | 6911.6 | 11820.3 | 9130.6 |
| AY197659.1 | 86835 | 4734.0 | 5725.2 | 7182.7 | 5649.6 | 5643.9 | 5074.0 |
| GU184174.1 | 591979 | 4737.2 | 5692.7 | 6836.7 | 5656.1 | 5692.0 | 5190.7 |
| GU184185.1 | 565984 | 6477.5 | 7334.7 | 7453.8 | 6454.4 | 7001.2 | 6272.8 |
| GU184175.1 | 575585 | 5801.3 | 6656.3 | 5248.6 | 5457.2 | 6759.6 | 5905.9 |
| GU184177.1 | 538789 | 5874.8 | 7008.5 | 6727.8 | 6189.3 | 7312.6 | 7006.3 |
| GU184186.1 | 584389 | 4159.4 | 5219.7 | 4514.8 | 4166.3 | 5561.4 | 4356.8 |
| EF661582.1 | 242473 | 6312.0 | 7864.5 | 5374.0 | 6115.7 | 6920.9 | 6036.8 |
| DQ842529.1 | 163675 | 10593.2 | 10112.7 | 7421.3 | 8519.3 | 10076.0 | 8548.9 |
| EU026213.1 | 245559 | 1621.3 | 2280.6 | 3835.5 | 2060.4 | 5766.6 | 3204.1 |
| DQ286706.1 | 149401 | 3519.7 | 4770.1 | 4508.4 | 4921.5 | 6670.0 | 4654.3 |
| DQ286704.1 | 148438 | 695.1 | 1062.0 | 1774.6 | 1901.9 | 1859.5 | 1345.0 |
| DQ842525.1 | 173631 | 9734.7 | 8934.4 | 9398.8 | 8745.2 | 8430.3 | 7217.7 |
| DQ842531.1 | 167990 | 1769.5 | 2135.7 | 1921.9 | 2548.8 | 3586.7 | 2867.5 |
| DQ842527.1 | 172269 | 3663.6 | 3888.9 | 2939.3 | 6015.6 | 9152.9 | 7297.7 |
| DQ286702.1 | 148239 | 5899.8 | 5777.8 | 6152.4 | 8350.7 | 10397.7 | 5179.3 |
| AY572031.1 | 102515 | 9505.8 | 10133.3 | 9746.6 | 10509.5 | 7502.3 | 7815.9 |
| AY572030.1 | 102350 | 397.0 | 604.1 | 1203.8 | 1505.5 | 1102.8 | 918.9 |
| DQ842528.1 | 173235 | 1677.1 | 2169.7 | 2019.5 | 2359.8 | 3615.7 | 3027.9 |
| DQ842532.1 | 171211 | 802.7 | 1190.3 | 1611.9 | 2062.7 | 1717.9 | 1228.8 |
| DQ286707.1 | 145483 | 3710.9 | 3530.7 | 2656.9 | 5006.4 | 4132.1 | 3561.4 |
| DQ286701.1 | 147292 | 2844.1 | 3301.1 | 2645.2 | 4005.6 | 2776.6 | 2177.7 |
| DQ286705.1 | 146262 | 2692.3 | 3731.1 | 6361.4 | 4567.4 | 1280.7 | 2675.8 |
| AY572029.2 | 108988 | 17199.5 | 16439.9 | 11622.5 | 13700.4 | 18290.8 | 13896.6 |
| DQ842530.1 | 169291 | 2004.1 | 2124.9 | 2419.6 | 2994.6 | 2680.9 | 2306.2 |
| AF248956.1 | 69018 | 4253.3 | 4111.8 | 3658.6 | 4874.3 | 4886.1 | 5231.4 |
| DQ321822.2 | 145208 | 5089.5 | 5868.2 | 3730.9 | 4017.5 | 4004.8 | 3556.8 |

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

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| AY192577.1 | 79786 | 4867.9 | 5206.5 | 4677.3 | 4734.9 | 4378.8 | 4324.8 |
| EF186824.1 | 183787 | 6031.0 | 4697.6 | 6037.8 | 7116.6 | 3197.0 | 3479.1 |
| AY197649.1 | 86755 | 6529.1 | 7597.9 | 5607.1 | 6587.7 | 8311.0 | 7104.8 |
| AY197648.1 | 87980 | 2241.5 | 2563.7 | 4753.3 | 3361.3 | 2041.8 | 2424.4 |
| AY197654.1 | 87732 | 2429.9 | 2887.9 | 3105.0 | 2900.5 | 4541.2 | 3035.5 |
| EU333400.1 | 278893 | 4052.4 | 4846.5 | 3745.2 | 3641.2 | 3222.7 | 4040.7 |
| EU333397.1 | 278326 | 4042.3 | 4847.1 | 3988.5 | 3632.9 | 3215.2 | 4033.4 |
| EU333398.1 | 279421 | 4011.1 | 4523.2 | 3988.9 | 3595.8 | 3219.8 | 4018.2 |
| EU003536.1 | 244948 | 13067.5 | 9671.4 | 5764.6 | 9961.3 | 12673.9 | 11753.3 |
| EU003537.1 | 243480 | 130.4 | 216.0 | 599.3 | 284.9 | 549.8 | 410.7 |
| EF474451.2 | 235777 | 154.0 | 280.7 | 442.1 | 217.4 | 502.0 | 307.6 |
| X80117.1 | 15647 | 3848.9 | 3284.2 | 4032.1 | 3828.8 | 5519.5 | 3688.6 |
| FJ226072.1 | 575096 | 2723.1 | 3462.4 | 2502.1 | 2712.2 | 1231.5 | 2171.0 |
| AY197643.1 | 86864 | 4520.8 | 5191.9 | 7508.4 | 5969.8 | 6842.8 | 6458.2 |
| AB010425.2 | 32876 | 42.8 | 50.1 | 113.3 | 70.4 | 69.5 | 30.6 |
| AB242433.1 | 169824 | 5117.3 | 5908.5 | 3558.3 | 4072.7 | 4015.9 | 3582.0 |
| Y18052.1 | 15588 | 6567.8 | 5940.6 | 4828.2 | 7680.7 | 4846.8 | 5547.8 |
| DQ459438.1 | 157077 | 1390.0 | 1555.7 | 960.9 | 1652.1 | 668.8 | 1086.5 |
| AF370120.1 | 66821 | 373.1 | 505.3 | 689.3 | 420.1 | 1159.6 | 971.6 |
| DQ286953.1 | 144993 | 1987.2 | 2136.1 | 1578.0 | 1404.6 | 1320.4 | 1223.5 |
| AY863003.1 | 109692 | 5089.3 | 5868.3 | 3729.6 | 4014.4 | 4003.6 | 3791.8 |
| EU375834.1 | 259943 | 5095.8 | 5990.9 | 3806.2 | 4034.1 | 4039.4 | 3616.7 |
| EU371934.1 | 260301 | 5355.0 | 4751.0 | 5365.9 | 6230.0 | 7102.1 | 7045.1 |
| EF050071.1 | 177441 | 4041.7 | 4463.1 | 3000.3 | 2940.1 | 3970.8 | 3422.1 |
| DQ645635.1 | 161008 | 3678.2 | 3617.7 | 3301.2 | 4606.3 | 3231.7 | 3071.8 |
| AY204549.1 | 107635 | 204.4 | 236.1 | 950.1 | 129.9 | 101.5 | 104.0 |
| GU361756.1 | 538151 | 5047.7 | 5494.8 | 3724.1 | 3970.9 | 3999.1 | 3768.9 |
| AY180950.1 | 101862 | 7657.4 | 7968.6 | 6768.4 | 6470.6 | 16749.8 | 12122.9 |
| AY180946.1 | 106611 | 6506.0 | 7708.7 | 5425.6 | 5659.6 | 5629.5 | 5511.7 |
| AY075038.1 | 55023 | 4240.6 | 4739.6 | 3449.7 | 3491.4 | 3919.7 | 3694.2 |
| EF534205.1 | 258469 | 8451.5 | 8159.1 | 7957.2 | 6968.9 | 8491.7 | 7657.4 |
| AF305198.1 | 69629 | 3414.7 | 3357.6 | 5012.8 | 4734.2 | 3527.7 | 2527.2 |
| DQ286574.1 | 142079 | 50.1 | 67.7 | 52.1 | 166.1 | 543.8 | 33.6 |
| AY270156.1 | 82781 | 5305.5 | 4776.8 | 4162.9 | 1896.9 | 6684.9 | 6490.6 |
| EF493020.1 | 226498 | 2015.7 | 1722.7 | 1288.1 | 3495.2 | 1556.2 | 1860.0 |
| AY685055.1 | 98886 | 10094.5 | 11039.6 | 8118.4 | 8980.0 | 13044.8 | 10291.1 |
| DQ164212.1 | 170032 | 6607.4 | 4096.4 | 6164.0 | 5346.9 | 9240.2 | 5427.9 |
| AF244363.1 | 17222 | 2925.2 | 3714.5 | 2412.0 | 3470.9 | 3485.5 | 3757.9 |
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AY495702.1 gg_id:99151 polystachya phytoplasma str. Aphanamixis yellows
EF432569.1 gg_id:254955 Bischofia polycarpa witches'-broom phytoplasma
AF455039.1 gg_id:68807 Almond witches'-broom phytoplasma str. AlmWB4 phytoplasma
AJ289192.2 gg_id:69575 Stylosanthes little leaf phytoplasma
AJ289191.1 gg_id:41747 Pigeon pea little leaf phytoplasma
EU999740.1 gg_id:328637 Jujube witches'-broom phytoplasma str. ZY1
FN257485.1 gg_id:544411 Chandigarh periwinkle phytoplasma
AJ548787.2 gg_id:150071 Flavescence doree phytoplasma str. FD1487
AF438413.1 gg_id:60303 Omani alfalfa witches'-broom phytoplasma
DQ305979.2 gg_id:546804 Leptodelphax dymas phytoplasma
FJ432664.1 gg_id:369928 Salt cedar witches'-broom phytoplasma str. SCWB1
AY389822.2 gg_id:100290 Aster yellows phytoplasma str. AY-BD2
DQ286577.1 gg_id:143334 Ocimum basilicum phytoplasma
DQ321821.1 gg_id:145420 Carludovica palmata leaf yellowing phytoplasma str. CPY
X76560.1 gg_id:15602 Mycoplasma sp str. FD flavescence doree
AJ289195.1 gg_id:25555 Vigna little leaf phytoplasma
Y16390.1 gg_id:15625 Italian alfalfa witches-broom phytoplasma
AY725211.2 gg_id:103733 Bolivia alfalfa phytoplasma
EF634457.1 gg_id:246840 Chrysanthemum yellows phytoplasma str. CY
AY725231.2 gg_id:200942 Conyza phytoplasma
AY265212.1 gg_id:102027 Aster yellows phytoplasma str. CVB
EU375835.1 gg_id:277015 Periwinkle yellows phytoplasma str. Hainan
X92869.1 gg_id:15651 Phytoplasma sp.
DQ302722.1 gg_id:144066 Garden beet witches'-broom phytoplasma str. YCH500
EU999741.1 gg_id:351684 Jujube witches'-broom phytoplasma str. TA1
DQ318241.1 gg_id:145644 Coconut lethal yellowing phytoplasma str. CLY-DR
EU549768.1 gg_id:263110 Coconut lethal yellowing phytoplasma str. M-182
EF050085.1 gg_id:180292 Periwinkle virescence phytoplasma str. CICY7
EF186822.1 gg_id:181552 Lethal yellowing phytoplasma str. LYja
DQ431843.1 gg_id:151644 Sesamum phyllody phytoplasma
AB076404.1 gg_id:80823 Potato witches'-broom phytoplasma
X83432.1 gg_id:15624 mollicute str. FAB (faba bean phyllody)
AY742330.1 gg_id:107557 Sorghum phytoplasma
AF147708.1 gg_id:54260 Candidatus Phytoplasma brasiliense
DQ378279.1 gg_id:151592 Coconut lethal yellowing phytoplasma str. Nevis (LYN 18-3)
AY197644.1 gg_id:87547 Flavescence doree phytoplasma str. FD-D
FN257484.1 gg_id:568424 Himachal periwinkle phytoplasma
AY204548.1 gg_id:107488 Sweet potato little leaf phytoplasma str. SPLL-Uga
AY147038.1 gg_id:106863 Argentinian alfalfa witches'-broom phytoplasma str. 16SrVII-C
EU099559.1 gg_id:277355 Cactus witches'-broom phytoplasma str. YN14
DQ431842.1 gg_id:153316 Chrysanthemum witches'-broom phytoplasma

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| AY495702.1 | 99151 | 2989.5 | 3174.4 | 3559.0 | 2308.7 | 4047.6 | 3799.8 |
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| AF455039.1 | 68807 | 6099.0 | 4931.0 | 2924.3 | 5398.4 | 5527.7 | 4124.1 |
| AJ289192.2 | 69575 | 6129.2 | 5574.5 | 6109.0 | 5578.6 | 5419.2 | 5770.2 |
| AJ289191.1 | 41747 | 1417.4 | 1909.5 | 2284.2 | 1205.3 | 353.8 | 588.9 |
| EU999740.1 | 328637 | 5055.0 | 5660.6 | 6822.3 | 6013.8 | 6058.5 | 5480.7 |
| FN257485.1 | 544411 | 5087.8 | 5867.2 | 3738.6 | 4009.7 | 3997.5 | 3553.5 |
| AJ548787.2 | 150071 | 4721.7 | 4912.1 | 8075.1 | 6495.8 | 4239.4 | 4531.6 |
| AF438413.1 | 60303 | 3252.0 | 2783.5 | 2422.1 | 3549.8 | 3622.3 | 4703.2 |
| DQ305979.2 | 546804 | 10429.9 | 9668.2 | 8114.6 | 10466.6 | 13826.6 | 14361.8 |
| FJ432664.1 | 369928 | 4647.2 | 4298.4 | 3693.9 | 7075.6 | 5387.6 | 3985.6 |
| AY389822.2 | 100290 | 4244.9 | 4698.8 | 4310.5 | 3390.0 | 4095.5 | 3698.0 |
| DQ286577.1 | 143334 | 13285.0 | 13307.4 | 8670.9 | 9352.1 | 20381.6 | 15661.3 |
| DQ321821.1 | 145420 | 454.1 | 978.7 | 1759.2 | 679.8 | 1614.6 | 1909.2 |
| X76560.1 | 15602 | 3958.6 | 3935.1 | 6921.2 | 5731.4 | 3456.2 | 3290.6 |
| AJ289195.1 | 25555 | 982.1 | 1006.7 | 929.9 | 1143.8 | 119.6 | 319.9 |
| Y16390.1 | 15625 | 2286.1 | 3435.1 | 1709.0 | 2358.7 | 275.8 | 538.1 |
| AY725211.2 | 103733 | 3664.4 | 3267.4 | 1851.3 | 4844.9 | 8827.2 | 6375.2 |
| EF634457.1 | 246840 | 7389.8 | 10704.3 | 7723.5 | 7199.3 | 10194.2 | 8440.2 |
| AY725231.2 | 200942 | 3036.0 | 3144.3 | 4555.5 | 4430.5 | 5330.5 | 4170.4 |
| AY265212.1 | 102027 | 5191.6 | 8417.2 | 3981.3 | 5085.7 | 4357.2 | 3520.6 |
| EU375835.1 | 277015 | 2611.4 | 2855.2 | 5836.6 | 3561.1 | 1407.5 | 1374.8 |
| X92869.1 | 15651 | 2185.2 | 2554.7 | 1681.7 | 1759.2 | 2396.1 | 2043.8 |
| DQ302722.1 | 144066 | 13736.3 | 9622.2 | 6484.9 | 10451.8 | 12440.6 | 12220.9 |
| EU999741.1 | 351684 | 3553.9 | 4020.0 | 4022.6 | 4257.3 | 5168.2 | 2856.1 |
| DQ318241.1 | 145644 | 668.9 | 1088.4 | 1669.4 | 1165.5 | 1878.8 | 1406.0 |
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| AY742330.1 | 107557 | 1437.5 | 1289.8 | 2802.9 | 1193.9 | 2624.2 | 1964.7 |
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| AY197644.1 | 87547 | 4118.4 | 4297.7 | 5997.5 | 5912.3 | 3998.7 | 4198.3 |
| FN257484.1 | 568424 | 6367.2 | 7063.2 | 5455.9 | 5490.3 | 3920.9 | 3841.0 |
| AY204548.1 | 107488 | 1603.8 | 1343.2 | 4049.0 | 1973.5 | 2022.1 | 2187.5 |
| AY147038.1 | 106863 | 13959.8 | 13228.5 | 14618.8 | 11895.7 | 13733.8 | 10403.2 |
| EU099559.1 | 277355 | 423.7 | 842.1 | 356.1 | 371.6 | 158.5 | 165.7 |
| DQ431842.1 | 153316 | 5750.6 | 8539.4 | 6230.9 | 5230.5 | 3529.0 | 4244.5 |

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

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| EF153634.1 | 186762 | 1819.7 | 2867.1 | 2803.5 | 2667.4 | 3753.8 | 3585.2 |
| FJ226076.1 | 550833 | 8587.6 | 7547.2 | 7595.7 | 8778.2 | 6390.2 | 6706.3 |
| FJ226074.1 | 566707 | 11023.3 | 10676.6 | 7849.8 | 10638.9 | 11618.3 | 12283.8 |
| EU333395.1 | 278466 | 2998.5 | 3315.6 | 3188.6 | 2545.3 | 3154.7 | 3845.1 |
| AF248960.1 | 55663 | 222.2 | 280.5 | 1696.8 | 219.6 | 115.1 | 142.7 |
| AF147706.1 | 54971 | 1028.8 | 1182.7 | 939.9 | 735.8 | 1409.6 | 1588.3 |
| AY265220.1 | 106715 | 5088.4 | 5864.0 | 3506.8 | 4015.0 | 4002.5 | 3556.9 |
| EU999742.1 | 326955 | 4721.5 | 5805.6 | 5250.4 | 5018.0 | 6302.0 | 5546.4 |
| GU361757.1 | 551933 | 2040.5 | 2261.5 | 1835.8 | 1959.7 | 1842.5 | 1645.7 |
| AY197647.1 | 87317 | 4654.7 | 4678.5 | 1572.5 | 6475.8 | 8067.5 | 7719.2 |
| GU113147.1 | 589201 | 11451.3 | 15301.8 | 11885.8 | 9451.0 | 11280.3 | 10012.6 |
| EU057983.1 | 237448 | 2057.5 | 2440.5 | 2092.2 | 2553.0 | 4094.0 | 3354.1 |
| EU241515.1 | 254449 | 2174.5 | 2902.9 | 1646.1 | 3155.4 | 5253.5 | 2236.4 |
| Y16393.1 | 15581 | 1762.7 | 2311.3 | 1150.8 | 1323.1 | 545.1 | 394.3 |
| EF186828.1 | 181939 | 600.4 | 1044.1 | 1093.7 | 591.9 | 158.6 | 341.2 |
| DQ318244.1 | 147021 | 4015.3 | 4001.1 | 3487.1 | 4844.1 | 3941.9 | 3112.4 |
| AY739024.1 | 100418 | 12626.1 | 12675.4 | 5621.4 | 13084.1 | 14960.8 | 12356.1 |
| AY180953.1 | 102314 | 6297.6 | 7577.6 | 5404.0 | 5652.4 | 5609.5 | 5869.0 |
| AF331973.1 | 112027 | 532.4 | 1131.0 | 807.5 | 426.5 | 237.7 | 231.2 |
| DQ318242.1 | 147649 | 3956.1 | 3833.1 | 3558.9 | 4834.8 | 3645.5 | 3059.6 |
| AY265210.1 | 101708 | 13077.2 | 16918.6 | 11046.3 | 12427.5 | 15218.0 | 12568.6 |
| FJ217385.1 | 340797 | 10499.0 | 10114.8 | 10045.2 | 9763.9 | 13088.0 | 9334.5 |
| GU113145.1 | 568778 | 3403.4 | 4076.7 | 1743.4 | 2700.1 | 1328.0 | 1338.7 |
| AF173558.1 | 15599 | 1426.6 | 1801.4 | 1428.6 | 1248.6 | 2561.2 | 2466.5 |
| AY787136.4 | 201507 | 7800.8 | 10139.2 | 7517.8 | 6347.6 | 10201.3 | 8515.4 |
| AY180944.1 | 106289 | 6272.7 | 6914.8 | 3008.5 | 6499.5 | 11913.8 | 8012.4 |
| AY377876.1 | 102155 | 9396.9 | 8961.0 | 7089.6 | 8733.5 | 6774.3 | 6517.5 |
| EU333396.1 | 279028 | 6184.6 | 9279.2 | 7203.6 | 5467.4 | 9122.5 | 7214.5 |
| AM180882.1 | 187579 | 2168.9 | 2189.0 | 2288.9 | 2564.8 | 737.5 | 1290.7 |
| DQ384857.1 | 151119 | 6888.7 | 8387.8 | 10181.7 | 9366.2 | 8623.6 | 9009.9 |
| X68373.1 | 15687 | 17274.3 | 18467.7 | 8009.9 | 14255.6 | 16252.5 | 13335.8 |
| DQ321820.1 | 145945 | 8025.2 | 7489.8 | 7185.8 | 5965.9 | 7013.4 | 6567.1 |
| AF279271.1 | 21611 | 5089.7 | 5818.1 | 4540.6 | 3907.8 | 4157.8 | 3518.9 |
| Y08173.1 | 15618 | 11928.7 | 8798.8 | 3714.5 | 7395.7 | 13052.3 | 14245.5 |
| AY180954.1 | 102473 | 3174.3 | 3985.1 | 3564.1 | 2271.6 | 4536.7 | 3503.5 |
| AF509322.1 | 63017 | 25.0 | 54.1 | 31.9 | 67.3 | 60.4 | 25.7 |
| AY265213.1 | 102179 | 2356.3 | 2957.2 | 1479.9 | 2195.6 | 1286.4 | 1437.2 |
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EU170353.1 gg_id:239724 Sweet potato little leaf phytoplasma 2&3Vtrio
FJ154847.1 gg_id:312556 Jujube witches'-broom phytoplasma str. ZQ
U16758.1 gg_id:15696 Mycoplasma feliminutum str. ATCC 25749
EU006252.1 gg_id:257027 Salmonella enterica serovar typhimurium exploits inflammation compete intestinal r
EU456203.1 gg_id:314291 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S
FJ681157.1 gg_id:529539 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU794312.1 gg_id:354444 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_L44
EF604794.1 gg_id:228310 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EU774401.1 gg_id:315971 mammals their gut microbes Eastern Black and White Colobus feces clone COL_aai1!
M25050.1 gg_id:15703 Anaeroplasma abactoclasticum
EF604918.1 gg_id:231986 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EU344682.1 gg_id:262497 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad
EU794279.1 gg_id:305348 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_G18
FJ683969.1 gg_id:528228 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
GQ897174.1 gg_id:555555 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons
DQ797091.1 gg_id:185593 human fecal clone RL386_aao86h04
DQ797049.1 gg_id:179979 human fecal clone RL386_aao86c09
NR_028691.1 gg_id:591314 Entomoplasma freundtii str. BARC318; ATCC 51999
GQ275106.1 gg_id:581987 gut symbionts are tightly linked herbivory ants extract single ant clone #130
AE017263.1 gg_id:100309 Mesoplasma florum L1 str. L1; ATCC 33453
AY187288.1 gg_id:79099 Mesoplasma tabanidae str. BARC 857; ATCC 49584
AF042194.1 gg_id:15792 Mycoplasma monodon str. Australiain
AY168929.2 gg_id:75831 Mesoplasma corruscae str. ATCC 49579
AY166704.1 gg_id:76006 Mesoplasma chauliocola str. ATCC 49578
DQ157864.1 gg_id:139255 Mycoplasma capricolum str. 700
U26055.1 gg_id:15786 Mycoplasma putrefaciens str. KS-1
AY155670.1 gg_id:75155 Entomoplasma luminosum str. ATCC 49195; PIMN-1
GQ275109.1 gg_id:568610 gut symbionts are tightly linked herbivory ants extract single ant clone #133
GQ275144.1 gg_id:555846 gut symbionts are tightly linked herbivory ants extract single ant clone #168
AY538169.1 gg_id:104104 Acholeplasma multilocale str. PN525
AF303132.1 gg_id:71794 Mesoplasma lactucae str. 831-C4; ATCC 49193 ATCC
DQ861915.1 gg_id:168652 Spiroplasma cantharicola str. Q-6
X63781.1 gg_id:15803 Spiroplasma citri str. R8A2HP
DQ112020.1 gg_id:130516 Spiroplasma citri str. Car6
AJ006775.1 gg_id:41072 Spiroplasma sp
NR_025706.1 gg_id:534716 Spiroplasma lampyridicola str. PUP-1; ATCC 43206
AY189309.1 gg_id:99424 Spiroplasma syrphidicola str. ATCC 33826; EA-1
AY189132.1 gg_id:101796 Spiroplasma helicoides str. ATCC 51746; TABS-2
AY345990.1 gg_id:93470 Entomoplasma melaleucae str. M1
AY189125.1 gg_id:106072 Spiroplasma alleghenense str. ATCC 51752; PLHS-1
EF151267.1 gg_id:202191 Spiroplasma sp. str. CRW-1

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| EU170353.1 | 239724 | 2937.9 | 3519.2 | 2115.4 | 3617.5 | 2064.3 | 2417.5 |
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| U16758.1 | 15696 | 430.2 | 526.2 | 1207.4 | 728.6 | 586.5 | 354.6 |
| EU006252.1 | 257027 | 2765.3 | 3418.6 | 1007.7 | 2555.7 | 2440.2 | 1805.7 |
| EU456203.1 | 314291 | 13806.0 | 17120.8 | 5827.9 | 11156.9 | 15863.7 | 12299.3 |
| FJ681157.1 | 529539 | 4698.4 | 5792.2 | 5487.6 | 4711.8 | 6805.2 | 6114.8 |
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| EU774401.1 | 315971 | 345.1 | 596.1 | 1207.5 | 680.8 | 424.3 | 605.0 |
| M25050.1 | 15703 | 23.3 | 35.4 | 43.8 | 62.9 | 56.3 | 32.9 |
| EF604918.1 | 231986 | 13422.7 | 13332.5 | 8230.8 | 14011.6 | 16106.4 | 14227.3 |
| EU344682.1 | 262497 | 5047.1 | 6318.4 | 5581.4 | 6641.1 | 9589.5 | 7234.8 |
| EU794279.1 | 305348 | 6258.6 | 7003.7 | 10448.1 | 6232.7 | 9042.7 | 8220.5 |
| FJ683969.1 | 528228 | 230.6 | 490.9 | 867.3 | 275.9 | 552.2 | 1033.0 |
| GQ897174.1 | 555555 | 4110.7 | 5539.1 | 3304.0 | 4195.9 | 5134.0 | 6246.1 |
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| DQ797049.1 | 179979 | 9398.1 | 10256.7 | 11765.3 | 8444.6 | 8437.2 | 10737.1 |
| NR_028691.1 | 591314 | 176.3 | 247.3 | 273.0 | 123.6 | 92.3 | 175.3 |
| GQ275106.1 | 581987 | 3514.2 | 3247.7 | 3455.0 | 841.0 | 1808.7 | 2227.4 |
| AE017263.1 | 100309 | 1766.1 | 3002.6 | 2199.3 | 1066.8 | 3682.1 | 2416.1 |
| AY187288.1 | 79099 | 1770.8 | 3051.5 | 2217.1 | 1068.3 | 3681.7 | 2412.1 |
| AF042194.1 | 15792 | 31.1 | 47.3 | 140.3 | 65.0 | 71.7 | 159.9 |
| AY168929.2 | 75831 | 4572.0 | 5434.2 | 3791.0 | 6470.0 | 6564.0 | 6090.2 |
| AY166704.1 | 76006 | 834.6 | 1176.3 | 2063.4 | 993.0 | 1704.1 | 1522.3 |
| DQ157864.1 | 139255 | 15.5 | 31.9 | 14.4 | 60.6 | 49.2 | 19.0 |
| U26055.1 | 15786 | 1707.0 | 1898.5 | 2206.9 | 2187.5 | 1100.1 | 2214.1 |
| AY155670.1 | 75155 | 509.1 | 475.8 | 347.6 | 346.3 | 304.6 | 352.7 |
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| GQ275144.1 | 555846 | 710.8 | 1647.7 | 2201.9 | 368.2 | 228.6 | 927.8 |
| AY538169.1 | 104104 | 36.1 | 79.2 | 99.7 | 79.9 | 97.3 | 72.7 |
| AF303132.1 | 71794 | 74.4 | 84.9 | 74.6 | 120.8 | 146.5 | 59.6 |
| DQ861915.1 | 168652 | 2854.1 | 3753.6 | 3850.3 | 3053.3 | 7176.4 | 4680.7 |
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| AY189125.1 | 106072 | 57.6 | 70.8 | 52.4 | 134.9 | 96.8 | 124.4 |
| EF151267.1 | 202191 | 1835.9 | 2358.2 | 1562.0 | 2256.4 | 1958.6 | 2391.7 |

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| s__unclassified | 71076 |
| s__unclassified | 71092 |
| s__unclassified | 71158 |
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| s__Candidatus Mycoplasma haematoparvum | 75792 |
| s__Candidatus Mycoplasma haemobos | 75428 |
| s__Candidatus Mycoplasma turicensis | 74635 |
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| s__Mycoplasma agalactiae | 73522 |
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| s__Mycoplasma agalactiae | 74331 |
| s__Mycoplasma agassizii | 73843 |
| s__Mycoplasma alvi | 71129 |
| s__Mycoplasma amphoriforme | 71058 |
| s__Mycoplasma amphoriforme | 71110 |
| s__Mycoplasma arginini | 73735 |
| s__Mycoplasma arthritidis | 73296 |
| s__Mycoplasma canis | 73560 |
| s__Mycoplasma citelli | 74324 |
| s__Mycoplasma conjunctivae | 73818 |
| s__Mycoplasma flocculare | 73650 |
| s__Mycoplasma gallisepticum | 71164 |
| s__Mycoplasma gallopavonis | 73653 |
| s__Mycoplasma genitalium | 70742 |
| s__Mycoplasma haemocanis | 74767 |
| s__Mycoplasma haemocanis | 75158 |
| s__Mycoplasma haemocanis | 75391 |
| s__Mycoplasma haemocanis | 75880 |

DQ860100.1 gg_id:164807 Spiroplasma lineolae str. TALS-2
AY189133.1 gg_id:101955 Spiroplasma insolitum str. ATCC 33502; M55
DQ917756.1 gg_id:258655 Spiroplasma mirum
GQ051079.1 gg_id:429439 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ275102.1 gg_id:558391 gut symbionts are tightly linked herbivory ants extract single ant clone #126
AY772395.1 gg_id:108248 Spiroplasma phoeniceum str. P40
AY189318.1 gg_id:104368 Spiroplasma sp. str. TIUS-1
AY189129.1 gg_id:106700 Spiroplasma culicicola str. ATCC 35112; AES-1
DQ860101.1 gg_id:166158 Spiroplasma platyhelix str. PALS-1
AY189305.1 gg_id:107782 Spiroplasma leptinotarsae str. ATCC 43213; LD-1B
NR_025703.1 gg_id:544767 Spiroplasma floricola str. 23-6; ATCC 29989
DQ319068.1 gg_id:148669 Spiroplasma kunkelii str. CR2-3x
GQ275136.1 gg_id:567222 gut symbionts are tightly linked herbivory ants extract single ant clone #160
AY325304.1 gg_id:100058 Spiroplasma melliferum str. BC-3
NR_025709.1 gg_id:565097 Spiroplasma montanense str. HYOS-1; ATCC 51745
AY189310.1 gg_id:103192 Spiroplasma turonicum str. ATCC 700271; Tab-4c
NR_025713.1 gg_id:561932 Spiroplasma velocicrescens str. MQ-4; ATCC 35262
GQ129114.1 gg_id:526608 Prevalence geographical canine hemotropic mycoplasma infections Mediterranean
EF424082.1 gg_id:209237 Mycoplasma sp. China-1
AY831867.1 gg_id:133123 Mycoplasma sp. 'feline hemotropic Switzerland'
DQ825454.1 gg_id:222355 Worldwide occurrence feline hemoplasma infections wild felid species Tanzania
NC_009497.1 gg_id:233772 Mycoplasma agalactiae str. PG2
AF332745.1 gg_id:73703 Mycoplasma agalactiae str. 396/12
AF332751.1 gg_id:70015 Mycoplasma agalactiae str. 35
AF060821.1 gg_id:15907 Mycoplasma agassizii str. K120
NR_025985.1 gg_id:565268 Mycoplasma alvi str. Isley; NCTC 10157
AY531656.1 gg_id:111859 Mycoplasma amphoriforme str. M5572
FJ226575.1 gg_id:326725 Mycoplasma amphoriforme str. A39
NR_029180.1 gg_id:550692 Mycoplasma gateae str. ATCC 23392
CP001047.1 gg_id:308649 Mycoplasma arthritidis str. 158L3-1
AF340023.1 gg_id:74000 Mycoplasma canis str. PG14
AF412973.1 gg_id:70402 Mycoplasma citelli str. RG-2C(T)
FJ226571.1 gg_id:310264 Mycoplasma conjunctivae str. Goat 655
GU227404.1 gg_id:579318 Mycoplasma flocculare str. USP9T
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AF412980.1 gg_id:72545 Mycoplasma gallopavonis str. WR1(T)
AY466443.1 gg_id:107609 Mycoplasma genitalium str. M2288
DQ825438.1 gg_id:217964 Mycoplasma haemofelis 111
EU930823.1 gg_id:340543 Mycoplasma haemofelis Porto Alegre
AY150985.1 gg_id:58418 Mycoplasma haemofelis UK no. 6
AY150973.1 gg_id:71517 Mycoplasma haemocanis Germany Munich no. 1

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| DQ860100.1 | 164807 | 129.0 | 348.3 | 522.0 | 119.7 | 91.1 | 904.7 |
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| DQ917756.1 | 258655 | 8906.5 | 7959.3 | 10520.6 | 11416.4 | 10387.9 | 9274.8 |
| GQ051079.1 | 429439 | 8834.6 | 7484.8 | 5873.3 | 8949.2 | 12337.0 | 10602.9 |
| GQ275102.1 | 558391 | 8071.3 | 7763.2 | 6461.7 | 11486.0 | 7078.8 | 6754.4 |
| AY772395.1 | 108248 | 16004.0 | 16919.6 | 13274.1 | 12925.4 | 10783.0 | 10148.5 |
| AY189318.1 | 104368 | 104.1 | 190.5 | 193.4 | 276.6 | 185.4 | 188.7 |
| AY189129.1 | 106700 | 2933.9 | 2710.6 | 4470.3 | 4532.5 | 6023.0 | 3193.3 |
| DQ860101.1 | 166158 | 140.9 | 97.3 | 32.0 | 67.5 | 85.7 | 57.6 |
| AY189305.1 | 107782 | 56.7 | 64.2 | 50.3 | 77.2 | 132.8 | 50.2 |
| NR_025703.1 | 544767 | 6056.3 | 6892.0 | 2338.8 | 7592.7 | 6035.6 | 5467.6 |
| DQ319068.1 | 148669 | 4564.1 | 5434.2 | 3924.2 | 5543.1 | 6135.5 | 3304.0 |
| GQ275136.1 | 567222 | 946.0 | 2443.2 | 3144.0 | 948.0 | 3019.5 | 4025.2 |
| AY325304.1 | 100058 | 7921.2 | 8868.7 | 6340.0 | 7461.4 | 7973.8 | 5489.8 |
| NR_025709.1 | 565097 | 6759.0 | 5934.9 | 5824.5 | 6296.1 | 7925.2 | 6570.9 |
| AY189310.1 | 103192 | 4319.2 | 6646.2 | 6278.0 | 3671.1 | 5610.8 | 4327.8 |
| NR_025713.1 | 561932 | 355.0 | 499.4 | 766.9 | 285.4 | 1706.2 | 916.8 |
| GQ129114.1 | 526608 | 16.7 | 36.2 | 46.8 | 48.4 | 61.9 | 26.1 |
| EF424082.1 | 209237 | 152.1 | 87.9 | 37.7 | 104.1 | 227.6 | 83.9 |
| AY831867.1 | 133123 | 4658.3 | 4814.5 | 2221.5 | 4086.2 | 4898.7 | 4321.6 |
| DQ825454.1 | 222355 | 6272.6 | 6509.1 | 2720.4 | 5696.1 | 826.4 | 1778.8 |
| NC_009497.1 | 233772 | 2621.2 | 3013.0 | 1356.3 | 1396.4 | 2209.6 | 1949.0 |
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| AF332751.1 | 70015 | 2944.1 | 3212.8 | 1765.5 | 1671.6 | 2086.1 | 2020.0 |
| AF060821.1 | 15907 | 313.5 | 454.5 | 1996.3 | 536.4 | 495.1 | 611.3 |
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| AY531656.1 | 111859 | 2170.9 | 2735.7 | 1291.6 | 2734.5 | 4290.7 | 3017.4 |
| FJ226575.1 | 326725 | 5430.6 | 5648.3 | 4062.6 | 4361.5 | 6485.4 | 4593.4 |
| NR_029180.1 | 550692 | 3052.2 | 3171.5 | 4046.2 | 4671.2 | 4281.3 | 4071.6 |
| CP001047.1 | 308649 | 10012.6 | 8922.7 | 7772.0 | 9345.6 | 8480.9 | 8255.0 |
| AF340023.1 | 74000 | 564.4 | 1813.3 | 1253.7 | 598.6 | 465.8 | 792.0 |
| AF412973.1 | 70402 | 74.5 | 88.9 | 211.1 | 103.6 | 87.6 | 58.3 |
| FJ226571.1 | 310264 | 4811.0 | 2197.4 | 2941.6 | 4248.2 | 748.4 | 1471.0 |
| GU227404.1 | 579318 | 240.4 | 302.6 | 963.0 | 440.6 | 1107.8 | 235.0 |
| L08896.4 | 15854 | 22.5 | 24.2 | 24.5 | 42.4 | 50.7 | 23.6 |
| AF412980.1 | 72545 | 1440.9 | 5770.4 | 3101.4 | 1451.9 | 1109.1 | 2084.0 |
| AY466443.1 | 107609 | 3697.9 | 3196.2 | 2627.4 | 4497.0 | 3839.9 | 2981.5 |
| DQ825438.1 | 217964 | 287.2 | 317.7 | 165.8 | 142.9 | 722.7 | 333.9 |
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| s__Mycoplasma microti | 70814 |
| s__Mycoplasma mobile | 73728 |
| s__Mycoplasma neurolyticum | 74358 |
| s__Mycoplasma opalescens | 73929 |
| s__Mycoplasma ovipneumoniae | 74293 |
| s__Mycoplasma penetrans | 70798 |
| s__Mycoplasma phocicerebrale | 74410 |
| s__Mycoplasma phocidae | 73167 |
| s__Mycoplasma phocirhinis | 73482 |
| s__Mycoplasma pneumoniae | 70867 |
| s__Mycoplasma pulmonis | 74201 |
| s__Mycoplasma spumans | 73225 |
| s__Mycoplasma suis | 75153 |
| s__Mycoplasma synoviae | 74078 |
| s__Mycoplasma testudineum | 74459 |
| s__Mycoplasma wenyonii | 75044 |
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| s__unclassified | 73272 |

AJ002268.1 gg_id:40026 Mycoplasma hominis str. P2
EU643797.1 gg_id:278892 Mycoplasma hyorhinis LuSIV
AF121890.1 gg_id:15878 Mycoplasma hyorhinis str. ATCC VR-2580
GU227374.1 gg_id:593611 Mycoplasma hyorhinis str. USP10T
NR_025064.1 gg_id:562555 Mycoplasma iners str. PG30; ATCC 19705
EF447273.1 gg_id:210500 Mycoplasma iowae str. HTL04-4846A
AF221116.1 gg_id:47885 Mycoplasma maculosum PG15(T)
U22415.1 gg_id:15832 Mycoplasma microti str. IL-372
AE017308.1 gg_id:103527 Mycoplasma mobile str. 163K
FJ655919.1 gg_id:565101 Mycoplasma neurolyticum str. T15
AF538961.1 gg_id:71629 Mycoplasma opalescens str. MHS408
U44771.1 gg_id:15870 Mycoplasma ovipneumoniae str. Y-98
BA000026.2 gg_id:107845 Mycoplasma penetrans str. HF-2
DQ840513.1 gg_id:166698 Mycoplasma phocicerebrale str. CSL 5195S2
EU827597.1 gg_id:349932 Mycoplasma phocidae str. CSL 7498-2
EU827598.1 gg_id:315295 Mycoplasma phocirhinis str. CSL 7475-4
NC_000912.1 gg_id:108728 Mycoplasma pneumoniae str. M129
AL445565.1 gg_id:58394 Mycoplasma pulmonis str. UAB CTIP
AF538684.1 gg_id:59733 Mycoplasma spumans
FJ263944.1 gg_id:316748 Mycoplasma suis str. HN
AE017245.1 gg_id:200524 Mycoplasma synoviae str. 53
U19768.1 gg_id:202917 Mycoplasma str. H3110
EU367963.1 gg_id:258287 Mycoplasma wenyonii cattle no. 48
DQ530428.1 gg_id:233952 Mycoplasma zalophi str. CSL 5195
AY571416.1 gg_id:114530 termite gut clone RsaHf232
GQ502581.1 gg_id:590759 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf4-
AB089055.1 gg_id:78062 termite gut homogenate clone Rs-G80
U09788.1 gg_id:15851 Mycoplasma str. ATCC 43263
NR_029165.1 gg_id:567958 Mycoplasma pirum str. 70-159; ATCC 25960
AB089054.1 gg_id:77956 termite gut homogenate clone Rs-B54
AB192228.1 gg_id:142809 termite gut homogenate clone RsTu1-65
AF125879.1 gg_id:15849 Mycoplasma cavipharyngis str. 117C(T)
AB089057.1 gg_id:77895 termite gut homogenate clone Rs-E42
AY571419.1 gg_id:114509 termite gut clone RsaHf283
EU859984.1 gg_id:344923 Mycoplasma sp. str. CSL7529-conjunctiva
AF221113.1 gg_id:71570 Mycoplasma columbinum MMP-1(T)
L24105.1 gg_id:15949 Mycoplasma gallinarum str. PG16
FM165074.1 gg_id:329837 Mycoplasma sp. C3T str. C3
AF221119.1 gg_id:19645 Mycoplasma spermatophilum AH159(T)
AM182894.1 gg_id:199102 Mycoplasma sp. str. 15CL2
AF221111.1 gg_id:73061 Mycoplasma caviae G122(T)

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| AJ002268.1 | 40026 | 6138.4 | 5353.3 | 8111.6 | 7163.6 | 7053.9 | 6279.9 |
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| AF121890.1 | 15878 | 10881.0 | 14170.3 | 4806.9 | 8771.1 | 9195.3 | 7280.0 |
| GU227374.1 | 593611 | 96.5 | 147.8 | 57.6 | 128.3 | 123.8 | 100.2 |
| NR_025064.1 | 562555 | 2597.9 | 1676.8 | 2040.2 | 1779.9 | 1052.4 | 1228.0 |
| EF447273.1 | 210500 | 5701.0 | 6259.0 | 5929.6 | 7833.6 | 8387.1 | 6643.5 |
| AF221116.1 | 47885 | 10164.1 | 9283.9 | 8402.7 | 10507.2 | 3159.9 | 4706.0 |
| U22415.1 | 15832 | 2788.4 | 3995.9 | 4945.2 | 4617.8 | 5065.1 | 7269.3 |
| AE017308.1 | 103527 | 6171.5 | 4773.7 | 9358.9 | 8779.1 | 5819.2 | 5147.9 |
| FJ655919.1 | 565101 | 124.6 | 93.1 | 177.6 | 121.0 | 103.7 | 79.2 |
| AF538961.1 | 71629 | 21.0 | 27.3 | 28.9 | 56.2 | 67.2 | 27.1 |
| U44771.1 | 15870 | 4714.9 | 5097.5 | 5398.1 | 5346.6 | 6546.8 | 6335.9 |
| BA000026.2 | 107845 | 31.6 | 50.3 | 168.6 | 88.1 | 61.3 | 34.0 |
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| EU827597.1 | 349932 | 7313.3 | 6848.2 | 8448.5 | 8508.8 | 6937.8 | 7818.8 |
| EU827598.1 | 315295 | 263.2 | 372.4 | 789.8 | 530.9 | 430.5 | 481.9 |
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| AL445565.1 | 58394 | 5691.7 | 4438.8 | 3828.0 | 5050.9 | 1785.1 | 2471.9 |
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| FJ263944.1 | 316748 | 11855.2 | 12210.7 | 7012.9 | 12792.5 | 13972.4 | 11366.1 |
| AE017245.1 | 200524 | 40.2 | 41.7 | 44.9 | 62.7 | 65.3 | 40.5 |
| U19768.1 | 202917 | 6283.4 | 5882.5 | 5120.5 | 6324.8 | 8894.4 | 7418.4 |
| EU367963.1 | 258287 | 5041.9 | 5696.3 | 2361.5 | 4742.4 | 6023.6 | 5147.1 |
| DQ530428.1 | 233952 | 6551.9 | 7027.8 | 5626.8 | 5690.1 | 5414.7 | 5669.7 |
| AY571416.1 | 114530 | 8475.7 | 9506.3 | 6600.7 | 8472.6 | 11225.2 | 8487.8 |
| GQ502581.1 | 590759 | 8637.8 | 8513.2 | 7459.5 | 7374.0 | 10933.3 | 9107.2 |
| AB089055.1 | 78062 | 134.8 | 189.8 | 365.7 | 166.4 | 141.8 | 178.4 |
| U09788.1 | 15851 | 28.3 | 56.1 | 34.3 | 68.9 | 68.1 | 18.0 |
| NR_029165.1 | 567958 | 1726.6 | 3401.0 | 1973.6 | 1321.8 | 155.7 | 359.1 |
| AB089054.1 | 77956 | 41.5 | 70.1 | 178.1 | 89.0 | 124.3 | 67.0 |
| AB192228.1 | 142809 | 24.0 | 31.4 | 28.6 | 50.0 | 63.0 | 28.0 |
| AF125879.1 | 15849 | 215.1 | 381.0 | 840.6 | 679.2 | 777.4 | 370.7 |
| AB089057.1 | 77895 | 96.5 | 98.7 | 363.2 | 86.4 | 79.0 | 44.1 |
| AY571419.1 | 114509 | 17.6 | 34.2 | 28.8 | 46.2 | 68.1 | 28.8 |
| EU859984.1 | 344923 | 457.0 | 490.3 | 4369.8 | 1775.3 | 152.8 | 122.8 |
| AF221113.1 | 71570 | 18.0 | 22.3 | 20.9 | 49.2 | 39.9 | 10.9 |
| L24105.1 | 15949 | 830.7 | 314.1 | 1745.8 | 960.9 | 470.5 | 1205.9 |
| FM165074.1 | 329837 | 1268.9 | 1236.5 | 999.9 | 1402.0 | 571.8 | 442.3 |
| AF221119.1 | 19645 | 483.5 | 358.3 | 572.3 | 862.9 | 283.4 | 754.6 |
| AM182894.1 | 199102 | 16402.7 | 13879.3 | 14334.3 | 14047.7 | 19310.2 | 16607.7 |
| AF221111.1 | 73061 | 39.2 | 49.9 | 45.6 | 59.0 | 62.1 | 31.0 |

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AF125590.1 gg_id:15901 Mycoplasma faucium str. DC333(T)
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AF412977.1 gg_id:32469 Mycoplasma crocodyli str. MP145(T)
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DQ223546.1 gg_id:144780 Mycoplasma sp. str. Ms02
EF510778.1 gg_id:224463 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aerug
AF221118.1 gg_id:48246 Mycoplasma primatum HRC292(T)
DQ223545.1 gg_id:142935 Mycoplasma sp. str. Ms01
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AF412970.1 gg_id:71789 Mycoplasma anatis str. 1340(T)
AF332757.1 gg_id:73175 Mycoplasma bovis str. 422/88
AF332748.1 gg_id:73746 Mycoplasma agalactiae str. L9
NR_024978.1 gg_id:548556 Mycoplasma equirhinis str. M432/72; ATCC 29420
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FJ959657.1 gg_id:555715 bottlenose dolphin upper respiratory tract blowhole clone D896_262
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L08054.1 gg_id:15918 Mycoplasma corogypsi str. BV1
U73903.1 gg_id:15913 Mycoplasma edwardii str. PG24
NR_024981.1 gg_id:573950 Mycoplasma subdolum str. TB; ATCC 29870
AY121109.1 gg_id:72631 Mycoplasma bovigenitalium 398/87
FJ226566.1 gg_id:349001 Mycoplasma sp. str. LR5794
FM165076.1 gg_id:325252 Mycoplasma sp. 2F1AT str. 2F1A
U58997.1 gg_id:15931 Mycoplasma hyopharyngis
EF510714.1 gg_id:224150 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aerug
EU859973.1 gg_id:328570 Mycoplasma iguanae str. 2327
NR_029183.1 gg_id:594001 Mycoplasma hyosynoviae str. S-16; ATCC 25591
AF538681.1 gg_id:56134 Mycoplasma collis str. 58B
FM165075.1 gg_id:344619 Mycoplasma sp. A1802T str. A1802
AF221112.1 gg_id:70343 Mycoplasma columbinasale 694(T)
AM774638.1 gg_id:239999 Mycoplasma canimucosale str. 1642
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FM878637.1 gg_id:553341 Mycoplasma sp. str. 38104
DQ340199.1 gg_id:147129 Dominance Mycoplasma guts Long-Jawed Mudsucker Gillichthys mirabilis five Califo
U44766.1 gg_id:15912 Mycoplasma bovirhinis str. PG43
AM182891.1 gg_id:184771 Mycoplasma sp. str. 13CL

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| AF125590.1 | 15901 | 2321.0 | 1617.6 | 5765.4 | 3132.2 | 2574.8 | 2441.3 |
| U16759.1 | 15916 | 24.7 | 30.2 | 206.4 | 72.2 | 82.2 | 34.9 |
| GU227407.1 | 579601 | 4837.8 | 4940.4 | 5020.6 | 4838.7 | 5692.2 | 6076.8 |
| AF412977.1 | 32469 | 44.6 | 47.7 | 24.2 | 76.9 | 95.1 | 54.7 |
| EF510696.1 | 220331 | 2694.7 | 3341.8 | 1671.4 | 4534.3 | 3594.8 | 5848.2 |
| DQ223546.1 | 144780 | 2109.6 | 2652.5 | 1206.8 | 2342.5 | 1944.6 | 1697.2 |
| EF510778.1 | 224463 | 3029.4 | 4282.1 | 5652.8 | 3292.5 | 5463.1 | 6390.4 |
| AF221118.1 | 48246 | 1858.5 | 2242.5 | 802.2 | 920.6 | 293.1 | 481.5 |
| DQ223545.1 | 142935 | 589.8 | 1093.0 | 863.7 | 1281.3 | 742.4 | 1003.6 |
| U44768.1 | 15865 | 5278.6 | 4885.0 | 9289.5 | 5977.1 | 3913.4 | 6336.8 |
| U22013.1 | 15920 | 45.3 | 47.2 | 38.1 | 66.1 | 89.1 | 64.4 |
| EF036469.1 | 179109 | 2849.3 | 2917.1 | 4124.7 | 3260.2 | 3937.0 | 3305.9 |
| EF510860.1 | 225935 | 2392.3 | 1807.5 | 4071.1 | 5461.2 | 2425.6 | 2508.1 |
| AF412970.1 | 71789 | 48.0 | 109.8 | 102.7 | 65.3 | 131.5 | 41.3 |
| AF332757.1 | 73175 | 68.7 | 143.9 | 280.2 | 180.5 | 132.3 | 244.5 |
| AF332748.1 | 73746 | 765.0 | 912.2 | 404.0 | 359.2 | 128.6 | 252.3 |
| NR_024978.1 | 548556 | 2679.2 | 2867.9 | 6754.6 | 4490.6 | 6928.3 | 6586.6 |
| AM182896.1 | 186205 | 8690.7 | 10495.2 | 8070.3 | 7601.5 | 8713.0 | 8376.0 |
| EF510818.1 | 217758 | 13084.6 | 14203.2 | 15094.3 | 12058.5 | 16087.5 | 14364.4 |
| FJ959657.1 | 555715 | 1583.7 | 1245.7 | 1193.6 | 1350.9 | 507.3 | 635.0 |
| U67943.1 | 15941 | 5744.8 | 4745.0 | 5376.1 | 5004.0 | 3956.0 | 3789.8 |
| L08054.1 | 15918 | 7893.6 | 10067.3 | 6521.9 | 4443.0 | 3417.5 | 4596.8 |
| U73903.1 | 15913 | 313.2 | 2018.5 | 1435.4 | 777.9 | 542.9 | 1029.3 |
| NR_024981.1 | 573950 | 4353.7 | 3219.4 | 5495.4 | 5746.7 | 4286.4 | 4021.6 |
| AY121109.1 | 72631 | 96.0 | 193.9 | 454.4 | 218.6 | 918.7 | 2268.4 |
| FJ226566.1 | 349001 | 1087.0 | 1796.5 | 1291.8 | 2845.3 | 632.1 | 703.4 |
| FM165076.1 | 325252 | 2679.8 | 2737.1 | 1767.2 | 2360.2 | 1079.2 | 1626.1 |
| U58997.1 | 15931 | 57.9 | 91.1 | 72.7 | 102.2 | 57.2 | 84.5 |
| EF510714.1 | 224150 | 6209.7 | 7081.2 | 5197.1 | 8057.2 | 12451.5 | 10622.1 |
| EU859973.1 | 328570 | 20.5 | 16.1 | 12.3 | 50.2 | 72.6 | 29.8 |
| NR_029183.1 | 594001 | 6913.3 | 5592.3 | 9745.8 | 9098.0 | 5423.7 | 6193.7 |
| AF538681.1 | 56134 | 9159.9 | 8063.0 | 2744.4 | 8920.3 | 6354.4 | 6385.8 |
| FM165075.1 | 344619 | 2255.6 | 2918.1 | 4379.8 | 2461.2 | 6214.1 | 5605.4 |
| AF221112.1 | 70343 | 15.2 | 21.2 | 21.1 | 41.5 | 68.7 | 15.8 |
| AM774638.1 | 239999 | 1065.2 | 1529.6 | 2802.9 | 1690.0 | 4277.2 | 5123.5 |
| AY246564.1 | 85218 | 2528.5 | 2840.0 | 5823.8 | 3369.0 | 3690.5 | 3161.5 |
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| FM878637.1 | 553341 | 235.0 | 519.1 | 1170.8 | 409.1 | 1064.1 | 480.3 |
| DQ340199.1 | 147129 | 4031.8 | 3951.6 | 654.3 | 2345.2 | 636.3 | 521.0 |
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FJ655917.1 gg_id:588056 Mycoplasma vulturii str. Gb-V33
NR_025186.1 gg_id:543508 Mycoplasma moatsii str. MK405; ATCC 27625
AF412974.1 gg_id:28253 Mycoplasma collis str. 58B(T)
AY050170.1 gg_id:60547 Mycoplasma timone
AF412989.1 gg_id:28733 Mycoplasma verecundum str. GIH(T)
FM878042.1 gg_id:557236 Mycoplasma sp. str. 51CL
EF510815.1 gg_id:219506 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aerug
AF125591.1 gg_id:15897 Mycoplasma falconis str. H/T1(T)
DQ340198.1 gg_id:146814 Dominance Mycoplasma guts Long-Jawed Mudsucker Gillichthys mirabilis five Califo
AF150495.1 gg_id:15925 Mycoplasma sp. str. 94630
AF412981.1 gg_id:70918 Mycoplasma glycophilum str. 486(T)
NR_024982.1 gg_id:567316 Mycoplasma gypis str. B1/T1; ATCC 51370
NR_025914.1 gg_id:557285 Mycoplasma meleagridis str. 17529; ATCC 25294
EF510816.1 gg_id:227513 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aerug
AF412971.1 gg_id:69777 Mycoplasma buteonis str. BbT2g(T)
M24582.1 gg_id:15954 Mycoplasma californicum
U15795.1 gg_id:15943 Mycoplasma felifaucium str. ATCC 43428
EF510786.1 gg_id:220695 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aerug
FM196534.1 gg_id:331374 Mycoplasma sp. str. Zaradi2
U09787.1 gg_id:15917 Mycoplasma felis str. ATCC 23391
AM182893.1 gg_id:190324 Mycoplasma sp. str. 11CL2
U16760.1 gg_id:15944 Mycoplasma leopharyngis str. ATCC 49889
AF170102.1 gg_id:15921 Mycoplasma capricolum
AF221115.1 gg_id:19295 Mycoplasma lipofaciens R171(T)
NR_025182.1 gg_id:555208 Mycoplasma dispar str. 462/2; ATCC 27140
AY492086.1 gg_id:136766 Mycoplasma suis str. Guangdong
AF178676.1 gg_id:51934 Candidatus Mycoplasma haemodidelphidis Illinois
AF306346.1 gg_id:136331 Candidatus Mycoplasma haemolamae str. Michigan
EU165510.1 gg_id:339052 Mycoplasma ovis Mo-Hu-3-05.2007
AY171918.1 gg_id:87318 Mycoplasma coccoides
EF221880.1 gg_id:206167 Mycoplasma wenyonii str. CGXD
U82963.1 gg_id:15860 Mycoplasma haemomuris str. Shizuoka
EU134687.1 gg_id:255073 tallgrass prarie soil clone FFCH10627
GU293201.1 gg_id:568172 Microbial contents and mucus yel catfish (Pelteobagrus fulvidraco) stomach content
EF516576.1 gg_id:219640 grassland soil clone FCPT702
AY500249.1 gg_id:102371 Candidatus Hepatoplasma crinochetorum clone 48
EU646193.1 gg_id:285164 Host-specificity transmitted Mycoplasma-like isopod symbionts hepatopancreas clor
EU646198.1 gg_id:280566 Host-specificity transmitted Mycoplasma-like isopod symbionts hepatopancreas clor
AF001173.1 gg_id:15899 Candidatus Mycoplasma ravipulmonis
U62937.2 gg_id:15831 Ureaplasma gallorale str. ATCC 43346
GU227393.1 gg_id:580923 Ureaplasma sp. str. USP S/N

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| FJ655917.1 | 588056 | 2949.7 | 1691.9 | 236.2 | 284.7 | 93.0 | 88.2 |
| NR_025186.1 | 543508 | 161.2 | 143.2 | 130.8 | 197.6 | 70.2 | 75.9 |
| AF412974.1 | 28253 | 9774.9 | 11594.2 | 5823.7 | 8465.6 | 8666.5 | 9643.2 |
| AY050170.1 | 60547 | 6887.3 | 6273.6 | 8549.0 | 7517.9 | 6084.5 | 6029.1 |
| AF412989.1 | 28733 | 17.7 | 12.4 | 11.3 | 56.7 | 66.8 | 22.9 |
| FM878042.1 | 557236 | 1365.3 | 1778.8 | 1385.7 | 441.7 | 1938.6 | 644.2 |
| EF510815.1 | 219506 | 7192.2 | 7344.5 | 6396.8 | 9375.1 | 11493.9 | 10780.9 |
| AF125591.1 | 15897 | 1297.7 | 2463.3 | 5248.4 | 1262.2 | 6292.8 | 5055.2 |
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| AF150495.1 | 15925 | 485.2 | 492.7 | 344.7 | 578.2 | 408.1 | 201.4 |
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| NR_024982.1 | 567316 | 11550.9 | 11316.7 | 12454.8 | 11802.7 | 6679.4 | 6631.0 |
| NR_025914.1 | 557285 | 356.8 | 850.8 | 292.1 | 247.7 | 327.5 | 509.7 |
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| AF412971.1 | 69777 | 5048.9 | 9122.4 | 7164.5 | 4620.4 | 4746.5 | 5146.7 |
| M24582.1 | 15954 | 22.6 | 26.0 | 11.4 | 50.2 | 65.8 | 17.9 |
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| EF510786.1 | 220695 | 1909.7 | 1944.1 | 2349.9 | 3712.6 | 2667.8 | 2806.6 |
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| U09787.1 | 15917 | 8205.3 | 9326.7 | 3907.7 | 5576.5 | 3575.7 | 3853.2 |
| AM182893.1 | 190324 | 6408.5 | 5654.0 | 5985.7 | 6291.0 | 3960.9 | 3977.7 |
| U16760.1 | 15944 | 8809.0 | 8443.6 | 7251.0 | 9286.5 | 11218.2 | 9291.6 |
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| AF178676.1 | 51934 | 122.8 | 128.8 | 70.8 | 119.9 | 235.8 | 99.9 |
| AF306346.1 | 136331 | 229.2 | 711.6 | 157.4 | 274.6 | 59.7 | 82.5 |
| EU165510.1 | 339052 | 6859.0 | 6895.7 | 3428.3 | 6280.8 | 7233.8 | 6270.8 |
| AY171918.1 | 87318 | 1676.7 | 2185.5 | 1890.0 | 2611.8 | 309.8 | 500.0 |
| EF221880.1 | 206167 | 12706.6 | 12219.6 | 6581.8 | 12801.1 | 13971.2 | 11365.4 |
| U82963.1 | 15860 | 51.3 | 88.4 | 46.5 | 58.5 | 90.0 | 35.4 |
| EU134687.1 | 255073 | 14301.4 | 15301.7 | 14750.0 | 13611.0 | 13721.3 | 12983.0 |
| GU293201.1 | 568172 | 3415.0 | 3070.3 | 3342.4 | 5021.0 | 1164.2 | 1842.0 |
| EF516576.1 | 219640 | 26.6 | 28.5 | 18.3 | 53.7 | 51.4 | 23.7 |
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| EU646193.1 | 285164 | 9220.9 | 8545.7 | 4940.9 | 5979.2 | 2728.4 | 4143.1 |
| EU646198.1 | 280566 | 6449.9 | 5362.0 | 6557.7 | 7658.7 | 3276.8 | 4709.7 |
| AF001173.1 | 15899 | 219.5 | 88.2 | 130.7 | 127.7 | 130.1 | 61.2 |
| U62937.2 | 15831 | 6298.6 | 9000.6 | 4855.8 | 4151.7 | 5005.7 | 4487.9 |
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g__Ureaplasma
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| s__Ureaplasma parvum | 70842 |
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| s__unclassified | 71632 |

NR_025877.1 gg_id:551749 Ureaplasma canigenitalium str. D6P-C; ATCC 51252
D78649.1 gg_id:15829 Ureaplasma cati str. F2
L08642.1 gg_id:15811 Ureaplasma urealyticum str. 27
U06097.1 gg_id:15816 Ureaplasma urealyticum str. 354 (serovar 5)
EU844042.1 gg_id:310545 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
EU459553.1 gg_id:294314 capybara feces clone CAP_aah99g08
FJ172803.1 gg_id:348767 Qinghai Yak Ruminal and Fungi China rumen clone RB-3C9
EU382038.1 gg_id:268757 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase
FJ366886.1 gg_id:370110 feces adult twins and mothers; TS28 clone TS28_a01a06
FJ671998.1 gg_id:521062 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
AF371530.1 gg_id:21652 swine intestine clone p-1735-b3
DQ805924.1 gg_id:175271 human fecal clone RL306aal92g01
GQ167173.1 gg_id:567437 Effects Hydraulic Retention Time on Anaerobic Hydrogenation Performance Microbi
GQ897787.1 gg_id:578177 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons
GQ448417.1 gg_id:576850 Microbiome neonatal calves: shedding microorganisms fecal clone calf783_10wks_g
GU303669.1 gg_id:561959 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c
AM275414.2 gg_id:234959 fecal microbiota irritable bowel syndrome patients significantly that healthy subject
EF445243.1 gg_id:207023 dairy cow rumen clone NED5C1
FJ681340.1 gg_id:519348 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
AM275475.2 gg_id:233848 fecal microbiota irritable bowel syndrome patients significantly that healthy subject
GQ896843.1 gg_id:569244 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do
FJ673493.1 gg_id:515507 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ684684.1 gg_id:529404 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
GQ897386.1 gg_id:585199 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do
EU474506.1 gg_id:292635 bighorn sheep feces clone BHSD_aaa03h12.Contig2
GU303586.1 gg_id:566240 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c
EU850597.1 gg_id:311889 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF427
AY985740.1 gg_id:117030 human stool clone C771
GQ451187.1 gg_id:513605 Fecal Yunnan snub-nosed monkey feces clone J19
FJ673434.1 gg_id:518672 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EF445272.1 gg_id:213966 dairy cow rumen clone NED4E12
DQ057362.1 gg_id:131450 chicken ileum/cecum clone cc106
EU773287.1 gg_id:306877 BigHorn sheep feces clone BH1_aao27e05
DQ326418.1 gg_id:148285 Metagenomic gut microbiome healthy human stool clone C469
FJ673790.1 gg_id:515508 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU844544.1 gg_id:325403 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
FJ680415.1 gg_id:515855 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ673176.1 gg_id:527857 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU344185.1 gg_id:277047 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad
EU475428.1 gg_id:297545 springbok feces clone SBSD_aaa04g12
EU850542.1 gg_id:342412 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF336

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|---|---|---|---|---|---|---|---|
| NR_025877.1 | 551749 | 2069.5 | 4412.2 | 1447.2 | 1866.4 | 1530.7 | 1467.4 |
| D78649.1 | 15829 | 6578.4 | 6106.6 | 3115.7 | 5971.1 | 2618.5 | 3857.8 |
| L08642.1 | 15811 | 21411.3 | 20684.3 | 19091.7 | 17170.2 | 21206.8 | 18344.9 |
| U06097.1 | 15816 | 2799.7 | 4660.9 | 1988.6 | 1728.0 | 2553.6 | 2242.1 |
| EU844042.1 | 310545 | 7441.8 | 7861.9 | 8030.3 | 6271.5 | 5257.9 | 4662.5 |
| EU459553.1 | 294314 | 4273.9 | 4298.0 | 3670.9 | 4434.9 | 4441.9 | 3175.4 |
| FJ172803.1 | 348767 | 1737.1 | 1922.4 | 1523.4 | 1402.4 | 385.8 | 736.0 |
| EU382038.1 | 268757 | 1802.2 | 2651.6 | 3905.0 | 2171.6 | 3751.8 | 3740.9 |
| FJ366886.1 | 370110 | 4687.4 | 5128.6 | 3995.3 | 4459.2 | 3604.0 | 3891.3 |
| FJ671998.1 | 521062 | 6610.6 | 7398.2 | 6941.6 | 6669.7 | 6072.5 | 7708.1 |
| AF371530.1 | 21652 | 33.1 | 30.3 | 71.1 | 57.0 | 57.5 | 19.9 |
| DQ805924.1 | 175271 | 2469.7 | 3597.9 | 1527.7 | 1836.3 | 2232.3 | 2026.4 |
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| GQ897787.1 | 578177 | 947.1 | 1237.2 | 1610.3 | 1347.7 | 1360.3 | 1362.7 |
| GQ448417.1 | 576850 | 11215.4 | 10134.4 | 7104.9 | 11517.1 | 12828.1 | 11385.6 |
| GU303669.1 | 561959 | 655.2 | 1499.2 | 1363.5 | 745.7 | 2511.3 | 1534.6 |
| AM275414.2 | 234959 | 3825.3 | 5758.7 | 363.2 | 975.6 | 1825.2 | 1986.6 |
| EF445243.1 | 207023 | 3000.1 | 2650.1 | 2322.4 | 3618.8 | 3442.8 | 3900.3 |
| FJ681340.1 | 519348 | 12060.5 | 15074.0 | 11066.4 | 11443.1 | 11556.1 | 11431.8 |
| AM275475.2 | 233848 | 250.5 | 185.9 | 334.1 | 221.5 | 164.0 | 267.0 |
| GQ896843.1 | 569244 | 26.0 | 35.2 | 28.8 | 54.8 | 62.3 | 19.6 |
| FJ673493.1 | 515507 | 6104.0 | 5675.4 | 3361.7 | 7005.8 | 7131.6 | 2827.7 |
| FJ684684.1 | 529404 | 8280.0 | 8972.7 | 7331.9 | 6777.4 | 8832.0 | 8306.6 |
| GQ897386.1 | 585199 | 8819.0 | 7572.8 | 4946.8 | 7761.7 | 6675.0 | 6224.6 |
| EU474506.1 | 292635 | 6521.7 | 6040.4 | 4274.7 | 4019.0 | 6696.7 | 5013.2 |
| GU303586.1 | 566240 | 1528.4 | 2604.0 | 3816.8 | 2159.1 | 5199.3 | 4013.9 |
| EU850597.1 | 311889 | 7323.8 | 7830.9 | 3817.0 | 8129.0 | 5632.9 | 4365.7 |
| AY985740.1 | 117030 | 47.4 | 57.3 | 42.1 | 72.8 | 114.7 | 81.0 |
| GQ451187.1 | 513605 | 736.7 | 564.5 | 2737.2 | 1029.1 | 413.9 | 545.8 |
| FJ673434.1 | 518672 | 1304.9 | 1820.0 | 1816.3 | 1913.8 | 753.8 | 1881.4 |
| EF445272.1 | 213966 | 574.4 | 399.8 | 1303.2 | 635.8 | 132.3 | 292.1 |
| DQ057362.1 | 131450 | 3629.0 | 4208.0 | 3661.7 | 5944.5 | 3921.6 | 5243.1 |
| EU773287.1 | 306877 | 4694.0 | 3981.2 | 7182.9 | 6923.6 | 4817.9 | 5224.1 |
| DQ326418.1 | 148285 | 8458.5 | 8426.4 | 7035.5 | 7066.2 | 16274.6 | 12257.4 |
| FJ673790.1 | 515508 | 3476.0 | 4030.1 | 3665.5 | 5674.0 | 1297.7 | 2412.4 |
| EU844544.1 | 325403 | 2946.1 | 2694.7 | 6376.7 | 3648.7 | 1646.5 | 2535.5 |
| FJ680415.1 | 515855 | 11826.5 | 12147.2 | 8010.4 | 9477.4 | 10077.9 | 8429.6 |
| FJ673176.1 | 527857 | 6626.4 | 6820.2 | 6558.6 | 7918.4 | 7263.4 | 5755.4 |
| EU344185.1 | 277047 | 4077.4 | 4698.2 | 1718.5 | 3355.3 | 2627.6 | 3323.7 |
| EU475428.1 | 297545 | 848.6 | 1000.0 | 1547.1 | 502.1 | 340.7 | 356.5 |
| EU850542.1 | 342412 | 1836.2 | 1972.6 | 3242.8 | 2642.6 | 7888.3 | 5097.8 |

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