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EU535251.1 gg_id:280823 profile human microbiota antecubital fossa (inner elbow) skin clone nbt172g09 EU535
GQ032573.1 gg_id:406089 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ032
EU169150.1 gg_id:237348 Pseudomonas tolaasii str. B48 EU169
FN599522.1 gg_id:565116 Pseudomonas fulva str. YMC09/4/B4619 FN599
EU511892.1 gg_id:262376 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_aaf10f12 EU511
FJ950618.1 gg_id:440750 Pseudomonas fluorescens str. c120 FJ9506
EU538898.1 gg_id:280517 profile human microbiota antecubital fossa (inner elbow) skin clone nbt96e11 EU538
FJ893841.1 gg_id:553685 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B1E; ear pu FJ8938
EU539842.1 gg_id:283035 profile human microbiota antecubital fossa (inner elbow) skin clone nbt106b04 EU539
DQ117554.1 gg_id:155221 structure (Citrullus vulgaris SCHARD.) -based approaches and terminal fragment len DQ117
AJ576246.1 gg_id:88635 Pseudomonas fluorescens 10CW AJ5762
FJ894143.1 gg_id:568601 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B1E; ear pu FJ8941
FJ605386.1 gg_id:454217 Pseudomonas poae str. AceR-3 FJ6053
DQ178219.1 gg_id:140655 Pseudomonas mendocina str. PC1 DQ178
EU538548.1 gg_id:284117 profile human microbiota antecubital fossa (inner elbow) skin clone nbt231f05 EU538
EU538115.1 gg_id:285323 profile human microbiota antecubital fossa (inner elbow) skin clone nbt82c09 EU538
FJ894501.1 gg_id:565829 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B2E; ear pu FJ8945
DQ318864.1 gg_id:154493 Pseudomonas syringae str. 8534 DQ318
EU537937.1 gg_id:280598 profile human microbiota antecubital fossa (inner elbow) skin clone nbt227f02 EU537
FJ976605.1 gg_id:559208 Pseudomonas putida FJ9766
FJ893686.1 gg_id:574564 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota WT3; ear p FJ8936
AB180734.1 gg_id:102043 Pseudomonas putida str. MT4 AB180
FJ950650.1 gg_id:467776 Pseudomonas putida str. d61 FJ9506
EU537214.1 gg_id:282093 profile human microbiota antecubital fossa (inner elbow) skin clone nbt68f04 EU537
EF016110.1 gg_id:177261 Pseudomonas sp. str. BJSX EF0161
FJ892925.1 gg_id:563436 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota HM2; ear p FJ8929
FJ893603.1 gg_id:553179 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota WT3; ear p FJ8936
EU434560.1 gg_id:271676 Pseudomonas fluorescens str. b33 EU4345
AM229082.1 gg_id:147892 Pseudomonas fluorescens str. C7R12 AM229
EU539097.1 gg_id:284787 profile human microbiota antecubital fossa (inner elbow) skin clone nbt98c04 EU539
EU540304.1 gg_id:285316 profile human microbiota antecubital fossa (inner elbow) skin clone nbt114g10 EU540
AJ492827.1 gg_id:63919 Pseudomonas cannabina str. CFBP 2341 AJ4928
EU540573.1 gg_id:283457 profile human microbiota antecubital fossa (inner elbow) skin clone nbt120b02 EU540
EU537625.1 gg_id:283084 profile human microbiota antecubital fossa (inner elbow) skin clone nbt73g10 EU537
AM184090.1 gg_id:152763 Pseudomonas syringae str. 1 AM184
DQ084459.1 gg_id:128081 Pseudomonas fluorescens str. FLM05-1 DQ084
AF137359.1 gg_id:8710 Pseudomonas fluorescens AF1373
AB167245.1 gg_id:107953 Pseudomonas syringae str. c121 AB167

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EU169146.1 gg_id:245783 Pseudomonas brenneri str. B46 EU1691
FJ893732.1 gg_id:548088 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota WT3; ear p FJ8937
EU539860.1 gg_id:284811 profile human microbiota antecubital fossa (inner elbow) skin clone nbt106g03 EU5398
EU169179.1 gg_id:253450 Pseudomonas fluorescens str. B73 EU1691
DQ095893.1 gg_id:130252 Pseudomonas plecoglossicida str. S4 DQ095
FJ950610.1 gg_id:425507 Pseudomonas sp. str. c156 FJ9506
AF064458.1 gg_id:8588 Pseudomonas monteilii str. CIP 104883 AF0644
AY303311.1 gg_id:132103 Pseudomonas sp. str. ps6-16 AY3033
EU540402.1 gg_id:283690 profile human microbiota antecubital fossa (inner elbow) skin clone nbt114d10 EU5404
EU539954.1 gg_id:282412 profile human microbiota antecubital fossa (inner elbow) skin clone nbt108d06 EU5399
EU111725.2 gg_id:558591 Pseudomonas migulae str. CT14 EU1117
AF348508.1 gg_id:74250 Pseudomonas corrugata str. ND9L AF3485
AY625608.1 gg_id:106509 Pseudomonas sp. str. E2.2 AY6256
EU538196.1 gg_id:283086 profile human microbiota antecubital fossa (inner elbow) skin clone nbt82e10 EU5381
FJ588703.1 gg_id:565803 Pseudomonas fluorescens str. HDY-9 FJ5887
EU534971.1 gg_id:281416 profile human skin microbiota ear punch biopsy female C57BL/6J mouse clone nbt18 EU5349
FJ893154.1 gg_id:549797 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota HM3; ear p FJ8931
EF154270.1 gg_id:188602 Pseudomonas cannabina str. 30 EF1542
EU239464.1 gg_id:253435 Pseudomonas putida str. XJUHX-1 EU2394
AF447394.1 gg_id:33976 Pseudomonas putida str. DLL-E4 AF4473
FJ894001.1 gg_id:570570 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B1E; ear pu FJ8940
EU169171.1 gg_id:250792 Pseudomonas fluorescens str. B20 EU1691
EU537043.1 gg_id:281302 profile human microbiota antecubital fossa (inner elbow) skin clone nbt219e06 EU5370
AF112477.1 gg_id:8726 Azospirillum sp AF1124
AY303254.1 gg_id:133637 Pseudomonas sp. str. ps10-13 AY3032
GQ260082.1 gg_id:545388 Pseudomonas fluorescens str. ICIRC97 GQ260
EU538363.1 gg_id:280933 profile human microbiota antecubital fossa (inner elbow) skin clone nbt87d05 EU5383
AY303243.1 gg_id:132705 Pseudomonas sp. str. pcs19 AY3032
EU538992.1 gg_id:286283 profile human microbiota antecubital fossa (inner elbow) skin clone nbt98c10 EU5389
EU538181.1 gg_id:280147 profile human microbiota antecubital fossa (inner elbow) skin clone nbt81f12 EU5381
EU538555.1 gg_id:283206 profile human microbiota antecubital fossa (inner elbow) skin clone nbt231f12 EU5385
AM933495.1 gg_id:321985 Pseudomonas antarctica FB1 AM933
EU535368.1 gg_id:286102 profile human microbiota antecubital fossa (inner elbow) skin clone nbt02b04 EU5353
AJ012712.1 gg_id:8701 Pseudomonas borealis MA342 AJ0127
DQ536514.1 gg_id:160709 Pseudomonas trivialis str. BIHB 736 DQ536
FJ892816.1 gg_id:567266 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota HM1; ear p FJ8928
AM262973.1 gg_id:159153 Pseudomonas oryzihabitans str. IAM 1568 AM262
FJ005063.1 gg_id:351681 feasibility and indigenous moderate-thermophilic bioleaching which old Pb/Zn smelti FJ0050
FJ607150.1 gg_id:555195 Pseudomonas syringae pv. morsprunorum str. ICMP 4991 FJ6071

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EU536420.1 gg_id:283843 profile human microbiota antecubital fossa (inner elbow) skin clone nbt213f02 EU5364
EU538972.1 gg_id:281795 profile human microbiota antecubital fossa (inner elbow) skin clone nbt96c06 EU5389
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AY303306.1 gg_id:135272 Pseudomonas sp. str. ps4-49 AY3033
AY970952.1 gg_id:115366 Pseudomonas moraviensis str. 1B4 AY9709
FJ893108.1 gg_id:546592 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota HM3; ear p FJ8931
FJ893415.1 gg_id:552313 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota WT1; ear p FJ8934
FJ405364.1 gg_id:368656 Pseudomonas sp. str. SPe FJ4053
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EF623836.1 gg_id:245159 Pseudomonas putida str. GIST-MRP44-1 EF6238
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AM933518.1 gg_id:309848 Pseudomonas antarctica FB27 AM933
EU540148.1 gg_id:283193 profile human microbiota antecubital fossa (inner elbow) skin clone nbt246b06 EU5401
EU046271.1 gg_id:253171 Pseudomonas takelamaensis str. HR2 EU0462
DQ981457.1 gg_id:203619 Pseudomonas fluorescens SB2 DQ981
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EU159479.1 gg_id:310066 Pseudomonas fluorescens str. A7 EU1594
FJ972536.1 gg_id:433249 Pseudomonas fluorescens str. NO7 FJ9725
AB181497.1 gg_id:109263 wastewater biofilm clone HSN-95 AB1814
EU537190.1 gg_id:286488 profile human microbiota antecubital fossa (inner elbow) skin clone nbt68b06 EU5371
DQ076645.1 gg_id:131495 Pseudomonas sp. str. LDC-25 DQ076
AY303320.1 gg_id:135251 Pseudomonas sp. str. ps6-47 AY3033
AF494092.1 gg_id:67520 Burkholderia caryophylli str. YS13 AF4940
AM411057.1 gg_id:191934 Pseudomonas sp. str. Z49zhy AM411
EU008575.1 gg_id:257715 Pseudomonas putida str. PS13 EU0085
EU439420.1 gg_id:547800 Pseudomonas putida str. LH-R1 EU4394
AF094732.1 gg_id:47203 Pseudomonas fluorescens str. ATCC 49642 AF0947
EU539155.1 gg_id:285112 profile human microbiota antecubital fossa (inner elbow) skin clone nbt101a08 EU5391
EU540291.1 gg_id:284613 profile human microbiota antecubital fossa (inner elbow) skin clone nbt114b02 EU5402
FJ893413.1 gg_id:547116 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota WT1; ear p FJ8934
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AB234274.1 gg_id:147927 Biotransformation Polychlorinated Dioxins Microbial Dynamics Sediment Microcosm AB2342
AF494091.1 gg_id:67521 Pseudomonas nitroreducens str. 0802 AF4940

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AB234275.1 gg_id:146760 Biotransformation Polychlorinated Dioxins Microbial Dynamics Sediment Microcosm AB2342
GU057052.1 gg_id:582539 Pseudomonas sp. str. VSR GU057
AY486367.1 gg_id:202697 Pseudomonas aeruginosa str. AU4594 AY4863
X06684.1 gg_id:8424 Pseudomonas aeruginosa str. DSM50071 X06684
EU537871.1 gg_id:286843 profile human microbiota antecubital fossa (inner elbow) skin clone nbt226a07 EU5378
AF140011.1 gg_id:8525 Pseudomonas pseudoalcaligenes str. ML-A04 AF1400
AY486371.1 gg_id:99682 Pseudomonas aeruginosa str. AU5056 AY4863
FJ675201.1 gg_id:518305 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6752
FJ658037.1 gg_id:533358 Metalworking Fluids and Aerosols Metallurgy Plant metalworking fluid clone Winter_ FJ6580
DQ350823.1 gg_id:147528 Pseudomonas aeruginosa str. B13 DQ350
FM992407.1 gg_id:574081 Pseudomonas sp. JPM-2009-2 FM992
AJ550306.1 gg_id:81887 Pseudomonas aeruginosa OK1 AJ5503
EF515555.1 gg_id:218565 Electricigen Enrichment MFC full-scale anaerobic bioreactor sludge treating brewery EF5155
GU217696.1 gg_id:536568 Pseudomonas sp. str. ljh-16 GU217
EF208965.1 gg_id:175605 Pseudomonas mendocina str. B6-1 EF2089
EF179862.1 gg_id:198175 Pseudomonas sp. KM-B4 str. B4 EF1798
FJ556919.1 gg_id:586137 Pseudomonas aeruginosa str. NGKCTS FJ5569
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DQ256334.1 gg_id:142026 subsurface water clone EV818BHEB5102502DRLWq27f062 DQ256
EU370415.1 gg_id:260507 Pseudomonas sp. str. 117S1 EU3704
FJ226424.1 gg_id:356153 Pseudomonas aeruginosa str. NAPCC-1 FJ2264
EU195558.1 gg_id:237500 Pseudomonas aeruginosa str. LP8 EU1955
FJ152919.1 gg_id:320016 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX4CI FJ1529
AY947918.1 gg_id:141280 Synchrony and seasonality two temperate rivers USA: Massachusetts Ipswich River c AY9479
EF200115.1 gg_id:202547 mine sulfur-cycling assemblage subpermafrost fracture waters Arctic gold mines clon EF2001
DQ916277.2 gg_id:161990 Pseudomonas lindanilytica str. IPL-1 DQ916
EU538163.1 gg_id:280131 profile human microbiota antecubital fossa (inner elbow) skin clone nbt81b11 EU5381
EU274299.1 gg_id:251989 Azotobacter chroococcum str. AZO2 EU2742
DQ149582.1 gg_id:160454 Pseudomonas aeruginosa str. HS-D38 DQ149
GU391472.1 gg_id:572803 Pseudomonas fluorescens str. Gd2F GU391
FJ169986.1 gg_id:344935 Pseudomonas sp. str. E505-11 FJ1699
AF140013.1 gg_id:23182 Pseudomonas pseudoalcaligenes str. ML-A09 AF1400
GQ149776.1 gg_id:565857 Burkholderia cepacia str. BCC933 GQ149
FJ675469.1 gg_id:531082 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6754
EU365515.1 gg_id:261544 Pseudomonas sp. str. BSs20085 EU3655
EU600372.1 gg_id:271714 Pseudomonas poae str. RT5RP2 EU6003

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EU434518.1 gg_id:265493 Pseudomonas fluorescens str. b225 EU4345
EU841537.1 gg_id:324692 Pseudomonas sp. str. 218 EU8415
EF053508.2 gg_id:328163 Pseudomonas aeruginosa MCCB 103 EF0535
GU395986.1 gg_id:520012 Pseudomonas aeruginosa str. SU-3 GU395
AY880297.1 gg_id:111387 Pseudomonas sp. str. M2-1 AY8802
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EU534823.1 gg_id:283071 profile human skin microbiota ear punch biopsy female C57BL/6J mouse clone nbt21 EU5348
GQ388959.1 gg_id:511710 quality deterioration drinking system during serious red water outbreak clone J135 GQ388
EF509283.1 gg_id:219801 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aerug EF5092
EF559215.1 gg_id:220548 mesophilic anaerobic digester clone A35_D28_L_B_B08 EF5592
AM111047.1 gg_id:140795 Pseudomonas sp. str. 7070 AM111
FJ901022.1 gg_id:513124 Polymorphism microbial reservoirs water cut stage oil field clone G-68 FJ9010
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AF140009.1 gg_id:8526 Pseudomonas pseudoalcaligenes str. ML-A02 AF1400
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EU187489.1 gg_id:252214 Pseudomonas pseudoalcaligenes str. W-20 EU1874
DQ318861.1 gg_id:152555 Pseudomonas syringae str. 8532 DQ318
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FJ950669.1 gg_id:387747 Pseudomonas sp. str. d130 FJ9506
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EU169149.1 gg_id:245779 Pseudomonas tolaasii str. B37 EU1691
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AF094735.1 gg_id:73739 Pseudomonas oleovorans str. ATCC 8062 AF0947
AF139996.1 gg_id:53457 Pseudomonas sp. str. ML-120 AF1399
EF586018.1 gg_id:240439 Methanol-assimilating anaerobic solid waste digester fed methanol clone M35_D20_ EF5860
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DQ279822.1 gg_id:144098 Pseudomonas sp. str. D14 DQ279
AY689052.1 gg_id:100960 Pseudomonas sp. str. 6C_12 AY6890
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FJ853495.1 gg_id:539000 Pseudomonas aeruginosa str. ZSL-2 FJ8534
EF608177.1 gg_id:573436 Pseudomonas aeruginosa str. HT25 EF6081
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EU272857.1 gg_id:363576 Pseudomonas aeruginosa str. MK50 EU2728
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FN429930.1 gg_id:584843 Pseudomonas sp. C2(2009) str. C2 FN4299
DQ984615.1 gg_id:253301 LY oil-contaminated soil clone LYC240 DQ984
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EU857418.1 gg_id:314447 Pseudomonas putida str. BF-S5 EU8574
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EU579530.1 gg_id:263193 Pseudomonas pseudoalcaligenes str. R32 EU5795

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AJ278107.1 gg_id:66198 Pseudomonas sp. str. KI AJ2781
FJ657973.1 gg_id:543148 Metalworking Fluids and Aerosols Metallurgy Plant metalworking fluid clone Winter_ FJ6579
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EF509416.1 gg_id:220349 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aerug EF5094
X92133.1 gg_id:71972 Lake Elmenteita isolate 45E3 X92133
EU888911.1 gg_id:312742 Pseudomonas sp. str. CL-AP6 EU888
EU538380.1 gg_id:286403 profile human microbiota antecubital fossa (inner elbow) skin clone nbt88h01 EU5383
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AF225956.1 gg_id:28841 Pseudomonas aeruginosa AF2259
FJ830845.1 gg_id:540820 Pseudomonas alcaligenes str. Y34 FJ8308
FJ674304.1 gg_id:526122 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6743
EU034723.1 gg_id:571092 Pseudomonas aeruginosa str. swu31-2 EU0347
AF118398.2 gg_id:66758 Pseudomonas sp. str. AST1 AF1183
FJ893914.1 gg_id:536878 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B1E; ear pu FJ8939
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AB361591.1 gg_id:267729 Pseudomonas aeruginosa str. 841 AB3615
GQ222267.1 gg_id:552840 Pseudomonas reactans str. AS1 GQ222
FJ901156.1 gg_id:541120 Polymorphism microbial reservoirs water cut stage oil field clone Z-85 FJ9011
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AY443041.1 gg_id:105353 Pseudomonas sp. str. HS5322 AY4430
DQ420635.1 gg_id:151159 Pseudomonas aeruginosa str. PGSL 03 DQ420
AM697417.1 gg_id:225569 sequencing libraries indoor dust clone BF0001D032 AM697
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EU780001.1 gg_id:326591 Pseudomonas pseudoalcaligenes str. 23 EU7800
EU252491.1 gg_id:237266 Pseudomonas sp. str. AM3 EU2524
AB021419.1 gg_id:8561 Pseudomonas denitrificans str. IAM 12023 AB0214
X92134.1 gg_id:43286 Lake Nakuru isolate 52N3 X92134
DQ140184.1 gg_id:139321 Pseudomonas sp. LJLP1-15 DQ140
AM088480.1 gg_id:142278 Pseudomonas citronellolis str. BG 6903 AM088
FJ893386.1 gg_id:548779 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota WT1; ear p FJ8933
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AJ853507.1 gg_id:110023 landfill leachate clone GZKB12 AJ8535
AB088116.1 gg_id:78808 Pseudomonas thermaerum str. T1 AB0881
FJ937924.1 gg_id:513078 Pseudomonas sp. str. LS197 FJ9379
FJ901066.1 gg_id:513913 Polymorphism microbial reservoirs water cut stage oil field clone G-104 FJ9010
EU661707.1 gg_id:283175 Pseudomonas aeruginosa str. NBRAJG91 EU6617
FJ675280.1 gg_id:527897 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6752
GQ388992.1 gg_id:587812 quality deterioration drinking system during serious red water outbreak clone J40 GQ388
AY699593.1 gg_id:106717 soil contaminated with polyaromatic hydrocarbons clone SAL2d7 AY6995
EU931560.1 gg_id:336985 Pseudomonas aeruginosa str. ZFJ-5 EU9315
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GQ241352.1 gg_id:570943 Pseudomonas sp. str. C23 GQ241
AF237678.1 gg_id:18018 Pseudomonas aeruginosa str. M2E AF2376
DQ481477.1 gg_id:157307 Pseudomonas putida str. VTs-34 DQ481
EU536369.1 gg_id:285992 profile human microbiota antecubital fossa (inner elbow) skin clone nbt62e06 EU5363

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EU214613.1 gg_id:328976 Pseudomonas fluorescens yb126 EU2146
EU734169.1 gg_id:461530 Pseudomonas plecoglossicida EU7341
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FJ892842.1 gg_id:559778 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota HM1; ear p FJ8928
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FJ607147.1 gg_id:513959 Pseudomonas syringae pv. actinidiae str. ICMP 9853 FJ6071
EF515714.1 gg_id:223417 Electricigen Enrichment MFC full-scale anaerobic bioreactor sludge treating brewery EF5157
AY206685.1 gg_id:82206 Pseudomonas jessenii str. PS06 AY2066
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AY970951.1 gg_id:115314 Pseudomonas vranovensis str. 2B2 AY9709
DQ868767.1 gg_id:165580 Pseudomonas tuomuerense str. Yuhua Xin DQ868
GQ200823.1 gg_id:533247 Pseudomonas plecoglossicida str. SP8 GQ200
AY054374.1 gg_id:105822 Pseudomonas pavonaceae AY0543
EU538192.1 gg_id:282127 profile human microbiota antecubital fossa (inner elbow) skin clone nbt82b02 EU5381
EF561642.1 gg_id:228381 Pseudomonas veronii str. T1/1 EF5616
AF074383.1 gg_id:8628 Pseudomonas migulae str. CIP 105470 AF0743
FJ894073.1 gg_id:534048 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B1E; ear pu FJ8940
EU540285.1 gg_id:282167 profile human microbiota antecubital fossa (inner elbow) skin clone nbt113h06 EU5402
GU185861.1 gg_id:577433 Pseudomonas koreensis str. PBRs7 GU185
EU797470.1 gg_id:350105 sediment station DBSE Northern Bering Sea clone 130D73 EU7974
AY622320.1 gg_id:102554 Pseudomonas putida str. AS90 AY6223
EF011017.1 gg_id:362986 Pseudomonas putida str. WP090 EF0110
FM864215.1 gg_id:362580 Pseudomonas tolaasii str. LPPA 532 FM864
EU826028.1 gg_id:333541 Pseudomonas putida str. SRI156 EU8260
EU538858.1 gg_id:284602 profile human microbiota antecubital fossa (inner elbow) skin clone nbt95c02 EU5388
GU391485.1 gg_id:537184 Pseudomonas sp. str. Pd1T GU391
FJ894574.1 gg_id:555704 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B2E; ear pu FJ8945
EU536488.1 gg_id:285516 profile human microbiota antecubital fossa (inner elbow) skin clone nbt214f08 EU5364
FJ893512.1 gg_id:572521 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota WT2; ear p FJ8935
EU538922.1 gg_id:281466 profile human microbiota antecubital fossa (inner elbow) skin clone nbt95c04 EU5389
EU620069.1 gg_id:269290 Pseudomonas putida str. GNA5 EU6200
EU434528.1 gg_id:264077 Pseudomonas fluorescens str. b338 EU4345

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X99541.1 gg_id:8521 Pseudomonas anguilliseptica str. 1123/5 X99541
EU434493.1 gg_id:261872 Pseudomonas fluorescens str. b361 EU434
DQ117553.1 gg_id:138228 structure (Citrullus vulgaris SCHARD.) -based approaches and terminal fragment len DQ117
AY690672.1 gg_id:98925 Pseudomonas sp. str. GC06 AY690
FM213380.2 gg_id:335840 Pseudomonas antarctica str. KJPB54 FM213
EU460330.1 gg_id:301237 polar bear feces clone PB1_aai26f10 EU460
EU539906.1 gg_id:284493 profile human microbiota antecubital fossa (inner elbow) skin clone nbt107f04 EU539
EU538024.1 gg_id:280553 profile human microbiota antecubital fossa (inner elbow) skin clone nbt225a12 EU538
FJ893055.1 gg_id:566846 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota HM2; ear p FJ8930
AM689948.1 gg_id:217808 Pseudomonas sp. str. SBC-3 AM689
AM933517.1 gg_id:340813 Pseudomonas migulae FB26 AM933
AJ308306.1 gg_id:37605 Pseudomonas fluorescens str. Biotype F ICMP 13616; ATCC 12983 AJ3083
EF428993.1 gg_id:217131 Pseudomonas sp. str. GIST-WP4s2 EF4289
EU536354.1 gg_id:284460 profile human microbiota antecubital fossa (inner elbow) skin clone nbt61e08 EU536
FJ405303.1 gg_id:360957 Edwardsiella tarda str. K14 FJ4053
AY741159.1 gg_id:170404 Pseudomonas fulva str. S29 AY741
FJ675430.1 gg_id:532272 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6754
AJ132994.1 gg_id:201265 Pseudomonas sp H171 AJ1329
AJ299216.1 gg_id:25364 Pseudomonas mevalonii str. M AJ2992
FJ893123.1 gg_id:539941 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota HM3; ear p FJ8931
DQ279335.1 gg_id:141206 Dynamic during maturation Tuber magnatum Pico ascoma Pseudomonas clone TM1 DQ279
FJ950541.1 gg_id:416614 Pseudomonas putida str. c252 FJ9505
AF534212.1 gg_id:60329 soil clone Phe41 AF5342
EU536746.1 gg_id:286175 profile human microbiota antecubital fossa (inner elbow) skin clone nbt250c09 EU536
NR_029051.1 gg_id:581450 Pseudomonas salomonii str. CFBP 2022 NR_02
EU540306.1 gg_id:283879 profile human microbiota antecubital fossa (inner elbow) skin clone nbt114h04 EU540
FJ893304.1 gg_id:538132 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota WT1; ear p FJ8933
AY091631.1 gg_id:123196 Pseudomonas sp. str. PH-05 AY0916
EU071502.1 gg_id:238253 and resistance microorganisms European clean room ESTEC HYDRA facility clone EHF EU0715
EU538018.1 gg_id:282396 profile human microbiota antecubital fossa (inner elbow) skin clone nbt225a06 EU538
AY538264.1 gg_id:111611 Pseudomonas fluorescens str. PC20 AY5382
X86623.1 gg_id:8602 Pseudomonas sp str. 2E-14 2A X86623
EU538325.1 gg_id:285758 profile human microbiota antecubital fossa (inner elbow) skin clone nbt83d10 EU538
EU537274.1 gg_id:282810 profile human microbiota antecubital fossa (inner elbow) skin clone nbt72c03 EU537
DQ318866.1 gg_id:156064 Pseudomonas pv. syringae str. NCPPB 281; 8511 DQ318
FJ950621.1 gg_id:434785 Pseudomonas putida str. c144 FJ9506
EU834281.1 gg_id:324211 Pseudomonas brassicacearum str. DS67 EU834
FJ894807.1 gg_id:544342 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota BME; ear p FJ8948
FJ893018.1 gg_id:534589 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota HM2; ear p FJ8930

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EU536280.1 gg_id:280556 profile human microbiota antecubital fossa (inner elbow) skin clone nbt62a02 EU536
AY321588.1 gg_id:88851 Pseudomonas fluorescens str. CCUG32456A AY3215
EU539168.1 gg_id:280377 profile human microbiota antecubital fossa (inner elbow) skin clone nbt102a09 EU539
EF428995.1 gg_id:216433 Pseudomonas fluorescens EF4289
EU538158.1 gg_id:285771 profile human microbiota antecubital fossa (inner elbow) skin clone nbt81a05 EU538
EU538367.1 gg_id:284298 profile human microbiota antecubital fossa (inner elbow) skin clone nbt87f04 EU538
DQ234206.2 gg_id:143653 determined library mangrove clone DS123 DQ234
FJ894557.1 gg_id:565334 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B2E; ear pu FJ8945
FJ894984.1 gg_id:560160 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota BME; ear p FJ8949
EU538332.1 gg_id:286926 profile human microbiota antecubital fossa (inner elbow) skin clone nbt83g07 EU538
FJ799903.2 gg_id:556353 Proteus vulgaris str. 4Bi FJ7999
EU537643.1 gg_id:285279 profile human microbiota antecubital fossa (inner elbow) skin clone nbt74h03 EU537
GU191929.1 gg_id:588639 Pseudomonas putida str. SB 3051 GU191
GU191927.1 gg_id:584485 Pseudomonas monteilii str. SB 3078 GU191
FJ894054.1 gg_id:566587 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B1E; ear pu FJ8940
AY472116.1 gg_id:99985 Pseudomonas fluorescens AY4721
Z76654.1 gg_id:8607 Pseudomonas amygdali str. LMG 2123T () Z76654
NR_025174.1 gg_id:564254 Pseudomonas extremorientalis str. KMM 3447 NR_025
EU538955.1 gg_id:284428 profile human microbiota antecubital fossa (inner elbow) skin clone nbt95h10 EU538
GQ169380.1 gg_id:588287 Pseudomonas thivervalensis str. IEHa GQ169
GQ900590.1 gg_id:574251 Pseudomonas putida str. MPR 4 GQ900
EU539535.1 gg_id:283940 profile human microbiota antecubital fossa (inner elbow) skin clone nbt241d05 EU539
EF194768.1 gg_id:203364 Pseudomonas putida str. PM1 EF1947
EU538937.1 gg_id:282205 profile human microbiota antecubital fossa (inner elbow) skin clone nbt95e09 EU538
EU536583.1 gg_id:282830 profile human microbiota antecubital fossa (inner elbow) skin clone nbt63c09 EU536
EU118771.1 gg_id:236931 Pseudomonas lutea str. AGL 2 EU118
EU538944.1 gg_id:283825 profile human microbiota antecubital fossa (inner elbow) skin clone nbt95f09 EU538
EF061900.1 gg_id:189806 Pseudomonas sp. str. M191 EF0619
FJ950560.1 gg_id:429741 Pseudomonas putida str. c53 FJ9505
FJ894025.1 gg_id:554071 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B1E; ear pu FJ8940
NR_028987.1 gg_id:542667 Pseudomonas trivialis str. P 513/19; DSM 14937; LMG 21464 NR_028
EU538393.1 gg_id:282501 profile human microbiota antecubital fossa (inner elbow) skin clone nbt88f02 EU538
FJ424813.1 gg_id:364673 Pseudomonas sp. str. MS-3 FJ4248
EF010981.1 gg_id:184602 Pseudomonas putida str. PM15 EF0109
FJ893331.1 gg_id:564098 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota WT1; ear p FJ8933
AJ871471.1 gg_id:110332 Pseudomonas luteola CP155-2 AJ8714
AF430121.1 gg_id:66816 Pseudomonas sp. str. VKM B-2265 dcm4 AF4301

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EU348741.1 gg_id:272086 Pseudomonas putida soil EU3487
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AF511511.1 gg_id:65394 Pseudomonas syringae SaU8 AF5115
FJ607148.1 gg_id:573718 Pseudomonas syringae pv. papulans str. ICMP 4044 FJ6071
DQ095887.1 gg_id:134099 Pseudomonas plecoglossicida str. R25 DQ095
FJ893902.1 gg_id:560794 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B1E; ear pu FJ8939
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AM933508.1 gg_id:324712 Pseudomonas antarctica FB16 AM933
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EU538994.1 gg_id:286958 profile human microbiota antecubital fossa (inner elbow) skin clone nbt98f12 EU5389
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AJ297354.1 gg_id:70736 Pseudomonas sp. str. FAIR/BE/F/GH39 AJ2973
AY771716.1 gg_id:108690 Pseudomonas aeruginosa str. S2-77 AY7717
FJ892791.1 gg_id:574101 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota HM1; ear p FJ8927
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AY690691.1 gg_id:99958 Pseudomonas sp. str. MaT03 AY6906
FJ465156.2 gg_id:575465 Pseudomonas fluorescens str. FY32 FJ4651
AB126621.2 gg_id:104655 Pseudomonas japonica str. IAM 15071 AB1266
AB060137.1 gg_id:62341 Pseudomonas cremoricolorata str. IAM 1541T AB0601
EU537931.1 gg_id:285392 profile human microbiota antecubital fossa (inner elbow) skin clone nbt227e04 EU5379
AM495723.1 gg_id:217056 Pseudomonas syringae str. ISF FR1 AM495

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EU465095.1 gg_id:289664 African elephant feces clone AFYEL_aaj68a05 EU4650
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FJ807483.1 gg_id:537835 Pseudomonas fulva str. TY16 FJ8074
EU539850.1 gg_id:284339 profile human microbiota antecubital fossa (inner elbow) skin clone nbt106d09 EU5398
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FJ005054.1 gg_id:326078 Pseudomonas grimontii str. R1 FJ0050
DQ365566.1 gg_id:149449 Pseudomonas poae str. JA01 DQ365
FJ894067.1 gg_id:544310 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B1E; ear pı FJ8940
EF079867.1 gg_id:174369 Pseudomonas sp. str. MY1412 EF0798
EU537635.1 gg_id:284554 profile human microbiota antecubital fossa (inner elbow) skin clone nbt74c03 EU5376
EU708321.1 gg_id:309775 Pseudomonas pv. syringae str. BBK3 EU7083
FJ894204.1 gg_id:535083 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B2E; ear pı FJ8942
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EU538346.1 gg_id:285713 profile human microbiota antecubital fossa (inner elbow) skin clone nbt84e03 EU5383
FJ893112.1 gg_id:543418 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota HM3; ear p FJ8931
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AM259177.1 gg_id:198385 Pseudomonas fluorescens pdm AM259

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AY271793.1 gg_id:109330 Pseudomonas fluorescens str. VKM B-2168 AY2717
FJ894374.1 gg_id:539676 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B2E; ear pu FJ8943
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EU169169.1 gg_id:251990 Pseudomonas aurantiaca str. B23 EU1691
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AY303305.1 gg_id:130588 Pseudomonas sp. str. ps4-45 AY3033
EU169168.1 gg_id:244420 Pseudomonas lini str. B25 EU1691
EF513773.1 gg_id:220219 Pseudomonas putida str. JB-1 EF5137
DQ536517.1 gg_id:159873 Pseudomonas trivialis str. BIHB 747 DQ536
EU647538.1 gg_id:282969 recovered Xidatan Tanggula and Yuzhufeng glaciers glacial snow glacier Tin Plateau c EU6475
EU536806.1 gg_id:283384 profile human microbiota antecubital fossa (inner elbow) skin clone nbt222a08 EU5368
EU101096.1 gg_id:252064 Sulfide/oxygen supply ratio predicts outcome competition among sulfur-oxidizing wa EU1010
EU464759.1 gg_id:294113 Hartmann's mountain zebra feces clone AFZEB_aaj70c09 EU4647
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EU252490.1 gg_id:236335 Pseudomonas sp. AM2(2007) str. AM2 EU2524
EF608541.1 gg_id:234990 predatory Poecilus chalcites their response lab rearing and antibiotic treatment diges EF6085
AM403206.1 gg_id:172703 Nitrate-reducing and Denitrifying Marine Aqua Biofilter marine aqua AM403
DQ824723.1 gg_id:194608 human fecal clone RL185_aaj72c07 DQ824
DQ339144.1 gg_id:149280 Pseudomonas pohangensis str. H3-R18 DQ339
EU143343.1 gg_id:238940 Salinisphaera sp. str. C1 EU1433
GU452539.1 gg_id:528872 Salinisphaera sp. str. T31B1 GU452
EF988634.1 gg_id:235478 Salinisphaera dokdoensis str. CL-ES53 EF9886
AJ421425.1 gg_id:64239 Salinisphaera shabanensis str. E1L3A AJ4214
EU740416.1 gg_id:464939 Salinisphaera hydrothermalis str. EPR70 EU7404
DQ015776.1 gg_id:139798 Antarctic lake water clone ELB25-046 DQ015
EF157203.1 gg_id:244546 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon EF1572
FJ752438.1 gg_id:530747 endosymbionts Loripes lacteus and Anodontia fragilis gill symbiont clone 2A FJ7524
U77478.1 gg_id:7623 endosymbiont Riftia pachyptila U77478
FJ752447.1 gg_id:517886 endosymbionts and Anodontia fragilis Loripes lacteus gill symbiont clone 2C FJ7524
AY542558.1 gg_id:113155 Gulf Mexico seafloor sediment clone GoM GB425 12B-13 AY5425
AM883183.1 gg_id:337155 Endosymbioses between and deep-sea siboglinid tubeworms arctic cold seep (Haak AM883
DQ394953.1 gg_id:152604 harbor sediment clone VHS-B3-62 DQ394
AB530204.1 gg_id:586339 Monitoring Suez and Tokyo bays based on analyses marine sediment clone Tokyo..B AB5302
AM040102.1 gg_id:148469 sandy sediments clone Sylt 6 AM040
AB189713.2 gg_id:104039 Ifremeria nautilei gill symbiont AB1897
AF165909.1 gg_id:7577 Escarpia spicata endosymbiont 'Alvin #2837' Alvin #2837 endosymbiont AF1659
X84980.1 gg_id:7606 Lucina pectinata gill symbiont X84980
EU488600.1 gg_id:535578 lucinid bivalve- symbiotic system: significance geochemical habitat on and gill symbi EU4886
U62131.1 gg_id:32280 Solemya terraeregina gill symbiont U62131
AM236336.1 gg_id:169677 thiotrophic endosymbiont Lucinoma aff. kazani AM236
U77480.1 gg_id:7624 endosymbiont Ridgeia piscesae U77480
AY129089.1 gg_id:81760 Seepiophila jonesi symbiont AY1290
L25707.1 gg_id:7583 Lucina floridana gill symbiont L25707
EF646140.1 gg_id:241188 Potential interactions particle- anammox and archaeal partners namibian Namibian u EF6461
AB073120.1 gg_id:67480 Endosymbiont Lamellibrachia satsuma clone TUB163 AB0731

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EU487821.1 gg_id:545897 lucinid bivalve- symbiotic system: significance geochemical habitat on and gill symbi EU4878
EU487848.1 gg_id:571610 lucinid bivalve- symbiotic system: significance geochemical habitat on and gill symbi EU4878
EU487790.1 gg_id:538251 lucinid bivalve- symbiotic system: significance geochemical habitat on and gill symbi EU4877
AF420355.1 gg_id:74333 hydrothermal sediment clone AF420355 AF4203
DQ394903.1 gg_id:154047 harbor sediment clone VHS-B1-30 DQ394
AY129088.1 gg_id:81293 unclassified escarpiid symbiont AY1290
DQ513106.1 gg_id:160275 Microbial life fluids ridge flank crustal fluid clone FS275-64B-03 DQ513
EU487817.1 gg_id:569845 lucinid bivalve- symbiotic system: significance geochemical habitat on and gill symbi EU4878
EU487849.1 gg_id:557080 lucinid bivalve- symbiotic system: significance geochemical habitat on and gill symbi EU4878
EU290681.1 gg_id:241066 microbial structure biogeochemical contrasting shelf sediments Namibian upwelling EU2906
AF170359.1 gg_id:7586 Dechloromarinus chlorophilus str. NSS AF1703
X84979.1 gg_id:7598 Codakia orbicularis gill symbiont X84979
EU580679.1 gg_id:269980 Autotrophic Thiomicrospira denitrificans-Like Catalyst Coupled Denitrification and Su EU5806
AM882519.1 gg_id:331064 Structure along hydrocarbon contamination coastal sediment oil polluted water pet AM882
EU287120.1 gg_id:235979 Pacific arctic surface sediment clone P13-27 EU2871
EF117913.1 gg_id:198462 Thiohalomonas denitrificans str. HLD 14 EF1179
DQ836238.1 gg_id:168486 Thiohalomonas nitratireducens str. HRHd 3sp DQ836
EF455919.1 gg_id:217101 Thiohalomonas denitrificans str. HLD 15 EF4559
EU374712.1 gg_id:274344 Thiohalorhabdus denitrificans str. HLD 10 EU3747
EU246256.1 gg_id:255672 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-P5-H08 EU2462
AY054370.1 gg_id:105206 marine ascidian symbiont clone AY054370 AY0543
GQ346935.1 gg_id:561050 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ346
AY805307.1 gg_id:124180 Dermacentor variabilis symbiont AY8053
AY243027.1 gg_id:84287 Francisella philomiragia str. 2669 AY2430
L26085.1 gg_id:7731 Francisella philomiragia L26085
AJ698862.1 gg_id:112014 Francisella philomiragia str. ATCC 25015 AJ6988
Z21931.1 gg_id:7757 Francisella tularensis str. lvs ATCC 6223 FSC 155 Z21931
EF153479.1 gg_id:208502 Francisella philomiragia str. DSM 7535 EF1534
AM403242.1 gg_id:192162 Francisella piscicida str. 2006-Chile AM403
AB001522.1 gg_id:7749 Ornithodoros moubata symbiote B AB0015
EU924183.1 gg_id:323152 sequences ticks USA: south-central Pennsylvania clone DA2 EU9241
FJ425613.1 gg_id:365486 communnities healthy and diseased colonies Caribbean coral Montastrea faveolata C FJ4256
FJ202233.1 gg_id:340201 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2022
FJ202510.1 gg_id:319177 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2025
FJ202975.1 gg_id:314000 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2029
FJ202678.1 gg_id:337559 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2026
FJ202250.1 gg_id:330874 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2022

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AY102612.1 gg_id:64552 Caedibacter taeniospiralis AY1026
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AB176554.1 gg_id:98992 Thiotrichales CML28 AB1765
DQ660912.1 gg_id:225063 Methylophaga sp. str. DMS002 DQ660
AY128533.1 gg_id:86185 Methylophaga natronica str. Bur2 AY1285
EU328072.1 gg_id:278985 dynamics during bioremediation crude oil contaminated moderate saline soil clone Y EU3280
DQ400508.1 gg_id:160152 Methylophaga marina str. KM5 DQ400
FJ172066.1 gg_id:333882 Microbial athalassohaline Tirez lagoon (Spain) water clone MJW9 FJ1720
AF384373.1 gg_id:66020 Methylophaga alcalica str. M39 AF3843
AY694421.1 gg_id:99935 Methylophaga murata str. Kr3 AY6944
EU287295.1 gg_id:254176 Pacific arctic surface sediment clone S11-112 EU2872
AY375062.1 gg_id:97463 deep sea sediment clone B92 AY3750
EU287249.1 gg_id:246106 Pacific arctic surface sediment clone S11-66 EU2872
EU287255.1 gg_id:239634 Pacific arctic surface sediment clone S11-72 EU2872
AJ704666.1 gg_id:109271 marine sediment clone HMMVCen-13 AJ7046
EU236405.1 gg_id:290767 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg92D11 EU2364
EU287300.1 gg_id:255354 Pacific arctic surface sediment clone S11-117 EU2873
FJ155021.1 gg_id:353468 seasonal fluctuation coastal Bohai Bay sequencing and RFLP soil clone D21 FJ1550
DQ521546.1 gg_id:191569 Antarctic lake ice cover clone ANTLV7_H05 DQ521
AY212648.1 gg_id:99225 water 20 m upstream manure clone 195up AY2126
GQ007716.1 gg_id:501947 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ007
AY542557.1 gg_id:113736 Gulf Mexico seafloor sediment clone GoM GB425 12B-8 AY5425
EU919781.1 gg_id:340144 Kongsfjorden western Spitsbergen Svalbard ocean water clone b59 EU9197
EU287118.1 gg_id:257905 Pacific arctic surface sediment clone P13-25 EU2871
AY375084.1 gg_id:97200 deep sea sediment clone B132 AY3750
AF532772.1 gg_id:60454 marine sediment clone Limfjorden L22 AF5327
AF035956.1 gg_id:7511 Beggiatoa sp. 'Bay Concepcion' str. Bay Concepcion 'Bay AF0359
FJ875195.1 gg_id:573955 Coexistence Beggiatoa spp. Epsilonproteobacteria and Fusibacter organically-enriche FJ8751
AF532775.1 gg_id:60451 marine sediment clone Limfjorden L9 AF5327
AY580013.1 gg_id:111119 Beggiatoa sp. 'Carmel Canyon' Carmel Canyon AY5800
AY883933.1 gg_id:137953 Juan de Fuca filamentous AY8839
AF532774.1 gg_id:60452 marine sediment clone Limfjorden L8 AF5327
AB108786.1 gg_id:84651 marine sediment clone Tokyo Bay D AB1087
AF532773.1 gg_id:60453 marine sediment clone Limfjorden L6 AF5327
FM203381.1 gg_id:432832 Biogeography filamentous and epsilonproteobacterial ectosymbionts vent shrimp e FM203
FM203400.1 gg_id:407753 Biogeography filamentous and epsilonproteobacterial ectosymbionts vent shrimp e FM203
EU086765.1 gg_id:286899 Siboglinum fiordicum and Endosymbionts Siboglinidae (Annelida) Norway: Ypsesund EU0867
EU086760.1 gg_id:285854 Siboglinum fiordicum and Endosymbionts Siboglinidae (Annelida) Norway: Ypsesund EU0867
EU491817.1 gg_id:271093 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU4918
FJ497604.1 gg_id:533041 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun FJ4976

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EU086767.1 gg_id:280842 Siboglinum fiordicum and Endosymbionts Siboglinidae (Annelida) Norway: Skoge Inle EU086
EU491836.1 gg_id:263959 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU491
EU592359.1 gg_id:581185 Seasonal changes Salton Sea hypersaline water clone SSW84Ap EU592
AB252051.1 gg_id:170060 Oligobrachia mashikoi endosymbiont AB252
FN397818.1 gg_id:421635 geomicrobiological investigation sediments Gulf Cadiz GeoB 9072-1 anoxic sub-surfa FN397
EU617743.1 gg_id:311740 Seasonal variation microbial Yel Sea sediment clone D13S-152 EU617
AB476179.1 gg_id:559576 Compositional and functional transition epibiotic microbial hydrothermal vent galath AB476
EU265784.1 gg_id:273851 epibiotic assemblage recently described Yeti Kiwa hirsuta (Kiwidae) surface crab hyc EU265
DQ351782.1 gg_id:149662 Microbial Adherent Sediment Particles Heavy Metal Contaminated North Sea Surfac DQ351
AB440173.1 gg_id:546279 Farming and harvesting filamentous vent- galatheid crab (Decapoda; Anomura) vent AB440
AM883178.1 gg_id:349801 Endosymbioses between and deep-sea siboglinid tubeworms arctic cold seep (Haak AM883
EU652549.1 gg_id:278683 Seasonal variation microbial Yel Sea sediment clone A8S-100 EU652
FJ712487.1 gg_id:522744 and Archaea Gas Hydrate Sediments (East Sea) Kazan Mud Volcano Anaximander Mo FJ7124
AY922216.1 gg_id:114239 whalefall clone 131703 AY922
AB476177.1 gg_id:535260 Compositional and functional transition epibiotic microbial hydrothermal vent galath AB476
EU617742.1 gg_id:317335 Seasonal variation microbial Yel Sea sediment clone D13S-1 EU617
EF687220.1 gg_id:280984 Biogeochemistry iron- and sulfur-precipitating microbial mats (Nile Mediterranean) ir EF6872
FJ712552.1 gg_id:520020 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) k FJ7125
DQ925898.1 gg_id:254275 Microbes and Thermal Gradients Temperature Hydrothermal Chimneys hydrotherm DQ925
AM176844.1 gg_id:160888 Recovery mangrove sediment clone SZB76 AM176
AB239761.1 gg_id:148717 isotopic evidence ectosymbiosis between filamentous and stalked barnacle (Cirriped AB239
EU652547.1 gg_id:277645 Seasonal variation microbial Yel Sea sediment clone C8S-96 EU652
AB271123.1 gg_id:165803 Oligobrachia mashikoi endosymbiont E AB271
AY225630.1 gg_id:98216 Mid-Atlantic Ridge hydrothermal sediment clone AT-s43 AY225
AY531559.1 gg_id:107157 Indian Ocean hydrothermal vent clone SF_C7-H11 AY531
FJ905702.1 gg_id:555129 s Tonga-Kermadec iron oxide sediments Volcano 1 Tonga Arc clone V1F22b FJ9057
FM242244.1 gg_id:345341 sequences sediment clone 81 T0h-oil FM242
EU707297.1 gg_id:349336 sulfur oxidizing Wadden Sea sediments Janssand intertidal sandy sediment 0 3 cm de EU707
EU025026.1 gg_id:252006 Leucothrix mucor str. LJS0601 EU025
EU265790.1 gg_id:260040 epibiotic assemblage recently described Yeti Kiwa hirsuta (Kiwidae) surface crab hyc EU265
DQ925906.1 gg_id:249236 Microbes and Thermal Gradients Temperature Hydrothermal Chimneys hydrotherm DQ925
AJ441234.1 gg_id:57450 hydrothermal vent polychaete mucous clone P. palm A 79 AJ4412
FJ712548.1 gg_id:527446 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) k FJ7125
AB476202.1 gg_id:559867 Compositional and functional transition epibiotic microbial hydrothermal vent galath AB476
AM883179.1 gg_id:350065 Endosymbioses between and deep-sea siboglinid tubeworms arctic cold seep (Haak AM883
AM040128.1 gg_id:145294 sandy sediments clone Sylt 32 AM040
AY327876.2 gg_id:89122 surface vent snail foot clone SF_C7-E4 AY327
EU491039.1 gg_id:272243 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount South Rift X EU491
EU265791.1 gg_id:267469 epibiotic assemblage recently described Yeti Kiwa hirsuta (Kiwidae) surface crab hyc EU265
EU555124.1 gg_id:260421 Microbial Sulfide Hydrothermal Vent Field Juan de Fuca Ridge Dudley hydrothermal EU555
EU652546.1 gg_id:278109 Seasonal variation microbial Yel Sea sediment clone B8S-13 EU652

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AB042542.1 gg_id:18561 Thiothrix eikelboomii str. COM- AB042
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GU269554.1 gg_id:546547 Thiothrix fructosivorans str. Q GU269
FJ769459.1 gg_id:513774 Changes Methanogenic Microbial After Sludge Pre-treatment full-scale municipal ana FJ7694
AM490765.1 gg_id:586481 Linking and functional nutrient spiraling mats (USA) microbial mat sulfidic cave sprir AM490
DQ413126.1 gg_id:151073 Microbial -dependent and Approaches Anaerobic/Aerobic SBR Reactor EBPR sludge DQ413
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DQ067608.1 gg_id:138619 Thiothrix sp. str. FBR0112 DQ067
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FM174322.1 gg_id:564802 biotrickling filter treating loads H2S biology tools clone H2SRC127 FM174
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AB166732.1 gg_id:99902 Thiothrix sp. str. KRN-B2 AB166
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DQ676306.1 gg_id:219763 Archaeal sediment and plankton freshwater pond suboxic freshwater-pond clone M DQ676
EU662352.1 gg_id:566153 Productivity- Chemolithoautotrophically Based Sulfidic Karst Systems microbial mat (EU662
AF110276.1 gg_id:81307 Beggiatoa sp. str. MS-81-1c AF110
GQ441309.1 gg_id:568660 and dynamic mat present vs. active nitrogen-fixing microorganisms marine microbia GQ441
GU117706.1 gg_id:552714 Beggiatoa sp. Arauama I GU117
FJ516903.1 gg_id:562971 semiarid 'Tablas de Daimiel National Park' wetland (Central Spain) unravelled upper s FJ5169
EF428583.1 gg_id:255153 Beggiatoa sp. 'Chiprana' EF4285
AF110275.1 gg_id:81842 Beggiatoa sp. str. AA5A AF110
EU015402.1 gg_id:241048 Beggiatoa sp. str. LPN EU015
AF110274.1 gg_id:81779 Beggiatoa alba str. B18LD; ATCC 33555 AF110
AF110277.1 gg_id:81107 Beggiatoa sp. str. MS-81-6 AF110
AM259850.1 gg_id:212023 Spatial sponge- Mediterranean Tethya aurantium sponge cortex clone TAA-10-90 AM259
EU491871.1 gg_id:261085 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU491
FJ542932.1 gg_id:511554 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone B FJ5429
EF471637.1 gg_id:269523 Fast Screening and Estuarine Operon Libraries whole surface water Chesapeake Bay (EF4716
GU230347.1 gg_id:568157 Multilevel approach along Rio de la Plata-South Atlantic Ocean coastal sediment clo GU230
FJ905691.1 gg_id:575131 s Tonga-Kermadec iron oxide chimney-like structure on Volcano 19 Tonga Arc clone V FJ9056
DQ988300.1 gg_id:193694 Microbial lab-scale A1-A2-O fixed biofilm system coking wastewater treatment with DQ988
DQ451463.1 gg_id:156946 forest soil clone FAC24 DQ451
EU369126.1 gg_id:346345 libraries oyster shell clone MBIOS-10 EU369
EU335403.1 gg_id:252003 Changes microbial metabolic and along hydrogeochemically variable profile unsatura EU335
EU104116.1 gg_id:336069 Evidence Comamonadaceae determinants settling performance activated sludge clo EU104
EU800820.1 gg_id:327533 It's all ranking aquatic Delaware Bay NJ clone 2C229038 EU800
AB013257.1 gg_id:8011 deep-sea sediment clone NKB5 AB013

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FM179868.1 gg_id:333458 Biogeochemical processes microbial Gullfaks and Tommeliten methane seeps (Nortl FM179
CU467466.1 gg_id:352266 Prokaryotic Tunisian saltern Saltern solar multipond clone CU467
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AJ504486.1 gg_id:62635 sewage sludge clone AJ5044
CU922396.1 gg_id:567904 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU922

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EU652542.1 gg_id:278509 Seasonal variation microbial Yel Sea sediment clone C8S-35 EU652
AB250579.1 gg_id:160900 and ecology Grotta Azzurra Palinuro Cape (Salerno Italy) microbial mat clone #6-4 AB250
FJ712512.1 gg_id:529452 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) k FJ7125
FJ497283.1 gg_id:575773 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun FJ4972
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GQ062984.1 gg_id:385334 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw96c02c GQ062
EF679186.1 gg_id:254988 sewage anaerobic sludge mediator-less MFC clone ASP-21 EF6791
GQ060276.1 gg_id:372558 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ060
AB286529.1 gg_id:207647 Reducing production and domination comamonadaceae reducing oxygen supply was AB286
GQ060660.1 gg_id:438403 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw03g09 GQ060
GQ062191.1 gg_id:455804 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv GQ062
GQ062255.1 gg_id:374917 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv GQ062
AB286547.1 gg_id:203983 Reducing production and domination comamonadaceae reducing oxygen supply was AB286
AF406529.1 gg_id:60643 bacterioplankton clone AEGEAN_165 AF4065
GQ337214.1 gg_id:552282 Hydrography shapes biogeography deep Arctic Ocean water depth 400m clone CB1 GQ337
GQ350551.1 gg_id:535210 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ350

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AF406536.1 gg_id:60638 bacterioplankton clone AEGEAN_243 AF4065
AACY01030334.1 gg_id:99301 Sargasso Sea AACY0
AB186988.1 gg_id:103264 Mariana trough hydrothermal vent water 0.2micro-m filterable fraction clone MT-NE AB1869
FJ826243.1 gg_id:510441 Succession during spring diatom bloom Sea filtered surface sea water contrasting nor FJ8262
GQ348876.1 gg_id:581691 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ348
AY700614.1 gg_id:109443 Australia: Great Barrier Reef clone PDB-OTU7 AY7006
EF571905.1 gg_id:230907 Coco's Island site 23 marine clone S23_4 EF5719
EU491486.1 gg_id:270695 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X4 clone EU4914
EU287407.1 gg_id:241556 Pacific arctic surface sediment clone S26-107 EU2874
FJ873329.1 gg_id:539933 Vertical and archaea methane-rich cold seep located base sediments Okhotsk Sea clo FJ8733
EU817105.1 gg_id:345886 Biological Haliclona (gellius) sp.: Sponge and Microbial Symbionts Pacific Ocean 13 m EU8171
EU652530.1 gg_id:278243 Seasonal variation microbial Yel Sea sediment clone C8S-47 EU6525
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GQ348494.1 gg_id:541236 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ348
GQ350244.1 gg_id:571396 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ350
GQ347632.1 gg_id:548782 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ347
FJ628318.1 gg_id:588621 transition and zone within near-shore basin: brackish water anoxic fjord Nitinat Lake (FJ6283
FJ203248.1 gg_id:351002 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c FJ2032
FJ203316.1 gg_id:314846 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c FJ2033
FJ959819.1 gg_id:558909 bottlenose dolphin upper respiratory tract blowhole clone D8A8_170 FJ9598
FJ203252.1 gg_id:309645 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c FJ2032
AB212895.1 gg_id:132694 The Mini plant Run 6 of the Nippon Steel Research and Engineering Center clone nsn AB2128
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DQ337067.1 gg_id:146995 subsurface water clone EV818SWSAP22 DQ337
GU208326.1 gg_id:568293 Study on Sediment Dongping Lake sediment clone Se2-23 GU208
AM935235.1 gg_id:552890 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM935
EF608532.1 gg_id:231765 predatory Poecilus chalcites their response lab rearing and antibiotic treatment diges EF6085
FJ612598.1 gg_id:511469 Orbus hercynius str. CN3 FJ6125
DQ837611.1 gg_id:173383 structures honeybee intestines and their response insecticidal proteins gut clone HB DQ837
AY942754.1 gg_id:147853 but species richness marine sponge Cymbastela concentrica clone Cc007 AY9427
EF076133.1 gg_id:240090 Sponge- microorganisms: ecology and biotechnological potential Bahamas: Little San EF0761
GU118596.1 gg_id:548103 Threatened Corals Provide Microbial Habitats clone Mfav_B05 GU118
EU799507.1 gg_id:339161 It's all ranking aquatic Newport Harbour RI clone 1C227115 EU7995
EU799990.1 gg_id:309275 It's all ranking aquatic Newport Harbour RI clone 1C227670 EU7999
EU799493.1 gg_id:333893 It's all ranking aquatic Newport Harbour RI clone 1C227099 EU7994
GQ441315.1 gg_id:554466 and dynamic mat present vs. active nitrogen-fixing microorganisms marine microbia GQ441
EF632661.1 gg_id:253267 Unique microbial contrasting aquatic altitude Andean Altiplano (northern Chile) sedir EF6326
DQ269079.1 gg_id:199419 marine macro-alga surface clone DPC097 DQ269
CU466822.1 gg_id:328710 Evry wastewater treatment plant anoxic basin clone CU466

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EF092261.1 gg_id:268390 Persistent Axinella corrugata clone BH1_G11 EF0922
AJ581350.1 gg_id:92419 Mediterranean sponge clone E01-9C-15 AJ5813
AB286554.1 gg_id:204859 Reducing production and domination comamonadaceae reducing oxygen supply was AB2865
FJ940806.1 gg_id:388951 Aeromonas punctata str. 4pM30 FJ9408
DQ270618.1 gg_id:144237 hydrothermal carbonate chimney clone LC1133B-43 DQ270
FJ497530.1 gg_id:592807 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun FJ4975
FJ655515.1 gg_id:583817 symbiont FJ6555
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AY292922.1 gg_id:101121 Vibrio fischeri EM17 AY2929
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CP000020.1 gg_id:129275 Vibrio fischeri str. ES114 CP0000
AY628647.1 gg_id:103863 Vibrio wodanis AY6286
DQ146991.1 gg_id:146962 Vibrio sp. str. V776 DQ146
AB497068.1 gg_id:546558 Aliivibrio logei str. 11-2 AB4970
EU185820.1 gg_id:398431 Aliivibrio logei str. WHSW1 EU1858
AY292934.1 gg_id:106476 Vibrio logei str. SR181 AY2929
EU862333.1 gg_id:580068 Aliivibrio sp. str. BV040308-21 EU8623
EU257749.1 gg_id:551220 Aliivibrio logei AV05/2007 EU2577
AY292928.1 gg_id:102104 Vibrio logei str. SL101 AY2929
EU091322.1 gg_id:314982 Aliivibrio salmonicida PB3-7rrnB EU0913
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EU091323.1 gg_id:304361 Aliivibrio salmonicida PB1-8rrnA EU0913
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FJ654064.1 gg_id:511531 Coral Reef Fish Feces and Gut Microbial Assemblages gut contents distal intestine clo FJ6540
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AY576761.1 gg_id:139186 Photobacterium sp. str. 26III/A02/220 AY5767
AY745814.1 gg_id:108596 Vibrio sp. str. JL-73 AY7458
Z19106.1 gg_id:9131 Cryptosaras couesi symbiont Z19106
NR_025574.1 gg_id:535720 Grimontia hollisae str. 75-80; LMG 17719 NR_025
AY292951.1 gg_id:107197 Photobacterium leiognathi str. SN2B AY2929
EF635307.1 gg_id:246572 Photobacterium subsp. damselae HQ061227-1 EF6353
AY642160.1 gg_id:111666 Photobacterium phosphoreum str. NZ-11D AY6421
AY642161.1 gg_id:111692 Photobacterium phosphoreum str. calba.1.1 AY6421
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AY341442.1 gg_id:106555 Photobacterium mandapamensis str. ATCC 33981 AY3414
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AY551089.1 gg_id:102788 Ferrania halotolerans str. MACL01	AY551
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AB470940.1 gg_id:567653 Vibrio sp. str. r42	AB470
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DQ923438.1 gg_id:176420 Vibrio sp. W-4	DQ923
AY960847.1 gg_id:114914 Photobacterium ganghwensis str. FR1311	AY9608
EU153251.1 gg_id:243117 Photobacterium sp. str. P16011A	EU1532
GQ231487.1 gg_id:582132 Vibrio natriegens str. T5	GQ231
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AY264923.1 gg_id:105451 Vibrio harveyi str. ACMM 642	AY2649

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GQ391944.1 gg_id:517522 Vibrio sp. str. PaH1.39

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FJ200649.1 gg_id:345203 Vibrio lentus str. I 80 FJ2006
EU188117.1 gg_id:318402 Uncultivated oceanic unicellular N2-fixing cyanobacteria are picoplankton unusual 7(EU188
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EF584085.1 gg_id:232685 Vibrio sp. str. TUN8	EF584
EU517645.1 gg_id:263861 Vibrio sp. str. 5D9	EU517
AM921804.1 gg_id:253912 Vibrio alginolyticus	AM921
EF645832.1 gg_id:247677 Vibrio parahaemolyticus str. H040823-1	EF6458
EU517643.1 gg_id:258894 Vibrio sp. str. 4C3	EU517
EU854911.1 gg_id:312073 Vibrio sp. 6D1	EU854
EU043382.1 gg_id:254129 Vibrio sinaloensis str. CAIM 636; LMG 21563	EU043
EU419926.1 gg_id:259946 Vibrio fortis str. RW39	EU419
GQ391945.1 gg_id:524646 Vibrio sp. str. PaH2.01a1	GQ391
EU517638.1 gg_id:274062 Vibrio sp. str. 4H2	EU517
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FJ605240.1 gg_id:561761 Vibrio harveyi str. HS08001	FJ6052
DQ097524.1 gg_id:132459 Vibrio litoralis str. mano22p	DQ097
EU854895.1 gg_id:346295 Vibrio sp. 6B2	EU8548
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AF218244.1 gg_id:19456 Vibrio sp	AF2182
DQ269211.1 gg_id:141139 Vibrio alginolyticus str. SR1	DQ269
GQ281380.1 gg_id:579117 Vibrio sp. str. KTW-12	GQ281
AY562192.1 gg_id:113713 Vibrio parahaemolyticus str. Sh06	AY5621
FM204856.1 gg_id:367994 Vibrio campbellii str. R1311	FM204
AB457058.1 gg_id:319566 Vibrio sp. str. SB-I1	AB457
FJ024709.1 gg_id:346035 Copper affects reduction and genetic enriched sulfate reducing coastal sediments exp	FJ0247
EU833997.1 gg_id:568897 Vibrio alginolyticus str. UST981101-032	EU8339
EU854908.1 gg_id:314683 Vibrio sp. 6E2	EU854
EF219054.1 gg_id:214480 Vibrio alginolyticus str. H050815-1	EF2190
EU854929.1 gg_id:344477 Vibrio sp. 6G11	EU854
FJ172044.1 gg_id:512369 Vibrio parahaemolyticus str. RW1	FJ1720
FJ457435.1 gg_id:511250 Vibrio sp. str. S2321	FJ4574
AY928014.1 gg_id:112649 Vibrio harveyi	AY9280
GQ260161.1 gg_id:584728 Vibrio tapetis str. C11.25	GQ260
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X97988.1 gg_id:9232 Vibrio sp str. VI966/26	X97988
FJ176451.1 gg_id:563362 Vibrio natriegens str. J-C2-40	FJ1764
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EU854951.1 gg_id:340143 Vibrio sp. 7B4	EU854

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EU660319.1 gg_id:299937 Vibrio parahaemolyticus str. CM2	EU6603
X97989.1 gg_id:9241 Vibrio sp str. VI1067/44	X97989
EU579452.1 gg_id:273618 Vibrio pomeroyi str. 929	EU5794
EU073023.1 gg_id:237745 Vibrio penaeicida HC051105-6	EU0730
GQ203114.1 gg_id:544229 Vibrio alginolyticus str. 23-6PIN	GQ203
EU517646.1 gg_id:263182 Vibrio sp. str. 5E9	EU5176
AB038029.1 gg_id:17434 Vibrio sp. str. OM02	AB0380
NC_009783.1 gg_id:471497 Vibrio harveyi BAA-1116 str. ATCC BAA-1116; BB120	NC_009
U57919.1 gg_id:9278 Vibrio cyclitrophicus str. 2P44	U57919
EU082035.1 gg_id:252648 Vibrio sp. str. cn83	EU0820
AY654760.1 gg_id:99936 Oculina mucus isolate 11	AY6547
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EF488080.1 gg_id:224355 Vibrio porteresiae str. MSSRF31	EF4880
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AM422800.1 gg_id:238361 Vibrio harveyi str. 04101	AM422
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EF584041.1 gg_id:231968 Vibrio sp. str. DS7	EF5840
DQ856554.1 gg_id:245610 intestinal microflora Chinese mitten crab (Eriocheir sinensis) clone C3S	DQ856
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DQ173157.1 gg_id:139193 Vibrio alginolyticus str. zouA	DQ173
AB038030.1 gg_id:47694 Vibrio splendidus str. ATCC33789	AB0380
EU854912.1 gg_id:353304 Vibrio sp. 6D10	EU8549
EF584056.1 gg_id:232714 Vibrio sp. str. HE3	EF5840
EU854944.1 gg_id:308043 Vibrio sp. 7A10(2008)	EU8549
GU194174.1 gg_id:524536 Vibrio cyclitrophicus str. Col 15	GU194
EU636230.1 gg_id:286820 Vibrio natriegens str. V6	EU6362
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X74701.1 gg_id:9315 Vibrio diazotrophicus str. ATCC 33466T	X74701
FJ866782.1 gg_id:557937 Rhodobacter capsulatus str. PSB-03	FJ8667
NZ_ACFN01000147.1 gg_id:580234 Vibrio parahaemolyticus str. AQ4037	NZ_AC
EU373091.1 gg_id:268687 Vibrio harveyi str. BB170	EU3730
EU854946.1 gg_id:351124 Vibrio sp. 7A12(2008)	EU8549
NC_009783.1 gg_id:471498 Vibrio harveyi BAA-1116 str. ATCC BAA-1116; BB120	NC_009
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AJ874360.1 gg_id:111259 Vibrio splendidus str. 01/104	AJ8743
EU517633.1 gg_id:262574 Vibrio sp. str. 4D5	EU5176

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EU372922.1 gg_id:272836 Vibrio sp. str. S16	EU3729
EU854947.1 gg_id:316417 Vibrio sp. 7A1	EU8549
AF493803.1 gg_id:93679 Vibrio sp. str. 167	AF4938
EU854829.1 gg_id:332034 Vibrio sp. 1A2	EU8548
AJ316167.1 gg_id:73319 Vibrio coralliilyticus str. LMG 10953	AJ3161
AF513465.1 gg_id:60374 Vibrio sp. str. PH19	AF5134
X74720.1 gg_id:9240 Vibrio parahaemolyticus str. ATCC 17802T	X74720
Z31657.1 gg_id:9268 Vibrio splendidus	Z31657
EU699809.1 gg_id:335968 Vibrio sp. str. F-6	EU6998
AY332566.1 gg_id:91317 Vibrio alginolyticus str. EcGS021001	AY3325
EU854930.1 gg_id:323930 Vibrio sp. 6G7	EU8549
AAWP01000045.1 gg_id:256024 Vibrio harveyi str. HY01	AAWP0
X74698.1 gg_id:9313 Vibrio cincinnatiensis str. ATCC 35912T	X74698
AY911394.1 gg_id:112657 Vibrio parahaemolyticus str. SW-1	AY9113
FJ202676.1 gg_id:344716 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k	FJ2026
AB470933.1 gg_id:556034 Vibrio sp. str. r27	AB4709
AM941185.1 gg_id:286468 Microbes enriched seawater after addition coral mucus and reef waters mixture1-8	AM941
EU854897.1 gg_id:306077 Vibrio sp. 6B3	EU8548
NZ_ACFO01000050.1 gg_id:577439 Vibrio parahaemolyticus str. -5034	NZ_AC
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AF513447.1 gg_id:55336 Vibrio alginolyticus str. LA6	AF5134
DQ146990.1 gg_id:149211 Vibrio sp. str. V759	DQ146
AY785255.1 gg_id:108413 microbial fuel cell anode clone 19	AY7852
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FJ952769.1 gg_id:410605 Vibrio sp. str. 1ta5	FJ9527
EU854825.1 gg_id:307164 Vibrio sp. 1B10(2008)	EU8548
EF584054.1 gg_id:230635 Vibrio sp. str. HE1	EF5840
EU246793.1 gg_id:243190 polyphasic description Pocillopora meandrina Palmyra Atoll Calcinus obscurus abdon	EU2467
FJ154796.1 gg_id:311946 Vibrio harveyi str. WG1702	FJ1547
NC_009783.1 gg_id:471500 Vibrio harveyi BAA-1116 str. ATCC BAA-1116; BB120	NC_009
EU854926.1 gg_id:322675 Vibrio sp. 6G9	EU8549
AY426982.1 gg_id:101603 Vibrio ezurae str. HDV1-1	AY4269
EU517647.1 gg_id:274949 Vibrio sp. str. 4G11	EU5176
X97990.1 gg_id:9224 Vibrio sp str. VI1964/75	X97990
FM995173.1 gg_id:568021 digestive gland QX infected and naive Sydney rock oysters Saccostrea glomerata Vib	FM995
AY967727.1 gg_id:115357 Vibrio alginolyticus IS3	AY9677
AY785254.1 gg_id:108410 microbial fuel cell anode clone 17	AY7852
EU854824.1 gg_id:318618 Vibrio sp. 1G1	EU8548

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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
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EU660311.1 gg_id:295546 Vibrio parahaemolyticus str. V1
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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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EU031646.1 gg_id:235697 Vibrio harveyi str. AK1

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AY254041.1 gg_id:82765 Vibrio hispanicus str. LMG 13211
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AB257339.2 gg_id:196408 Vibrio kanaloae str. Do-155
AB257330.2 gg_id:175599 Vibrio kanaloae str. Do-40
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DQ978993.1 gg_id:196541 Vibrio sp. S-12
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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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GQ327
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s__Vibrio shilonii	6265
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s__Vibrio tapetis	6277
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s__Vibrio vulnificus	6301
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AY897206.2 gg_id:122102 Vibrio ponticus str. RP30 AY8972
DQ005880.1 gg_id:128085 Vibrio sp. str. A358 DQ005
AJ630102.1 gg_id:109158 Vibrio ponticus str. CECT 5870 AJ6301
AF513463.1 gg_id:60376 Vibrio proteolyticus str. PH8 AF5134
NR_026128.1 gg_id:554644 Vibrio proteolyticus str. ATCC 15338 NR_02
DQ995521.1 gg_id:190831 Vibrio proteolyticus str. A2G-5B DQ995
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EU123937.1 gg_id:342373 Ulcerative enteritis Homarus americanus: case report and intestinal aerobic apparen EU123
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EF584027.1 gg_id:229162 Vibrio sp. str. BS11 EF584
AY911395.1 gg_id:112524 Vibrio shilonii str. SW-2 AY9113
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FN554604.2 gg_id:548927 Vibrio tapetis str. HJ4 FN554
AY800099.1 gg_id:255639 Vibrio tapetis str. UK6 AY800
AY129278.1 gg_id:78597 Vibrio tapetis str. LP2 AY1292
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EF546280.1 gg_id:279479 Polymorphisms Vibrio vulnificus clone 05_C08 EF5462
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AJ515220.1 gg_id:69396 Vibrio splendidus str. LMG 10952 AJ5152
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FJ457370.1 gg_id:545463 Vibrio sp. str. S1132 FJ4573
AY363245.1 gg_id:94021 Hydrocarboniphaga effusa str. AP103; ATCC BAA-332 AY3632
EU313812.1 gg_id:256598 Hydrocarboniphaga sp. str. B2-9 EU3138
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GU205299.1 gg_id:516554 unusual Microbial Venezuelan Tepui (Orthoquartzite) Cave: Dominance Chloroflexal GU205
FJ466262.1 gg_id:546919 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea FJ4662
AB257720.1 gg_id:158622 Panacagrimonas perspica str. Gsoil 142 AB257
GQ389062.1 gg_id:536669 quality deterioration drinking system during serious red water outbreak clone S18 GQ389
EU328045.1 gg_id:278173 dynamics during bioremediation crude oil contaminated moderate saline soil clone B EU328
GQ389123.1 gg_id:575267 quality deterioration drinking system during serious red water outbreak clone S76 GQ389
AJ867659.1 gg_id:109705 melted-ice water clone JFJ-ICE-Bact-31 AJ8676
GQ389067.1 gg_id:538784 quality deterioration drinking system during serious red water outbreak clone S22 GQ389

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

s__Solimonas soli	15913
s__unclassified	15934
s__unclassified	16067
s__unclassified	16158
s__unclassified	16413
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s__unclassified	16487
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s__Dokdonella koreensis	16704
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s__unclassified	16192
s__unclassified	16255
s__unclassified	16281
s__unclassified	16513
s__unclassified	16667
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s__unclassified	17175
s__unclassified	17392
s__Dyella ginsengisoli	17021
s__Dyella ginsengisoli	17397
s__Dyella japonica	17167
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s__Frateuria aurantia	16282
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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 EF0678
AB074648.1 gg_id:78370 pea aphid symbiont clone APe2_11 AB0746
GQ009435.1 gg_id:500228 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw77 GQ009
EU542470.1 gg_id:269231 Effects chemical structure concentration on pathways microbial during dechlorinatio EU5424
GQ009794.1 gg_id:499871 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw77 GQ009
AJ318170.1 gg_id:37497 waste-gas biofilter clone BIrii5 AJ3181
AM935172.1 gg_id:541995 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM935
GQ009827.1 gg_id:499839 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw77 GQ009
AY544768.1 gg_id:101731 Aquamonas vora str. BPTSA20 AY5447
AF445723.1 gg_id:33015 travertine hot spring clone SM2D10 AF4457
AF445726.1 gg_id:18696 travertine hot spring clone SM2E10 AF4457
DQ239766.1 gg_id:143429 Rhodanobacter sp. str. CC-JY-1 DQ239
EF589679.1 gg_id:233714 Dokdonella koreensis str. NML 01-0233 EF5896
EU276578.1 gg_id:370138 -DGGE and Approaches Analyze Effect Agricultural Practices on Soil agricultural soil c EU2765
CU466843.1 gg_id:354759 Evry wastewater treatment plant anoxic basin clone CU466
EF516860.1 gg_id:223206 grassland soil clone FCPS392 EF5168
EF125947.1 gg_id:571774 Biofilm-reactor Based Enrichment Utilizing Oligotrophic Concentrations Acyl-homose EF1259
EU150285.1 gg_id:279341 acidobacteria and dry meadow soil Niwot Ridge LTER clone Ni_H08_DMDN EU150
EU708508.1 gg_id:293748 and Situ Quantification Arsenite Oxidizing Denitrifying Enrichment anoxic arsenite ox EU7085
AM981201.1 gg_id:266974 Dokdonella sp. str. PYM5-11 AM981
FJ971728.1 gg_id:462787 microbial autrotrophic denitrification granular sludge clone R1-B4 FJ9717
AB245362.1 gg_id:149239 Dokdonella ginsengisoli str. Gsoil 191 AB2453
AB245367.1 gg_id:146494 Dyella ginsengisoli str. Gsoil 3046 AB2453
EF191353.1 gg_id:199169 Dyella ginsengisoli str. LA-3 EF1913
AB110496.1 gg_id:102417 Dyemonas todaii str. XD10 AB1104
DQ451515.1 gg_id:156994 forest soil clone FAC76 DQ451
EU682683.1 gg_id:329236 Frateuria sp. str. VA24 EU6826
DQ378209.1 gg_id:154251 oil-polluted soil clone F47_Pitesti DQ378
AB091195.1 gg_id:105821 Frateuria aurantia str. IFO3247 AB0911
AB091196.1 gg_id:105973 Frateuria aurantia str. IFO3249 AB0911
AB091198.1 gg_id:106286 Frateuria aurantia str. IFO13329 AB0911
AB091194.1 gg_id:105669 Frateuria aurantia str. IFO3245 AB0911
AY792283.1 gg_id:120471 Humic Lake clone CrystalBog571C8 AY7922
GU458291.1 gg_id:522526 Dyella sp. str. ST6D GU458
AY913255.1 gg_id:114384 forest soil clone DUNssu037 (-2A) (OTU#012) AY9132
AY884571.1 gg_id:112345 Dyella soli str. BB4 AY8845
AJ252143.1 gg_id:47724 Schineria larvae str. L1/68 AJ2521
EU008091.1 gg_id:370121 Ignatzschineria sp. str. C2H18 EU0080
DQ337535.1 gg_id:148917 Schineria sp. CHNDP40 DQ337
AM397063.1 gg_id:170943 Schineria sp. str. S5 AM397
AJ580498.1 gg_id:99030 Luteibactor rhizovicina str. LJ96 AJ5804

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g__Luteibacter
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g__Pseudoxanthomonas

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s__Pseudoxanthomonas mexicana	17143
s__Pseudoxanthomonas taiwanensis	16460
s__Pseudoxanthomonas taiwanensis	17172
s__unclassified	15908

DQ984591.1 gg_id:242890 Mt. Nan-Jen litterfall clone IYF125 DQ984
DQ986460.1 gg_id:192082 Luteibacter sp. str. MDA0897 DQ986
DQ532183.1 gg_id:165763 Geographical Variation Microbial Burden and Spacecraft Assembly Johnson Space Ce DQ532
AB433628.1 gg_id:275651 Luteimonas mephitis AB4336
DQ337599.1 gg_id:146003 Luteimonas sp. CHNTR51 DQ337
AJ012228.1 gg_id:7793 Luteimonas mephitis str. B1953/27.1 AJ0122
AB246805.2 gg_id:150537 Luteimonas sp. str. Q-1 AB2468
AY500144.1 gg_id:104583 Luteimonas sp. H10 str. H10; AS 1.3529 AY5001
FJ750462.1 gg_id:510835 Luteimonas sp. str. EM0590 FJ7504
DQ323663.1 gg_id:146080 Lysobacter taiwanensis str. DD-1133 DQ323
AB299978.2 gg_id:258113 Lysobacter spongicola str. KMM 329 AB2999
AY599704.1 gg_id:101000 fungal ascocarp clone Cl-11-TB4-II AY5997
GQ003601.1 gg_id:506057 Topographical and Temporal Human Skin Microbiome skin alar crease clone nbu54h GQ003
GU361114.1 gg_id:524518 Lysobacter enzymogenes str. T226 GU361
EU440727.1 gg_id:557970 Soil are Changed Agricultural Practices agricultural soil clone Plot17-C01 EU4407
AY642571.1 gg_id:151984 and carbonate precipitation giant microbialites ly alkaline Lake Van Turkey microbiali AY6425
EF173350.1 gg_id:199667 Options situ remediation contaminated mixture chlorinated hydrocarbons hydrocarb EF1733
EU244029.1 gg_id:359969 16SrRNA probes river Leine sediment clone sls1316 EU2440
DQ191178.1 gg_id:140061 Lysobacter sp. str. GH 1-9 DQ191
DQ532277.1 gg_id:163869 Geographical Variation Microbial Burden and Spacecraft Assembly Johnson Space Ce DQ532
AM930380.1 gg_id:245194 Lysobacter enzymogenes str. 3.1T8 AM930
AY557615.1 gg_id:101503 Silanimonas lenta str. 25-4 AY5576
EU908051.1 gg_id:326693 Lysobacter sp. str. ZLD-17 EU9080
FJ674447.1 gg_id:520058 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6744
EU236311.1 gg_id:296150 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg1bA3 EU2363
DQ129253.1 gg_id:138668 microarray level air two cities Texas urban aerosol clone AKIW751 DQ129
EU800949.1 gg_id:353183 It's all ranking aquatic Delaware Bay NJ clone 2C229208 EU8009
AY599709.1 gg_id:101824 fungal ascocarp clone Cl-106-TB4-II AY5997
EU881196.1 gg_id:333628 Karst region natural restoration land soil clone KNR200711-002 EU8811
AJ534675.1 gg_id:75877 ground water deep-well injection disposal site radioactive wastes Tomsk-7 clone S15A AJ5346
AM111012.1 gg_id:140927 Lysobacter sp. str. 3070 AM111
AJ582198.1 gg_id:93932 soil near uranium mill tailings clone Gitt-GS-126 AJ5821
AB166878.1 gg_id:100144 Lysobacter sp. str. Dae16 AB1668
EU662609.1 gg_id:567662 Productivity- Chemolithoautotrophically Based Sulfidic Karst Systems floating microb EU6626
FN357197.1 gg_id:541979 Lysobacter capsici str. 10.4.5 FN3571
AB008507.1 gg_id:7875 Pseudoxanthomonas japonensis str. 12-3 AB0085
GQ480839.1 gg_id:537693 Pseudoxanthomonas mexicana str. L2 GQ480
AF273082.1 gg_id:41720 Pseudoxanthomonas mexicana str. AMX 26B AF2730
AM932276.1 gg_id:276970 Pseudoxanthomonas taiwanensis str. S22-49 AM932
AF427039.2 gg_id:72795 Pseudoxanthomonas taiwanensis str. CB-226 AF4270
GQ263885.1 gg_id:572981 Structure Simulated Level Waste Site simulated level waste site clone WC2_134 GQ263

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GQ263804.1 gg_id:561211 Structure Simulated Level Waste Site simulated level waste site clone WC1_b45	GQ263
GQ263736.1 gg_id:539166 Structure Simulated Level Waste Site simulated level waste site clone WC1_a52	GQ263
AY686710.1 gg_id:99791 Pseudoxanthomonas johnstonii str. JA40	AY686
AB271140.1 gg_id:165390 Pseudoxanthomonas suwonensis str. MX8-2	AB271
GQ264214.1 gg_id:532909 Structure Simulated Level Waste Site simulated level waste site clone WW1_a91	GQ264
EU589254.1 gg_id:276619 China Ningxia rice paddy field soil clone 1_A10	EU589
AM418384.1 gg_id:191835 Pseudoxanthomonas spadix str. IMMIB AFH-5	AM418
AB245360.1 gg_id:149042 Pseudoxanthomonas ginsengisoli str. Gsoil 175	AB245
AJ581600.1 gg_id:93887 soil near uranium mill tailings clone KCM-B-65	AJ5816
DQ419968.1 gg_id:155699 Frateuria sp. DM-HM	DQ419
DQ370020.1 gg_id:154977 Rhodanobacter lindaniclasticus str. czh-131	DQ370
AY495959.1 gg_id:101644 Frateuria sp. str. WJ69	AY495
AF312216.1 gg_id:28808 South Africa: KwaZulu-Natal Province Pietermaritzburg clone Y14-2 bacterium	AF312
AY081991.1 gg_id:68655 atrazine-catabolizing microbial absence methanol clone KRA30-20	AY081
GQ047745.1 gg_id:430929 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor	GQ047
EU818793.1 gg_id:354823 Rhodanobacter sp. str. LQ-2	EU818
DQ837296.1 gg_id:256803 Archaeal and pristine National Park Spain Donana coastal aquifer clone 49S1_1B_51	DQ837
EF166075.1 gg_id:196704 Rhodanobacter ginsengisoli str. GR17-7	EF166
FJ167498.1 gg_id:305737 microbiology granular sludge under autotrophic mixotrophic and heterotrophic denit	FJ1674
GQ250431.2 gg_id:593647 Rhodanobacter sp. str. MJ01	GQ250
AY218756.1 gg_id:81132 penguin droppings sediments clone KD6-20	AY218
GU134907.1 gg_id:582647 Acid-tolerant microaerophilic oxdizing enhance Fe(III) accumulation Fe(II) oxidizing e	GU134
AY218745.1 gg_id:81880 penguin droppings sediments clone KD6-1	AY218
AY218667.1 gg_id:81461 penguin droppings sediments clone KD9-36	AY218
AY188308.1 gg_id:79780 marine? clone KD3-82	AY188
AB286179.1 gg_id:182472 Rhodanobacter thiooxidans str. LCS2	AB286
AB100608.1 gg_id:79383 Swingsiella fulva str. Jip2	AB100
DQ125745.1 gg_id:133703 uranium contaminated soil clone AKAU3857	DQ125
EF166076.1 gg_id:192094 Rhodanobacter terrae str. GP18-1	EF166
EU332829.1 gg_id:256674 Rhodanobacter sp. str. LnR5-47	EU332
DQ125806.1 gg_id:133317 uranium contaminated soil clone AKAU3949	DQ125
AY218740.1 gg_id:82238 penguin droppings sediments clone KD5-73	AY218
FJ538158.1 gg_id:560044 metagenomics study rice treated milk vetch and no-tillage paddy field soil clone MBM	FJ5381
FJ405366.1 gg_id:359626 Rhodanobacter terrae str. SPg	FJ4053
AY188317.1 gg_id:79298 penguin droppings sediment clone KD5-51	AY188
FJ466329.1 gg_id:511559 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea	FJ4663
AY218719.1 gg_id:81363 penguin droppings sediments clone KD7-89	AY218
EU196307.1 gg_id:253030 Rhodanobacter sp. NP47	EU196
AY218723.1 gg_id:81676 penguin droppings sediments clone KD5-100	AY218

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AF376025.1 gg_id:50262 Frateuria sp. str. NO-16	AF376
AY218606.1 gg_id:82101 penguin droppings sediments clone KD3-139	AY218
DQ230920.1 gg_id:143831 Stenotrophomonas maltophilia str. KB2	DQ230
DQ912806.1 gg_id:242976 Stenotrophomonas maltophilia str. ZX-PKU-003	DQ912
FM213382.2 gg_id:332451 Stenotrophomonas maltophilia str. MN6	FM213
AY641540.1 gg_id:100214 Stenotrophomonas maltophilia str. BK	AY641
AY738260.1 gg_id:106659 Stenotrophomonas maltophilia str. TKW1	AY738
AB194323.1 gg_id:138821 Stenotrophomonas maltophilia str. BL-12	AB194
DQ192172.1 gg_id:139973 Stenotrophomonas maltophilia str. flds	DQ192
AB299977.1 gg_id:224930 Stenotrophomonas maltophilia str. 26-3 (= KMM 3045)	AB299
EU857419.1 gg_id:344187 Stenotrophomonas maltophilia str. BF-S6	EU857
EU239471.1 gg_id:239046 Pseudomonas geniculata str. XJUHX-9	EU239
EF102868.1 gg_id:245040 Stenotrophomonas maltophilia str. G-5-5-1	EF1028
DQ077704.1 gg_id:132159 Stenotrophomonas maltophilia FLX	DQ077
DQ327729.1 gg_id:146179 Stenotrophomonas maltophilia str. DHHJ	DQ327
EU239465.1 gg_id:243036 Pseudomonas geniculata str. XJUHX-2	EU239
EU239476.1 gg_id:257977 Pseudomonas geniculata str. XJUHX-18	EU239
FM213378.2 gg_id:314300 Stenotrophomonas maltophilia str. KJPB14	FM213
FJ976090.1 gg_id:426140 Stenotrophomonas maltophilia str. ATCC 53510	FJ9760
GU265557.1 gg_id:577388 Stenotrophomonas acidaminiphila str. BTY	GU265
DQ864512.1 gg_id:170684 Stenotrophomonas maltophilia	DQ864
EF174242.1 gg_id:192384 direct activated 1st maturation stage sludge clone B17-814	EF1742
DQ824702.1 gg_id:174317 human fecal clone RL185_aaj72a04	DQ824
DQ824618.1 gg_id:185994 human fecal clone RL185_aaj70e05	DQ824
FJ268981.1 gg_id:366073 unculturable rhizospheric soil Phragmites cummunis growing wetland ecosystem dist	FJ2689
EU434427.1 gg_id:276010 Stenotrophomonas koreensis str. a197	EU434
DQ824602.1 gg_id:175201 human fecal clone RL185_aaj70c07	DQ824
DQ824541.1 gg_id:179102 human fecal clone RL185_aaj69d09	DQ824
AJ012229.1 gg_id:7812 Stenotrophomonas nitritireducens str. L2	AJ0122
FJ950643.1 gg_id:396619 Stenotrophomonas maltophilia str. c199	FJ9506
FJ405360.1 gg_id:360816 Stenotrophomonas maltophilia str. SPa	FJ4053
DQ469587.1 gg_id:158226 Stenotrophomonas maltophilia Sm777	DQ469
FM178869.1 gg_id:310433 Acetobacter pasteurianus str. CCM 3606	FM178
AJ131782.1 gg_id:7817 Stenotrophomonas maltophilia str. LMG 10873	AJ1317
GQ268318.1 gg_id:589026 Stenotrophomonas maltophilia str. Y1	GQ268
AF511522.1 gg_id:65384 Stenotrophomonas maltophilia SaO5lg	AF511
AJ293466.1 gg_id:39173 Stenotrophomonas maltophilia str. e-p20	AJ2934
AJ293469.1 gg_id:50487 Stenotrophomonas maltophilia str. c20	AJ2934
FJ347998.1 gg_id:334679 Stenotrophomonas sp. str. GGC-D7A	FJ3479
EU239472.1 gg_id:253725 Pseudomonas geniculata str. XJUHX-10	EU239
EU779483.1 gg_id:349163 Hartmann's Mountain Zebra feces clone AFZEB_aaj71b07	EU779

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EF620464.1 gg_id:246737 Stenotrophomonas maltophilia str. ISSDS-774
AY484506.1 gg_id:106950 Stenotrophomonas maltophilia
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AB547226.1 gg_id:514890 Stenotrophomonas maltophilia str. NCCP-45
EU934076.1 gg_id:344292 Stenotrophomonas maltophilia str. FR2_1con
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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
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EF221776.1 gg_id:201486 Stenotrophomonas sp. str. tap-8
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EF620455.1 gg_id:249332 Stenotrophomonas maltophilia str. ISSDS-585
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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AJ293470.1 gg_id:20877 Stenotrophomonas maltophilia str. e-a21 AJ2934
GQ267816.1 gg_id:540690 Stenotrophomonas maltophilia str. PSM-5 GQ267
AJ306833.1 gg_id:71314 Stenotrophomonas maltophilia ON2 AJ3068
EU627172.1 gg_id:278738 Stenotrophomonas maltophilia str. NH.300 EU627
DQ223428.2 gg_id:143204 Stenotrophomonas maltophilia str. ZJUB-041 DQ223
U62646.1 gg_id:7795 Stenotrophomonas maltophilia str. MGB U6264
AJ243605.1 gg_id:74547 Stenotrophomonas sp AJ2436
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FN395263.1 gg_id:392327 Stenotrophomonas maltophilia str. FR-W4Ba FN395
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AJ131909.1 gg_id:7832 Stenotrophomonas maltophilia str. LMG 11003 AJ1319
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DQ079059.1 gg_id:128053 Stenotrophomonas maltophilia SA Ant15 DQ079
EF690418.1 gg_id:242975 Stenotrophomonas maltophilia M17-5 EF6904
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GU186115.1 gg_id:552717 Stenotrophomonas maltophilia str. IHB B 1365 GU186
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AJ131115.1 gg_id:7808 Stenotrophomonas maltophilia str. LMG 10991 AJ1311
DQ186643.2 gg_id:168391 Stenotrophomonas maltophilia str. KNUC161 DQ186
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AF508105.1 gg_id:66237 Thermomonas haemolytica N22 AF508
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NR_025265.1 gg_id:572324 Thermomonas hydrothermalis str. SGM-6; DSM 14834 NR_02
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EU104238.1 gg_id:341846 Evidence Comamonadaceae determinants settling performance activated sludge clo EU104
EU202907.1 gg_id:342175 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo EU2029
EU202899.1 gg_id:345071 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo EU2028
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EU662613.1 gg_id:539739 Productivity- Chemolithoautotrophically Based Sulfidic Karst Systems floating microb EU662
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AM936180.1 gg_id:537205 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM936
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CU466816.1 gg_id:339285 Evry wastewater treatment plant anoxic basin clone CU466
GU332843.1 gg_id:593908 Arenimonas sp. str. NA-09 GU332
AJ619045.1 gg_id:102209 Brewery bottling plant clone MTAC25 AJ6190
EU449635.1 gg_id:535385 Soil are Changed Agricultural Practices agricultural soil clone Plot4-2E09 EU449
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AF140004.1 gg_id:50378 Xanthomonas sp. str. ML-168b AF140
DQ984626.1 gg_id:251179 YK oil-contaminated soil clone YK_62 DQ984
AB240283.1 gg_id:143176 microbial structure Phragmites rhizosphere biofilm reed bed reactor laboratory clone AB240
GQ354936.1 gg_id:566599 structure between two geochemically distinct springs Alum Rock Park spring clone M GQ354
AY922114.1 gg_id:113915 farm soil clone AKYH1464 AY922
DQ856527.1 gg_id:240149 intestinal microflora Chinese mitten crab (Eriocheir sinensis) clone C2G DQ856
FJ538122.1 gg_id:555549 metagenomics study rice treated milk vetch and no-tillage paddy field soil clone MBT FJ5381
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AM932272.1 gg_id:275388 Luteimonas sp. str. S22-40 AM932
FJ671430.1 gg_id:524537 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6714
DQ846687.1 gg_id:168681 Cibimonas vasta str. CC-YY255 DQ846
AM939778.1 gg_id:263341 Dyella marensis str. CS5-B2 AM939
DQ125662.1 gg_id:130301 uranium contaminated soil clone AKAU3728 DQ125
AM229325.1 gg_id:151541 Xanthomonas sp. str. T7-07 AM229
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EF018705.1 gg_id:209670 aspen rhizosphere clone Amb_16S_1156 EF0187
AY328765.1 gg_id:88178 drinking water system simulator clone DSSD67 AY328
AM936392.1 gg_id:563988 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM936
AM935846.1 gg_id:566333 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM935
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EU202908.1 gg_id:331342 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo EU202
AB161360.1 gg_id:99159 Lysobacter brunescens str. KCTC 12130 AB161
GU250851.1 gg_id:571730 Anaerobic biodegradation branched hydrocarbon biomarker analog pristane waste GU250
GQ039397.1 gg_id:430138 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbu GQ039
EU276577.1 gg_id:362681 -DGGE and Approaches Analyze Effect Agricultural Practices on Soil agricultural soil c EU276
AM934790.1 gg_id:572655 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM934
AM980880.1 gg_id:272797 Aspromonas sp. UK-29 AM980
FJ612198.1 gg_id:550784 and Biogeochemistry Dongping Lake Ecosystems lake water clone DP3.5.36 FJ6121
GQ264123.1 gg_id:585780 Structure Simulated Level Waste Site simulated level waste site clone WC3_60 GQ264
EF174287.1 gg_id:177737 direct activated sludge last compost maturation stage clone J56-814 EF1742
EU015100.1 gg_id:244451 Investigation estrogen-degrading bioreactors membrane bioreactor suspension and EU015
EF540404.1 gg_id:222135 oil-shale semi-coke solid waste clone 3_16MK EF5404
EU421886.1 gg_id:260668 Un-culturable Indian Himalayas soil under glacier Lahaul-Spiti Valley clone KC-84 EU421
AB008508.1 gg_id:7884 ultramicrobacterium str. DY01 AB008
AY963358.1 gg_id:156208 structures and correlated ecological factors soils two evergreen broad-leaved forests AY9633
EF660758.1 gg_id:256944 Luteimonas aestuarii str. B9 EF6607
DQ984608.1 gg_id:253110 LY oil-contaminated soil clone LYC172 DQ984
AY218631.1 gg_id:203227 Penguin Droppings Sediments Ardley Island Antarctica clone KD4-32 AY2186
EU150258.1 gg_id:278696 acidobacteria and soil Niwot Ridge LTER clone Ni_D2P1 EU150
AJ604540.1 gg_id:102773 Collembola-associated clone za04 AJ6045

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FJ380131.1 gg_id:369488 ornithogenic Ross Sea region Antarctica AB1 soil clone 1/2/2D FJ3801
AY372931.1 gg_id:142723 marine sponge Pseudoceratina clavata symbiont AY372!
GQ396926.1 gg_id:592861 Functional unvegetated perhumid recently-deglaciated soils do not correlate shifts s GQ396
AB274846.1 gg_id:163937 Variation predominant microbial consortium N.22 d on medium containg aromatic a AB274!
FN563156.1 gg_id:590307 Impact changing HRT OLR on prokaryotes involved biomethanizitaion and fuzzy logic FN563
FJ380132.1 gg_id:367350 ornithogenic Ross Sea region Antarctica AB1 soil clone 1/2/4D FJ3801
EU236277.1 gg_id:297307 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone HgCo4 EU236
GU208439.1 gg_id:559226 Study on Sediment Dongping Lake sediment clone Fr3-6 GU208
GU444064.1 gg_id:514899 Effects amendments on fertility and microbial structure cucumber Cucumis sativus L GU444
AM490086.1 gg_id:202402 Xanthomonas sp. str. P2-12-1 AM490
GQ009333.1 gg_id:500330 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ009
DQ228359.1 gg_id:142243 microbial compositions two subglacial possible role microbes chemical weathering p DQ228
AJ311653.1 gg_id:71415 Fulvimonas soli str. LMG 19981T AJ3116
X95919.1 gg_id:7871 Xanthomonas axonopodis str. LMG 538-T X95919
AM991237.1 gg_id:279266 Microbial groundwater and their potential use biomonitoring karst spring water clo AM991
AF523890.1 gg_id:63325 forested wetland clone RCP1-10 AF5238
GU250856.1 gg_id:580658 Anaerobic biodegradation branched hydrocarbon biomarker analog pristane waste GU250
EU237492.1 gg_id:241713 Lysobacter sp. str. XM415 EU237
GQ250435.1 gg_id:585059 Xanthomonas sp. str. MJ09 GQ250
EU662625.1 gg_id:583425 Productivity- Chemolithoautotrophically Based Sulfidic Karst Systems floating microb EU662
EU134744.1 gg_id:253642 tallgrass prarie soil clone FFCH13468 EU134
DQ458014.1 gg_id:158419 acid mine drainage clone DX17 DQ458
AB288902.1 gg_id:202916 termite gut homogenate clone BOf5-13 AB288
DQ001634.1 gg_id:157598 Microbial seeps asphalt seep clone E91-46 DQ001
DQ660840.1 gg_id:238846 DongChuan copper pyrites PRC determined acid mine drainage (AMD) clone DCN-I-1 DQ660
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AB245363.1 gg_id:147794 Lysobacter ginsengisoli str. Gsoil 357 AB245
EU104170.1 gg_id:351052 Evidence Comamonadaceae determinants settling performance activated sludge clo EU104
FJ674765.1 gg_id:516410 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6747
EU834776.1 gg_id:513843 methods extraction nucleic acid activated lab scale EBPR-activated sludge clone L68 EU834
EU449638.1 gg_id:575082 Soil are Changed Agricultural Practices agricultural soil clone Plot4-2H07 EU449
AJ307936.1 gg_id:50142 derived microbial 'pearl'- community clone sipK9 AJ3079
EF157085.1 gg_id:237178 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon EF157
EF492981.1 gg_id:235704 Iron-manganese Nodule and Its Surrounding Soil soil around iron-manganese nodule EF4929
GU208447.1 gg_id:580506 Study on Sediment Dongping Lake sediment clone Fr2-6 GU208
GU208400.1 gg_id:539242 Study on Sediment Dongping Lake sediment clone Fh2-4 GU208
EF648150.1 gg_id:257386 dynamics during produced water treatment aerobic activated sludge clone XJ100 EF6481
EU134776.1 gg_id:244985 tallgrass prarie soil clone FFCH9956 EU134
GU169062.1 gg_id:584355 Biofilms formed on substances: response f conditions and carbon concentrations sy GU169

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EU134748.1 gg_id:249305 tallgrass prarie soil clone FFCH14140 EU134
GQ129910.1 gg_id:457990 Genetic inventory 'JPL-SAF' during MSL mission spacecraft assembly clean room floc GQ129
GQ396811.1 gg_id:511988 Functional unvegetated perhumid recently-deglaciated soils do not correlate shifts s GQ396
FJ598363.1 gg_id:512980 Study Prokaryotic Some Selected Niches Western Ghats India water clone BCWCWP1 FJ5983
AB118236.1 gg_id:100967 Halothiobacillus sp. str. SO07 AB118
FJ947035.1 gg_id:542102 Study Prokaryotic Some Selected Niches Western Ghats India sediment clone BCWCS FJ9470
GU144259.1 gg_id:542178 Xanthomonas arboricola pv. poinsettiicola str. LMG 8675 GU144
Y10754.1 gg_id:7889 Xanthomonas hyacinthi str. LMG 739 T Y10754
AY247064.1 gg_id:83056 Xanthomonas translucens pv. graminis AY247
AF000946.1 gg_id:7876 Xanthomonas pv. campestris str. Xc17 AF000
Y10766.1 gg_id:7862 Xanthomonas sacchari str. LMG 471 T Y10766
Y10756.1 gg_id:7878 Xanthomonas melonis str. LMG 8670 T Y10756
NR_029332.1 gg_id:587741 Xanthomonas theicola str. TC1; LMG 8684 NR_02
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X99298.1 gg_id:7880 Xanthomonas campestris str. LMG 726 X99298
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AY253329.1 gg_id:85823 Xanthomonas translucens pv. poae AY2533
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Y10761.1 gg_id:7857 Xanthomonas vesicatoria str. LMG 911 T Y10761
Y10764.1 gg_id:7856 Xanthomonas bromi str. LMG 947 T Y10764
X95922.1 gg_id:7861 Xanthomonas populi str. LMG 5743-T X95922
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EU741037.1 gg_id:338929 Xanthomonas sp. str. FeL06 EU741
AY576651.1 gg_id:105820 Xanthomonas axonopodis pv. syngonii str. X191 AY5766
AY576639.1 gg_id:105873 Xanthomonas axonopodis pv. dieffenbachiae str. LMG8664 AY5766
AY576652.1 gg_id:105970 Xanthomonas axonopodis pv. syngonii str. LMG9055 AY5766
AF442744.1 gg_id:68801 Xanthomonas axonopodis pv. citri str. Lw AF4427
EF101979.1 gg_id:191402 Xanthomonas axonopodis str. MSF EF1019
Y10765.1 gg_id:7883 Xanthomonas codiaei str. LMG 8678 T Y10765
AF442739.1 gg_id:68804 Xanthomonas axonopodis pv. aurantifolii str. X84 pv. AF4427

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AJ864722.1 gg_id:199736 Pseudomonas boreopolis str. S2-s-PMWA-6 AJ8647
AF203388.1 gg_id:21170 Xylella fastidiosa str. PL.788; ATCC35871 AF2033
AF203392.1 gg_id:25098 Xylella fastidiosa str. PE.PLS AF2033
EU526732.1 gg_id:259129 Xylella fastidiosa str. EO EU5267
AF159572.1 gg_id:7844 Xylella fastidiosa str. PCE-FG; ATCC35881 AF1595
EF433940.1 gg_id:214495 Xylella fastidiosa CaVc3 EF4339
EF433931.1 gg_id:208471 Xylella fastidiosa VvIIc2 EF4339
DQ991191.1 gg_id:197140 Xylella fastidiosa str. 4BD7 DQ991
AF159576.1 gg_id:7848 Xylella fastidiosa str. Mul-2 AF1595
EF157080.1 gg_id:243037 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon EF1570
EF095437.1 gg_id:579168 Application and DGGE fingerprinting detection microbial Malaysian sweet crude oil cl EF0954
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EF571979.1 gg_id:230588 Coco's Island site 23 marine clone S23_78 EF5719
GQ259226.1 gg_id:570167 Microbial activities coastal marine sediments and column Svalbard deep water clone GQ259
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GQ347305.1 gg_id:592130 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ347
GQ347277.1 gg_id:538806 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ347
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AY907769.1 gg_id:137410 identification picoplankton contrasting waters Arabian Sea water clone A712021 AY907
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GQ259264.1 gg_id:576577 Microbial activities coastal marine sediments and water column Svalbard deep sedi GQ259
FJ716273.1 gg_id:568134 Chlorobi dominate shal chemocline Bahamas Sawmill Sink column 10.3 m water dept FJ7162
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EU385747.1 gg_id:259814 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S EU385
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FJ746183.1 gg_id:563570 Microbial oligotrophic marine sediments: South Pacific Gyre ocean sediment 5306 m FJ7461
EU181491.1 gg_id:255266 Prokaryotic enhanced organic matter remineralization continental margin marine se EU181
DQ513074.1 gg_id:161026 Microbial life fluids ridge flank crustal fluid clone FS266-18B-03 DQ513
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AY907781.1 gg_id:137211 identification picoplankton contrasting waters Arabian Sea water clone A712049 AY907
GQ351198.1 gg_id:579754 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Eastern GQ351
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AF406551.1 gg_id:103827 complex marine community d at depth 200 m North Aegean Sea (Station 3) clone AE AF406
GQ337246.1 gg_id:568401 Hydrography shapes biogeography deep Arctic Ocean water depth 1000m clone CB GQ337
GQ375271.1 gg_id:515331 Hydrography shapes biogeography deep Arctic Ocean water depth 1000 m clone CB GQ375

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GQ337265.1 gg_id:590436 Hydrography shapes biogeography deep Arctic Ocean water depth 428m clone CB1 GQ337
AB187008.1 gg_id:106295 Suiyo seamount hydrothermal vent water 0.2micro-m filterable fraction clone SSM-N AB187
AB187006.1 gg_id:105980 Suiyo seamount hydrothermal vent water 0.2micro-m filterable fraction clone SSM-N AB187
FJ746090.1 gg_id:567620 Microbial oligotrophic marine sediments: South Pacific Gyre ocean sediment 5306 m FJ7460
EF573230.1 gg_id:231910 Coco's Island site 23 marine clone S23_1329 EF5732
DQ889875.1 gg_id:171291 natural product producing octocoral Erythropodium caribaeorum clone EC214 DQ889
EU491524.1 gg_id:270326 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR4C EU491
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EF494370.1 gg_id:222885 Nunnock River granitic landscape clone NR.1.116 EF4943
AM997686.1 gg_id:571356 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A AM997
FJ205353.1 gg_id:510135 Prokaryotic deep-sea hydrothermal region East Lau Spreading Centre deep marine se FJ2053
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EU048632.1 gg_id:245214 Microbial surface marine sediment Xisha Trough South China Sea clone MD2902-B28 EU048
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DQ395515.1 gg_id:151247 deep-sea octacoral clone ctg_CGOCA20 DQ395
EU135311.1 gg_id:246322 tallgrass prarie soil clone FFCH7260 EU1353
GU454958.1 gg_id:530796 Understanding short-chain fatty acids accumulation enhanced alkaline digestion: kir GU454
AY218601.1 gg_id:81510 penguin droppings sediments clone KD3-113 AY2186
AJ863240.1 gg_id:120514 poplar tree microcosm bulk soil flooded clone 26BSF3 AJ8632
DQ248296.1 gg_id:143458 carbon tetrachloride contaminated soil clone TF2 DQ248
GQ116329.1 gg_id:384169 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw691e0 GQ116
GQ002367.1 gg_id:507292 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu176f02 GQ002
FJ455888.1 gg_id:512694 Variations archaeal and sulfate-methane transition zone continental margin sediment FJ4558
EU048664.1 gg_id:246357 and archaeal surface marine sediment Slope South China Sea clone MD2896-B3 EU048
AF254404.1 gg_id:41280 4MB-degrading consortium clone UASB_TL26 AF2544
EU344940.1 gg_id:262115 Hepialus gonggaensis guts equalized library larval gut clone Hg5-30 EU3449
DQ990931.2 gg_id:184899 Microbial Rock Varnish Yungay Atacama Desert Chile rock varnish clone AYRV1-033 DQ990
EF516747.1 gg_id:225432 grassland soil clone FCPS434 EF5167
EF018189.1 gg_id:206828 aspen rhizosphere clone Amb_16S_532 EF0181
EF018382.1 gg_id:205209 aspen rhizosphere clone Amb_16S_760 EF0183
AB179676.1 gg_id:200752 Clones Deep-Groundwater Microorganisms That Pass through 0.2-Micrometer-Pore- AB1796
EU246293.1 gg_id:250492 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-P6-E01 EU2462
EF018234.1 gg_id:213599 aspen rhizosphere clone Amb_16S_585 EF0182
EU335431.1 gg_id:250861 Changes microbial metabolic and along hydrogeochemically variable profile unsatura EU3354

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EF018239.1 gg_id:204896 aspen rhizosphere clone Amb_16S_590 EF0182
FJ479051.1 gg_id:590993 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4790
AJ519639.1 gg_id:77042 uranium tailings soil clone Sh765B-AG-45 AJ5196
EF516922.1 gg_id:220959 grassland soil clone FCPO411 EF5169
AM991193.1 gg_id:279508 Microbial groundwater and their potential use biomonitoring karst spring water clo AM991
FJ478673.1 gg_id:534321 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4786
FJ478543.1 gg_id:578866 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4785
FJ479426.1 gg_id:570387 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4794
EU881156.1 gg_id:306708 Karst region primary forest soil clone KPF200711-139 EU881
DQ298285.1 gg_id:152331 studies on and nifH Lasiurus sindicus Sewan grass Thar Desert Rajasthan India rhizos DQ298
GU444065.1 gg_id:525151 Effects amendments on fertility and microbial structure cucumber Cucumis sativus L GU444
AB487162.1 gg_id:592058 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNIR0 AB487
AF234126.1 gg_id:44346 arid soil clone #0319-6A21 AF2341
EU135321.1 gg_id:249043 tallgrass prarie soil clone FFCH6980 EU1353
AB120010.1 gg_id:100441 Brachyspira aalborgi str. HISM16/5/02 AB1200
FM178385.1 gg_id:350706 Brachyspira aalborgi str. HIS1 Human intestinal spirochaetosis patient 1 FM178
EF455559.1 gg_id:206262 Brachyspira alvinipulli str. C1; ATCC 51933 EF4555
AY349941.1 gg_id:93018 Brachyspira canis str. CN 129 AY3499
EU819059.1 gg_id:369616 Brachyspira corvi str. AN968/4/04 EU8190
EU819065.1 gg_id:369752 Brachyspira corvi str. AN1876/1/04 EU8190
AY349944.1 gg_id:92367 Brachyspira pilosicoli str. Dog 17 AY3499
AB120007.1 gg_id:105392 Brachyspira pilosicoli str. CD2S AB1200
DQ473575.1 gg_id:209655 Brachyspira suanatina str. 4859/03 DQ473
AB093305.1 gg_id:84017 Brachyspira innocens D3D/6/15 AB0933
AB093307.1 gg_id:83843 Brachyspira innocens D7D/6/15 AB0933
AY349949.1 gg_id:92347 Brachyspira aalborgi str. W3b AY3499
AY514024.1 gg_id:100496 Brachyspira pilosicoli Br1622 AY5140
AY312492.1 gg_id:88867 Brachyspira murdochii str. 56-150 AY3124
AB092969.1 gg_id:86423 Brachyspira innocens D1D/6/15 AB0929
EF517541.1 gg_id:257834 Brachyspira hyodysenteriae P134/99 EF5175
U14933.1 gg_id:3783 Brachyspira innocens str. 983-90 (group II) U14933
DQ922565.1 gg_id:171642 Brachyspira hyodysenteriae str. 91507-8x/01 (T21) DQ922
U14930.1 gg_id:3768 Brachyspira hyodysenteriae str. B78 U14930
U14915.1 gg_id:3753 Brachyspira innocens str. 1023-90 (group III) U14915
EF164984.1 gg_id:235829 Brachyspira pulli AN2929/1/03 EF1649
EF164966.1 gg_id:254733 Brachyspira intermedia AN3536/03 EF1649
AB093323.1 gg_id:84667 Brachyspira innocens D1A/11/9 AB0933
AB093308.1 gg_id:82681 Brachyspira innocens D9D/6/15 AB0933
AB093314.1 gg_id:83734 Brachyspira innocens D1A/10/5 AB0933
AB093304.1 gg_id:84263 Brachyspira innocens D2A/6/15 AB0933

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g__sfA
g__sfA
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g__sfB
g__sfA
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g__Leptospira
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s__Leptospira biflexa	76467
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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
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AB093320.1 gg_id:85067 Brachyspira innocens D6B/10/25 AB093
U14920.1 gg_id:3770 Brachyspira innocens str. B256 (group III) U1492
EF164976.1 gg_id:240387 Brachyspira innocens AN4113/03 EF1649
AB079583.1 gg_id:77935 Brachyspira ibaraki str. HIS24/11/99 AB0795
EF164969.1 gg_id:257537 Brachyspira intermedia AN5112/03 EF1649
FJ461892.1 gg_id:569032 Microbial ecology industrial digestor mesophilic anaerobic reactor fed effluent chemi FJ4618
EU245543.1 gg_id:249265 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M2-H0 EU2455
AY605147.1 gg_id:104927 microbial mat clone IF004 AY6051
AY605151.1 gg_id:100106 microbial mat clone IF025 AY6051
AY605148.1 gg_id:105069 microbial mat clone IF007 AY6051
EU245476.1 gg_id:250068 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M2-A0 EU2454
DQ329632.1 gg_id:159296 Guerrero Negro hypersaline microbial mat clone 05D2Z42 DQ329
Z21632.1 gg_id:4396 Leptonema illini str. 3055 Z21632
DQ991481.1 gg_id:186857 Leptospira alexanderi serovar Mengla str. A85 DQ991
NC_010842.1 gg_id:304981 Leptospira biflexa serovar strain 'Patoc (Ames)' str. Patoc 1 (Ames) NC_01
Z12821.1 gg_id:4383 Leptospira biflexa serovar str. patoc Patoc 1 Z12821
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EF537007.1 gg_id:229607 Leptospira borgpetersenii serovar Javanica 969 EF5370
FJ154592.1 gg_id:343791 Leptospira borgpetersenii serovar Mini str. Sari FJ1545
Z21630.1 gg_id:4348 Leptospira borgpetersenii str. JAVANICA VELDRAT BATAVIA 46 Z21630
AY631891.1 gg_id:107131 Leptospira inadai serovar Aguarana str. MW-4 AY6318
AM050566.1 gg_id:138386 Leptospira interrogans serovar Canicola str. Utrecht V AM050
FJ154562.1 gg_id:343537 Leptospira kirschneri serovar str. Kambale FJ1545
FJ154560.2 gg_id:330258 Leptospira kirschneri serovar Erinaceiauriti str. Erinaceus Auritus 670 FJ1545
EF596782.1 gg_id:231150 Leptospira interrogans L1207 EF5967
FJ154570.1 gg_id:350766 Leptospira kirschneri serovar Grippotyphosa str. Mandemarkers FJ1545
EF612285.1 gg_id:233710 Leptospira licerasiae serovar Varillal str. CEH010 EF6122
EF612287.1 gg_id:233288 Leptospira licerasiae serovar Varillal str. MMD835 EF6122
Z21635.1 gg_id:4347 Leptospira noguchii str. PANAMA CZ 214 Z21635
DQ991493.1 gg_id:195575 Leptospira santarosai serovar str. Alice DQ991
U12673.1 gg_id:4307 Leptospira weilii str. serogroup Icterohaemorrhagiae s WB46 U12673
Z21631.1 gg_id:4382 Leptospira biflexa serovar Canela str. CANELA Z21631
EF025496.1 gg_id:190457 Leptospira wolffi str. Korat-H2 EF0254
U12670.2 gg_id:4306 Leptospira borgpetersenii str. serovar hardjo strain Hardjo bo BD50 U12670
EF205465.1 gg_id:211824 among geographically regions central Tibet geothermal spring mat clone YCB65 EF2054
FJ660552.1 gg_id:562022 Correlation functional stability and dynamics full-scale wastewater treatment plant a FJ6605
AY631880.1 gg_id:101978 Leptospira alexanderi serovar Manhao 3 str. L 60 AY6318
Z21633.1 gg_id:4381 Leptospira biflexa serovar Jequitaia str. JEQUITAIA Z21633
Z26969.1 gg_id:4372 Leptospira biflexa str. tororo TORORO MUTANT STRAIN PARENT Z26969
DQ066980.1 gg_id:134767 Lake Washington sediment clone pLW-94 DQ066
Z21649.1 gg_id:4305 Leptospira santarosai str. SHERMANI 1342 K Z21649

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g__Leptospira
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s__Borrelia carolinensis	76524
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s__Borrelia turdi	76098
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CP000348.1 gg_id:176749 Leptospira borgpetersenii serovar Hardjo-bovis str. L550 CP0003
Z21634.1 gg_id:4346 Leptospira inadai str. LYME Z21634
Z21629.1 gg_id:4370 Leptospira biflexa serovar Ancona str. ANCONA PORTO Z21629
AY631885.1 gg_id:102755 Leptospira fainei serovar Hurstbridge str. BUT 6 AY6318
AB279549.1 gg_id:181283 Leptospira kmetyi serovar Malaysia str. Bejo-Iso9 AB2795
U60594.1 gg_id:4349 Leptospira fainei str. Hurstbridge U60594
X17547.1 gg_id:4333 Leptospira interrogans str. serovar canicola strain Moulton X17547
GQ441345.1 gg_id:584418 and dynamic mat present vs. active nitrogen-fixing microorganisms marine microbia GQ441
AE016823.1 gg_id:149405 Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130 AE0168
EU358706.1 gg_id:334061 structure archaeal denaturing gel electrophoresis and sequencing mesophilic biogas EU3587
EU887797.1 gg_id:317015 and RFLP anaerobes Nisargruna biogas plant anaerobic digester clone 48IVSN EU8877
AB447738.1 gg_id:550451 Microbial Structure and Dynamics Granules Expanded Granular Sludge Bed (EGSB) R AB4477
AB089124.1 gg_id:77837 termite gut homogenate clone Rs-H88 AB0891
AB244313.1 gg_id:143845 Microbial mesophilic chemostat cultivation long-chain fatty acids-degrading methan AB2443
AB191983.1 gg_id:143791 termite gut homogenate clone M1PT4-10 AB1919
AY293856.1 gg_id:88155 Leptospira parva str. H; NCTC 11395 AY2938
AB191844.1 gg_id:141715 termite gut homogenate clone M1NP2-04 AB1918
EF454943.2 gg_id:217661 termite hindgut clone 290cost002-P3L-731 EF4549
AB191843.1 gg_id:141819 termite gut homogenate clone M2PT2-76 AB1918
EF586003.1 gg_id:243633 Methanol-assimilating anaerobic solid waste digester fed methanol clone M35_D8_L EF5860
EU358680.1 gg_id:352774 structure archaeal denaturing gel electrophoresis and sequencing mesophilic biogas EU3586
EU462396.1 gg_id:288748 Sumatran orangutan feces clone orang1_aai53g01 EU4623
AF357916.2 gg_id:28706 Spirochaeta sp. str. Buddy AF3579
AJ698092.1 gg_id:105838 Spirochaeta sp. str. SPN1 AJ6980
AM982634.1 gg_id:277877 microbial and slurry pig saw dust spent bedding clone PISD-AJA01 AM982
DQ833400.1 gg_id:172254 Sphaerochaeta sp. str. TQ1 DQ833
X85194.1 gg_id:4173 Borrelia afzelii str. DK4 X85194
NZ_ABGJ01000002.1 gg_id:270217 Borrelia burgdorferi str. 72a NZ_AB
EU085407.1 gg_id:560956 Borrelia carolinensis SCW-22 EU0854
AF210136.1 gg_id:38090 Borrelia coriaceae CA435 AF2101
AY342029.1 gg_id:99035 Borrelia garinii str. SIKA1 AY3420
AY342031.1 gg_id:102963 Borrelia garinii str. PD89 AY3420
U42292.1 gg_id:4241 Borrelia hermsii U42292
L40598.1 gg_id:4269 Borrelia japonica str. IKA2 L40598
AY166715.1 gg_id:76818 Borrelia lonestari AY1667
U23211.1 gg_id:4172 Borrelia lonestari str. Texas 20 U23211
AB022101.2 gg_id:4288 Borrelia sinica str. CMN3 AB0221
D67024.1 gg_id:4215 Borrelia turdi str. Ac502 D67024
AB113315.1 gg_id:104671 Borrelia duttonii VS4 AB1133
X85189.1 gg_id:4157 Borrelia burgdorferi str. 272 X85189

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EU246071.1 gg_id:240820 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-P2-G11 EU246
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FM242277.1 gg_id:320359 sequences sediment clone 6bis T0h-oil FM242
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AY605171.1 gg_id:101310 microbial mat clone LH042 AY605
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AM493256.1 gg_id:348409 Multiple symbionts two species co-occurring gutless oligochaete worms Mediterrar AM493
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AB244312.1 gg_id:143685 Microbial mesophilic chemostat cultivation long-chain fatty acids-degrading methan AB2443
EU073764.1 gg_id:256394 Microbial subsurface beds and methanogenic s coal enrichment clone ObedB-2A EU0737
AF050549.1 gg_id:3966 contaminated aquifer clone WCHB1-40 AF0505
AY426468.1 gg_id:107508 full-scale anaerobic UASB bioreactor treating paper mill wastewater clone E3 AY4264
EF515259.1 gg_id:219657 Electricigen Enrichment MFC upf microbial fuel cell anode clone 22a12 EF5152
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EU245482.1 gg_id:255522 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M2-B0 EU245
AB177323.1 gg_id:128374 seafloor methane hydrate clone ODP1251B20.23 AB177
FJ516894.1 gg_id:548153 semiarid 'Tablas de Daimiel National Park' wetland (Central Spain) unravelled upper s FJ5168
AY605142.1 gg_id:104169 microbial mat clone IE071 AY605
NR_027585.1 gg_id:560417 Spirochaeta smaragdinae str. SEBR 4228; DSM 11293 NR_02
FJ203346.1 gg_id:320773 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h FJ2033
AB088873.1 gg_id:77729 termite gut homogenate clone Rs-D16 sp. AB088
EU245577.1 gg_id:237886 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M3-C0 EU245
EU245839.1 gg_id:242567 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M7-A1 EU245
AY605137.1 gg_id:99854 microbial mat clone IE046 AY605
AY605176.1 gg_id:102131 microbial mat clone LH079 AY605
AY605141.1 gg_id:104007 microbial mat clone IE070 AY605
GU117988.1 gg_id:577654 Threatened Corals Provide Microbial Habitats clone Acer_D05 GU117
FM242378.1 gg_id:306448 sequences sediment clone 78 T9d+oil FM242
EU245233.1 gg_id:251576 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-H4-E05 EU245
AM236337.1 gg_id:168305 Evidence chemoautotrophic symbiosis Mediterranean cold seep clam (Bivalvia: Luci AM236
DQ329738.1 gg_id:159150 Guerrero Negro hypersaline microbial mat clone 05D2Z88 DQ329
AF507855.1 gg_id:62701 Mono Lake at depth 23 m station 6 July 2000 clone ML623J-23 bacterium AF507
FJ462030.1 gg_id:570445 Microbial ecology industrial digestor mesophilic anaerobic reactor fed effluent chemi FJ4620
EF031095.1 gg_id:182638 Prokaryotic Tirez La Macha Spain endorheic hypersaline atalasohaline lake clone SalB EF031
AY605165.1 gg_id:105791 microbial mat clone LG016 AY605
EU245551.1 gg_id:244538 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M3-A0 EU245
AY922180.1 gg_id:112885 whalefall clone 131573 AY922
FJ203063.1 gg_id:347941 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c FJ2030
AY605131.1 gg_id:98915 microbial mat clone IE024 AY605
X97096.1 gg_id:3801 peat bog clone TM3 X97096
EU385698.1 gg_id:262150 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S EU385
EF203193.1 gg_id:212910 phylotypes sediments Lake Kastoria Greece sediment clone Kas148B EF2031
EU488038.1 gg_id:540607 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU488

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EU048676.1 gg_id:250799 and archaeal surface marine sediment Slope South China Sea clone MD2896-B17 EU0486
AY605145.1 gg_id:104643 microbial mat clone IE094 AY6051
DQ329747.1 gg_id:159087 Guerrero Negro hypersaline microbial mat clone 072DZ15 DQ329
FJ748821.1 gg_id:582122 Vertical and sulfate-reducing prokaryotes estuarine Southern China Pearl River Estuar FJ7488
X89050.1 gg_id:4043 termite hindgut clone mpsp2 X89050
AJ458944.1 gg_id:83652 Mixotricha paradoxa is flagellate hindgut Mastotermes darwiniensis clone mp1 of AJ4589
AJ458945.1 gg_id:83413 Mixotricha paradoxa is flagellate hindgut Mastotermes darwiniensis clone mp3 of AJ4589
X89052.1 gg_id:4082 termite hindgut clone mpsp16 X89052
X89044.1 gg_id:4038 termite hindgut clone sp5_18 X89044
GU432215.1 gg_id:573932 Human Oral Microbiome oral cavity GU432
FJ976389.1 gg_id:573319 Interindividual healthy human oral microbiota mouth clone 24B016 FJ9763
GU408851.1 gg_id:574066 Human Oral Microbiome oral cavity GU408
AF385536.1 gg_id:29328 swab advanced noma lesion clone BZ013 AF3855
NR_025141.1 gg_id:570521 Treponema azotonutricium str. ZAS-9; DSM 13862 NR_025
AB088874.1 gg_id:77582 termite gut homogenate clone Rs-D40 sp. AB0888
AB088888.1 gg_id:77749 termite gut homogenate clone Rs-E64 sp. AB0888
D85438.1 gg_id:3915 Treponema denticola str. ATCC33520 D85438
X87139.1 gg_id:63015 Treponema lecithinolyticum periodontitis patient PFB4G X87139
FJ204241.1 gg_id:317194 Treponema medium subsp. bovis str. T52B FJ2042
M88726.1 gg_id:3964 Treponema pallidum M8872
AF302938.1 gg_id:30574 Treponema parvum str. OMZ842 AF3029
EF061267.1 gg_id:199343 Treponema pedis str. T354A EF0612
EF061263.1 gg_id:197926 Treponema bovis str. T323C EF0612
AB088896.1 gg_id:78075 termite gut homogenate clone Rs-B05 sp. AB0888
AY571472.1 gg_id:114451 termite gut clone RsaP136 AY5714
AB231032.1 gg_id:147653 termite gut wall clone HsW01-016 AB2310
AB231029.1 gg_id:146387 termite gut wall clone HsW01-003 AB2310
AF068334.1 gg_id:4047 termite gut homogenate clone RFS11 AF0683
AF068420.1 gg_id:4099 termite gut homogenate clone RFS7 AF0684
AF093251.1 gg_id:4009 Treponema primitia str. ZAS-1 AF0932
AB088916.1 gg_id:78032 termite gut homogenate clone Rs-Q68 AB0889
DQ009704.2 gg_id:141895 termite gut homogenate clone R38A5 DQ009
AB015889.1 gg_id:3841 Treponema subsp. socranskii 128B AB0158
AB191946.1 gg_id:143013 termite gut homogenate clone M2PT2-10 AB1919
AB085159.1 gg_id:72109 termite gut clone NkS-Dev14 AB0851
EF454259.2 gg_id:222608 termite hindgut clone 290cost002-P3L-1859 EF4542
X79548.1 gg_id:4015 Spirochaeta species X79548
AJ458946.1 gg_id:86557 Mixotricha paradoxa is flagellate hindgut Mastotermes darwiniensis clone mp4 of AJ4589
EU773678.1 gg_id:342601 Capybara feces clone CAP_aai00b06 EU7736

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AF061347.1 gg_id:3931 Treponema sp. I:Q:AT20 str. AT20 AF061
AB088881.1 gg_id:78047 termite gut homogenate clone Rs-D57 sp. AB088
GQ502611.1 gg_id:582361 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf7- GQ502
AF068405.1 gg_id:4094 termite gut homogenate clone ZAS89 AF068
EF454213.1 gg_id:220388 termite hindgut clone 290cost002-P3L-1803 EF4542
EF453852.2 gg_id:218658 termite hindgut clone 290cost002-P3L-1216 EF4538
AF023029.1 gg_id:3906 Treponema sp. str. III:13:D94 AF023
AB234361.1 gg_id:150211 termite gut homogenate clone MgMjD-028 AB2343
AB192147.1 gg_id:141512 termite gut homogenate clone RsTz-89 AB192
AB192141.1 gg_id:142334 termite gut homogenate clone RsTz-84 AB192
AB231057.1 gg_id:146440 termite gut wall clone NkW01-009 AB231
EF453913.2 gg_id:218561 termite hindgut clone 290cost002-P3L-1301 EF4539
GQ502615.1 gg_id:536096 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf7- GQ502
EF454897.2 gg_id:226681 termite hindgut clone 290cost002-P3L-619 EF4548
EF454832.1 gg_id:217886 termite hindgut clone 290cost002-P3L-484 EF4548
AJ419816.1 gg_id:22449 Spirochaeta sp AJ4198
AB191964.1 gg_id:141888 termite gut homogenate clone M1NP2-77 AB1919
AB088905.1 gg_id:77877 termite gut homogenate clone Rs-A09 sp. AB0889
AB231063.1 gg_id:147373 termite gut wall clone NkW01-044 AB231
AB084952.1 gg_id:69074 termite gut clone NkS1 AB0849
EU794266.1 gg_id:346741 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_P10 EU7942
AB062832.1 gg_id:31994 termite gut homogenate clone BCf6-15 AB0628
AB360375.1 gg_id:265198 Identification endosymbiotic methanogen and ectosymbiotic spirochetes protists ter AB3603
AF068341.1 gg_id:4087 termite gut homogenate clone RFS41 AF0683
AB088901.1 gg_id:78179 termite gut homogenate clone Rs-C91 sp. AB0889
AM942448.1 gg_id:302412 Evidence multiple Treponema phylotypes involved bovine shown 16rDNA and fluore AM942
EU771469.1 gg_id:354983 Hamadryas Baboon feces clone AFBAB_aai04f02 EU7714
AY571478.1 gg_id:114784 termite gut clone RsaHf303 AY5714
AB088882.2 gg_id:77600 termite gut homogenate clone Rs-P25 sp. AB0888
AF023063.1 gg_id:3947 Treponema sp. str. I:N:D47 AF023
AF068345.1 gg_id:4049 termite gut homogenate clone CFS6 AF0683
AF371928.1 gg_id:68837 swine intestine clone p-2159-s959-3 AF3719
AB192251.1 gg_id:143974 termite gut homogenate clone RPK-14 AB1922
EF454122.2 gg_id:220481 termite hindgut clone 290cost002-P3L-1667 EF4541
EF454300.2 gg_id:223993 termite hindgut clone 290cost002-P3L-1914 EF4543
EF454181.2 gg_id:222160 termite hindgut clone 290cost002-P3L-1759 EF4541
AY212749.1 gg_id:105320 equine manure clone wet198 AY2127
EU794214.1 gg_id:316624 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_S39 EU7942
EF562545.1 gg_id:251512 stable microbial consortia capable degrading complex organic matter paper pulp colu EF5625

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AB084965.1 gg_id:74426 termite gut clone NkS50 AB084
GU408735.1 gg_id:557008 Human Oral Microbiome oral cavity GU408
AF023052.1 gg_id:3939 Treponema sp. str. I:G:C1 AF023
AF023053.1 gg_id:3940 Treponema sp. str. I:F:D13 AF023
AF023031.1 gg_id:3908 Treponema sp. str. II:C:T1 AF023
GQ502617.1 gg_id:545719 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf7- GQ502
EF454600.2 gg_id:219918 termite hindgut clone 290cost002-P3L-2386 EF4546
AB192144.1 gg_id:142525 termite gut homogenate clone RsTz-02 AB192
AM182455.1 gg_id:146784 Treponema sp. str. SPIT5 AM182
AB360374.1 gg_id:276247 Identification endosymbiotic methanogen and ectosymbiotic spirochetes protists ter AB360
AB062823.1 gg_id:48891 termite gut homogenate clone BCf4-14 AB062
EU358687.1 gg_id:313606 structure archaeal denaturing gel electrophoresis and sequencing mesophilic biogas EU358
AY735103.1 gg_id:102578 Spirochaeta taiwanensis str. K1LY AY735
AB192255.1 gg_id:143026 termite gut homogenate clone RPK-39 AB192
GQ068618.1 gg_id:417534 Topographical and Temporal Human Skin Microbiome skin nare clone nbw152g06c1 GQ068
GU408631.1 gg_id:564057 Human Oral Microbiome oral cavity GU408
AB088908.1 gg_id:78092 termite gut homogenate clone Rs-D13 sp. AB088
AB191856.1 gg_id:144192 termite gut homogenate clone M1NP1-86 AB191
AB191941.1 gg_id:143947 termite gut homogenate clone M2PT2-47 AB191
AB255896.1 gg_id:165815 Localization Cell Morphologies Members Candidate TG3 and Subphylum Phylum Fibr AB2558
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EF453804.1 gg_id:223738 termite hindgut clone 290cost002-P3L-1157 EF4538
AM980448.1 gg_id:301091 Treponema sp. PT9 PT8 AM980
AF068347.1 gg_id:4118 termite gut homogenate clone CFS121 AF0683
AB062834.1 gg_id:46398 termite gut homogenate clone BCf6-24 AB0628
AF068342.1 gg_id:3984 termite gut homogenate clone RFS6 AF0683
AB189699.1 gg_id:112977 termite gut homogenate clone Tc-69 AB189
EU472054.1 gg_id:294974 francois langur feces clone FL_1aaa01h05 EU472
GQ039064.1 gg_id:441410 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbu41 GQ039
AB191917.1 gg_id:141191 termite gut homogenate clone M2PB4-42 AB191
AB198448.1 gg_id:135888 termite gut wall fraction clone RsW01-008 AB198
AB192242.1 gg_id:141806 termite gut homogenate clone RPK-17 AB192
AB084968.1 gg_id:69543 termite gut clone NkS83 AB084
GQ502646.1 gg_id:555083 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf7- GQ502
GQ502659.1 gg_id:565920 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf7- GQ502
EU471602.1 gg_id:295386 Asiatic elephant feces clone AE1_aaa04f01 EU471
EF454215.2 gg_id:226149 termite hindgut clone 290cost002-P3L-1805 EF4542
AB088900.1 gg_id:77591 termite gut homogenate clone Rs-Q78 sp. AB088

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AB299520.1 gg_id:241126 Motility Symbiont Termite Gut Flagellate Caduceia versatilis Member 'Synergistes' G AB2995
AB231059.1 gg_id:145031 termite gut wall clone NkW01-018 AB2310
EF454250.2 gg_id:217773 termite hindgut clone 290cost002-P3L-1848 EF4542
AF068416.1 gg_id:4098 termite gut homogenate clone RFS52 AF0684
AB088894.1 gg_id:78213 termite gut homogenate clone Rs-A19 AB0888
AB231025.1 gg_id:146570 termite gut wall clone HsW01-020 AB2310
AB088891.1 gg_id:77621 termite gut homogenate clone Rs-B29 sp. AB0888
AB192151.1 gg_id:143612 termite gut homogenate clone RsTz-90 AB1921
NR_029348.1 gg_id:572161 Treponema brennaborense str. DD5/3; DSM 12168 NR_029
EU464306.1 gg_id:295712 hamadryas baboon feces clone AFBAB_aai02c04 EU4643
DQ003618.1 gg_id:124523 human mouth clone MB2_G19 DQ003
EF454942.2 gg_id:225337 termite hindgut clone 290cost002-P3L-730 EF4549
EF453933.2 gg_id:221957 termite hindgut clone 290cost002-P3L-1334 EF4539
AB191865.1 gg_id:142763 termite gut homogenate clone M2PB4-83 AB1918
GU408605.1 gg_id:562976 Human Oral Microbiome oral cavity GU408
EF454221.1 gg_id:223424 termite hindgut clone 290cost002-P3L-1811 EF4542
AB032009.1 gg_id:25824 protist termite clone HsDiSp319 clone AB0320
AB231031.1 gg_id:145132 termite gut wall clone HsW01-012 AB2310
AM420109.1 gg_id:248721 Noma subgingival plaque clone 303F01(oral) AM420
GQ502650.1 gg_id:573443 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf7- GQ502
AJ419821.1 gg_id:40667 Spirochaeta sp AJ4198
EF454883.2 gg_id:218947 termite hindgut clone 290cost002-P3L-590 EF4548
AB088911.1 gg_id:78206 termite gut homogenate clone Rs-J58 sp. AB0889
EF453968.2 gg_id:225557 termite hindgut clone 290cost002-P3L-1386 EF4539
AB231058.1 gg_id:148743 termite gut wall clone NkW01-016 AB2310
AB191854.1 gg_id:143614 termite gut homogenate clone M1PL1-31 AB1918
AY341822.1 gg_id:93141 Treponema genomosp. P1 AY3418
AF068426.1 gg_id:4127 termite gut homogenate clone RFS18 AF0684
AB299519.1 gg_id:252938 Motility Symbiont Termite Gut Flagellate Caduceia versatilis Member 'Synergistes' G AB2995
EF453971.2 gg_id:222007 termite hindgut clone 290cost002-P3L-1390 EF4539
AB084956.1 gg_id:73924 termite gut clone NkS8 AB0849
AF068346.1 gg_id:4117 termite gut homogenate clone CFS124 AF0683
EU748341.1 gg_id:339907 neotropical folivorous flying bird adult hoatzin crop clone hoa5_07h09 EU7483
AB255898.1 gg_id:171504 Localization Cell Morphologies Members Candidate TG3 and Subphylum Phylum Fibr AB2558
EF454202.2 gg_id:227383 termite hindgut clone 290cost002-P3L-1791 EF4542
AM420288.1 gg_id:239628 Noma subgingival plaque clone 703018(oral) AM420
AB541984.1 gg_id:585733 Spirochaeta stenostrepta str. JCM 16534 AB5419
AF023051.1 gg_id:3938 Treponema sp. str. I:B:C7 AF0230
AB191908.1 gg_id:142284 termite gut homogenate clone M1NP1-85 AB1919
DQ065758.1 gg_id:134428 Treponema zioleckii str. kT DQ065
EF454917.2 gg_id:221675 termite hindgut clone 290cost002-P3L-663 EF4549

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AB191817.1 gg_id:141230 termite gut homogenate clone M1PT4-88 AB1918
AB231061.1 gg_id:149915 termite gut wall clone NkW01-037 AB2310
AY518274.1 gg_id:104346 Treponema sp. str. 14V28 AY5182
AY178844.1 gg_id:104881 Treponema sp. str. Sy24 AY1788
GQ502618.1 gg_id:536459 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf7- GQ502
AB192139.1 gg_id:142969 termite gut homogenate clone RsTz-33 AB1921
EF453877.2 gg_id:227094 termite hindgut clone 290cost002-P3L-1254 EF4538
AB062839.1 gg_id:27323 termite gut homogenate clone BCf7-24 AB0628
AY369252.1 gg_id:94775 Treponema vincentii str. OMZ 861 AY3692
AF182831.1 gg_id:3955 Treponema sp. str. I:V:AU076 AF1828
AB062840.1 gg_id:38586 termite gut homogenate clone BCf8-03 AB0628
EU473593.1 gg_id:299900 Somali wild ass feces clone WA_aaa02d10 EU4735
EF454129.2 gg_id:226390 termite hindgut clone 290cost002-P3L-1681 EF4541
AB198654.1 gg_id:135860 termite gut fluid and protists fraction clone RsC01-085 AB1986
AM980447.1 gg_id:299619 Treponema sp. PT8 AM980
AY369247.1 gg_id:95168 Treponema sp. str. OMZ 839 AY3692
EF453952.2 gg_id:220850 termite hindgut clone 290cost002-P3L-1363 EF4539
EF454455.2 gg_id:227278 termite hindgut clone 290cost002-P3L-2160 EF4544
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GQ502639.1 gg_id:536207 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf7- GQ502
AB255894.1 gg_id:162987 Localization Cell Morphologies Members Candidate TG3 and Subphylum Phylum Fibr AB2558
FJ976308.1 gg_id:558616 Interindividual healthy human oral microbiota mouth clone 10B549 FJ9763
GQ502652.1 gg_id:591066 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf7- GQ502
AY571470.1 gg_id:114589 termite gut clone RsaHf241 AY5714
AB085158.1 gg_id:72963 termite gut clone NkS-Dev1 AB0851
AB243262.1 gg_id:149532 acetone-preserved termite gut clone M2PB4a-025 AB2432
DQ307690.1 gg_id:144644 termite intestinal tract clone MTG-91 DQ307
GU304073.1 gg_id:541314 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU304
EF454406.2 gg_id:222609 termite hindgut clone 290cost002-P3L-2077 EF4544
EF453999.2 gg_id:226973 termite hindgut clone 290cost002-P3L-1424 EF4539
EF454271.2 gg_id:225517 termite hindgut clone 290cost002-P3L-1873 EF4542
AB084973.1 gg_id:73490 termite gut clone NkS97 AB0849
AB191834.1 gg_id:141753 termite gut homogenate clone M1PT4-49 AB1918
AB191848.1 gg_id:142623 termite gut homogenate clone M1NP1-75 AB1918
AB088915.1 gg_id:78017 termite gut homogenate clone Rs-Q13 sp. AB0889
AF068423.1 gg_id:4053 termite gut homogenate clone RFS94 AF0684
AB085166.1 gg_id:69238 termite gut clone NkS-Oxy25 AB0851
GQ502657.1 gg_id:589527 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf7- GQ502
DQ003625.1 gg_id:121373 human mouth clone MB4_G11 DQ003
AF357565.1 gg_id:71422 mpn-isolate group 17 AF3575

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AB191824.1 gg_id:143359 termite gut homogenate clone M1NP1-15 AB191
AB192253.1 gg_id:143938 termite gut homogenate clone RPK-33 AB192
GQ502658.1 gg_id:590884 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf7- GQ502
GQ422733.1 gg_id:565720 Human Oral Microbiome dental plaque GQ422
AY005081.1 gg_id:45933 subgingival dental plaque clone AF068 AY005
AB191928.1 gg_id:144853 termite gut homogenate clone M1PL1-51 AB191
EU464271.1 gg_id:302795 hamadryas baboon feces clone AFBAB_aai01e01 EU464
EU794206.1 gg_id:324511 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_N44 EU794
AB088903.1 gg_id:77948 termite gut homogenate clone Rs-E21 sp. AB088
GQ039162.1 gg_id:400332 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbu41 GQ039
AB191968.1 gg_id:141054 termite gut homogenate clone M1NP2-94 AB191
EU471558.1 gg_id:291957 Asiatic elephant feces clone AE1_aaa04b06 EU471
AF068336.1 gg_id:4116 termite gut homogenate clone RFS15 AF068
GQ502644.1 gg_id:543504 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf7- GQ502
GQ502653.1 gg_id:547244 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf7- GQ502
AM420275.1 gg_id:240104 Noma subgingival plaque clone 702D05(oral) AM420
AY134898.1 gg_id:59569 oral periodontitis clone EX137 AY134
AB062768.1 gg_id:21434 termite gut homogenate clone BCf1-01 AB062
AF182836.1 gg_id:3922 Treponema sp. str. 3:E:AT013 AF182
GU408692.1 gg_id:546393 Human Oral Microbiome oral cavity GU408
AB088889.1 gg_id:78084 termite gut homogenate clone Rs-A43 sp. AB088
GU428680.1 gg_id:538832 Human Oral Microbiome oral cavity GU428
AB084969.1 gg_id:70817 termite gut clone NkS85 AB084
AB234367.1 gg_id:146849 termite gut homogenate clone MgMjD-036 AB234
AB191868.1 gg_id:144495 termite gut homogenate clone M2PT2-95 AB191
AB032000.1 gg_id:36987 protist termite clone HsPySp16 clone AB032
EF454895.2 gg_id:226214 termite hindgut clone 290cost002-P3L-616 EF454
AB234372.1 gg_id:148779 termite gut homogenate clone MgMjR-079 AB234
AB085163.1 gg_id:70117 termite gut clone NkS-Oxy1 AB085
AB084955.1 gg_id:69510 termite gut clone NkS7 AB084
GQ502640.1 gg_id:539398 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf7- GQ502
AB192247.1 gg_id:143443 termite gut homogenate clone RPK-13 AB192
AB084954.1 gg_id:74331 termite gut clone NkS5 AB084
EF559163.1 gg_id:220887 mesophilic anaerobic digester clone G35_D8_L_B_C07 EF559
GQ502642.1 gg_id:584558 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf7- GQ502
GQ426550.1 gg_id:552289 Treponema sp. str. S GQ426
AF275918.1 gg_id:46681 anaerobic digester clone AA14 AF275
AB191836.1 gg_id:143094 termite gut homogenate clone M1NP1-56 AB191
AB088880.1 gg_id:77953 termite gut homogenate clone Rs-B10 sp. AB088
AY337320.1 gg_id:106877 Spirochaeta sp. str. B AY337

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AY337319.1 gg_id:103241 Spirochaeta sp. str. M6 AY3373
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AF166259.1 gg_id:37803 Spironema culicis str. BR91 AF166
EU448140.1 gg_id:266509 Spirochaeta sp. str. SIP1 EU448
EU245914.1 gg_id:251213 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M8-B0 EU245
AB192150.1 gg_id:142321 termite gut homogenate clone RsTz-71 AB192
GQ406200.1 gg_id:583561 Benthic submerged sinkhole ecosystems sediment clone -45-14 GQ406
AB088897.1 gg_id:77774 termite gut homogenate clone Rs-B68 sp. AB088
EU385774.1 gg_id:273317 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S EU385
EU245152.1 gg_id:240123 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-H3-B03 EU245
GU139329.1 gg_id:593443 lactate formate propionate hydrogen donors reductive dehalogenation trichloroeth GU139
GU139313.1 gg_id:542335 lactate formate propionate hydrogen donors reductive dehalogenation trichloroeth GU139
EF602483.1 gg_id:233469 metabolic phylum Planctomycetes anaerobic sulfide and sulfur-rich spring (Zodletone EF6024
AJ278165.1 gg_id:65483 anaerobic bioreactor clone SHA-116 AJ2781
AF286040.1 gg_id:51888 saltmarsh clone LCP-5 AF286
CU918232.1 gg_id:568533 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU918
AB248650.1 gg_id:146622 mesophilic anaerobic butyrate-degrading reactor clone BHB21 AB248
CU918313.1 gg_id:562644 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU918
CU918359.1 gg_id:540776 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU918
EU887773.1 gg_id:336104 and RFLP anaerobes Nisargruna biogas plant anaerobic digester clone 8SN EU887
FJ825527.1 gg_id:561904 Microbial during start-up mesophilic biogas plant clone 42B_BS1_4 FJ8255
EF515598.1 gg_id:222084 Electricigen Enrichment MFC full-scale anaerobic bioreactor sludge treating brewery EF5155
CU917471.1 gg_id:560582 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU917
EU639140.1 gg_id:356001 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU639
CT574476.1 gg_id:154406 major candidate division within anaerobic sludge digester Evry municipal wastewate CT5744
CR933095.1 gg_id:110532 municipal wastewater treatment plant clone 029C09_P_DI_P15 CR933
CT574479.1 gg_id:150885 major candidate division within anaerobic sludge digester Evry municipal wastewate CT5744
CT574480.1 gg_id:153806 major candidate division within anaerobic sludge digester Evry municipal wastewate CT5744
EU638532.1 gg_id:348562 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU638
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EU639264.1 gg_id:339506 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU639
GQ461620.1 gg_id:567190 Coupling -ITS Clone Libraries and Automated Intergenic Spacer Microbial TCE Bioren GQ461

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CU927274.1 gg_id:539547 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU927
AB175393.1 gg_id:99923 mesophilic anaerobic BSA digester clone BSA2B-21 AB1753
EU864445.1 gg_id:335847 structures under selection pressure levels antibiotics Xiao River receiving treated ox EU8644
CU923797.1 gg_id:567700 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU923
AB513440.1 gg_id:566297 Removal dioxins semi-aerobic fed-batch composting biostimulation 'Dehalococcoide AB5134
AJ306785.1 gg_id:66916 DCP-dechlorinating consortium clone SHA-4 AJ3067
AY426469.1 gg_id:107649 full-scale anaerobic UASB bioreactor treating paper mill wastewater clone E30 AY4264
EF602475.1 gg_id:256047 metabolic planctomycetes anaerobic sulfide- and sulfur-rich zodletone spring oklaho EF6024
EF602476.1 gg_id:227609 metabolic phylum Planctomycetes anaerobic sulfide and sulfur-rich spring (Zodletone EF6024
EU381859.1 gg_id:271582 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU3818
EU474681.1 gg_id:290320 Indian rhinoceros feces clone IR_aaa02b12 EU4746
AB231045.1 gg_id:203507 termite gut wall clone HsW01-043 AB2310
EU283584.1 gg_id:278222 Model Early Earth Harbors Deeply Divergent Divisions Anderson Lake clone A1104 EU2835
EU101271.1 gg_id:242859 Sulfide/oxygen supply ratio predicts outcome competition among sulfur-oxidizing wa EU1012
EU681994.1 gg_id:287458 microflora imbalances intestine dogs inflammatory bowel disease duodenum health EU6819
AF255601.1 gg_id:74652 hot spring clone SRI-24 AF2556
EU635940.1 gg_id:278855 Microbiology geochemistry great boiling and mud springs sediment hot spring; temp EU6359
CU926426.1 gg_id:573323 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU9264
CU926777.1 gg_id:558738 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU9267
AF129869.1 gg_id:1641 anaerobic digestor clone BB48 AF1298
NZ_ACJX02000009.1 gg_id:484357 Anaerobaculum hydrogeniformans str. ATCC BAA-1850 NZ_AC
EU878334.1 gg_id:565884 Investigation factors influencing production large-scale municipal biogas plant therm EU8783
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U50711.1 gg_id:1634 Anaerobaculum thermoterrnum U50711
EU639374.1 gg_id:343828 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU6393
EU276415.1 gg_id:290298 Anaerobaculum thermoterrnum str. YWT-2 EU2764
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GU357466.1 gg_id:574739 Crude biodegraded under thermophilic conditions methanogenic consortia enriched GU357
AB175377.1 gg_id:99359 mesophilic anaerobic BSA digester clone BSA2B-05 AB1753
EU234248.1 gg_id:249038 river and un techniques downstream Wang Yang River receiving penicillin G producti EU2342
AF069287.1 gg_id:1649 Aminobacterium colombiense AF0692
EF559198.1 gg_id:218020 mesophilic anaerobic digester clone A35_D28_L_B_E01 EF5591
AF234542.1 gg_id:71455 Dethiosulfovibrio marinus str. sr12; DSM 12538 AF2345
AY005466.1 gg_id:72749 Dethiosulfovibrio acidaminovorans str. sr15 (DSM 12590) AY0054
CU917598.1 gg_id:543835 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU9175
AY953224.1 gg_id:114635 anaerobic swine lagoon clone A-2G AY9532
CU925573.1 gg_id:553988 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU9255
EF436500.1 gg_id:204216 Jonquetella anthropi str. ADV126 EF4365
CU920428.1 gg_id:539058 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU9204
EU462629.1 gg_id:302106 Sumatran orangutan feces clone orang2_aai66c11 EU4626

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AB288913.1 gg_id:199975 termite gut homogenate clone BOf7-16 AB288
DQ085087.1 gg_id:132438 goat rumen clone A13 DQ085
AF125200.1 gg_id:1643 oral cavity clone D084 AF1252
AF125199.2 gg_id:1642 oral cavity clone BH017 AF1251
GU410680.1 gg_id:540821 Human Oral Microbiome oral cavity clone _D059 GU410
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AB062836.1 gg_id:38526 termite gut homogenate clone BCf7-04 AB0628
AB192113.1 gg_id:142452 termite gut homogenate clone M2PB4-76 AB1921
AB192116.1 gg_id:143824 termite gut homogenate clone M1PL1-68 AB1921
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AB192115.1 gg_id:144260 termite gut homogenate clone M1PL1-49 AB1921
AB231081.1 gg_id:146679 termite gut wall clone NkW01-046 AB2310
AB189694.1 gg_id:113993 termite gut homogenate clone Tc-61 AB1896
AB299558.1 gg_id:237398 Motility Symbiont Termite Gut Flagellate Caduceia versatilis Member 'Synergistes' G AB2995
CU463952.1 gg_id:276742 Cloacibacillus evryensis str. 158 CU4639
EF551160.1 gg_id:230271 Synergistes sp. NML96A088 EF5511
DQ412721.1 gg_id:162959 Synergistes sp. str. RMA 16290 DQ412
CP001818.1 gg_id:523250 Thermanaerovibrio acidaminovorans str. DSM 6589 CP0018
CU927653.1 gg_id:568704 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU927
CU924623.1 gg_id:558424 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU924
EU234149.1 gg_id:247916 receiving river and un techniques anaerobic process WWTP treating penicillin G prod EU2341
CU919451.1 gg_id:575488 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU9194
EU471574.1 gg_id:296843 Asiatic elephant feces clone AE1_aaa01b03 EU4715
CU920720.1 gg_id:536647 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU9207
EU471563.1 gg_id:290654 Asiatic elephant feces clone AE1_aaa04b01 EU4715
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CU923733.1 gg_id:575163 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU9237
CT573946.1 gg_id:156047 Evry municipal wastewater treatment plant clone 009G09_B_SD_P15 CT5739
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CU925055.1 gg_id:568648 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU9250
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CU927313.1 gg_id:571181 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU9273
GQ377129.1 gg_id:547330 structure two reactive PCE degrading enrichment s stimulated OU Duck Pond Norm GQ377
CU920532.1 gg_id:559188 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU9205
CU924981.1 gg_id:573012 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU9249
CU919042.1 gg_id:563832 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU9190
AM933660.1 gg_id:276480 Enrichment dioxin-dehalogenating two-liquid phase s anaerobic enrichment clone M AM933

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EU721809.1 gg_id:568879 microbial production water Alaskan mesothermic petroleum reservoir two methods EU721
AB195868.1 gg_id:109151 Anaerobic sludge clone N42 AB195
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AB175356.1 gg_id:107021 mesophilic anaerobic BSA digester clone BSA1B-02 AB1753
EU887988.1 gg_id:329262 Microbial structure hydrolytic stage two-stage anaerobic digestion grass silage leach EU887
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EU504523.1 gg_id:273270 cecal contents Mus musculus strain C57BL/6J; myd1 clone myd1_aaa01g09
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EU509052.1 gg_id:258746 cecal contents Mus musculus strain C57BL/6J; MD7 clone MD7_aap42f09 EU509
EU509587.1 gg_id:270157 cecal contents Mus musculus strain C57BL/6J; WD10 clone WD10_aak45c10 EU509
EU511456.1 gg_id:274825 cecal contents Mus musculus strain C57BL/6J; WD8 clone WD8_aak20f03 EU511
EU507812.1 gg_id:277029 cecal contents Mus musculus strain C57BL/6J; MD24 clone MD24_aaa01c03 EU507
EU511344.1 gg_id:276457 cecal contents Mus musculus strain C57BL/6J; WD8 clone WD8_aak18g01 EU511
EU508445.1 gg_id:263759 cecal contents Mus musculus strain C57BL/6J; MD2 clone MD2_aap33f03 EU508
EU505392.1 gg_id:259805 cecal contents Mus musculus strain C57BL/6J; myd4 clone myd4_aaa03g02 EU505
EU508551.1 gg_id:261932 cecal contents Mus musculus strain C57BL/6J; MD2 clone MD2_aap35c06 EU508
EU505649.1 gg_id:261890 cecal contents Mus musculus strain C57BL/6J; myd5 clone myd5_aaa04a10 EU505
EU511197.1 gg_id:273662 cecal contents Mus musculus strain C57BL/6J; WD7 clone WD7_aal04c05 EU511
AJ417075.1 gg_id:98789 Allobaculum stercoricanis str. DSM 13632T AJ417
FJ880109.1 gg_id:404034 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8801
FJ880453.1 gg_id:385422 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8804
FJ881278.1 gg_id:371453 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8812
FJ880804.1 gg_id:438839 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8808
FJ879085.1 gg_id:454212 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8790
FJ881066.1 gg_id:443722 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8810
DQ113686.1 gg_id:134101 dog colon clone C5-42 DQ113
FJ881120.1 gg_id:389961 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8811
FJ879538.1 gg_id:396494 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8795
EU503550.1 gg_id:260405 cecal contents Mus musculus strain C57BL/6J; CRWD2 clone CRWD2_aaa01a12 EU503
FJ880589.1 gg_id:393599 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8805
FJ880248.1 gg_id:409717 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8802
FJ879685.1 gg_id:386583 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8796
FJ881144.1 gg_id:425371 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8811
AB018187.1 gg_id:42372 Eubacterium cylindroides str. JCM 7787 AB018
FJ681704.1 gg_id:529292 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6817
FJ681342.1 gg_id:528410 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6813
DQ805198.1 gg_id:193516 human fecal clone RL249_aaj82h06 DQ805
EU467401.1 gg_id:297126 chimpanzee feces clone CHIMP12_c08_1 EU467
FJ683962.1 gg_id:528905 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6839
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DQ325889.1 gg_id:150312 Metagenomic gut microbiome healthy human stool clone B703 DQ325
DQ325904.1 gg_id:148077 Metagenomic gut microbiome healthy human stool clone B725 DQ325
DQ796045.1 gg_id:190736 human fecal clone RL202_aai50f11 DQ796
DQ801091.1 gg_id:194446 human fecal clone RL387_aao92a09 DQ801
DQ796640.1 gg_id:195652 human fecal clone RL179aan76d10 DQ796
DQ796955.1 gg_id:184237 human fecal clone RL179_aao56h09 DQ796
FJ673811.1 gg_id:526513 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6738
FJ675938.1 gg_id:521444 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6759

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FJ674214.1 gg_id:522991 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6742
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DQ325818.1 gg_id:150015 Metagenomic gut microbiome healthy human stool clone B551 DQ325
DQ325686.1 gg_id:147618 Metagenomic gut microbiome healthy human stool clone B287 DQ325
DQ796023.1 gg_id:198115 human fecal clone RL202_aai50d06 DQ796
DQ810113.1 gg_id:178347 human fecal clone RL184_aao68c01 DQ810
FJ677579.1 gg_id:529596 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6775
FJ672990.1 gg_id:522129 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6729
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EU467482.1 gg_id:292065 Sumatran orangutan feces clone orang1_h04_1 EU467
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DQ326393.1 gg_id:150448 Metagenomic gut microbiome healthy human stool clone C428 DQ326
DQ326047.1 gg_id:148356 Metagenomic gut microbiome healthy human stool clone BA25 DQ326
EU762827.1 gg_id:342647 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU762
EU474482.1 gg_id:296794 bighorn sheep feces clone BHSD_aaa04h07 EU474
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Z36271.1 gg_id:15722 Bulleidia extructa str. 1365 Z36271
AF220064.1 gg_id:31844 Bulleidia extructa str. DSM 13220 AF220
FJ833972.1 gg_id:542406 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P2Q202_46F06 FJ8339
EU776314.1 gg_id:323045 Red Kangaroo feces clone KO1_aai41a05 EU776
AB218311.1 gg_id:146880 Fecal microbial (dugong dugon) determined genes Dugong feces clone dgA-88 AB218
DQ325832.1 gg_id:147485 Metagenomic gut microbiome healthy human stool clone B577 DQ325
FJ832913.1 gg_id:559793 Microbial Ecology Crop Folivorous Hoatzin crop contents clone A1Q101_08H01 FJ8329
EU467125.1 gg_id:302200 mongoose lemur feces clone ML_aae88h01 EU467
FJ832594.1 gg_id:584753 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P3Q302_12D02 FJ8325
FJ833018.1 gg_id:576628 Microbial Ecology Crop Folivorous Hoatzin crop contents clone A1Q102_85E11 FJ8330
EU462550.1 gg_id:297719 Sumatran orangutan feces clone orang2_aai65a01 EU462
FJ832520.1 gg_id:537476 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P3Q201_73A10 FJ8325
AB031056.1 gg_id:21980 Bulleidia moorei str. JCM 10645 RCA59-74 AB031
EU774283.1 gg_id:340869 Chimpanzee feces clone CHIMP1_a07_1 EU774
EU344272.1 gg_id:275128 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU344
EU344303.1 gg_id:260783 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU344
FJ976219.1 gg_id:582816 Interindividual healthy human oral microbiota mouth clone 3688 FJ9762
AF371517.1 gg_id:54730 swine intestine clone p-2772-24E5 AF371
EU344300.1 gg_id:259168 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU344
DQ015346.1 gg_id:132391 mouse cecum clone M2_1g10_3 DQ015
AB030223.1 gg_id:33198 Catenibacterium mitsuokai str. JCM 10608 AB030
AB030222.1 gg_id:27171 Catenibacterium mitsuokai str. JCM 10607 AB030
AB030225.1 gg_id:21138 Catenibacterium mitsuokai str. JCM 10610 AB030
AB030221.1 gg_id:46764 Catenibacterium mitsuokai str. JCM 10606 AB030

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AB030226.1 gg_id:40839 Catenibacterium mitsuokai str. JCM 10611 AB030
DQ326116.1 gg_id:145343 Metagenomic gut microbiome healthy human stool clone BB76 DQ326
DQ326286.1 gg_id:145169 Metagenomic gut microbiome healthy human stool clone C247 DQ326
DQ325906.1 gg_id:150498 Metagenomic gut microbiome healthy human stool clone B730 DQ325
DQ325656.1 gg_id:150173 Metagenomic gut microbiome healthy human stool clone B225 DQ325
EU773418.1 gg_id:309852 Black lemur feces clone BKLE_g06_1 EU773
EU461777.1 gg_id:287510 mongoose lemur feces clone ML_aaj28g12 EU461
DQ325879.1 gg_id:146207 Metagenomic gut microbiome healthy human stool clone B679 DQ325
EU469507.1 gg_id:289377 black lemur feces clone BKLE_b06_2 EU469
EU459789.1 gg_id:295705 ring-tailed lemur feces clone RT_aai12h06 EU459
AY978040.1 gg_id:122153 human cecum mucosal biopsy clone LH84 AY978
EU530322.1 gg_id:274970 mucosa adherent and invasive microbes profile adenoma colorectal cancer clone M4 EU530
AY978152.1 gg_id:125309 human cecum mucosal biopsy clone LJ38 AY978
NZ_ACCK01000460.1 gg_id:469918 Catenibacterium mitsuokai str. DSM 15897 NZ_AC
EU469487.1 gg_id:298026 black lemur feces clone BKLE_g01_1 EU469
DQ325735.1 gg_id:146738 Metagenomic gut microbiome healthy human stool clone B383 DQ325
AY976273.1 gg_id:124283 human ascending colon mucosal biopsy clone LX20 AY976
DQ326095.1 gg_id:145882 Metagenomic gut microbiome healthy human stool clone BB39 DQ326
NR_026495.1 gg_id:550248 Clostridium cocleatum str. I50; DSM 1551 NR_02
NR_029247.1 gg_id:590150 Clostridium ramosum str. 113-1; DSM 1402 NR_02
EU462941.1 gg_id:300521 southern three-banded armadillo feces clone arma_aaj55d03 EU462
NZ_ABIK02000003.1 gg_id:259777 Clostridium spiroforme str. DSM 1552 NZ_AB
ABIK02000013.1 gg_id:270245 Clostridium spiroforme str. DSM 1552 ABIK02
X75908.1 gg_id:15715 Clostridium spiroforme str. ATCC 29900 X75908
X73441.1 gg_id:15716 Clostridium spiroforme str. DSM 1552 X73441
DQ825115.1 gg_id:193907 human fecal clone RL185_aan85e10 DQ825
FJ673628.1 gg_id:528507 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6736
DQ100445.1 gg_id:142563 Clostridium sp. str. SDG-Mt85-3Db DQ100
AJ576394.1 gg_id:100232 midgut homogenate Pachnoda ephippiata larva clone PeM34 AJ5763
GQ897372.1 gg_id:571478 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do GQ897
EU542496.1 gg_id:274239 Effects chemical structure concentration on pathways microbial during dechlorinatio EU542
FJ364978.1 gg_id:368625 feces adult twins and mothers; TS1 clone TS1_a01d09 FJ3649
DQ808012.1 gg_id:199138 human fecal clone RL180_aan70f06 DQ808
AB288920.1 gg_id:200664 termite gut homogenate clone BOf9-07 AB288
DQ793967.1 gg_id:187634 human fecal clone RL176_aah45h09 DQ793
FJ365022.1 gg_id:368528 feces adult twins and mothers; TS1 clone TS1_a01h09 FJ3650
DQ326867.1 gg_id:149994 Metagenomic gut microbiome healthy human stool clone E349 DQ326
FJ363684.1 gg_id:357024 feces adult twins and mothers; TS14 clone TS14_a02b01 FJ3636
FJ676587.1 gg_id:516871 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6765
EU134663.1 gg_id:251385 tallgrass prarie soil clone FFCH17703 EU134
FJ678331.1 gg_id:515661 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6783

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DQ794080.1 gg_id:183083 human fecal clone RL176_aan57g03 DQ794
AY982801.1 gg_id:115534 human descending colon mucosal biopsy clone KZ46 AY982
FJ677018.1 gg_id:516022 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6770
DQ441352.1 gg_id:191030 human intestinal biopsy clone CD101 DQ441
DQ057480.1 gg_id:136526 str. ic1391 DQ057
GQ492588.1 gg_id:580597 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
DQ798465.1 gg_id:181284 human fecal clone RL181_aan97a10 DQ798
FJ679216.1 gg_id:521524 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6792
FJ678731.1 gg_id:514684 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6787
GQ898739.1 gg_id:570735 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do GQ898
GQ491637.1 gg_id:588666 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
EF071177.1 gg_id:190872 library survey and quantitative measurement major mucosa- IBD human colonic muc EF0711
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AY975735.1 gg_id:116787 human ascending colon mucosal biopsy clone Y182 AY975
DQ797930.1 gg_id:180338 human fecal clone RL302_aal93e08 DQ797
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FJ371039.1 gg_id:370335 feces adult twins and mothers; TS5 clone TS5_a04c01 FJ3710
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GQ046231.1 gg_id:427628 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw GQ046
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FJ370764.1 gg_id:362087 feces adult twins and mothers; TS5 clone TS5_a01a04 FJ3707
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FJ368229.1 gg_id:358899 feces adult twins and mothers; TS3 clone TS3_a01g05 FJ3682
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FJ370922.1 gg_id:358586 feces adult twins and mothers; TS5 clone TS5_a02h01 FJ3709
AM277455.2 gg_id:229069 fecal microbiota irritable bowel syndrome patients significantly that healthy subject AM277
DQ804182.1 gg_id:198054 human fecal clone RL187_aah69h03 DQ804
GQ492759.1 gg_id:587530 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
DQ440561.1 gg_id:156898 Clostridium innocuum str. Ulm 12 DQ440
GQ492977.1 gg_id:586813 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
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DQ803568.1 gg_id:177504 human fecal clone RL251_aaj87e08 DQ803

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GQ448197.1 gg_id:585386 Microbiome neonatal calves: shedding microorganisms fecal clone calf32_6wks_grp GQ448
GQ175408.1 gg_id:509861 Chicken intestinal microbiota modulations various feed supplementations DGGE anc GQ175
AM275546.2 gg_id:231985 fecal microbiota irritable bowel syndrome patients significantly that healthy subject AM275
FJ368343.1 gg_id:368662 feces adult twins and mothers; TS3 clone TS3_a03b11 FJ3683
AM275478.2 gg_id:233953 fecal microbiota irritable bowel syndrome patients significantly that healthy subject AM275
DQ801017.1 gg_id:191700 human fecal clone RL387_aao91a01 DQ801
EU507257.1 gg_id:276227 cecal contents Mus musculus strain C57BL/6J; MD22 clone MD22_aaa04e02 EU507
FJ676717.1 gg_id:510237 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6767
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FJ680914.1 gg_id:515268 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6809
FJ681460.1 gg_id:519377 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6814
FJ681610.1 gg_id:512366 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6816
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AB540983.1 gg_id:581050 Erysipelothrix tonsillarum str. JCM 8533 AB540
AJ550617.1 gg_id:88075 Erysipelothrix inopinata str. 143-02 AJ5506
EU748014.1 gg_id:306059 neotropical folivorous flying bird adult hoatzin crop clone hoa12_36D05 EU748
Y11466.1 gg_id:15728 Holdemania filiformis str. ATCC 51649 Y11466
FJ369019.1 gg_id:367215 feces adult twins and mothers; TS4 clone TS4_a03c12 FJ3690
EU761816.1 gg_id:341803 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1 EU7618
FJ371255.1 gg_id:366464 feces adult twins and mothers; TS6 clone TS6_a02g10 FJ3712
EU461496.1 gg_id:296385 black rhinoceros feces clone RH_aaj91a04 EU461
FJ833665.1 gg_id:583224 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J1Q402_90B12 FJ8336
EU471859.1 gg_id:292053 Asiatic elephant feces clone AE3_aaa04h07 EU4718
FJ364883.1 gg_id:356807 feces adult twins and mothers; TS19 clone TS19_a04c08 FJ3648
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EU470295.1 gg_id:293994 Grevy's zebra feces clone GZ_aaa03h02 EU470
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EU470473.1 gg_id:299480 Grevy's zebra feces clone GZ_aaa01g09 EU470
EU462969.1 gg_id:297568 southern three-banded armadillo feces clone arma_aaj55h06 EU462
EU467550.1 gg_id:294524 southern three-banded armadillo feces clone arma_h07 EU467
AJ629069.1 gg_id:188919 Eubacterium sp. Pei061 AJ6290
AY953174.1 gg_id:114580 anaerobic swine lagoon clone B-1F AY953
EU981243.1 gg_id:332976 sulfate reducing living bench scale aquifer packed bed clone D7_FB EU981
FJ382687.1 gg_id:562083 Potentially pathogenic and air stem cell transplant summer hospital shower water BN FJ3826
EU104057.1 gg_id:355578 Evidence Comamonadaceae determinants settling performance activated sludge clo EU104
FJ382255.1 gg_id:513876 Potentially pathogenic and air stem cell transplant summer hospital shower water BN FJ3822
AY297808.1 gg_id:89878 waterlogged archaeological wood clone pACH93 AY2978

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AY953244.1 gg_id:114755 anaerobic swine lagoon clone B-4D AY953
FM178530.1 gg_id:350518 Monitoring abundance and expression 'dehalococcoides' species chloroethene-redu FM178
AB210825.1 gg_id:168842 Lactobacillus vitulinus str. JCM 1143 AB210
EU458708.1 gg_id:300437 Goeldi's marmoset feces clone CAL_g06 EU458
EU458757.1 gg_id:289892 Goeldi's marmoset feces clone CAL_e12_1 EU458
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AB192060.1 gg_id:200153 termite gut homogenate clone M2PT2-44 AB192
AB018186.1 gg_id:49837 Eubacterium cylindroides str. JCM 7786 AB018
FJ371145.1 gg_id:360344 feces adult twins and mothers; TS6 clone TS6_a01e02 FJ3711
DQ353903.1 gg_id:148303 Fecal Wild Gorilla (Gorilla beringei) wild gorilla feces clone Z5 DQ353
GQ016276.1 gg_id:493391 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw GQ016
AF371514.1 gg_id:49369 swine intestine clone p-1763-b3 AF3715
EU510761.1 gg_id:276677 cecal contents Mus musculus strain C57BL/6J; WD5 clone WD5_aak40h01 EU510
AM405127.2 gg_id:565289 percent G+C fraction libraries number Actinobacteria human faecal clone AP11K.78 AM405
EU461077.1 gg_id:288677 red kangaroo feces clone KO1_aai43g04 EU461
EU458788.1 gg_id:289655 Goeldi's marmoset feces clone CAL_e07_2 EU458
GQ175443.1 gg_id:539382 Chicken intestinal microbiota modulations various feed supplementations DGGE anc GQ175
EU504762.1 gg_id:262375 cecal contents Mus musculus strain C57BL/6J; myd2 clone myd2_aaa01g05 EU504
L34683.1 gg_id:15729 Eubacterium tortuosum L34683
EF071180.1 gg_id:195355 library survey and quantitative measurement major mucosa- IBD human colonic muc EF0711
EU850490.1 gg_id:346727 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF257 EU850
AB009222.1 gg_id:15714 rumen clone RFN74 bacterium AB009
EU009857.1 gg_id:256237 intestinal microbiota domestic and wild turkeys turkey cecum clone WTB_Y12 EU009
GQ377117.1 gg_id:585892 structure two reactive PCE degrading enrichment s stimulated OU Duck Pond Norm GQ377
EU459459.1 gg_id:294991 capybara feces clone CAP_aah97e09 EU459
CU922014.1 gg_id:541244 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU922
EU009820.1 gg_id:248473 intestinal microbiota domestic and wild turkeys turkey cecum clone WTB_J26 EU009
EU407216.1 gg_id:259697 household biogas digester clone GW-33 EU407
EF445265.1 gg_id:211927 dairy cow rumen clone NED5E6 EF4452
EU473447.1 gg_id:297865 Somali wild ass feces clone WA_aaa02f10 EU473

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EU871420.1 gg_id:308656 Genetic Bovine (Bos taurus) Rumen Thailand clone CF413 EU871
EU463746.1 gg_id:301292 domesticated horse feces clone horsej_aai92a12 EU463
EU871344.1 gg_id:346271 Genetic Bovine (Bos taurus) Rumen Thailand clone CF16 EU871
FJ681865.1 gg_id:529472 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6818
EU842625.1 gg_id:352686 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
EF515475.1 gg_id:221660 Electricigen Enrichment MFC upf microbial fuel cell anode clone 24h04 EF5154
DQ456144.1 gg_id:158774 pre-adolescent turkey cecum clone CFT114H9 DQ456
EU464340.1 gg_id:293385 hamadryas baboon feces clone AFBAB_aai03a08 EU464
FJ680789.1 gg_id:518054 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6807
FJ205803.1 gg_id:335171 microbial integrating library sequences and metagenome data obtained 454-pyroseq FJ2058
EU794282.1 gg_id:317703 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_K38 EU794
FJ684918.1 gg_id:530177 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6849
EU219944.1 gg_id:257268 study prokaryotic approach landfill soil 5.5 ft. depth clone C81B EU219
FJ717180.1 gg_id:511931 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United King FJ7171
EU050916.1 gg_id:236166 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_07_32 EU050
EU142042.1 gg_id:243175 Methyl sulfides intermediates anaerobic oxidation methane seep sediment clone SR EU142
EU570894.1 gg_id:545311 transition and zone within near-shore anoxic basin: Nitinat Lake depth 13 m clone Ni EU570
FJ366283.1 gg_id:360268 feces adult twins and mothers; TS25 clone TS25_a04h01 FJ3662
EF434374.1 gg_id:204256 human infant gastrointestinal tract microbiota stool mother babies 13 and 14 7 mont EF4343
FJ366026.1 gg_id:366738 feces adult twins and mothers; TS25 clone TS25_a01h02 FJ3660
CU924120.1 gg_id:551818 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU924
CU921361.1 gg_id:552601 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU921
AJ853619.1 gg_id:110120 landfill leachate clone GZKB127 AJ8536
FN436127.1 gg_id:559693 Molekularbiologische Charakterisierung der bakteriellen Populationsdynamik eines t FN436
AY862794.2 gg_id:160460 prokaryotic genetic Salar de Atacama Northern Chile athalassohaline lake water clon AY8627
AF507895.1 gg_id:62666 Mono Lake at depth 2m station 6 July 2000 clone ML602J-25 G+C AF5078
EU778068.1 gg_id:313232 feces clone RL117_aae91b10 EU778
AM947541.1 gg_id:268726 Minor changes detected microbial structure and after three week thermophilic dige AM947
AM947531.1 gg_id:265685 Minor changes detected microbial structure and after three week thermophilic dige AM947
GU196243.1 gg_id:581038 Bioaugmentation improved recovery digesters after toxicant exposure lab-scale ana GU196
GQ448397.1 gg_id:588815 Microbiome neonatal calves: shedding microorganisms fecal clone calf783_6wks_gr GQ448
AF412968.1 gg_id:21971 Acholeplasma axanthum str. S-743(T) AF412
FJ226570.1 gg_id:355090 Acholeplasma laidlawii str. Haig 179L FJ2265
AY257485.1 gg_id:83638 Mesoplasma pleciae str. ATCC 49582; PS-1 AY2574
CP000896.1 gg_id:243946 Acholeplasma laidlawii str. PG-8A CP000
U14905.1 gg_id:15691 Acholeplasma laidlawii str. PG8 ATCC 23206 U1490
AY785356.1 gg_id:108386 Acholeplasma sp. str. CODA 1G AY7853
FJ590762.1 gg_id:568272 Acholeplasma sp. DM-2009 str. Lorelei FJ5907
EU517562.1 gg_id:274442 methanogenic microbial consortia mature oil sands tailings clone 12-7C EU517
DQ337019.1 gg_id:145365 subsurface water clone EV818CFSSAHH219 DQ337

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AY538163.1 gg_id:103238 Acholeplasma brassicae str. 0502 AY538
AM950255.1 gg_id:540644 Sulphide oxidation elemental sulphur membrane bioreactor: Performance and selec AM950
L33734.1 gg_id:15688 Acholeplasma palmae str. ATCC49389; J233 L33734
AY538168.1 gg_id:103956 Acholeplasma morum str. 72-043 AY538
FJ876262.1 gg_id:556175 Acholeplasma oculi str. Panangala 59 FJ8762
FJ825517.1 gg_id:542107 Microbial during start-up mesophilic biogas plant clone 86_BS1_21 FJ8255
AM982581.2 gg_id:278258 microbial and slurry pig saw dust spent bedding clone PISD-AIG02 AM982
DQ337046.1 gg_id:148755 subsurface water clone EV818EB5CPSAJJ46 DQ337
AY538170.1 gg_id:107774 Acholeplasma parvum str. H23M AY538
EF586009.1 gg_id:252219 Methanol-assimilating anaerobic solid waste digester fed methanol clone M35_D8_L EF586
AB369182.1 gg_id:235282 Microbiological Assessment Circulation Mud Fluids During First Operation Drilling De AB369
AY538167.1 gg_id:103806 Acholeplasma hippikon str. C1 AY538
AY538164.1 gg_id:103388 Acholeplasma cavigenitalium str. GP3 AY538
DQ989179.1 gg_id:235828 Artemisia witches'-broom phytoplasma II DQ989
AF411592.1 gg_id:60512 Erigeron witches'-broom phytoplasma str. RPWB phytoplasma AF411
AY180931.1 gg_id:100768 Aster yellows phytoplasma str. OnionD2 AY180
AY180930.1 gg_id:100615 Aster yellows phytoplasma str. RgwdD1 AY180
AY180925.1 gg_id:105275 Aster yellows phytoplasma str. C..13 AY180
AY265216.1 gg_id:102638 Plantago virescence phytoplasma str. PVM AY265
AY180941.1 gg_id:105824 Aster yellows phytoplasma str. PLD1 AY180
AY180936.1 gg_id:101585 Aster yellows phytoplasma str. BtsvCarD6 AY180
AY180933.1 gg_id:101087 Aster yellows phytoplasma str. CarD4 AY180
AY180948.1 gg_id:106919 Aster yellows phytoplasma str. OnionD1 AY180
EU099556.1 gg_id:275610 Cactus witches'-broom phytoplasma str. YN11 EU099
EU099557.1 gg_id:271658 Cactus witches'-broom phytoplasma str. YN12 EU099
EU099549.1 gg_id:273742 Cactus witches'-broom phytoplasma str. YN04 EU099
EU099563.1 gg_id:275567 Cactus witches'-broom phytoplasma str. YN18 EU099
EU099555.1 gg_id:275102 Cactus witches'-broom phytoplasma str. YN10 EU099
EU099569.1 gg_id:274000 Cactus witches'-broom phytoplasma str. YN24 EU099
EU099566.1 gg_id:272756 Cactus witches'-broom phytoplasma str. YN21 EU099
AY377868.1 gg_id:106270 Strawberry virescence phytoplasma 3101 AY377
AB052872.1 gg_id:106149 Brachiaria grass white leaf phytoplasma str. BraWL-KK AB052
X68339.1 gg_id:15630 Phytoplasma sp str. ash yellows X68339
NC_011047.1 gg_id:345428 Candidatus Phytoplasma mali NC_01
AJ310849.2 gg_id:53611 Candidatus Phytoplasma pini str. PinG AJ3108
X68374.1 gg_id:15654 Phytoplasma sp str. German peach X68374
GQ403235.1 gg_id:561370 Grapevine stolbur phytoplasma str. GrIRAN08 GQ403
FJ376625.1 gg_id:582084 Poinsettia branch-inducing phytoplasma str. PoiBI-JR1 FJ3766
AY731819.1 gg_id:102742 Solanum quitoense machorreo phytoplasma AY731
AY081817.1 gg_id:58989 Chinaberry yellows phytoplasma AY081

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s__Cassava frogskin disease phytoplasma	74424
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s__Crotalaria witches-broom phytoplasma	74238
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s__Lethal yellowing phytoplasma	74521
s__Loofah witches-broom phytoplasma	73268
s__Onion yellows phytoplasma	74599

FJ376627.1 gg_id:566603 Goldenrod yellows phytoplasma str. GRY-GR1	FJ3766
AF495882.1 gg_id:67193 Chinaberry yellows phytoplasma str. CbY1	AF4958
DQ444264.1 gg_id:201671 Chinaberry yellows phytoplasma ChTYXIII-4	DQ444
AY787141.2 gg_id:108981 Morinda yellows phytoplasma	AY7871
DQ640501.1 gg_id:230702 Poa stunt phytoplasma str. PoaS	DQ640
DQ640502.1 gg_id:229957 Poa stunt phytoplasma str. PoaS	DQ640
AY669063.1 gg_id:137793 Ribes rubrum phytoplasma	AY6690
AY265218.1 gg_id:102937 Clover phyllody phytoplasma str. KVG	AY2652
DQ452416.1 gg_id:157195 Glycine tomentella witches'-broom phytoplasma str. WBGT	DQ452
EF193357.1 gg_id:202717 Sesame phyllody phytoplasma str. SEPN	EF1933
EU513212.1 gg_id:267241 Cleome witches'-broom phytoplasma str. ClWB-Hnsy	EU5132
AB257290.1 gg_id:183185 Jasmine witches'-broom phytoplasma	AB2572
EF990734.1 gg_id:256711 Pigeon pea witches'-broom phytoplasma M2	EF9907
GU184178.1 gg_id:583290 Jujube witches'-broom phytoplasma str. Yingbuluo	GU184
GU184173.1 gg_id:561436 Jujube witches'-broom phytoplasma str. Fupingdazao	GU184
AY197659.1 gg_id:86835 Cherry lethal yellows phytoplasma str. CLY-5	AY1976
GU184174.1 gg_id:591979 Jujube witches'-broom phytoplasma str. Dongzao	GU184
GU184185.1 gg_id:565984 Jujube witches'-broom phytoplasma str. Jinsimizao	GU184
GU184175.1 gg_id:575585 Jujube witches'-broom phytoplasma str. Pozao	GU184
GU184177.1 gg_id:538789 Jujube witches'-broom phytoplasma str. Baizao	GU184
GU184186.1 gg_id:584389 Jujube witches'-broom phytoplasma str. OT	GU184
EF661582.1 gg_id:242473 Jujube witches'-broom phytoplasma str. DL1	EF6615
DQ842529.1 gg_id:163675 Lethal yellowing phytoplasma M3	DQ842
EU026213.1 gg_id:245559 Lethal yellowing phytoplasma SN	EU0262
DQ286706.1 gg_id:149401 Lethal yellowing phytoplasma str. DJ7	DQ286
DQ286704.1 gg_id:148438 Lethal yellowing phytoplasma str. DJ10	DQ286
DQ842525.1 gg_id:173631 Lethal yellowing phytoplasma S4	DQ842
DQ842531.1 gg_id:167990 Lethal yellowing phytoplasma M2	DQ842
DQ842527.1 gg_id:172269 Lethal yellowing phytoplasma M4	DQ842
DQ286702.1 gg_id:148239 Lethal yellowing phytoplasma str. DJ4	DQ286
AY572031.1 gg_id:102515 Coconut lethal yellowing phytoplasma str. Jamaica	AY5720
AY572030.1 gg_id:102350 Coconut lethal yellowing phytoplasma	AY5720
DQ842528.1 gg_id:173235 Lethal yellowing phytoplasma C1	DQ842
DQ842532.1 gg_id:171211 Lethal yellowing phytoplasma M1	DQ842
DQ286707.1 gg_id:145483 Lethal yellowing phytoplasma str. DJ5	DQ286
DQ286701.1 gg_id:147292 Lethal yellowing phytoplasma str. DJ8	DQ286
DQ286705.1 gg_id:146262 Lethal yellowing phytoplasma str. DJ2	DQ286
AY572029.2 gg_id:108988 Coconut lethal yellowing phytoplasma	AY5720
DQ842530.1 gg_id:169291 Lethal yellowing phytoplasma M6	DQ842
AF248956.1 gg_id:69018 Loofah witches'-broom phytoplasma str. LfWB phytoplasma	AF2489
DQ321822.2 gg_id:145208 Ragweed yellows phytoplasma str. RwY	DQ321

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s__Paulownia witches-broom phytoplasma	73282
s__Pigeon pea witches-broom phytoplasma	74396
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AY192577.1 gg_id:79786 Paulownia witches'-broom phytoplasma AY1925
EF186824.1 gg_id:183787 Pigeon pea witches'-broom phytoplasma str. PPWBpr EF1868
AY197649.1 gg_id:86755 Rubus stunt phytoplasma str. Rus400 AY1976
AY197648.1 gg_id:87980 Rubus stunt phytoplasma str. RuS AY1976
AY197654.1 gg_id:87732 Hemp dogbane yellows phytoplasma str. HD1 AY1976
EU333400.1 gg_id:278893 Russian potato purple top phytoplasma str. Rus103-7 EU3334
EU333397.1 gg_id:278326 Russian potato purple top phytoplasma str. Rus103-2 EU3333
EU333398.1 gg_id:279421 Russian potato purple top phytoplasma str. Rus103-4 EU3333
EU003536.1 gg_id:244948 Sweet potato little leaf phytoplasma 14c EU0035
EU003537.1 gg_id:243480 Sweet potato little leaf phytoplasma 7E EU0035
EF474451.2 gg_id:235777 Identification Allocasuarina fraseriana little phytoplasma disease Allocasurina Kings P EF4744
X80117.1 gg_id:15647 Phytoplasma sp str. Coconut lethal yellowing disease X80117
FJ226072.1 gg_id:575096 Sweet pepper purple vein phytoplasma str. SwPPV3 FJ2260
AY197643.1 gg_id:86864 Flavescence doree phytoplasma str. FD70 AY1976
AB010425.2 gg_id:32876 -group I phytoplasma~synonym:Japanese Hydrangea phyllody phytoplasma japonicur AB0104
AB242433.1 gg_id:169824 Henon bamboo witches'-broom phytoplasma AB2424
Y18052.1 gg_id:15588 Knautia arvensis phyllody phytoplasma Y18052
DQ459438.1 gg_id:157077 Sugarcane grassy shoot phytoplasma Bidar DQ459
AF370120.1 gg_id:66821 Dandelion virescence phytoplasma str. DanVir AF3701
DQ286953.1 gg_id:144993 Broadbeam phytoplasma DQ286
AY863003.1 gg_id:109692 chinaberry yellows phytoplasma str. Vietnam AY8630
EU375834.1 gg_id:259943 Periwinkle little leaf phytoplasma EU3758
EU371934.1 gg_id:260301 Malaysian periwinkle virescence phytoplasma EU3719
EF050071.1 gg_id:177441 Sandal spike phytoplasma Karnataka EF0500
DQ645635.1 gg_id:161008 Coconut lethal yellowing phytoplasma str. LYC347 DQ645
AY204549.1 gg_id:107635 Periwinkle witches'-broom phytoplasma str. PerWB-FL AY2045
GU361756.1 gg_id:538151 Goosegrass yellows phytoplasma str. GGY1 GU361
AY180950.1 gg_id:101862 Aster yellows phytoplasma str. Btsv4C..2b AY1809
AY180946.1 gg_id:106611 Aster yellows phytoplasma str. ParsD4 AY1809
AY075038.1 gg_id:55023 Mulberry dwarf phytoplasma str. MD-ko AY0750
EF534205.1 gg_id:258469 Iranian safflower phyllody phytoplasma EF5342
AF305198.1 gg_id:69629 Virginia creeper phytoplasma str. VC-Fl AF3051
DQ286574.1 gg_id:142079 Parthenium histrophorus phytoplasma DQ286
AY270156.1 gg_id:82781 Centaurea solstitialis virescence phytoplasma CSV virescence AY2701
EF493020.1 gg_id:226498 Poinsettia flower distortion phytoplasma EF4930
AY685055.1 gg_id:98886 Peanut yellows phytoplasma AY6850
DQ164212.1 gg_id:170032 Dictamnus stunt phytoplasma str. DitS DQ164
AF244363.1 gg_id:17222 Black locust witches'-broom phytoplasma str. BLWB witches'-broom AF2443
EF529494.1 gg_id:219241 Chrysanthemum witches'-broom phytoplasma EF5294
FJ376629.1 gg_id:572583 Alaska potato purple top phytoplasma str. PPT-AK6 FJ3766
AF521672.1 gg_id:64303 Weeping tea tree witches'-broom phytoplasma tree AF5216

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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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Y16391.1 gg_id:15674 Bindweed yellows phytoplasma Y16391
EF363314.1 gg_id:573100 Cotton virescence phytoplasma EF3633
EF153634.1 gg_id:186762 Solanum malacoxylon new natural host stolbur phytoplasma R16F2n R16R2; _primer EF1536
FJ226076.1 gg_id:550833 Montana potato purple top phytoplasma str. PPT-MT117-3 FJ2260
FJ226074.1 gg_id:566707 Montana potato purple top phytoplasma str. PPT-MT117-1 FJ2260
EU333395.1 gg_id:278466 Coneflower phyllody phytoplasma str. ConPh MD3 EU3333
AF248960.1 gg_id:55663 Mexican periwinkle virescence phytoplasma str. MPV virescence AF2489
AF147706.1 gg_id:54971 Chayote witches'-broom phytoplasma str. ChWBIII(Ch10) phytoplasma AF1477
AY265220.1 gg_id:106715 Blueberry stunt phytoplasma str. BBS1 AY2652
EU999742.1 gg_id:326955 Jujube witches'-broom phytoplasma str. ZZH1 EU9997
GU361757.1 gg_id:551933 Persian violet stunt phytoplasma str. PVS1 GU361
AY197647.1 gg_id:87317 Alder yellows phytoplasma str. ALY1068 AY1976
GU113147.1 gg_id:589201 Periwinkle little leaf phytoplasma str. PLL-Hn1 GU113
EU057983.1 gg_id:237448 Lethal yellowing phytoplasma EU0579
EU241515.1 gg_id:254449 Coconut lethal yellowing phytoplasma str. BCT-C6 EU2415
Y16393.1 gg_id:15581 Picris echioides phyllody phytoplasma Y16393
EF186828.1 gg_id:181939 Lime witches'-broom phytoplasma str. LWB EF1868
DQ318244.1 gg_id:147021 Coconut lethal yellowing phytoplasma str. CLY-Hon DQ318
AY739024.1 gg_id:100418 Lethal wilt oil palm phytoplasma str. PC2.1014R AY7390
AY180953.1 gg_id:102314 Aster yellows phytoplasma str. DillD2 AY1809
AF331973.1 gg_id:112027 Cactus witches'-broom phytoplasma str. CWB1 AF3319
DQ318242.1 gg_id:147649 Coconut lethal yellowing phytoplasma str. CLY-Mexl DQ318
AY265210.1 gg_id:101708 Primrose virescence phytoplasma str. PRIVC AY2652
FJ217385.1 gg_id:340797 Tanzania coconut lethal disease phytoplasma str. LDT FJ2173
GU113145.1 gg_id:568778 Chinese periwinkle phyllody phytoplasma str. PP-Hn1 GU113
AF173558.1 gg_id:15599 Clover yel edge phytoplasma str. CYE-L AF1735
AY787136.4 gg_id:201507 Candidatus Phytoplasma lycopersici new phytoplasma species causing Morrenia littl AY7871
AY180944.1 gg_id:106289 Aster yellows phytoplasma str. Btsv2C..17 AY1809
AY377876.1 gg_id:102155 Napier grass phytoplasma 2002/19-5 AY3778
EU333396.1 gg_id:279028 Russian potato purple top phytoplasma str. Rus103-1 EU3333
AM180882.1 gg_id:187579 Sweet potato little leaf phytoplasma Aus1 AM180
DQ384857.1 gg_id:151119 Coconut lethal yellowing phytoplasma str. LYN 14-1 DQ384
X68373.1 gg_id:15687 Phytoplasma sp str. American aster yellows X68373
DQ321820.1 gg_id:145945 Carludovica palmata leaf yellowing phytoplasma str. CPY DQ321
AF279271.1 gg_id:21611 Paulownia witches'-broom phytoplasma AF2792
Y08173.1 gg_id:15618 Phytoplasma sp Y08173
AY180954.1 gg_id:102473 Aster yellows phytoplasma str. ParsD1 AY1809
AF509322.1 gg_id:63017 Sorghum bunchy shoot phytoplasma AF5093
AY265213.1 gg_id:102179 Blueberry stunt phytoplasma str. BBS3 AY2652
EF042898.1 gg_id:176840 Strawberry multiplier phytoplasma str. SMP-FL EF0428

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EU170353.1 gg_id:239724 Sweet potato little leaf phytoplasma 2&3Vtrio EU170
FJ154847.1 gg_id:312556 Jujube witches'-broom phytoplasma str. ZQ FJ1548
U16758.1 gg_id:15696 Mycoplasma feliminutum str. ATCC 25749 U16758
EU006252.1 gg_id:257027 Salmonella enterica serovar typhimurium exploits inflammation compete intestinal r EU006
EU456203.1 gg_id:314291 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU456
FJ681157.1 gg_id:529539 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6811
EU794312.1 gg_id:354444 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_L44 EU7943
EF604794.1 gg_id:228310 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6047
EU774401.1 gg_id:315971 mammals their gut microbes Eastern Black and White Colobus feces clone COL_aai1! EU7744
M25050.1 gg_id:15703 Anaeroplasma abactoclasticum M2505
EF604918.1 gg_id:231986 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6049
EU344682.1 gg_id:262497 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU3446
EU794279.1 gg_id:305348 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_G18 EU7942
FJ683969.1 gg_id:528228 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6839
GQ897174.1 gg_id:555555 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ897
DQ797091.1 gg_id:185593 human fecal clone RL386_aao86h04 DQ797
DQ797049.1 gg_id:179979 human fecal clone RL386_aao86c09 DQ797
NR_028691.1 gg_id:591314 Entomoplasma freundtii str. BARC318; ATCC 51999 NR_028
GQ275106.1 gg_id:581987 gut symbionts are tightly linked herbivory ants extract single ant clone #130 GQ275
AE017263.1 gg_id:100309 Mesoplasma florum L1 str. L1; ATCC 33453 AE0172
AY187288.1 gg_id:79099 Mesoplasma tabanidae str. BARC 857; ATCC 49584 AY1872
AF042194.1 gg_id:15792 Mycoplasma monodon str. Australiain AF0421
AY168929.2 gg_id:75831 Mesoplasma corruscae str. ATCC 49579 AY1689
AY166704.1 gg_id:76006 Mesoplasma chauliocola str. ATCC 49578 AY1667
DQ157864.1 gg_id:139255 Mycoplasma capricolum str. 700 DQ157
U26055.1 gg_id:15786 Mycoplasma putrefaciens str. KS-1 U26055
AY155670.1 gg_id:75155 Entomoplasma luminosum str. ATCC 49195; PIMN-1 AY1556
GQ275109.1 gg_id:568610 gut symbionts are tightly linked herbivory ants extract single ant clone #133 GQ275
GQ275144.1 gg_id:555846 gut symbionts are tightly linked herbivory ants extract single ant clone #168 GQ275
AY538169.1 gg_id:104104 Acholeplasma multilocale str. PN525 AY5381
AF303132.1 gg_id:71794 Mesoplasma lactucae str. 831-C4; ATCC 49193 ATCC AF3031
DQ861915.1 gg_id:168652 Spiroplasma cantharicola str. Q-6 DQ861
X63781.1 gg_id:15803 Spiroplasma citri str. R8A2HP X63781
DQ112020.1 gg_id:130516 Spiroplasma citri str. Car6 DQ112
AJ006775.1 gg_id:41072 Spiroplasma sp AJ0067
NR_025706.1 gg_id:534716 Spiroplasma lampyridicola str. PUP-1; ATCC 43206 NR_025
AY189309.1 gg_id:99424 Spiroplasma syrphidicola str. ATCC 33826; EA-1 AY1893
AY189132.1 gg_id:101796 Spiroplasma helicoides str. ATCC 51746; TABS-2 AY1891
AY345990.1 gg_id:93470 Entomoplasma melaleucae str. M1 AY3459
AY189125.1 gg_id:106072 Spiroplasma alleghenense str. ATCC 51752; PLHS-1 AY1891
EF151267.1 gg_id:202191 Spiroplasma sp. str. CRW-1 EF1512

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DQ917756.1 gg_id:258655 Spiroplasma mirum DQ917
GQ051079.1 gg_id:429439 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ051
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AY189318.1 gg_id:104368 Spiroplasma sp. str. TIUS-1 AY1893
AY189129.1 gg_id:106700 Spiroplasma culicicola str. ATCC 35112; AES-1 AY1891
DQ860101.1 gg_id:166158 Spiroplasma platyhelix str. PALS-1 DQ860
AY189305.1 gg_id:107782 Spiroplasma leptinotarsae str. ATCC 43213; LD-1B AY1893
NR_025703.1 gg_id:544767 Spiroplasma floricola str. 23-6; ATCC 29989 NR_025
DQ319068.1 gg_id:148669 Spiroplasma kunkelii str. CR2-3x DQ319
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NR_025709.1 gg_id:565097 Spiroplasma montanense str. HYOS-1; ATCC 51745 NR_025
AY189310.1 gg_id:103192 Spiroplasma turonicum str. ATCC 700271; Tab-4c AY1893
NR_025713.1 gg_id:561932 Spiroplasma velocicrescens str. MQ-4; ATCC 35262 NR_025
GQ129114.1 gg_id:526608 Prevalence geographical canine hemotropic mycoplasma infections Mediterranean GQ129
EF424082.1 gg_id:209237 Mycoplasma sp. China-1 EF4240
AY831867.1 gg_id:133123 Mycoplasma sp. 'feline hemotropic Switzerland' AY8318
DQ825454.1 gg_id:222355 Worldwide occurrence feline hemoplasma infections wild felid species Tanzania DQ825
NC_009497.1 gg_id:233772 Mycoplasma agalactiae str. PG2 NC_009
AF332745.1 gg_id:73703 Mycoplasma agalactiae str. 396/12 AF3327
AF332751.1 gg_id:70015 Mycoplasma agalactiae str. 35 AF3327
AF060821.1 gg_id:15907 Mycoplasma agassizii str. K120 AF0608
NR_025985.1 gg_id:565268 Mycoplasma alvi str. Isley; NCTC 10157 NR_025
AY531656.1 gg_id:111859 Mycoplasma amphoriforme str. M5572 AY5316
FJ226575.1 gg_id:326725 Mycoplasma amphoriforme str. A39 FJ2265
NR_029180.1 gg_id:550692 Mycoplasma gateae str. ATCC 23392 NR_029
CP001047.1 gg_id:308649 Mycoplasma arthritidis str. 158L3-1 CP0010
AF340023.1 gg_id:74000 Mycoplasma canis str. PG14 AF3400
AF412973.1 gg_id:70402 Mycoplasma citelli str. RG-2C(T) AF4129
FJ226571.1 gg_id:310264 Mycoplasma conjunctivae str. Goat 655 FJ2265
GU227404.1 gg_id:579318 Mycoplasma flocculare str. USP9T GU227
L08896.4 gg_id:15854 Mycoplasma gallisepticum str. A5969 L08896
AF412980.1 gg_id:72545 Mycoplasma gallopavonis str. WR1(T) AF4129
AY466443.1 gg_id:107609 Mycoplasma genitalium str. M2288 AY4664
DQ825438.1 gg_id:217964 Mycoplasma haemofelis 111 DQ825
EU930823.1 gg_id:340543 Mycoplasma haemofelis Porto Alegre EU9308
AY150985.1 gg_id:58418 Mycoplasma haemofelis UK no. 6 AY1509
AY150973.1 gg_id:71517 Mycoplasma haemocanis Germany Munich no. 1 AY1509

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AF121890.1 gg_id:15878 Mycoplasma hyorhinis str. ATCC VR-2580 AF1218
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NR_025064.1 gg_id:562555 Mycoplasma iners str. PG30; ATCC 19705 NR_02
EF447273.1 gg_id:210500 Mycoplasma iowae str. HTL04-4846A EF4472
AF221116.1 gg_id:47885 Mycoplasma maculosum PG15(T) AF221
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FJ655919.1 gg_id:565101 Mycoplasma neurolyticum str. T15 FJ6559
AF538961.1 gg_id:71629 Mycoplasma opalescens str. MHS408 AF5389
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EU827597.1 gg_id:349932 Mycoplasma phocidae str. CSL 7498-2 EU8275
EU827598.1 gg_id:315295 Mycoplasma phocirhinis str. CSL 7475-4 EU8275
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EU367963.1 gg_id:258287 Mycoplasma wenyonii cattle no. 48 EU3679
DQ530428.1 gg_id:233952 Mycoplasma zalophi str. CSL 5195 DQ530
AY571416.1 gg_id:114530 termite gut clone RsaHf232 AY5714
GQ502581.1 gg_id:590759 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf4- GQ502
AB089055.1 gg_id:78062 termite gut homogenate clone Rs-G80 AB089
U09788.1 gg_id:15851 Mycoplasma str. ATCC 43263 U09788
NR_029165.1 gg_id:567958 Mycoplasma pirum str. 70-159; ATCC 25960 NR_02
AB089054.1 gg_id:77956 termite gut homogenate clone Rs-B54 AB089
AB192228.1 gg_id:142809 termite gut homogenate clone RsTu1-65 AB192
AF125879.1 gg_id:15849 Mycoplasma cavipharyngis str. 117C(T) AF1258
AB089057.1 gg_id:77895 termite gut homogenate clone Rs-E42 AB089
AY571419.1 gg_id:114509 termite gut clone RsaHf283 AY5714
EU859984.1 gg_id:344923 Mycoplasma sp. str. CSL7529-conjunctiva EU8599
AF221113.1 gg_id:71570 Mycoplasma columbinum MMP-1(T) AF221
L24105.1 gg_id:15949 Mycoplasma gallinarum str. PG16 L24105
FM165074.1 gg_id:329837 Mycoplasma sp. C3T str. C3 FM165
AF221119.1 gg_id:19645 Mycoplasma spermatophilum AH159(T) AF221
AM182894.1 gg_id:199102 Mycoplasma sp. str. 15CL2 AM182
AF221111.1 gg_id:73061 Mycoplasma caviae G122(T) AF221

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GU227407.1 gg_id:579601 Mycoplasma hyopneumoniae str. USP14P GU227
AF412977.1 gg_id:32469 Mycoplasma crocodyli str. MP145(T) AF4129
EF510696.1 gg_id:220331 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aerug EF5106
DQ223546.1 gg_id:144780 Mycoplasma sp. str. Ms02 DQ223
EF510778.1 gg_id:224463 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aerug EF5107
AF221118.1 gg_id:48246 Mycoplasma primatum HRC292(T) AF2211
DQ223545.1 gg_id:142935 Mycoplasma sp. str. Ms01 DQ223
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U22013.1 gg_id:15920 Mycoplasma sturni str. UC/MF U22013
EF036469.1 gg_id:179109 Mycoplasma cricetuli str. CH EF0364
EF510860.1 gg_id:225935 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aerug EF5108
AF412970.1 gg_id:71789 Mycoplasma anatis str. 1340(T) AF4129
AF332757.1 gg_id:73175 Mycoplasma bovis str. 422/88 AF3327
AF332748.1 gg_id:73746 Mycoplasma agalactiae str. L9 AF3327
NR_024978.1 gg_id:548556 Mycoplasma equirhinis str. M432/72; ATCC 29420 NR_02
AM182896.1 gg_id:186205 Mycoplasma sp. str. 10T4 AM182
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FJ959657.1 gg_id:555715 bottlenose dolphin upper respiratory tract blowhole clone D896_262 FJ9596
U67943.1 gg_id:15941 Mycoplasma adleri str. G145 U67943
L08054.1 gg_id:15918 Mycoplasma corogypsi str. BV1 L08054
U73903.1 gg_id:15913 Mycoplasma edwardii str. PG24 U73903
NR_024981.1 gg_id:573950 Mycoplasma subdolum str. TB; ATCC 29870 NR_02
AY121109.1 gg_id:72631 Mycoplasma bovigenitalium 398/87 AY1211
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FM165076.1 gg_id:325252 Mycoplasma sp. 2F1AT str. 2F1A FM165
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EF510714.1 gg_id:224150 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aerug EF5107
EU859973.1 gg_id:328570 Mycoplasma iguanae str. 2327 EU8599
NR_029183.1 gg_id:594001 Mycoplasma hyosynoviae str. S-16; ATCC 25591 NR_02
AF538681.1 gg_id:56134 Mycoplasma collis str. 58B AF5386
FM165075.1 gg_id:344619 Mycoplasma sp. A1802T str. A1802 FM165
AF221112.1 gg_id:70343 Mycoplasma columbinasale 694(T) AF2211
AM774638.1 gg_id:239999 Mycoplasma canimucosale str. 1642 AM774
AY246564.1 gg_id:85218 Mycoplasma sp. str. VJC358 AY2465
L24104.1 gg_id:15922 Mycoplasma gallinaceum str. DD L24104
FM878637.1 gg_id:553341 Mycoplasma sp. str. 38104 FM878
DQ340199.1 gg_id:147129 Dominance Mycoplasma guts Long-Jawed Mudsucker Gillichthys mirabilis five Califo DQ340
U44766.1 gg_id:15912 Mycoplasma bovirhinis str. PG43 U44766
AM182891.1 gg_id:184771 Mycoplasma sp. str. 13CL AM182

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FJ655917.1 gg_id:588056 Mycoplasma vulturii str. Gb-V33 FJ6559
NR_025186.1 gg_id:543508 Mycoplasma moatsii str. MK405; ATCC 27625 NR_02
AF412974.1 gg_id:28253 Mycoplasma collis str. 58B(T) AF412
AY050170.1 gg_id:60547 Mycoplasma timone AY050
AF412989.1 gg_id:28733 Mycoplasma verecundum str. GIH(T) AF412
FM878042.1 gg_id:557236 Mycoplasma sp. str. 51CL FM878
EF510815.1 gg_id:219506 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aeru EF5108
AF125591.1 gg_id:15897 Mycoplasma falconis str. H/T1(T) AF125
DQ340198.1 gg_id:146814 Dominance Mycoplasma guts Long-Jawed Mudsucker Gillichthys mirabilis five Califo DQ340
AF150495.1 gg_id:15925 Mycoplasma sp. str. 94630 AF150
AF412981.1 gg_id:70918 Mycoplasma glycophilum str. 486(T) AF412
NR_024982.1 gg_id:567316 Mycoplasma gypis str. B1/T1; ATCC 51370 NR_02
NR_025914.1 gg_id:557285 Mycoplasma meleagridis str. 17529; ATCC 25294 NR_02
EF510816.1 gg_id:227513 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aeru EF5108
AF412971.1 gg_id:69777 Mycoplasma buteonis str. BbT2g(T) AF412
M24582.1 gg_id:15954 Mycoplasma californicum M2458
U15795.1 gg_id:15943 Mycoplasma felifaucium str. ATCC 43428 U1579
EF510786.1 gg_id:220695 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aeru EF5107
FM196534.1 gg_id:331374 Mycoplasma sp. str. Zaradi2 FM196
U09787.1 gg_id:15917 Mycoplasma felis str. ATCC 23391 U0978
AM182893.1 gg_id:190324 Mycoplasma sp. str. 11CL2 AM182
U16760.1 gg_id:15944 Mycoplasma leopharyngis str. ATCC 49889 U1676
AF170102.1 gg_id:15921 Mycoplasma capricolum AF170
AF221115.1 gg_id:19295 Mycoplasma lipofaciens R171(T) AF221
NR_025182.1 gg_id:555208 Mycoplasma dispar str. 462/2; ATCC 27140 NR_02
AY492086.1 gg_id:136766 Mycoplasma suis str. Guangdong AY492
AF178676.1 gg_id:51934 Candidatus Mycoplasma haemodidelphidis Illinois AF178
AF306346.1 gg_id:136331 Candidatus Mycoplasma haemolamae str. Michigan AF306
EU165510.1 gg_id:339052 Mycoplasma ovis Mo-Hu-3-05.2007 EU165
AY171918.1 gg_id:87318 Mycoplasma coccoides AY171
EF221880.1 gg_id:206167 Mycoplasma wenyonii str. CGXD EF2218
U82963.1 gg_id:15860 Mycoplasma haemomuris str. Shizuoka U8296
EU134687.1 gg_id:255073 tallgrass prarie soil clone FFCH10627 EU134
GU293201.1 gg_id:568172 Microbial contents and mucus yel catfish (Pelteobagrus fulvidraco) stomach content GU293
EF516576.1 gg_id:219640 grassland soil clone FCPT702 EF5165
AY500249.1 gg_id:102371 Candidatus Hepatoplasma crinochetorum clone 48 AY500
EU646193.1 gg_id:285164 Host-specificity transmitted Mycoplasma-like isopod symbionts hepatopancreas clor EU646
EU646198.1 gg_id:280566 Host-specificity transmitted Mycoplasma-like isopod symbionts hepatopancreas clor EU646
AF001173.1 gg_id:15899 Candidatus Mycoplasma ravipulmonis AF001
U62937.2 gg_id:15831 Ureaplasma gallorale str. ATCC 43346 U6293
GU227393.1 gg_id:580923 Ureaplasma sp. str. USP S/N GU227

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D78649.1 gg_id:15829 Ureaplasma cati str. F2 D7864
L08642.1 gg_id:15811 Ureaplasma urealyticum str. 27 L08642
U06097.1 gg_id:15816 Ureaplasma urealyticum str. 354 (serovar 5) U0609
EU844042.1 gg_id:310545 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
EU459553.1 gg_id:294314 capybara feces clone CAP_aah99g08 EU459
FJ172803.1 gg_id:348767 Qinghai Yak Ruminal and Fungi China rumen clone RB-3C9 FJ1728
EU382038.1 gg_id:268757 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU382
FJ366886.1 gg_id:370110 feces adult twins and mothers; TS28 clone TS28_a01a06 FJ3668
FJ671998.1 gg_id:521062 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6719
AF371530.1 gg_id:21652 swine intestine clone p-1735-b3 AF371
DQ805924.1 gg_id:175271 human fecal clone RL306aal92g01 DQ805
GQ167173.1 gg_id:567437 Effects Hydraulic Retention Time on Anaerobic Hydrogenation Performance Microbi GQ167
GQ897787.1 gg_id:578177 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ897
GQ448417.1 gg_id:576850 Microbiome neonatal calves: shedding microorganisms fecal clone calf783_10wks_g GQ448
GU303669.1 gg_id:561959 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU303
AM275414.2 gg_id:234959 fecal microbiota irritable bowel syndrome patients significantly that healthy subject AM275
EF445243.1 gg_id:207023 dairy cow rumen clone NED5C1 EF4452
FJ681340.1 gg_id:519348 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6813
AM275475.2 gg_id:233848 fecal microbiota irritable bowel syndrome patients significantly that healthy subject AM275
GQ896843.1 gg_id:569244 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do s GQ896
FJ673493.1 gg_id:515507 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6734
FJ684684.1 gg_id:529404 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6846
GQ897386.1 gg_id:585199 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do s GQ897
EU474506.1 gg_id:292635 bighorn sheep feces clone BHSD_aaa03h12.Contig2 EU474
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EU850597.1 gg_id:311889 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF427 EU850
AY985740.1 gg_id:117030 human stool clone C771 AY985
GQ451187.1 gg_id:513605 Fecal Yunnan snub-nosed monkey feces clone J19 GQ451
FJ673434.1 gg_id:518672 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6734
EF445272.1 gg_id:213966 dairy cow rumen clone NED4E12 EF4452
DQ057362.1 gg_id:131450 chicken ileum/cecum clone cc106 DQ057
EU773287.1 gg_id:306877 BigHorn sheep feces clone BH1_aao27e05 EU773
DQ326418.1 gg_id:148285 Metagenomic gut microbiome healthy human stool clone C469 DQ326
FJ673790.1 gg_id:515508 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6737
EU844544.1 gg_id:325403 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
FJ680415.1 gg_id:515855 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6804
FJ673176.1 gg_id:527857 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6731
EU344185.1 gg_id:277047 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU344
EU475428.1 gg_id:297545 springbok feces clone SBSD_aaa04g12 EU475
EU850542.1 gg_id:342412 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF336 EU850

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FJ367190.1 gg_id:367962 feces adult twins and mothers; TS28 clone TS28_a04e12 FJ3671
FJ678613.1 gg_id:531345 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6786
AY916353.1 gg_id:114378 human stool clone D051 AY9163
EU381774.1 gg_id:265197 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU381
FJ832322.1 gg_id:558715 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P1Q301_19C03 FJ8323
EU463631.1 gg_id:303133 domesticated horse feces clone horsej_aai90a12 EU463
FJ440078.1 gg_id:567506 Megamonas hypermegale colonization correlates Campylobacter jejuni exclusion pou FJ4400
FJ682646.1 gg_id:513042 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6826
EU844825.1 gg_id:327546 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8448
EU871410.1 gg_id:324570 Genetic Bovine (Bos taurus) Rumen Thailand clone CF378 EU8714
DQ456306.1 gg_id:158491 pre-adolescent turkey cecum clone CFT211G6 DQ456
EU381733.1 gg_id:265925 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid EU381
DQ353915.1 gg_id:146314 Fecal Wild Gorilla (Gorilla beringei) wild gorilla feces clone Z32 DQ353
EU843681.1 gg_id:325563 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
EU844239.1 gg_id:327857 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8442
AF001742.1 gg_id:15698 rumen clone RF9 AF0017
GQ451225.1 gg_id:545091 Fecal Yunnan snub-nosed monkey feces clone J128 GQ451
AM277561.2 gg_id:229533 fecal microbiota irritable bowel syndrome patients significantly that healthy subject AM277
GU303762.1 gg_id:580081 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU303
EU622737.1 gg_id:279179 -feed administered sub-therapeutic chlorotetracycline alters structure and but not a EU6227
AY916186.1 gg_id:114444 human ascending colon biopsy clone LW88 AY9161
EU344299.1 gg_id:271356 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU3442
FJ833479.1 gg_id:591398 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J1Q201_78F10 FJ8334
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EF406725.1 gg_id:211308 mouse colon clone infected_14days-B9 EF4067
EU842453.1 gg_id:316729 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU8424
AY986020.1 gg_id:127092 human stool clone D332 AY9860
EU764308.1 gg_id:341905 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1 EU7643
FJ172880.1 gg_id:352691 Qinghai Yak Ruminal and Fungi China rumen clone RB-2D1 FJ1728
EU844758.1 gg_id:347587 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8447
GU476604.1 gg_id:522127 microbial biogas fermentation enrichment clone BBMC-4 GU476
GU208279.1 gg_id:537538 Study on Sediment Dongping Lake sediment clone 6F1-3 GU208
EU358689.1 gg_id:325820 structure archaeal denaturing gel electrophoresis and sequencing mesophilic biogas EU3586
GQ458248.1 gg_id:513979 Microbial structure co-digestion anaerobic bioreactors treating cassava pulp and pig GQ458
AB192099.1 gg_id:143019 termite gut homogenate clone M1NP1-24 AB1920
AB192110.1 gg_id:144845 termite gut homogenate clone M1PT4-30 AB1921
AB255930.1 gg_id:164433 Localization Cell Morphologies Members Candidate TG3 and Subphylum Phylum Fibr AB2559
EF454354.2 gg_id:220027 termite hindgut clone 290cost002-P3L-1996 EF4543
EF454970.2 gg_id:227321 termite hindgut clone 290cost002-P3L-828 EF4549
AB243293.1 gg_id:149384 acetone-preserved termite gut clone M2PB4a-088 AB2432
FJ202893.1 gg_id:317953 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2028

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AAHE01000005.1 gg_id:134272 Deinococcus geothermalis str. DSM 11300 AAHE0
AY743256.1 gg_id:138843 Deinococcus hohokamensis str. KR-40 AY7432
AY743275.1 gg_id:138931 Deinococcus maricopensis str. KR-1 AY7432
AB264133.1 gg_id:171820 Deinococcus sp. str. TDMA-21 AB2641
AY743280.1 gg_id:138834 Deinococcus papagonensis str. KR-241 AY7432
AE000513.1 gg_id:146329 Deinococcus radiodurans str. R1 AE0005
AY743284.1 gg_id:138790 Deinococcus sonorensis str. KR-90 AY7432
GQ043868.1 gg_id:461798 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw97 GQ043
EF141348.1 gg_id:247857 Deinococcus peraridilitoris str. KR-200 EF1413
AY743267.1 gg_id:139200 Deinococcus apachensis str. KR-32 AY7432
AM988777.1 gg_id:568744 Deinococcus sp. str. K4.1 AM988
AF385541.1 gg_id:136570 Prevalent species and phylotypes advanced noma lesions Deinococcus oral clone CB(AF3855
DQ532354.2 gg_id:168505 Geographical Variation Microbial Burden and Spacecraft Assembly Kennedy Space C DQ532
EU834252.1 gg_id:347125 Deinococcus aquaticus str. DS27 EU8342
DQ883809.1 gg_id:163551 Deinococcus cellulolytica str. 5516J-15 DQ883
NR_026403.1 gg_id:562641 Deinococcus radiopugnans str. ATCC 19172 NR_02
EU029127.1 gg_id:238409 Deinococcus sp. str. 2A2 EU0291
EF635408.1 gg_id:285250 Deinococcus alpinitundrae str. ME-04-04-52 EF6354
GQ357648.1 gg_id:546802 Deinococcus sp. str. YIM 75723 GQ357
GQ441240.1 gg_id:556010 and dynamic mat present vs. active nitrogen-fixing microorganisms marine microbia GQ441
EU029130.1 gg_id:250755 Deinococcus sp. str. 3A5 EU0291
AB374383.1 gg_id:271722 sequences Weissenstein (white rock) / few millimeters be surface rock called 'Weiss AB3743
M21413.1 gg_id:1418 Deinococcus radiodurans M2141
EU626561.1 gg_id:282134 Deinococcus xinjiangensis str. X-82 EU6265
DQ022077.1 gg_id:136712 Truepera radiovictrix str. TU-8 DQ022
EU622978.1 gg_id:279041 Deinococcus sp. str. 5516T-9 EU6229
EU427464.1 gg_id:264010 Deinococcus sp. str. I-0 EU4274
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AY743279.1 gg_id:138901 Deinococcus yavapaiensis str. KR-236 AY7432
EU362143.1 gg_id:332198 and Mesquite Flats Site Death Valley dune sand clone 14 EU3621
EF522236.1 gg_id:219134 Endolithic Microbial Ecosystems Rocky Mountain endolithic sandstone clone FQSS01(EF5222
GQ058104.1 gg_id:395808 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw: GQ058
AM283039.1 gg_id:159842 Deinococcus sp. str. Han23 AM283
GQ072152.1 gg_id:389682 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw192g11 GQ072
AM292065.1 gg_id:249433 Deinococcus radiodurans zf-69-II AM292
GQ130053.1 gg_id:435637 Genetic inventory 'JPL-SAF' during MSL mission spacecraft assembly clean room floc GQ130

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DQ847439.1 gg_id:170011 human forearm skin clone GL2-41 DQ847
DQ366016.1 gg_id:152980 Dominant soils Marble Point and Wright Valley Victoria Land Antarctica soil clone 21 DQ366
EU622979.1 gg_id:279558 Deinococcus sp. str. 5516T-11 EU622
AB473897.1 gg_id:568788 sequences endolithic and archaea Weissenstein (white rock) / Albula pass few millim AB473
DQ883808.1 gg_id:169628 Deinococcus aeria str. 5516J-6 DQ883
GQ130015.1 gg_id:405062 Genetic inventory 'JPL-SAF' during MSL mission spacecraft assembly clean room floc GQ130
FJ444684.1 gg_id:562787 Cotton Rhizosphere cotton rhizosphere clone 2y-56 FJ4446
FJ176238.1 gg_id:307654 Deinococcus sp. str. ZLM-202 FJ1762
GQ026439.1 gg_id:453803 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl GQ026
EU029134.1 gg_id:250725 Deinococcus sp. str. 5A5 EU029
AM940971.1 gg_id:263628 Deinococcus aquatilis str. CCUG 53370 AM940
AJ585985.1 gg_id:95404 Deinococcus sp. str. AA69 AJ5859
GQ052823.1 gg_id:377731 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ052
DQ223543.2 gg_id:171337 Deinococcus sp. X2 DQ223
FM872722.1 gg_id:365101 occupant source house floor dust clone FB01A10 FM872
AY743278.1 gg_id:139150 Deinococcus pimensis str. KR-242 AY743
AY250871.1 gg_id:86556 lichen-dominated Antarctic cryptoendolithic community clone FBP266 bacterium AY250
GU214174.1 gg_id:593108 and biota slimes Canadian paper mills slime mill taken wet section around papermal GU214
DQ366015.1 gg_id:153959 Dominant soils Marble Point and Wright Valley Victoria Land Antarctica soil clone J3 DQ366
DQ130037.1 gg_id:137532 microbial biota normal forearm human skin clone GR66 DQ130
GQ023518.1 gg_id:486153 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu319e11 GQ023
DQ683348.1 gg_id:172621 Deinococcus piscis str. 3ax DQ683
NR_026421.1 gg_id:555743 Meiothermus cerbereus str. GY-1 NR_02
DQ916146.1 gg_id:167558 Meiothermus rosaceus str. WQBGR2-3 DQ916
NR_027614.1 gg_id:543137 Meiothermus ruber 1279 str. DSM 1279; ATCC 35948 NR_02
AJ871173.1 gg_id:114851 Meiothermus ruber str. SPS-242 AJ8711
X84211.1 gg_id:1405 Meiothermus silvanus str. V1-R2 X84211
AF418002.1 gg_id:20802 Meiothermus taiwanensis str. WR-220 AF418
AF418001.1 gg_id:26209 Meiothermus taiwanensis str. WR-30 AF418
AJ871171.1 gg_id:114643 Meiothermus timidus str. RQ-12 AJ8711
DQ899883.1 gg_id:238702 structure receiving long-term augmentations chromium contaminated wastes landfi DQ899
NR_026244.1 gg_id:540285 Meiothermus chliarophilus str. ALT-8; ATCC 700543; BCRC 17113 NR_02
AJ871172.1 gg_id:114775 Meiothermus ruber str. SPS-241 AJ8711
L37521.1 gg_id:1398 Thermus sp str. ac-2 L37521
FN178497.1 gg_id:573829 Meiothermus sp. str. CAL-12 FN178
EU249978.1 gg_id:239060 Polyphasic description Pocillopora mucus secreted Pacillopora meandrina coral color EU249
AB107956.1 gg_id:85579 Oceanithermus desulfurans str. St55B AB107
Y18412.1 gg_id:35343 Thermus antranikianii str. HE-5 Y18412
NR_026501.1 gg_id:533728 Thermus igniterrae str. RF-4; DSM 12459 NR_02

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EU214609.1 gg_id:323841 Thermus thermophilus yb60g EU214
EU616794.1 gg_id:273039 Thermus thermophilus str. WG EU616
AY557603.1 gg_id:105041 Thermus yunnanensis AY557
NR_025901.1 gg_id:535809 Thermus filiformis str. Wai33; ATCC 43280 NR_02
Y18409.1 gg_id:30085 Thermus brockianus str. 15038T Y18409
Y18416.1 gg_id:45920 Thermus oshimai str. SPS-17T Y18416
AF018197.1 gg_id:1324 temperature clone env.OPS 15 AF018
L09663.1 gg_id:1345 Thermus aquaticus L09663
AF331969.1 gg_id:41572 Thermus rehai str. RH99-02 AF331
FJ638543.1 gg_id:511615 Temperature dependent succession sulfate reducing muddy southwestern Taiwan hc FJ6385
GU233838.1 gg_id:537430 effects temperature pH salinity and sinter growth rate on microbial Icelandic waters GU233
AY861866.1 gg_id:112463 Obsidian Pool prime community clone OPPB146 AY861
AF020205.1 gg_id:1335 Thermus scotoductus str. SA-01 AF020
EU701067.3 gg_id:290466 Thermus sp. str. K-39 EU701
Y18408.1 gg_id:47782 Thermus igniterrae str. GE-2 Y18408
EU924248.1 gg_id:326104 Microbiology and geochemistry Little Hot Creek hot spring sediment temperature 8C EU924
AB071811.1 gg_id:24092 Thermus kawarayuensis str. KW11 AB071
EU753248.1 gg_id:352672 Thermus sp. str. PRI-2268 EU753
AY028380.1 gg_id:67904 Thermus sp. str. C4 AY028
AF521188.1 gg_id:63588 Thermus sp. str. RH-1514 AF521
L77877.1 gg_id:106875 Thermothrix thiopara L77877
L37522.1 gg_id:1357 Thermus sp str. ac-7 L37522
AF255591.1 gg_id:17962 Thermus sp. str. SRI-248 AF255
Y18410.1 gg_id:26144 Thermus scotoductus str. ITI-252T Y18410
AJ507298.1 gg_id:60062 Vulcanithermus mediatlanticus str. TR AJ5072
DQ832056.1 gg_id:165232 Geochemical Controls on Microbial Rainbow and Springs Yellowstone National Park . DQ832
DQ832059.1 gg_id:165655 Geochemical Controls on Microbial Rainbow and Springs Yellowstone National Park . DQ832
NR_028639.1 gg_id:540517 Marinithermus hydrothermalis str. T1; JCM 11576 NR_02
DQ832060.1 gg_id:173448 Geochemical Controls on Microbial Rainbow and Springs Yellowstone National Park . DQ832
DQ924664.1 gg_id:177658 Microbial Norris Geyser Basin Yellowstone National Park Cistern Hot Spring clone BV DQ924
DQ924670.1 gg_id:189281 Microbial Norris Geyser Basin Yellowstone National Park Cistern Hot Spring clone BV DQ924
EU435435.1 gg_id:273276 Thermodesulfatator sp. str. AT1325 EU435
AJ969460.1 gg_id:157635 Microbial black smoker s Mid Atlantic Ridge ecological implications rock fragments ch AJ9694
AY280428.1 gg_id:102075 exterior deep-sea hydrothermal vent sulfide chimney Juan de Fuca Ridge Pacific Oce AY2804
AB282756.1 gg_id:230931 Thermosulfidobacterium lithotrophicum str. ABI70S6 (= JCM13301 = DSM 17441 AB282
EU635930.1 gg_id:279109 Microbiology geochemistry great boiling and mud springs sediment hot spring; temp EU635
EF077228.1 gg_id:253157 Anaerobic oxidation short-chain hydrocarbons marine sulphate-reducing Guaymas B EF0772
AM712345.1 gg_id:247140 detection and ly microbial Brothers Seamount Kermadec Arc New Zealand biofilm h AM712
NR_025146.1 gg_id:570497 Thermodesulfobacterium hydrogeniphilum str. SL6; DSM 14290 NR_02
FJ638609.1 gg_id:537018 Temperature dependent succession sulfate reducing muddy southwestern Taiwan hc FJ6386
AF419676.1 gg_id:25647 Guaymas Basin hydrothermal sediment clone a2b002 AF419

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EU851047.2 gg_id:325520 Fervidobacterium sp. str. 1445t EU851
AF509468.1 gg_id:66261 Geotoga aestuarianus str. T3B AF5094
EU245202.1 gg_id:245616 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-H4-A11 EU245
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CP001634.1 gg_id:422862 Kosmotoga olearia str. TBF 19.5.1 CP001
CU918298.1 gg_id:557400 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU918
EU542473.1 gg_id:258468 Effects chemical structure concentration on pathways microbial during dechlorinatio EU542
FJ901103.1 gg_id:540611 Polymorphism microbial reservoirs water cut stage oil field clone Z-49 FJ9011
AB530678.1 gg_id:539611 Kosmotoga sp. str. S304 AB530
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AJ250439.1 gg_id:1220 Marinitoga camini MV1075 AJ2504
FM253687.1 gg_id:341893 Marinitoga sp. str. MC3 FM253
AJ431249.1 gg_id:79381 Thermotogales str. Dex60-32 AJ4312
DQ834030.1 gg_id:167691 Geochemical Controls on Microbial Rainbow and Springs Yellowstone National Park DQ834
CP000879.1 gg_id:256420 Petrotoga mobilis str. SJ95 CP000
EU999020.1 gg_id:321922 Predominance Methanolobus and Methanoculleus spp. Archaeal Saline Gas Field Fo EU999
GQ385331.1 gg_id:575997 Petrotoga sp. str. AR80 GQ385
NR_029058.1 gg_id:590603 Petrotoga mexicana str. Met-12; DSM 14811; CIP 107371 NR_02
EU878330.1 gg_id:550151 Investigation factors influencing production large-scale municipal biogas plant therm EU878
EU639044.1 gg_id:325788 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU639
EU639299.1 gg_id:338480 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU639
EU639355.1 gg_id:316749 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU639
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CP000716.1 gg_id:243559 Thermosipho melanesiensis str. BI429 CP000
AJ272022.2 gg_id:40837 Thermosipho geolei str. DSM 13256 AJ2720
AF491334.1 gg_id:83498 Thermosipho ferriphilus str. GB21 AF4913
AJ577471.1 gg_id:90392 Thermosipho atlanticus str. DV1140 AJ5774
AB024932.1 gg_id:1231 Thermosipho japonicus str. IHB1 AB024

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EU924246.1 gg_id:303956 Microbiology and geochemistry Little Hot Creek hot spring sediment temperature 8 EU924
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AY526506.1 gg_id:136778 Microbial thermophilic anaerobic sludge methanol-fed lab scale bioreactor clone H8 AY526
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FJ466109.1 gg_id:571249 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea FJ4661
FJ542881.1 gg_id:528972 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone A FJ5428
GU172187.1 gg_id:555087 Microbial Eucalyptus plantation soil clone DSM-R15 GU172
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AY571850.1 gg_id:107654 hydrocarbon-contaminated soil clone 342B AY5718
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AF507687.1 gg_id:111978 forest soil clone C129 AF5076
EU135387.1 gg_id:248392 tallgrass prarie soil clone FFCH16289 EU135
EU104333.1 gg_id:321742 Evidence Comamonadaceae determinants settling performance activated sludge clo EU104
DQ906081.1 gg_id:223958 nickel resistance genes metagenome Tinto River rhizosphere clone ERF-G10 DQ906
AM991156.1 gg_id:279572 Microbial groundwater and their potential use biomonitoring karst spring water clo AM991
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FJ542918.1 gg_id:515209 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone A FJ5429
EU703288.1 gg_id:566066 taxon richness -altitude lakes eastern tin plateau predominance Bacteroidetes and S EU703
EF688335.1 gg_id:238281 soil clone F1-127 EF6883
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DQ451478.1 gg_id:156885 forest soil clone FAC39 DQ451
DQ404603.1 gg_id:153216 contaminated sediment clone 656047 DQ404
AJ318136.1 gg_id:26128 Waste-gas biofilter clone BIgi18 AJ3181
DQ404740.1 gg_id:154332 contaminated sediment clone 655080 DQ404
EU381500.1 gg_id:275085 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid EU381
EU381884.1 gg_id:258263 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU381

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EU475226.1 gg_id:290144 bonobo feces clone BNO_aaa02b03 EU4752
FJ881207.1 gg_id:397321 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8812
DQ815554.1 gg_id:169081 mouse cecum clone aab42f07 DQ815
AM932658.1 gg_id:573677 microbiota Toll-like receptor 2 deficient mice exhibits lineage specific modifications AM932
DQ815839.1 gg_id:169901 mouse cecum clone aab23a06 DQ815
AF432141.1 gg_id:17020 oral clone FR058 AF4321
EU431764.1 gg_id:575675 Troglobitic (Cansiliella) on specialized feeding apparatus calcium carbonate (moonmi EU4317
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FJ470446.1 gg_id:537729 Chinese human cavities healthy oral cavity clone A_D_01_89 FJ4704
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CU917574.1 gg_id:569517 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU9175
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AF015925.1 gg_id:13724 hot spring clone OctSpA1-106 AF015
AF419683.1 gg_id:112352 Guaymas Basin hydrothermal sediment clone CS_B017 AF419
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AY661974.1 gg_id:136998 uranium-contaminated groundwater clone 300G-H06 AY661
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AJ575730.1 gg_id:96609 lake water clone SW59 AJ5757
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AB369179.1 gg_id:245910 Microbiological Assessment Circulation Mud Fluids During First Operation Drilling De AB369
GQ502665.1 gg_id:542290 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf9- GQ502
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FJ444768.1 gg_id:587631 Cotton Rhizosphere cotton rhizosphere clone 4y-121 FJ4447
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EU015115.1 gg_id:253831 Investigation estrogen-degrading bioreactors membrane bioreactor suspension and EU015
AB286360.1 gg_id:216828 Reducing production and domination comamonadaceae reducing oxygen supply was AB286
AB062814.1 gg_id:18774 termite gut homogenate clone BCf3-05 AB0628
EU135529.1 gg_id:246267 tallgrass prarie soil clone FFCH9358 EU135
AY622244.1 gg_id:107299 subsurface soil clone B-I12 AY622
DQ097276.1 gg_id:160664 Encapsulating and growing '' Majority mucus coral Fungia granulosa clone RS.Sph.0C DQ097
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AB299565.1 gg_id:241161 Motility Symbiont Termite Gut Flagellate Caduceia versatilis Member 'Synergistes' G AB299
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EU803670.1 gg_id:338096 It's all ranking aquatic Lake Gatun clone 5C231275 EU803
DQ302114.1 gg_id:153206 Rubromonas marinus gen. sp. nov. first marine representative subdivision one Verru DQ302
FM242275.1 gg_id:341545 sequences sediment clone 13bis T0h-oil FM242
GQ347889.1 gg_id:585626 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ347
U81738.2 gg_id:1556 anaerobic digestor clone vadinHA64 U81738
AY695840.1 gg_id:105129 Opitutus sp. str. SA-9 AY6958
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AJ240909.1 gg_id:74031 marine clone CHAB-II-49 AJ2409
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AB198611.1 gg_id:135899 termite gut fluid and protists fraction clone RsC01-040 AB198
EU283474.1 gg_id:278788 Model Early Earth Harbors Deeply Divergent Divisions Anderson Lake clone A210 EU2834
AB299566.1 gg_id:256775 Motility Symbiont Termite Gut Flagellate Caduceia versatilis Member 'Synergistes' G AB299
AB073978.1 gg_id:41135 Fucophilus fucoidanolyticus str. SI-1234 AB073
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AB192188.1 gg_id:143442 termite gut homogenate clone RsTz-69 AB192
FJ516822.1 gg_id:513750 semiarid 'Tablas de Daimiel National Park' wetland (Central Spain) unravelled biofilm FJ5168
AF075271.2 gg_id:9675 Alterococcus agarolyticus str. ADT3; CCRC17102 AF075
FJ717327.1 gg_id:535151 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United Kingc FJ7173
FJ717277.1 gg_id:511489 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United Kingc FJ7172
FJ717325.1 gg_id:510475 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United Kingc FJ7173
AY114312.1 gg_id:72268 anoxic marine sediment clone LD1-PA15 AY1143
AB189371.1 gg_id:114335 cold seep sediment clone JT75-134 AB189
AF449255.1 gg_id:61856 vent worm clone R76-B128 AF449

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FJ717311.1 gg_id:572386 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United Kingc FJ7173
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FJ717291.1 gg_id:548455 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United Kingc FJ7172
EU804364.1 gg_id:341372 It's all ranking aquatic 250 miles Panama City clone 6C232274 EU804
DQ513023.1 gg_id:160321 Microbial life fluids ridge flank crustal fluid clone FS142-12B-02 DQ513
AY222315.1 gg_id:113883 host hindgut caecum clone Ver 1 AY222
EF520620.1 gg_id:232855 structure lakes: what controls ? acid-impacted lake clone ADK-BTh02-31 EF5206
AJ575731.1 gg_id:97376 lake water clone NE06 AJ5757
EU703279.1 gg_id:554393 taxon richness -altitude lakes eastern tin plateau predominance Bacteroidetes and S EU703
EF520637.1 gg_id:231528 structure lakes: what controls ? acid-impacted lake clone ADK-HDh02-03 EF5206
AY752089.1 gg_id:99083 lake water clone P38.12 AY752
FJ543046.1 gg_id:519253 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone B FJ5430
FJ543079.1 gg_id:527379 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone B FJ5430
AJ863245.1 gg_id:127649 poplar tree microcosm, bulk soil, flooded clone 21BSF50 AJ8632
EF516165.1 gg_id:221896 grassland soil clone FCPP479 EF5161
FJ612408.1 gg_id:535790 and Biogeochemistry Dongping Lake Ecosystems lake water clone DP10.4.22 FJ6124
AY792308.1 gg_id:123679 Humic Lake clone CrystalBog1B6 AY7923
AB369162.1 gg_id:256945 Microbiological Assessment Circulation Mud Fluids During First Operation Drilling De AB369
AY388649.1 gg_id:108024 Chthoniobacter flavus AY3886
DQ450786.1 gg_id:160871 Microbial Alpine Tundra Wet Meadow Soil: Chloroflexi Cold Water-Saturated saturat DQ450
EF516096.1 gg_id:224503 grassland soil clone FCPT710 EF5160
EF515981.1 gg_id:220364 grassland soil clone FCPT465 EF5159
EF516968.1 gg_id:223379 grassland soil clone FCPS729 EF5169
FJ822655.1 gg_id:588551 and metagenomic Verrucomicrobia former agricultural grassland soil rhizosphere clor FJ8226
AY960766.1 gg_id:115027 Detection and Cultivation Soil Verrucomicrobia Ellin503 AY9607
EU135441.1 gg_id:251499 tallgrass prarie soil clone FFCH5517 EU1354
AB486453.1 gg_id:588961 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC AB486
AB374368.1 gg_id:270180 sequences Weissenstein (white rock) / few millimeters be surface rock called 'Weiss AB3743
GQ402701.1 gg_id:541789 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
EF516529.1 gg_id:221334 grassland soil clone FCPN729 EF5165
FJ822636.1 gg_id:535268 and metagenomic Verrucomicrobia former agricultural grassland soil rhizosphere clor FJ8226
GQ397058.1 gg_id:538238 Functional unvegetated perhumid recently-deglaciated soils do not correlate shifts s GQ397
FM877557.1 gg_id:358664 Microbial several mining wastes Bulgaria uranium mill tailings clone BuhD-321 FM877
AY960770.1 gg_id:114998 Detection and Cultivation Soil Verrucomicrobia Ellin507 AY9607

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EU131041.1 gg_id:236458 alkaline China coal mine soil clone SIP CM42 EU131
EU644180.1 gg_id:286072 and Samoylov Island Lena active layer -centred polygon near surface horizon; Rim_T EU644
EF018510.1 gg_id:214306 aspen rhizosphere clone Amb_16S_1148 EF0185
EF018524.1 gg_id:207125 aspen rhizosphere clone Amb_16S_784 EF0185
GQ264267.1 gg_id:511817 Structure Simulated Level Waste Site simulated level waste site clone WW1_b71 GQ264
FJ822653.1 gg_id:554650 and metagenomic Verrucomicrobia former agricultural grassland soil rhizosphere clor FJ8226
DQ228393.1 gg_id:142335 microbial compositions two subglacial possible role microbes chemical weathering p DQ228
EU135556.1 gg_id:249859 tallgrass prarie soil clone FFCH4930 EU135
AY212589.1 gg_id:104784 water 10 m downstream manure clone 139ds10 AY212
FM253596.1 gg_id:325609 Rock gold mine unusually microbial biofilm clone D07-1 FM253
AY960769.1 gg_id:115085 Detection and Cultivation Soil Verrucomicrobia Ellin506 AY960
EU881176.1 gg_id:354713 Karst region natural restoration land soil clone KNR200711-119 EU881
AY395330.1 gg_id:100320 pasture soil clone EB1011 AY395
AY326520.1 gg_id:136989 Amazon soil clone 28-1 AY326
AY218772.1 gg_id:82424 penguin droppings sediments clone KD6-84 AY218
AY395325.1 gg_id:104976 pasture soil clone EB1006 AY395
EF018259.1 gg_id:213922 aspen rhizosphere clone Amb_16S_615 EF0182
EF516966.1 gg_id:223148 grassland soil clone FCPS574 EF5169
EF494340.1 gg_id:222682 Nunnock River granitic landscape clone NR.1.035 EF4943
EF516048.1 gg_id:222701 grassland soil clone FCPS405 EF5160
FJ592654.1 gg_id:557191 Fumarole-supported islands biodiversity within hyperarid -elevation landscape on Pu FJ5926
Y07576.1 gg_id:1624 grassland soil clone DA101 Y07576
DQ298012.1 gg_id:143982 Microbial hydrocarbon contaminated soil clone UA4 DQ298
EU881274.1 gg_id:335630 (long-term grazing and burned annual) Karst region serious disturbance field soil clor EU881
EF018412.1 gg_id:213519 aspen rhizosphere clone Amb_16S_1028 EF0184
EU861826.1 gg_id:320598 effects chronic fertilization on alpine tundra microbial implications carbon and nitrog EU861
EU881282.1 gg_id:320201 (long-term grazing and burned annual) Karst region serious disturbance field soil clor EU881
EF494343.1 gg_id:227202 Nunnock River granitic landscape clone NR.1.076 EF4943
DQ404689.1 gg_id:154629 contaminated sediment clone 655902 DQ404
FJ822650.1 gg_id:582528 and metagenomic Verrucomicrobia former agricultural grassland rhizosphere soil clor FJ8226
EF019688.1 gg_id:214739 aspen rhizosphere clone Elev_16S_849 EF0196
EF516045.1 gg_id:217322 grassland soil clone FCPN578 EF5160
DQ395984.1 gg_id:155782 deep-sea octacoral clone ctg_CGOGA62 DQ395
EF019129.1 gg_id:212017 aspen rhizosphere clone Amb_16S_1762 EF0191
EF516305.1 gg_id:225899 grassland soil clone FCPN716 EF5163
EU335341.1 gg_id:241683 Changes microbial metabolic and along hydrogeochemically variable profile unsatura EU335
EF019121.1 gg_id:206632 aspen rhizosphere clone Amb_16S_1750 EF0191
FM877556.1 gg_id:359072 Microbial several mining wastes Bulgaria uranium mill tailings clone BuhD-107 FM877
EF018766.1 gg_id:206493 aspen rhizosphere clone Amb_16S_1227 EF0187
EF516889.1 gg_id:220177 grassland soil clone FCPO660 EF5168

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EF516261.1 gg_id:220494 grassland soil clone FCPO467 EF5162
EF019883.1 gg_id:211980 aspen rhizosphere clone Elev_16S_1248 EF0198
GQ356142.1 gg_id:594250 biomarkers ammonia oxidation activity anaerobic ammonium-oxidation (Anammox) GQ356
CU919143.1 gg_id:572340 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU919
CU918228.1 gg_id:549254 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU918
CU920760.1 gg_id:571409 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU920
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EU471776.1 gg_id:294166 Asiatic elephant feces clone AE2_aaa01b10 EU471
EU771419.1 gg_id:339447 Asiatic elephant feces clone AE1_aaa02h11 EU771
EU463717.1 gg_id:297614 domesticated horse feces clone horsej_aai91e11 EU463
EU471538.1 gg_id:291474 Asiatic elephant feces clone AE1_aaa02e02 EU471
EU471740.1 gg_id:291133 Asiatic elephant feces clone AE2_aaa04d02 EU471
EU473570.1 gg_id:300038 Somali wild ass feces clone WA_aaa01g06 EU473
EU775815.1 gg_id:338441 Horse feces clone horsem_aai95h08 EU775
EU471942.1 gg_id:292730 Asiatic elephant feces clone AE3_aaa04e08 EU471
EU471839.1 gg_id:298259 Asiatic elephant feces clone AE2_aaa02c03 EU471
EU471710.1 gg_id:288899 Asiatic elephant feces clone AE2_aaa01a07 EU471
EU773126.1 gg_id:349774 Banteng feces clone BG_aaa02h07.Contig1 EU773
AB185519.1 gg_id:99547 rumen clone F23-B04 AB185
EU470381.1 gg_id:298808 Grevy's zebra feces clone GZ_aaa02b08 EU470
EU776446.1 gg_id:326916 Red Kangaroo feces clone KO2_aai18a10 EU776
EU864491.1 gg_id:327984 structures under selection pressure levels antibiotics Xiao River receiving treated ox EU864
AB015546.1 gg_id:203309 deep-sea sediments depths clone BD2-18 AB015
AY114334.1 gg_id:63771 anoxic marine sediment clone LD1-PB20 AY114
CU920931.1 gg_id:556915 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU920
GQ259319.1 gg_id:534591 Microbial activities coastal marine sediments and water column Svalbard surface se GQ259
FN396736.1 gg_id:546665 constant flux thermophilic cold seabed Arctic marine surface sediment clone s5_8_II FN396
AY114328.1 gg_id:70013 anoxic marine sediment clone LD1-PA50 AY114
AY963317.1 gg_id:151682 structures and correlated ecological factors soils two evergreen broad-leaved forests AY963
EU881223.1 gg_id:333383 Karst region natural restoration land soil clone KNR200711-042 EU881
EU135433.1 gg_id:257941 tallgrass prarie soil clone FFCH3955 EU135
AM162463.1 gg_id:154318 and situ identification acidic sphagnum peat bog clone B69 AM162
EU135525.1 gg_id:236593 tallgrass prarie soil clone FFCH8458 EU135
EU135455.1 gg_id:240895 tallgrass prarie soil clone FFCH1225 EU135
EF516767.1 gg_id:220193 grassland soil clone FCPT575 EF5167
EU135479.1 gg_id:251458 tallgrass prarie soil clone FFCH10633 EU135
AF465651.1 gg_id:50325 thermal soil clone YNPRH34A AF465
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EF516676.1 gg_id:221568 grassland soil clone FCPO598 EF5166
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AY212643.1 gg_id:107428 water 20 m upstream manure clone 190up AY2126
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FM209351.1 gg_id:567812 Microbial Negev desert s sand soil clone 2031 FM209
AM162456.1 gg_id:155778 and situ identification acidic sphagnum peat bog clone B52 AM162
FJ625341.1 gg_id:551837 Influence lead contamination on boreal pine forest soil clone HF_NC_2 FJ6253
AM162459.1 gg_id:151165 and situ identification acidic sphagnum peat bog clone B129 AM162
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AJ617869.1 gg_id:110756 oxic-anoxic interphase flooded paddy soil clone D142114 AJ6178
EF516552.1 gg_id:217929 grassland soil clone FCPU600 EF5165
DQ125505.1 gg_id:132722 uranium contaminated soil clone AKAU3464 DQ125
FJ479069.1 gg_id:590252 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4790
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EF516075.1 gg_id:223550 grassland soil clone FCPT406 EF5160
DQ450782.1 gg_id:161263 Microbial Alpine Tundra Wet Meadow Soil: Chloroflexi Cold Water-Saturated satura DQ450
EU937949.1 gg_id:321753 Biogeochemistry Iron Oxidation Circumneutral Freshwater Habitat riparian iron oxidi EU937
EF515942.1 gg_id:225894 grassland soil clone FCPP485 EF5159
FJ468383.1 gg_id:585431 Bioaugmentation Pseudomonas sp. strain MHP41 promotes attenuation and changes FJ4683
EU135478.1 gg_id:250253 tallgrass prarie soil clone FFCH10577 EU135
EU135518.1 gg_id:253183 tallgrass prarie soil clone FFCH17360 EU135
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EF612425.1 gg_id:248066 historic semiarid lead-zinc mine tailings site soil clone OS-C04 EF6124
EF019315.1 gg_id:206560 aspen rhizosphere clone Elev_16S_510 EF0193
AM162462.1 gg_id:155827 and situ identification acidic sphagnum peat bog clone B64 AM162
GU444057.1 gg_id:523991 Effects amendments on fertility and microbial structure cucumber Cucumis sativus L GU444
AM162461.1 gg_id:151640 and situ identification acidic sphagnum peat bog clone B147 AM162
DQ521482.1 gg_id:186160 Antarctic lake ice cover clone ANTLV1_D01 DQ521
EU135543.1 gg_id:248805 tallgrass prarie soil clone FFCH18403 EU135
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EU135514.1 gg_id:257782 tallgrass prarie soil clone FFCH15477 EU1355
EF020079.1 gg_id:207326 aspen rhizosphere clone Elev_16S_1488 EF0200
FJ592707.1 gg_id:543327 Fumarole-supported islands biodiversity within hyperarid -elevation landscape on Pu FJ5927
EU335255.1 gg_id:241999 Changes microbial metabolic and along hydrogeochemically variable profile unsatura EU3352
EF516775.1 gg_id:218032 grassland soil clone FCPU668 EF5167
GQ348914.1 gg_id:560563 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ348
FJ155059.1 gg_id:318309 seasonal fluctuation coastal Bohai Bay sequencing and RFLP soil clone CB FJ1550
GQ348513.1 gg_id:542753 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ348
GQ348797.1 gg_id:535223 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ348
DQ302118.1 gg_id:156301 Rubromonas marinus gen. sp. nov. first marine representative subdivision one Verru DQ302
FJ628330.1 gg_id:513658 transition and zone within near-shore basin: brackish water anoxic fjord Nitinat Lake FJ6283
FJ615181.1 gg_id:544538 Microbial dynamics seasonally fjord: British Columbia Saanich Inlet depth 125m anoxi FJ6151
FJ615159.1 gg_id:557490 Microbial dynamics seasonally fjord: British Columbia Saanich Inlet depth 100m anoxi FJ6151
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AY028219.1 gg_id:32593 marine clone Arctic97B-4 AY0282
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GU061235.1 gg_id:574533 Evaluation culturing methods cultivate previously Yel Sea intertidal beach seawater GU061
GU208329.1 gg_id:570490 Study on Sediment Dongping Lake sediment clone Se2-17 GU208
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EU135432.1 gg_id:254690 tallgrass prarie soil clone FFCH13487 EU1354
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EU135494.1 gg_id:237927 tallgrass prarie soil clone FFCH12670 EU1354
EU937926.1 gg_id:337426 Biogeochemistry Iron Oxidation Circumneutral Freshwater Habitat riparian iron oxidi EU9379
AJ853567.1 gg_id:110302 landfill leachate clone GZKB73 AJ8535
CU917597.1 gg_id:546967 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU9175
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FM994912.1 gg_id:550907 springs Velingrad region Bulgaria hot spring Mizinka clone VS-21 FM994
EU104111.1 gg_id:310462 Evidence Comamonadaceae determinants settling performance activated sludge clo EU1041
DQ017913.1 gg_id:134130 upland stream clone S-Btb7_11 DQ017
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FJ905685.1 gg_id:535898 s Tonga-Kermadec iron oxide chimney-like structure on Volcano 19 Tonga Arc clone V FJ9056
EF516930.1 gg_id:225632 grassland soil clone FCPN502 EF5169
EF516856.1 gg_id:224253 grassland soil clone FCPS671 EF5168
EF018903.1 gg_id:212324 aspen rhizosphere clone Amb_16S_1397 EF0189
AY395425.1 gg_id:102024 pasture soil clone EB1106 AY3954
FJ478519.1 gg_id:536090 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4785

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DQ451523.1 gg_id:156917 forest soil clone FAC84 DQ451
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EF099597.1 gg_id:184418 mouse cecum clone SWPT4_aaa01f05 EF0995
EU459611.1 gg_id:291051 ring-tailed lemur feces clone RT_aai09c04 EU459
EF099110.1 gg_id:192171 mouse cecum clone SWPT2_aaa02d09 EF0991
CP001071.1 gg_id:278234 Akkermansia muciniphila str. ATCC BAA-835 CP001
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DQ805338.1 gg_id:177459 human fecal clone RL203_aai61d02 DQ805
EU508722.1 gg_id:262854 cecal contents Mus musculus strain C57BL/6J; MD4 clone MD4_aap49h09 EU508
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EF604904.1 gg_id:230139 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous(EF6049
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EU459638.1 gg_id:298839 ring-tailed lemur feces clone RT_aai09g05 EU459
EU763463.1 gg_id:345321 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A4 EU7634
EF604517.1 gg_id:234298 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous(EF6045
DQ793539.1 gg_id:178086 human fecal clone RL246_aai73b07 DQ793
AY977829.1 gg_id:118714 human cecum mucosal biopsy clone LF22 AY9778
EU506706.1 gg_id:261175 cecal contents Mus musculus strain C57BL/6J; MD20 clone MD20_aap54h02 EU506
DQ807201.1 gg_id:185152 human fecal clone RL244_aaj47e04 DQ807
DQ805485.1 gg_id:174822 human fecal clone RL203_aai63c06 DQ805
DQ805597.1 gg_id:177705 human fecal clone RL203_aai64g05 DQ805
EU506506.1 gg_id:274986 cecal contents Mus musculus strain C57BL/6J; MD19 clone MD19_aaa03b03 EU506
DQ805539.1 gg_id:185779 human fecal clone RL203_aai64a01 DQ805
FJ365265.1 gg_id:368894 feces adult twins and mothers; TS1 clone TS1_a04g10 FJ3652
AJ408970.1 gg_id:31006 human colonic clone HuCA18 AJ4089
EU507500.1 gg_id:258589 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_2aaa04b09 EU507
FJ364958.1 gg_id:359195 feces adult twins and mothers; TS1 clone TS1_a01c01 FJ3649
AY986145.1 gg_id:116910 human stool clone D491 AY986
EU006397.1 gg_id:255263 Salmonella enterica serovar typhimurium exploits inflammation compete intestinal r EU006
DQ805319.1 gg_id:195328 human fecal clone RL203_aai61b04 DQ805
EU763313.1 gg_id:334717 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A4 EU763
FJ365018.1 gg_id:365334 feces adult twins and mothers; TS1 clone TS1_a01h05 FJ3650
DQ803989.1 gg_id:181549 human fecal clone RL200_aai60g06 DQ803
DQ805473.1 gg_id:197876 human fecal clone RL203_aai63b03 DQ805

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EU939409.1 gg_id:335768 Fecal wild pygmy loris feces clone WF16S_131 EU939
DQ803720.1 gg_id:179163 human fecal clone RL200_aai57e09 DQ803
DQ803687.1 gg_id:177813 human fecal clone RL200_aai57b09 DQ803
EU763746.1 gg_id:346624 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU763
EF099090.1 gg_id:180789 mouse cecum clone SWPT2_aaa02b02 EF099
EF099511.1 gg_id:185740 mouse cecum clone SWPT3_aaa04b11 EF099
DQ805333.1 gg_id:187220 human fecal clone RL203_aai61c08 DQ805
EF099126.1 gg_id:181513 mouse cecum clone SWPT2_aaa02f08 EF099
FJ371231.1 gg_id:359222 feces adult twins and mothers; TS6 clone TS6_a02e02 FJ3712
FJ364037.1 gg_id:360894 feces adult twins and mothers; TS150 clone TS150_a02c03 FJ3640
FJ365015.1 gg_id:367987 feces adult twins and mothers; TS1 clone TS1_a01h02 FJ3650
EU768083.1 gg_id:340215 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C EU768
FJ364103.1 gg_id:366847 feces adult twins and mothers; TS150 clone TS150_a03a07 FJ3641
EF098492.1 gg_id:197822 mouse cecum clone SWPT15_aaa04b09 EF0984
DQ805416.1 gg_id:197098 human fecal clone RL203_aai62d02 DQ805
FJ371195.1 gg_id:361687 feces adult twins and mothers; TS6 clone TS6_a02a08 FJ3711
FJ366647.1 gg_id:361853 feces adult twins and mothers; TS27 clone TS27_a02b07 FJ3666
FJ363943.1 gg_id:359085 feces adult twins and mothers; TS150 clone TS150_a01b10 FJ3639
DQ793729.1 gg_id:185943 human fecal clone RL246_aai76c11 DQ793
FJ369647.1 gg_id:366053 feces adult twins and mothers; TS51 clone TS51_a03b08 FJ3696
FJ369644.1 gg_id:366982 feces adult twins and mothers; TS51 clone TS51_a03b04 FJ3696
EF099031.1 gg_id:188922 mouse cecum clone SWPT2_aaa01c10 EF099
FJ369652.1 gg_id:365331 feces adult twins and mothers; TS51 clone TS51_a03c03 FJ3696
EU768211.1 gg_id:349733 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C EU768
FJ364059.1 gg_id:368699 feces adult twins and mothers; TS150 clone TS150_a02e04 FJ3640
DQ803799.1 gg_id:180056 human fecal clone RL200_aai58e09 DQ803
DQ806904.1 gg_id:187104 human fecal clone RL198_aaj75b08 DQ806
EU768169.1 gg_id:344643 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C EU768
DQ803992.1 gg_id:185431 human fecal clone RL200_aai60g09 DQ803
FJ371678.1 gg_id:366631 feces adult twins and mothers; TS8 clone TS8_a01a06 FJ3716
FJ365028.1 gg_id:359843 feces adult twins and mothers; TS1 clone TS1_a02a04 FJ3650
EU506426.1 gg_id:277079 cecal contents Mus musculus strain C57BL/6J; MD19 clone MD19_aaa01e12 EU506
FJ371109.1 gg_id:358268 feces adult twins and mothers; TS6 clone TS6_a01a10 FJ3711
AY978065.1 gg_id:120670 human cecum mucosal biopsy clone LI24 AY978
DQ805371.1 gg_id:191984 human fecal clone RL203_aai61g09 DQ805
DQ805313.1 gg_id:185545 human fecal clone RL203_aai61a06 DQ805
FJ369694.1 gg_id:359376 feces adult twins and mothers; TS51 clone TS51_a03f11 FJ3696
FJ371129.1 gg_id:364544 feces adult twins and mothers; TS6 clone TS6_a01c08 FJ3711
EU509276.1 gg_id:263476 cecal contents Mus musculus strain C57BL/6J; MD8 clone MD8_aap47a09 EU509

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FJ365053.1 gg_id:361231 feces adult twins and mothers; TS1 clone TS1_a02c08 FJ3650
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EU506534.1 gg_id:260817 cecal contents Mus musculus strain C57BL/6J; MD19 clone MD19_aaa03e12 EU506
DQ795501.1 gg_id:182004 human fecal clone RL178_aan65b11 DQ795
EU006176.1 gg_id:255048 Salmonella enterica serovar typhimurium exploits inflammation compete intestinal r EU006
DQ806760.1 gg_id:178399 human fecal clone RL186_aao48d05 DQ806
DQ803815.1 gg_id:197646 human fecal clone RL200_aai58g02 DQ803
EF098337.1 gg_id:191825 mouse cecum clone SWPT15_aaa01a11 EF0983
EF099264.1 gg_id:191956 mouse cecum clone SWPT2_aaa04g06 EF0992
EF099136.1 gg_id:191681 mouse cecum clone SWPT2_aaa02g09 EF0991
EF602830.1 gg_id:234575 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6028
DQ803955.1 gg_id:174718 human fecal clone RL200_aai60d02 DQ803
DQ793678.1 gg_id:173820 human fecal clone RL246_aai75e04 DQ793
GQ493064.1 gg_id:577245 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493

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FJ367560.1 gg_id:365237 feces adult twins and mothers; TS2 clone TS2_a01a04 FJ3675
DQ823974.1 gg_id:179397 human fecal clone RL204_aaj57f06 DQ823
GQ491465.1 gg_id:537012 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
EU506850.1 gg_id:260295 cecal contents Mus musculus strain C57BL/6J; MD21 clone MD21_aar07c08 EU506
DQ797870.1 gg_id:196376 human fecal clone RL206_aaj16g12 DQ797
EU006464.1 gg_id:245541 Salmonella enterica serovar typhimurium exploits inflammation compete intestinal r EU006
FJ367593.1 gg_id:359766 feces adult twins and mothers; TS2 clone TS2_a01d01 FJ3675
DQ805310.1 gg_id:177858 human fecal clone RL203_aai61a03 DQ805
EF605156.1 gg_id:227800 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6051
EF603774.1 gg_id:233386 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6037
EF099020.1 gg_id:180596 mouse cecum clone SWPT2_aaa01b09 EF099
GQ491995.1 gg_id:584653 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
EU006396.1 gg_id:251790 Salmonella enterica serovar typhimurium exploits inflammation compete intestinal r EU006
EU006177.1 gg_id:253234 Salmonella enterica serovar typhimurium exploits inflammation compete intestinal r EU006
FJ371421.1 gg_id:363508 feces adult twins and mothers; TS6 clone TS6_a04g05 FJ3714
EU507388.1 gg_id:276012 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_2aaa02e06 EU507
EU507089.1 gg_id:266625 cecal contents Mus musculus strain C57BL/6J; MD22 clone MD22_aaa01a11 EU507
AY979494.1 gg_id:123265 human transverse colon mucosal biopsy clone M135 AY979
DQ824431.1 gg_id:176638 human fecal clone RL304_aal75h11 DQ824
GQ491867.1 gg_id:579826 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
DQ803761.1 gg_id:190136 human fecal clone RL200_aai58b01 DQ803
DQ793686.1 gg_id:182478 human fecal clone RL246_aai75f02 DQ793
DQ803743.1 gg_id:194760 human fecal clone RL200_aai57h03 DQ803
EF603613.1 gg_id:233237 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6036
EF602796.1 gg_id:232549 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6027
DQ803928.1 gg_id:176439 human fecal clone RL200_aai60a08 DQ803
GQ492726.1 gg_id:543645 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
GQ492710.1 gg_id:533891 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
EU469988.1 gg_id:289362 trancaspain urial feces clone TU1_aaa03b07 EU469
GQ491356.1 gg_id:589626 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
DQ793673.1 gg_id:177438 human fecal clone RL246_aai75d08 DQ793
GQ493744.1 gg_id:562137 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
DQ803674.1 gg_id:182771 human fecal clone RL200_aai57a07 DQ803
DQ824465.1 gg_id:199450 human fecal clone RL304_aal76c12 DQ824
EU451703.1 gg_id:316576 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83 EU451
EU006404.1 gg_id:254430 Salmonella enterica serovar typhimurium exploits inflammation compete intestinal r EU006
EF605151.1 gg_id:234253 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6051
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DQ803856.1 gg_id:179974 human fecal clone RL200_aai59b12 DQ803

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EU474343.1 gg_id:297296 western lowland gorilla feces clone GORSD_aaa02d12 EU4743
DQ803801.1 gg_id:175615 human fecal clone RL200_aai58e11 DQ803
EU508365.1 gg_id:262989 cecal contents Mus musculus strain C57BL/6J; MD27 clone MD27_aaa03h06 EU5083
FJ367694.1 gg_id:364483 feces adult twins and mothers; TS2 clone TS2_a02e02 FJ3676
DQ797786.1 gg_id:197591 human fecal clone RL206_aaj15g12 DQ797
DQ824257.1 gg_id:192313 human fecal clone RL304_aal73f01 DQ824
EF605153.1 gg_id:232422 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6051
EF603066.1 gg_id:230664 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6030
EF099628.1 gg_id:184620 mouse cecum clone SWPT4_aaa02b07 EF0996
EF099133.1 gg_id:198936 mouse cecum clone SWPT2_aaa02g06 EF0991
EU507293.1 gg_id:262054 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_2aaa01c03 EU5072
GQ493815.1 gg_id:568909 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
EU509193.1 gg_id:268293 cecal contents Mus musculus strain C57BL/6J; MD8 clone MD8_aap45f10 EU5091
GQ448638.1 gg_id:544288 Microbiome neonatal calves: shedding microorganisms fecal clone calf784_6wks_gr GQ448
EU474260.1 gg_id:294287 western lowland gorilla feces clone GORSD_aaa03a03 EU4742
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EF099038.1 gg_id:178077 mouse cecum clone SWPT2_aaa01d08 EF0990
EU459692.1 gg_id:300791 ring-tailed lemur feces clone RT_aai10h12 EU4596
EF603938.1 gg_id:227678 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6039
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DQ824314.1 gg_id:194496 human fecal clone RL304_aal74d01 DQ824
GQ491874.1 gg_id:550767 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
EU508387.1 gg_id:270147 cecal contents Mus musculus strain C57BL/6J; MD27 clone MD27_aaa04g02 EU5083
EF604791.1 gg_id:232493 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6047
GQ492159.1 gg_id:561627 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
EU451506.1 gg_id:353432 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU4515
EF604911.1 gg_id:227993 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6049
DQ807255.1 gg_id:187988 human fecal clone RL244_aaj48b11 DQ807
GQ493932.1 gg_id:570491 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
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EU474294.1 gg_id:294378 western lowland gorilla feces clone GORSD_aaa03b05 EU4742
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EU506595.1 gg_id:269033 cecal contents Mus musculus strain C57BL/6J; MD20 clone MD20_aap53a03 EU5065
EF099070.1 gg_id:175442 mouse cecum clone SWPT2_aaa01g10 EF0990
EF099675.1 gg_id:187986 mouse cecum clone SWPT4_aaa02g06 EF0996
EF602794.1 gg_id:228401 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6027
EF099117.1 gg_id:180918 mouse cecum clone SWPT2_aaa02e08 EF0991
GQ492323.1 gg_id:588591 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
DQ803906.1 gg_id:183355 human fecal clone RL200_aai59g07 DQ803

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EU506859.1 gg_id:275140 cecal contents Mus musculus strain C57BL/6J; MD21 clone MD21_aar07d09 EU506
DQ302110.1 gg_id:153007 Rubromonas marinus gen. sp. nov. first marine representative subdivision one Verru DQ302
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AB252090.1 gg_id:155636 entrapped Puruogangri ice core clone PIC-D19 AB252
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GU208316.1 gg_id:546058 Study on Sediment Dongping Lake sediment clone Ser1-21 GU208
AB154319.1 gg_id:105709 freshwater clone S9JA-40 AB1543
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FJ437966.1 gg_id:511993 Benthic okenone production Fayetteville New York Green Lake surface sediments 16. FJ4379
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NR_026024.1 gg_id:564314 Prosthecobacter fusiformis str. FC4; ATCC 25309 NR_02
U60012.1 gg_id:1588 Prosthecobacter dejongeii U6001
U60013.1 gg_id:1593 Prosthecobacter vanneervenii str. FC2 U6001
EU104166.1 gg_id:319751 Evidence Comamonadaceae determinants settling performance activated sludge clo EU104
FJ612153.1 gg_id:585360 and Biogeochemistry Dongping Lake Ecosystems lake water clone DP3.2.74 FJ6121
EU580493.1 gg_id:556878 Benthic diatoms Constance: functional interactions regarding growth and EPS-secret EU5804
AY922120.1 gg_id:113378 farm soil clone AKYH1486 AY9221
AB305640.1 gg_id:248402 Prosthecobacter sp. str. HAQ-1 AB3056
EF516716.1 gg_id:225469 grassland soil clone FCPT546 EF5167
AB297805.1 gg_id:246659 Rubritalea spongiae str. YM21-132 AB2978

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AB240273.1 gg_id:142471 microbial structure rhizosphere Phragmites bulk soil reed bed reactor laboratory clor AB240
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EU245399.1 gg_id:253042 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M1-B1: EU2453
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FM242339.1 gg_id:308686 sequences sediment clone 6 T9d-oil FM242
EU491715.1 gg_id:264509 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU4917
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FJ437978.1 gg_id:513669 Benthic okenone production Fayetteville New York Green Lake surface sediments 16. FJ4379
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AJ009463.1 gg_id:12396 chlorobenzene-degrading consortium clone SJA-43 AJ0094
EF515388.1 gg_id:224753 Electricigen Enrichment MFC upf microbial fuel cell anode clone 23g04 EF5153
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EU385957.1 gg_id:261806 Stratified microbes sediments Core MD05-2902 subseafloor sediment South China S EU385
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EU491860.1 gg_id:264692 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU491
EU734965.1 gg_id:332707 assemblages sediment station DBSE Northern Bering Sea clone 059D21 EU734
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GQ850584.1 gg_id:565629 bottom water northern Bering Sea clone d148 GQ850
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GQ433939.1 gg_id:567951 Subseafloor ocean crust microbial observatories: (F-through Osmo Colonization Syst GQ433
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DQ067002.1 gg_id:130730 Lake Washington sediment clone pLW-100 DQ067
DQ811950.1 gg_id:170215 mangrove soil clone MSB-4E2 DQ811
EU592418.1 gg_id:572696 Seasonal changes Salton Sea hypersaline sediment clone SSS7N EU592
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DQ330720.1 gg_id:159127 Guerrero Negro hypersaline microbial mat clone 08D2Z74 DQ330
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EU385924.1 gg_id:259885 Stratified microbes sediments Core MD05-2902 subseafloor sediment South China S EU385
AY114332.1 gg_id:63773 anoxic marine sediment clone LD1-PB19 AY1143
FJ716267.1 gg_id:563562 Chlorobi dominate shal chemocline Bahamas Sawmill Sink column 10.3 m water dept FJ7162
FJ712501.1 gg_id:526723 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) K FJ7125
AM745159.1 gg_id:290797 Impact oil er hydrocarbons on microbial and activity Gulf Mexico cold seep marine s AM745
DQ067003.1 gg_id:131050 Lake Washington sediment clone pLW-69 DQ067
GQ500696.1 gg_id:556217 Surveys Biofilms and Sediments Mammoth Cave Karst Aquifers Charon's Cascade sa GQ500
EU528261.1 gg_id:281647 Seasonal Dynamics Mudflat Mouth Major Kentucky Lake Reservoir Tributary sedime EU528
AJ854267.1 gg_id:211083 Impact flooding on (Populus sp.) trees poplar tree microcosm bulk soil unflooded clor AJ8542
AJ582051.1 gg_id:94268 soil near uranium mill tailings clone JG36-GS-103 AJ5820
AJ390482.1 gg_id:22777 soil clone PRR-12 AJ3904
FJ479218.1 gg_id:570966 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4792
EU135569.1 gg_id:240877 tallgrass prarie soil clone FFCH3040 EU135
FJ479480.1 gg_id:540938 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4794
EF032778.1 gg_id:185827 cyanobacterial mat in lava cave clone HAVOmat06 EF0327
FJ478598.1 gg_id:553028 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4785
AM991194.1 gg_id:277712 Microbial groundwater and their potential use biomonitoring karst spring water clo AM991
AJ863228.1 gg_id:125819 poplar tree microcosm bulk soil flooded clone 21BSF64 AJ8632
AJ390458.1 gg_id:28793 soil clone PBS-III-30 AJ3904
EU135567.1 gg_id:242108 tallgrass prarie soil clone FFCH1818 EU135
EU135572.1 gg_id:243244 tallgrass prarie soil clone FFCH12488 EU135
AY921903.1 gg_id:113334 farm soil clone AKYG868 AY921
FJ479290.1 gg_id:585878 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4792
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AF280852.1 gg_id:45661 bioreactor clone mle1-16 AF280
FJ712468.1 gg_id:525404 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) K FJ7124
FN396645.1 gg_id:541341 constant flux thermophilic cold seabed Arctic marine surface sediment clone s5_0_I FN396
FJ484438.1 gg_id:567353 microbial autonomous rover world's deepest phreatic sinkhole wall biomat El Zacator FJ4844
EF999394.1 gg_id:247500 Vertical and Methanotrophs Estuarine Sediments Pearl River Estuary sediments 50cn EF9993
EF602491.1 gg_id:228206 metabolic phylum Planctomycetes anaerobic sulfide and sulfur-rich spring (Zodletone EF6024
DQ521801.1 gg_id:161669 Anaerobic Methane Oxidizing ANME-1b Archaea Hypersaline Sediments Gulf Mexic DQ521
AY114325.1 gg_id:63782 anoxic marine sediment clone LD1-PA39 AY1143
FJ485054.1 gg_id:555839 microbial autonomous rover world's deepest phreatic sinkhole biomat El Zacaton 114 FJ4850
EU491142.1 gg_id:260737 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak EU491
DQ289929.2 gg_id:172911 Microbial Carbon and Nitrogen Cycling Sediments South Atlantic Bight Permeable Sh DQ289
FJ485078.1 gg_id:562684 microbial autonomous rover world's deepest phreatic sinkhole biomat El Zacaton 114 FJ4850
FJ902124.1 gg_id:552555 phreatic limestone sinkholes northeastern Mexico orange biomat 8m deep cenote Ca FJ9021
EF602497.1 gg_id:231901 metabolic phylum Planctomycetes anaerobic sulfide and sulfur-rich spring (Zodletone EF6024
EU135574.1 gg_id:248536 tallgrass prarie soil clone FFCH4663 EU135
AF317770.1 gg_id:136806 Nullarbor cave clone wb1_H11 AF3177

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EU652628.1 gg_id:279399 Seasonal variation microbial Yel Sea sediment clone A8S-81	EU652
GU208350.1 gg_id:580844 Study on Sediment Dongping Lake sediment clone Td3-9	GU208
GQ347695.1 gg_id:534156 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich	GQ347
EU721779.1 gg_id:550488 microbial production water Alaskan mesothermic petroleum reservoir two methods	EU721
GU112185.1 gg_id:590013 library biogas slurry anaerobic fermentation pig manure clone 180	GU112
DQ329651.1 gg_id:200370 Guerrero Negro hypersaline microbial mat clone 062DZ75	DQ329
DQ329650.1 gg_id:201943 Guerrero Negro hypersaline microbial mat clone 062DZ40	DQ329
FJ719034.1 gg_id:529088 Protozoan grazers alter metabolically active aquifer aquifier sediments clone p03_A0	FJ7190
EF516850.1 gg_id:218322 grassland soil clone FCPS649	EF5168
AY532578.1 gg_id:106562 uranium-contaminated aquifer clone 1013-28-CG38	AY5325
EF516449.1 gg_id:225148 grassland soil clone FCPT678	EF5164
AY850299.1 gg_id:135358 depending on what microbial treatment present soil clone c1	AY8502
AB089068.1 gg_id:78071 termite gut homogenate clone Rs-J96	AB089
EF454817.2 gg_id:218493 termite hindgut clone 290cost002-P3L-449	EF4548
EF454921.2 gg_id:225715 termite hindgut clone 290cost002-P3L-678	EF4549
AB192117.1 gg_id:141608 termite gut homogenate clone M2PT2-63	AB192
EF454187.2 gg_id:217932 termite hindgut clone 290cost002-P3L-1771	EF4541
AB188635.1 gg_id:113660 termite gut homogenate clone Pl-P1-21	AB188
GQ340261.1 gg_id:572828 Prokaryotic Marathonas Reservoir Greece water column clone A08-131-BAC	GQ340
DQ520188.1 gg_id:161631 shal China sequences hypertrophic freshwater lake clone ML-9-34.2	DQ520
DQ300591.1 gg_id:146168 microbial ocean's interior amplicon single fosmid library pool 130m depth HOT static	DQ300
GQ350069.1 gg_id:588419 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich	GQ350

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Community Analysis: Hybridization Intensities

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GQ354923.1 gg_id:540167 structure between two geochemically distinct springs Alum Rock Park spring clone M	GQ354
DQ676460.1 gg_id:220280 Archaeal sediment and plankton freshwater pond suboxic freshwater-pond clone M	DQ676
EU644237.1 gg_id:284266 and Samoylov Island Lena active layer -centred polygon near surface horizon; Rim_T	EU644
DQ676456.1 gg_id:224443 Archaeal sediment and plankton freshwater pond suboxic freshwater-pond clone M	DQ676
GQ339139.1 gg_id:528049 Comprehensive Investigation on Iron Cycling Freshwater Seep ing Microscopy Cultiv	GQ339
AB179495.1 gg_id:99699 sedimentary rock clone MIZ04	AB179
AB193900.1 gg_id:108824 deep-sea vent clone Mb-NB06	AB193
DQ676475.1 gg_id:223552 Archaeal sediment and plankton freshwater pond suboxic freshwater-pond clone M	DQ676
GQ346852.1 gg_id:562467 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich	GQ346
GQ348940.1 gg_id:577547 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich	GQ348
EU283579.1 gg_id:278529 Model Early Earth Harbors Deeply Divergent Divisions Anderson Lake clone A285	EU283
FJ234919.1 gg_id:346434 Microbial structure mesophilic biogas mesophil anaerobic reactors fed corne silage cl	FJ2349
GU196235.1 gg_id:578115 Bioaugmentation improved recovery digesters after toxicant exposure lab-scale ana	GU196
AJ543755.1 gg_id:96419 anoxic sediment Lake Cadagno clone 1	AJ5437
EF192905.1 gg_id:202214 sediments temperate artificial lake Rapel reservoir sediment clone Rap2_24C	EF1929
AJ290978.1 gg_id:112449 anaerobic bioreactor clone SHA-114	AJ2909
AB186797.1 gg_id:105224 polychlorinated dioxin dechlorinating microcosm clone TSBZ04	AB186
AY297964.1 gg_id:88282 thermophilic anaerobic terephthalate-degrading sludge clone TTA_B4	AY2979
EU385779.1 gg_id:267654 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S	EU385
AM712334.1 gg_id:254942 detection and ly microbial Brothers Seamount Kermadec Arc New Zealand biofilm h	AM712
AY592377.1 gg_id:106589 deep-sea mud volcano clone Amsterdam-2B-17; BC20-2B-17	AY5923
EU385806.1 gg_id:261876 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S	EU3858
EF492945.1 gg_id:241470 Iron-manganese Nodule and Its Surrounding Soil soil around iron-manganese nodule	EF4929
AF245036.1 gg_id:44004 soil metagenomic library clone 17F9	AF2450
FJ793158.1 gg_id:529323 Archaea and Hot Spring Thailand Tao Dam hot spring clone TDB13	FJ7931
EF516094.1 gg_id:226261 grassland soil clone FCPS413	EF5160
FJ004718.1 gg_id:561968 Acidobacteria former agricultural soil rhizosphere clone 1Fe	FJ0047
EU132222.1 gg_id:246947 tallgrass prarie soil clone FFCH14447	EU132
EU925922.1 gg_id:347057 sediments sediment station DBS1 northern Bering Sea clone 160I37	EU9259
Z95707.1 gg_id:1740 soil clone 11-14	Z95707
EU881247.1 gg_id:352805 (long-term grazing and burned annual) Karst region serious disturbance field soil clor	EU881
GU230433.1 gg_id:556512 Multilevel approach along Rio de la Plata-South Atlantic Ocean coastal sediment clo	GU230
AY703459.1 gg_id:138920 Detection and ly acidobacterial analyses Altamira Cave clone ALT24	AY7034
EF516178.1 gg_id:222997 grassland soil clone FCPT460	EF5161
FJ004643.1 gg_id:533715 Acidobacteria former agricultural bulk soil clone 72L1B	FJ0046
AY922011.1 gg_id:113257 farm soil clone AKYG433	AY9220
EF516869.1 gg_id:219766 grassland soil clone FCPU565	EF5168

Array Hybridization Intensity (normalized by										
B01	S01	S02	S03	S04	S05	S06	S08	S09		
8767.0	7813.7	6936.0	8092.7	7391.5	7925.3	8902.8	7504.0	6		23
363.2	4235.0	3031.0	2968.4	2045.1	3971.4	3406.1	3843.7	1		72
3619.1	5992.8	5649.8	6480.2	6144.1	5512.6	7488.7	5118.1	4		58
62.7	510.3	554.1	687.8	339.8	491.3	482.7	548.7	58.0	152.7	328.2
4864.0	9098.2	9097.0	9927.3	7570.8	8735.1	10143.5	8950.5	7831.5	5486.6	10250.9
39.8	1675.7	871.3	1013.5	675.0	1149.0	638.9	1013.2	267.6	236.7	644.9
51.5	3212.0	2203.4	3139.7	941.5	3284.4	1404.3	2576.1	354.1	480.8	2270.3
45.7	230.7	272.2	339.9	50.5	193.2	61.2	81.5	64.2	28.9	95.5
1960.6	11315.3	9418.5	10738.5	7943.6	9888.2	9895.1	9834.7	7146.9	6928.8	10004.8
3217.6	8325.7	7717.9	8442.9	7243.2	8356.6	8596.3	8159.2	6940.4	6892.2	9200.4
4017.3	8466.2	7086.8	7509.4	6268.5	7822.9	8712.4	7856.8	4691.9	4584.3	7423.6
432.2	9295.0	7318.8	8316.5	6277.7	8068.7	9352.3	8234.5	5514.3	3306.8	8053.0
5862.2	3036.7	3932.8	4088.4	4945.3	4553.5	5647.1	4349.5	3242.6	4488.0	3059.7
207.0	570.9	696.2	716.3	751.8	605.4	665.0	729.5	306.9	184.7	669.7
61.9	140.7	167.5	225.8	167.6	104.3	146.0	50.6	91.6	89.9	134.7
36.0	100.9	189.6	146.0	67.0	61.5	83.0	47.6	26.1	33.0	46.1
287.6	2074.3	2062.7	2578.3	2580.8	1846.2	3042.1	2017.1	923.7	556.8	1395.7
117.5	175.9	178.2	167.5	199.1	174.5	136.1	152.7	117.7	85.3	121.0
6868.1	6624.6	6878.2	6722.3	8211.5	6869.4	8878.6	6825.0	6047.4	5477.8	6668.8
680.7	3558.3	3744.9	3790.8	4220.8	4390.8	4601.4	3493.5	2719.5	1612.5	2531.2
48.6	435.0	468.5	399.7	620.1	354.2	415.0	382.0	332.7	131.1	281.3
441.7	1267.9	1197.1	1545.3	2252.6	1557.8	2186.7	1145.4	489.1	200.5	993.3
4155.9	2419.8	1729.6	2403.3	1832.9	2067.7	2074.3	1997.9	2728.5	1807.5	2645.3
2296.9	3945.7	3980.6	4669.7	5104.6	4231.8	5246.6	3910.8	3680.8	2509.3	3590.1
948.2	3139.6	2308.9	2825.8	2692.8	2712.7	2939.7	2372.5	2303.5	1922.6	2781.6
29.5	873.0	671.6	1185.6	1241.5	1180.9	1057.1	812.6	269.5	63.2	550.2
570.4	2659.2	3781.2	3943.5	3226.4	3425.0	2627.3	3947.6	2299.1	3268.5	1803.3
277.0	1018.5	1167.3	1810.2	1352.9	1386.0	1567.0	1991.0	1069.9	165.6	914.8
956.5	4135.1	4390.0	4204.2	5175.0	5144.2	4445.5	5060.1	2275.2	3121.7	4196.5
67.0	224.2	120.2	206.6	393.2	370.9	241.9	142.6	90.3	29.1	133.6
4502.8	5261.5	5033.4	5222.1	5505.3	4812.6	5428.0	6400.5	5788.3	2194.7	5020.0
391.3	3555.6	2779.0	3019.4	3552.5	3015.4	4155.6	2581.7	2487.9	1693.3	1684.3
493.8	1357.8	2100.9	2151.0	1990.5	1911.0	2226.8	2425.5	2002.9	868.3	1110.9
63.3	939.4	633.5	1090.6	1277.5	1052.8	1170.5	575.9	281.1	87.3	419.8
891.2	6739.3	6602.0	7442.8	7891.4	6716.6	8519.1	6515.6	4237.8	5175.5	5282.8
2629.4	3806.7	3757.3	5237.5	5785.7	4098.9	5623.4	4179.7	3488.2	2363.7	3886.0
168.5	980.5	694.6	913.4	1667.9	1524.6	1236.8	879.0	685.8	69.6	730.7

		.7
		.8
		.2
170.0	433.0	230.5
8506.6	9348.8	9071.6
417.5	1140.9	1408.5
1200.6	1211.1	1212.9
33.4	92.4	30.0
7560.0	7859.6	9791.3
8172.5	8268.2	9052.6
5880.7	7122.1	8295.3
5822.8	6571.3	7227.4
4117.9	4524.2	5588.1
357.1	555.0	559.2
103.4	216.1	143.6
46.2	72.9	98.9
1339.9	1442.4	2255.6
149.7	249.9	166.7
7112.2	7080.6	8671.5
3496.6	3470.9	5167.6
374.5	487.9	403.4
1065.3	1543.9	2596.6
1893.8	2022.0	3283.8
3725.2	3424.7	6946.9
2250.0	3049.6	5314.1
635.7	1328.8	3813.0
3610.3	4448.5	5611.6
2554.8	1960.0	4815.1
5039.3	5030.0	6518.1
97.8	358.7	1305.0
5637.0	5958.2	6386.0
2426.4	3509.2	7338.0
2903.0	1797.1	3422.0
533.7	1589.1	3116.2
6276.5	5857.3	8438.0
4212.4	4597.4	5277.0
568.0	2383.1	5192.5

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DQ906800.1 gg_id:240618 Oman subsurface soil clone 5A-4 DQ906
DQ984540.1 gg_id:240646 Mt. Nan-Jen soil clone IFD_04 DQ984
EF018279.1 gg_id:212863 aspen rhizosphere clone Amb_16S_639 EF0182
EU193029.1 gg_id:329690 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo EU193
DQ513087.1 gg_id:161093 Microbial life fluids ridge flank crustal fluid clone FS266-72B-03 DQ513
EF516647.1 gg_id:222528 grassland soil clone FCPU544 EF5166
DQ463182.1 gg_id:157927 Acid Drainage Tong Lushan Copper Mine China acid mine drainage clone tls1-4 DQ463
D26171.1 gg_id:3704 Acidobacterium capsulatum D2617
AJ292576.1 gg_id:38048 PCB-polluted soil clone WD217 AJ2925
NC_008009.1 gg_id:159436 Korebacter versatilis Ellin345 NC_00
EF020028.1 gg_id:211355 aspen rhizosphere clone Elev_16S_1423 EF020
AM934736.1 gg_id:564102 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM934
AB486931.1 gg_id:540833 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCOR AB486
AB240248.1 gg_id:143307 microbial structure rhizosphere Phragmites bulk soil reed bed reactor laboratory clo AB240
GQ402790.1 gg_id:535450 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
AY234523.1 gg_id:112314 soil isolate Ellin5106 AY2345
EF018237.1 gg_id:206267 aspen rhizosphere clone Amb_16S_588 EF0182
AB240373.1 gg_id:144577 microbial structure Phragmites rhizosphere biofilm reed bed reactor laboratory clon AB2403
EF516733.1 gg_id:222434 grassland soil clone FCPP762 EF5167
AY963401.1 gg_id:156032 structures and correlated ecological factors soils two evergreen broad-leaved forests AY9634
EU680441.1 gg_id:285726 unculturable forest Gaoligong Mountains Yunnan soil clone S5-14 EU6804
EU680442.1 gg_id:284815 unculturable forest Gaoligong Mountains Yunnan soil clone S5-16 EU6804
EF516334.1 gg_id:223904 grassland soil clone FCPO423 EF5163
AB307653.1 gg_id:267261 clay wall used Japanese traditional buildings clone B45 AB3076
AY963484.1 gg_id:150977 structures and correlated ecological factors soils two evergreen broad-leaved forests AY9634
DQ528761.1 gg_id:160117 Edaphobacter modestum str. Wbg-1 DQ528
AY963496.1 gg_id:155420 structures and correlated ecological factors soils two evergreen broad-leaved forests AY9634
AY326573.1 gg_id:136280 Amazon soil clone 81-2 AY3265
FJ466338.1 gg_id:571120 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea FJ4663
DQ660894.1 gg_id:162763 Terriglobus roseus str. KBS 68 DQ660
EF018694.1 gg_id:212239 aspen rhizosphere clone Amb_16S_988 EF0186
DQ532229.1 gg_id:168599 Geographical Variation Microbial Burden and Spacecraft Assembly Johnson Space C DQ532
EU035939.2 gg_id:320478 Insight microbial structure Norwegian deep-water Desmacidon sponge deep-sea cor EU0359
EF516123.1 gg_id:221631 grassland soil clone FCPN626 EF5161
FJ466377.1 gg_id:509471 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea FJ4663
EF492914.1 gg_id:243138 Iron-manganese Nodule and Its Surrounding Soil soil around iron-manganese nodule EF4929
EF516926.1 gg_id:220395 grassland soil clone FCPP741 EF5169
AY963394.1 gg_id:153608 structures and correlated ecological factors soils two evergreen broad-leaved forests AY9633
EU132221.1 gg_id:239485 tallgrass prarie soil clone FFCH14327 EU132
FJ902583.1 gg_id:587792 phreatic limestone sinkholes northeastern Mexico biofilm 1m deep hydrothermal ver FJ9025
EU440640.1 gg_id:540618 Soil are Changed Agricultural Practices agricultural soil clone Plot17-H09 EU440

38.8	189.8	97.8	143.0	453.8	118.0	172.3	52.0	33.5	31.6	211.6
628.2	2488.1	4044.8	4009.1	2716.5	4734.2	2010.1	4447.5	2462.5	5942.8	1791.3
45.9	79.6	58.9	99.5	114.6	134.0	90.5	62.8	42.6	25.2	45.9
1914.4	4042.6	3338.1	3760.6	3758.0	3909.4	3850.1	3378.0	3663.9	1309.2	1791.2
150.7	526.4	551.6	896.4	446.5	532.5	510.8	724.4	372.9	283.4	708.2
1650.1	5671.2	6460.2	7429.9	9585.8	6604.8	9259.4	6762.6	6824.7	1855.1	6260.4
58.7	2778.5	2860.0	3065.9	5433.3	2791.2	4105.0	2429.4	1272.6	426.0	1742.7
43.4	74.6	381.9	44.9	129.5	68.3	96.3	53.1	27.0	26.7	38.4
38.9	554.2	1477.9	1342.2	1228.8	678.6	847.9	1230.8	264.4	85.3	808.7
51.3	136.0	333.7	90.0	578.6	97.9	113.6	33.1	33.6	32.2	86.8
51.7	575.1	654.7	608.7	2200.0	678.2	1240.3	308.8	69.4	59.1	182.8
5427.2	6261.0	6615.0	6889.1	6427.4	6452.3	7026.6	7581.0	7076.1	5084.3	7634.1
33.7	537.6	786.9	622.0	752.4	716.2	621.1	614.1	245.6	69.8	333.2
464.7	2504.9	3199.2	2403.6	1511.2	1754.5	2041.5	2542.9	2059.0	1578.4	2260.8
69.5	1652.4	2083.7	1609.8	3393.7	2602.2	2052.8	1355.3	472.4	276.9	1456.1
48.9	255.8	680.6	305.9	913.9	405.0	792.2	291.3	127.5	41.3	163.4
168.0	2889.1	3303.5	2773.5	2764.8	2933.5	5097.8	4504.1	2664.5	854.3	3044.5
144.3	292.0	296.5	299.5	356.3	392.8	475.3	480.8	152.4	161.9	234.1
126.0	1825.0	1655.3	1878.1	3941.0	2720.1	2631.8	906.2	417.7	98.0	1105.6
34.2	750.0	1035.5	641.6	1974.4	1023.9	969.4	560.5	175.7	86.3	358.3
49.9	673.7	1092.3	1084.9	1425.7	900.9	1568.9	990.0	354.5	145.7	547.0
1105.8	6930.0	6773.7	7225.7	9071.2	6996.6	9107.6	6392.4	5061.5	2868.8	6936.3
23.7	344.6	590.1	338.3	739.6	607.5	498.1	292.6	86.5	30.7	154.1
74.1	2023.4	2096.8	1349.7	1058.1	1008.3	717.0	962.7	291.6	172.1	805.7
159.8	1380.4	2011.8	2205.3	2322.0	1948.7	2613.9	2036.2	741.9	362.1	1290.6
39.9	63.7	80.9	67.8	292.3	60.9	206.7	75.0	26.9	16.2	48.1
175.0	3247.0	3450.0	3706.2	4196.3	3137.2	4308.3	3096.2	2630.3	1202.0	3678.3
176.0	1567.5	1803.6	1710.3	1906.0	1489.5	1844.3	1978.0	962.9	488.8	1427.2
666.7	1510.5	2452.2	1669.7	2471.1	1753.2	2362.8	1950.6	830.6	986.2	1012.6
68.3	966.1	1337.6	728.5	2054.9	638.5	778.5	799.7	334.5	190.1	679.9
2148.3	2300.6	2789.5	3136.4	2924.3	2470.3	2850.6	3227.4	2153.8	826.2	2425.9
133.5	1497.8	1828.3	2195.3	3178.8	1984.0	2737.6	1772.0	757.2	199.1	1042.4
771.3	4903.3	4919.9	5698.9	6015.9	4393.6	6778.2	4364.5	3068.6	2357.6	3598.1
6337.8	1845.9	1380.1	1808.2	4138.7	2237.9	3627.0	982.1	641.4	173.5	622.5
78.2	391.6	522.3	390.7	607.6	474.6	636.8	442.3	252.7	132.6	343.9
8440.0	11127.6	10918.4	13149.0	14909.3	11628.4	15362.6	10088.8	9845.4	5770.0	10988.9
70.6	1737.5	1643.8	2150.7	2974.7	2279.8	3041.1	1259.2	437.1	270.6	786.1
6733.2	3027.2	3651.2	2959.7	4212.7	3138.8	3438.2	3542.9	2586.1	2411.4	2531.2
742.3	5764.3	5193.3	6531.7	7037.2	4657.8	5200.5	4422.6	3188.4	2289.8	3586.3
39936.5	11386.2	9454.0	11896.2	14592.9	10782.4	14187.7	10366.0	13998.9	11408.2	14916.8
7981.3	6578.6	5513.1	5981.9	7654.6	6884.7	7056.8	5819.4	5694.1	6092.6	5804.4

58.9	195.1	468.5
4768.8	5258.4	4233.9
39.7	124.2	287.7
3099.5	4472.2	6257.8
631.3	828.0	411.6
6051.9	8185.0	10296.6
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142.6	96.1	250.3
762.5	1441.4	2209.8
37.8	193.2	584.2
209.3	641.5	1737.2
6102.6	6486.5	7202.7
481.6	574.7	1102.6
1905.5	1564.3	1993.9
1367.5	2753.9	6103.8
197.1	655.8	1362.5
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379.6	650.4	471.4
1180.3	1570.4	4451.6
496.2	918.1	1941.7
873.5	1094.0	2478.3
7934.0	7516.4	9962.8
241.4	730.5	1456.0
487.8	949.7	2517.4
1466.0	2114.3	3929.7
43.1	83.4	99.5
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1612.3	2381.8	2991.1
732.4	807.9	2136.1
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3846.3	4064.9	5797.3
1735.9	2013.6	4325.5
381.0	679.1	583.7
10519.9	11785.2	16135.1
1052.3	1866.7	4962.0
3832.5	3490.5	5061.3
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GQ396810.1 gg_id:559480 Functional unvegetated perhumid recently-deglaciated soils do not correlate shifts s GQ396
AF465659.1 gg_id:41797 Acidobacterium group clone YNPRH72A AF4656
FJ269341.1 gg_id:588263 Microbes marine sponges sponge tissue clone XC1E08 FJ2693
EF019289.1 gg_id:209203 aspen rhizosphere clone Elev_16S_476 EF0192
EU491200.1 gg_id:262940 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak EU491
EU132218.1 gg_id:257702 tallgrass prarie soil clone FFCH13847 EU132
EF492905.1 gg_id:248553 Iron-manganese Nodule and Its Surrounding Soil soil around iron-manganese nodule EF4929
EF494349.1 gg_id:223415 Nunnock River granitic landscape clone NR.1.090 EF4943
AY395361.1 gg_id:106724 pasture soil clone EB1042 AY3953
AY913359.1 gg_id:114204 forest soil clone DUNssu152 (+7A) (OTU#097) AY9133
EU250262.1 gg_id:235484 acid mine drainage clone GXDC-48 EU250
EF612359.1 gg_id:245188 historic semiarid lead-zinc mine tailings site soil clone OS-C161 EF6123
DQ451440.1 gg_id:156686 forest soil clone FAC1 DQ451
AY922122.1 gg_id:113404 farm soil clone AKYH1493 AY9221
AY212587.1 gg_id:104490 water 10 m downstream manure clone 137ds10 AY2125
AM072423.1 gg_id:138534 Untersuchung Verschiebung der bakteriellen Populationen mit U(VI) inokulierten Bc AM072
AF465656.1 gg_id:46677 Acidobacterium group clone YNPRH46A AF4656
AF200698.1 gg_id:16327 soil clone UA2 AF2006
FJ536905.1 gg_id:535248 Linking performance microbiology biofilters treating dimethyl sulphide presence and FJ5369
DQ906061.1 gg_id:223389 nickel resistance genes metagenome Tinto River rhizosphere clone ERF-1H5 DQ906
DQ404598.1 gg_id:151613 contaminated sediment clone 656042 DQ404
FJ479257.1 gg_id:577226 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4792
AY395347.1 gg_id:106465 pasture soil clone EB1028 AY3953
AY587227.1 gg_id:102666 soil clone AY5872
AY326572.1 gg_id:136267 Amazon soil clone 1031-2 AY3265
AJ292587.1 gg_id:39070 PCB-polluted soil clone WD277 AJ2925
AY234608.1 gg_id:112338 soil isolate Ellin5257 AY2346
AB240272.1 gg_id:143367 microbial structure rhizosphere Phragmites bulk soil reed bed reactor laboratory clo AB240
GQ500876.1 gg_id:564241 Surveys Biofilms and Sediments Mammoth Karst Aquifers Bio-Sep beads containing GQ500
GQ264031.1 gg_id:592891 Structure Simulated Level Waste Site simulated level waste site clone WC3_122 GQ264
FM873307.1 gg_id:362254 occupant source house floor dust clone FD01E01 FM873
GU359061.1 gg_id:518576 rhizosphere soil peanut clone 1S9 GU359
GU134916.1 gg_id:584087 Acid-tolerant microaerophilic oxdizing enhance Fe(III) accumulation Fe(II) oxidizing e GU134
GQ487990.1 gg_id:556931 Microbial metal soil polluted heavy metals clone V20-30 GQ487
DQ395032.1 gg_id:151522 harbor sediment clone VHS-B5-13 DQ395
EU150215.1 gg_id:278437 acidobacteria and soil Niwot Ridge LTER; spruce fir forest clone NiA_SF_26 EU150
EU132259.1 gg_id:244025 tallgrass prarie soil clone FFCH8685 EU132
FJ478546.1 gg_id:582523 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4785
AY289389.1 gg_id:88072 soil clone ABS-318 AY2893
EU669640.1 gg_id:308898 soil clone S8-19 EU6696
AY225650.1 gg_id:97371 Mid-Atlantic Ridge hydrothermal sediment clone AT-s2-57 AY2256

13490.8	5667.1	5553.9	6380.1	9406.2	6009.2	9759.4	6391.6	4091.4	3913.0	3945.9
40.4	49.5	133.3	31.7	40.3	38.2	40.2	32.7	23.9	24.0	42.6
3743.0	4885.0	4437.9	5206.9	7076.5	4984.2	6919.4	5417.7	3331.6	1912.7	3935.8
47.1	277.1	163.4	329.8	1302.6	239.1	424.2	83.7	81.2	35.3	105.6
2047.4	5682.8	6355.9	6514.8	7876.9	6825.5	7058.1	6086.2	4600.3	4654.6	4843.4
1187.5	3181.3	2613.1	2830.5	4249.8	3234.1	4090.1	2419.5	1536.1	1404.3	1465.4
14942.3	8574.9	7716.2	8387.3	8903.3	8826.4	9668.3	7765.5	8787.4	8798.5	8374.9
49.6	35.5	96.6	24.7	54.6	27.4	32.0	25.3	19.9	15.0	34.9
319.8	1307.7	1446.0	1579.4	1537.2	1181.3	1332.4	1190.6	728.7	1148.0	1068.0
209.7	2754.1	3526.9	2760.7	3709.6	1849.8	3783.7	2800.7	2439.1	1353.2	2231.8
1321.7	3871.5	3803.7	4251.2	5424.3	4024.5	5274.8	4714.0	3696.8	3107.7	5601.2
207.3	5936.8	5012.4	6228.6	9246.4	3620.5	10086.2	3342.2	2768.4	998.6	2675.4
5939.8	2829.1	3138.5	2782.8	3624.6	3196.1	3221.2	2747.5	3072.3	2313.1	3442.4
220.8	6187.2	5675.2	6816.3	8780.8	4898.7	7682.6	4054.1	2294.2	2285.2	3126.1
1420.5	3574.0	2922.1	3728.7	4616.6	2753.6	3893.1	3108.1	1854.2	1537.3	1846.8
16452.5	6197.8	5328.3	5859.4	6542.5	5824.6	6862.0	5005.7	8705.1	5781.9	8166.6
36.7	181.6	278.7	107.5	157.4	161.6	123.0	143.0	60.8	30.8	91.9
4388.3	4972.8	3501.5	4662.8	6033.5	4495.8	5945.9	3963.7	3759.1	4264.4	3677.9
3411.2	3776.9	3894.4	3893.0	4932.0	4139.8	3495.3	3675.6	3585.2	1690.0	3927.3
14278.3	5112.8	5911.8	5684.1	6275.6	5073.0	6195.5	4757.1	8748.6	6770.3	5933.5
113.4	256.2	467.9	281.3	371.9	348.8	350.9	388.9	130.9	95.2	303.9
64.9	2165.1	1511.6	1663.3	6233.2	3562.8	2581.8	596.4	375.5	228.1	846.2
239.0	3523.8	3560.1	4122.2	5820.4	3549.6	7405.8	3237.8	1579.4	2124.5	2185.7
5390.5	7524.1	6938.7	7923.5	9187.6	6914.8	9603.2	7302.8	6461.2	5009.8	8436.7
184.8	2165.0	3448.9	2464.3	2465.1	2727.9	2852.6	2576.3	1657.6	1985.7	1649.6
455.2	2375.9	3016.8	2775.6	4598.4	2399.6	4609.4	2529.0	681.8	1009.1	1255.6
52.5	45.0	71.5	65.5	86.0	45.6	64.8	69.8	27.8	25.9	39.3
3296.1	6066.1	5738.8	7543.0	10857.3	6208.4	10308.4	5314.1	3302.2	6425.0	3409.6
369.7	6477.6	4931.6	6267.9	10530.5	6057.4	9170.8	6409.3	2580.8	2932.6	2879.2
316.1	11655.5	10045.6	12071.2	15417.6	11164.8	15231.8	10935.6	6963.5	7301.5	8895.9
1914.6	1843.6	2238.3	1855.6	2505.2	2057.5	2199.7	1730.9	2329.2	930.9	1703.1
3706.3	2919.2	2537.2	2097.0	4145.0	3132.0	4833.8	2327.1	939.8	362.6	1744.2
123.2	2661.2	3723.6	3484.5	3868.3	2773.0	4054.4	2965.8	1292.4	1139.2	2227.7
159.6	865.8	1121.8	864.2	1961.2	1980.9	953.8	924.5	393.5	196.1	696.8
98.2	919.9	1018.2	1146.0	1922.7	2553.7	2628.2	1242.6	313.7	237.3	515.0
422.9	1168.9	2173.5	1356.3	1705.5	1312.0	1170.4	1420.2	704.1	142.9	973.8
4653.5	6156.7	6565.7	7170.5	8719.5	6161.2	8223.5	5925.5	4274.8	3994.7	6321.7
4267.0	8502.6	8628.2	8997.8	10524.8	8745.8	9911.3	8398.1	9668.3	7495.9	8437.0
42.7	92.0	82.6	101.2	214.2	119.5	137.8	60.2	34.8	27.7	51.2
80.1	3968.7	3219.9	3996.2	6481.1	4422.6	5882.3	3611.7	1533.4	954.2	2601.1
67.4	230.4	269.8	267.1	615.7	259.0	361.5	141.1	62.1	59.3	113.9

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29.5	52.9	112.1
5697.1	5419.9	7974.0
130.1	195.0	431.6
6543.2	6341.7	7429.6
2474.0	2918.5	4536.7
7448.4	9020.2	9772.1
23.4	38.9	34.1
1126.8	1273.1	1915.7
3392.7	1935.7	3846.2
3885.7	5602.5	6622.8
2622.5	2571.6	6246.4
3431.0	3798.7	5267.0
4571.8	4698.7	7073.1
2987.1	3276.5	5235.6
5196.0	6484.9	6348.6
96.9	294.8	342.7
3632.5	5458.2	4932.4
4576.5	4785.9	5613.0
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204.6	551.1	733.5
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3274.9	3928.3	5911.1
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2117.6	2584.3	2644.9
2201.5	2777.2	3621.0
49.9	104.4	73.3
6409.9	5576.8	9948.7
7817.6	4592.9	8238.9
12785.0	9921.3	15114.4
1956.5	2292.9	2756.5
2507.4	3576.6	5216.7
2211.0	2821.2	4553.9
1448.7	1180.2	4131.4
1390.2	1626.9	2528.0
1091.4	1352.0	2104.6
5220.3	6186.5	10593.0
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AY922158.1 gg_id:113717 farm soil clone AKYH822 AY9221
FJ466048.1 gg_id:511685 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea FJ4660
EF018405.1 gg_id:212293 aspen rhizosphere clone Amb_16S_1019 EF0184
FJ810547.1 gg_id:405751 Subsurface ecosystem resilience: Long-term attenuation subsurface contaminants su FJ8105
GQ487992.1 gg_id:546910 Microbial metal soil polluted heavy metals clone V8-11 GQ487
FJ478777.1 gg_id:592157 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4787
EF018834.1 gg_id:211129 aspen rhizosphere clone Amb_16S_1315 EF0188
EF019762.1 gg_id:216690 aspen rhizosphere clone Elev_16S_943 EF0197
GQ500711.1 gg_id:557097 Surveys Biofilms and Sediments Mammoth Cave Karst Aquifers Charon's Cascade sa GQ500
GU363035.1 gg_id:543451 and archaeal biogeochemical cycling genes within Qiongdongnan basin Sea: pilot stu GU363
EU735013.1 gg_id:347978 assemblages sediment station DBSE Northern Bering Sea clone 109A50 EU735
DQ458047.1 gg_id:158731 acid mine drainage clone DX6 DQ458
FM872925.1 gg_id:369871 occupant source house floor dust clone FB04F12 FM872
AY922132.1 gg_id:114129 farm soil clone AKYH511 AY9221
FM872996.1 gg_id:359837 occupant source house floor dust clone FB02F09 FM872
AJ863211.1 gg_id:126401 poplar tree microcosm bulk soil unflooded clone 20BSU25 AJ8632
FM866297.1 gg_id:360249 Microbial several mining wastes Bulgaria uranium mill tailings clone BuhC-173 FM866
EU276526.1 gg_id:358489 -DGGE and Approaches Analyze Effect Agricultural Practices on Soil agricultural soil c EU2765
EU150201.1 gg_id:279537 acidobacteria and soil Niwot Ridge LTER; spruce fir forest clone NiA_SF_12 EU1502
AY493934.1 gg_id:136869 Fingerprinting aggregates soil clone 117 AY4939
EF516417.1 gg_id:227524 grassland soil clone FCPN713 EF5164
EU132307.1 gg_id:244850 tallgrass prarie soil clone FFCH7214 EU1323
EU491340.1 gg_id:271398 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X3 clone EU4913
AB252946.1 gg_id:162343 Identification Shibayama lagoon Ishikawa Japan iron-oxidation biofilm clone 033 AB2529
DQ395960.1 gg_id:155016 deep-sea octacoral clone ctg_CGOGA68 DQ395
EU335199.1 gg_id:241341 Changes microbial metabolic and along hydrogeochemically variable profile saturate EU3351
FJ203529.1 gg_id:352218 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h FJ2035
AY326582.1 gg_id:136930 Amazon soil clone 31-1 AY3265
EU665054.1 gg_id:541146 Soil are Changed Agricultural Practices agricultural soil clone Plot22-B06 EU6650
FJ466242.1 gg_id:547399 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea FJ4662
AF154085.1 gg_id:1813 hydrocarbon seep clone BPC015 AF1540
AY963491.1 gg_id:153165 structures and correlated ecological factors soils two evergreen broad-leaved forests AY9634
EF492949.1 gg_id:255562 Iron-manganese Nodule and Its Surrounding Soil soil around iron-manganese nodule EF4929
AM935750.1 gg_id:538422 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM935
EU881222.1 gg_id:336433 Karst region natural restoration land soil clone KNR200711-030 EU8812
AB192240.1 gg_id:144515 termite gut homogenate clone RsTu1-92 AB1922
EU250256.1 gg_id:257823 acid mine drainage clone GXDC-42 EU2502
EU335409.1 gg_id:253648 Changes microbial metabolic and along hydrogeochemically variable profile unsatura EU3354
EF018918.1 gg_id:213165 aspen rhizosphere clone Amb_16S_1420 EF0189
FJ478490.1 gg_id:568935 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4784

1163.4	1084.3	1172.5	1167.5	2666.5	1219.7	2706.4	1179.3	959.8	618.2	624.6
1053.7	3504.6	2750.1	3132.1	6748.4	3954.9	5344.5	3448.7	1389.0	998.7	2151.6
28.6	1939.4	1805.8	2066.4	2605.0	1605.6	2929.6	1303.4	353.1	187.9	724.5
1313.7	2691.3	2761.5	3070.9	2235.2	2577.1	3607.8	1565.2	2065.4	1563.3	2486.3
1799.2	1990.9	1759.5	1695.6	4223.3	2716.1	2171.7	1500.4	909.3	683.5	1946.0
88.0	2805.6	2512.6	2941.3	5378.9	2615.8	5133.1	2441.8	1247.1	1925.9	1341.1
4405.1	5501.1	4925.2	4069.9	7312.5	5477.1	6789.9	5436.3	4784.0	3818.7	7286.9
2255.0	620.5	574.3	462.7	958.0	705.0	1164.3	837.6	195.0	141.5	401.8
45.2	434.8	275.8	333.6	1324.0	602.2	572.9	140.6	110.4	25.6	212.0
18990.6	9044.3	8655.4	9500.6	11013.6	9074.6	10101.1	7939.5	10398.3	9711.1	9430.5
1266.0	4855.1	5780.5	5928.2	6629.6	4986.1	6957.3	4486.4	4447.8	3004.3	5928.1
5795.1	9202.6	9472.9	9641.8	11715.5	9370.8	11961.2	9683.6	7969.9	6558.5	12924.9
3501.4	2656.8	2634.6	2548.0	3378.0	2803.0	2679.5	2250.7	3076.4	2310.3	3101.0
696.3	4041.0	5613.5	4833.6	4748.5	4467.3	5029.7	5399.8	2918.9	2999.4	5909.7
224.0	2778.8	2116.2	3196.8	4598.4	2919.7	3971.6	1973.2	795.5	391.7	2013.8
16167.9	5761.0	5106.5	5385.0	6147.2	4962.5	6806.7	4499.1	7556.6	5871.9	7142.5
233.9	5341.7	5682.0	6117.7	7177.5	5060.6	7792.7	5319.6	8164.6	2950.8	4627.5
21.1	3460.9	1810.1	2542.3	5387.1	2481.3	2891.3	2384.7	602.1	339.6	1036.0
27953.4	9524.3	9439.4	10390.4	11114.4	9479.5	11535.7	9239.0	14065.4	10356.0	12878.3
40.0	941.2	1199.2	512.5	2539.1	856.2	739.9	320.5	242.4	132.4	558.4
5202.4	3854.1	3403.5	3992.2	4919.1	3372.4	4289.0	3883.7	2769.0	2290.6	2764.0
46.9	170.2	224.3	313.8	1238.7	176.1	809.4	313.8	72.3	32.5	108.5
8334.7	4016.6	4451.9	4399.2	4597.1	4072.1	4915.2	4509.5	4986.4	2654.7	4944.7
3012.1	2284.6	2264.6	2651.5	3627.9	2980.9	3495.7	3893.3	1325.9	1338.0	3216.5
58.9	1019.2	873.7	1034.6	1918.9	1135.2	1745.9	930.8	277.0	217.8	461.0
360.4	5359.0	5309.0	5657.6	9912.4	5536.8	9134.9	4568.8	3465.1	2195.8	4023.1
80.7	2580.2	2548.0	1990.3	4271.6	2945.3	2704.0	1505.3	1010.8	744.5	1974.7
4865.2	2030.4	2317.5	2567.5	3326.6	2149.5	3207.1	2340.4	1576.2	801.6	1544.2
1759.6	7360.8	6738.0	8463.8	7680.6	6819.8	7581.2	6183.8	11380.5	7433.7	8879.5
799.1	5843.2	6028.7	7288.8	11458.3	5825.6	10366.5	5045.6	2832.9	2524.2	3657.3
31750.3	5603.6	5275.0	6210.3	6019.0	5755.1	5006.2	4486.8	8136.6	7921.6	8031.6
4866.2	5963.4	5617.9	6825.5	7674.9	5207.6	6956.3	5087.5	3804.3	3347.3	5287.9
1521.8	4710.5	5872.9	6011.1	7331.3	5448.1	7160.3	4897.3	2877.7	3396.2	5137.1
3119.8	2280.9	2987.1	2474.3	2363.5	2370.9	2672.0	2282.2	2185.6	1631.7	2631.1
1310.9	5490.9	5218.0	6057.5	9693.4	5608.9	8758.0	5104.7	3305.1	2466.8	4050.8
179.1	4492.8	4239.1	5173.2	7075.3	4132.0	6898.9	4445.4	1885.7	1473.1	2358.4
66.3	246.3	430.3	278.8	225.3	252.0	296.4	281.2	109.5	72.3	187.5
9841.1	4256.8	4613.0	4638.3	5308.1	4477.6	5773.1	5332.9	4903.7	5075.6	4937.6
20461.7	7244.5	6487.8	7294.3	7090.7	6725.0	7292.3	5263.5	16225.3	7280.3	11023.5
61.7	3419.9	3151.3	3809.4	4432.9	3141.5	5210.2	3465.0	1144.9	824.5	2830.2
948.7	5596.5	6546.4	7074.3	7882.7	5997.6	8022.4	5459.4	5442.9	3085.2	5899.2

706.1	1675.6	1745.2
3137.8	4357.7	5966.3
1488.0	1342.8	3149.0
2321.7	2752.6	4017.1
1486.6	4361.3	9064.0
2693.7	2438.0	4308.5
5753.2	6172.4	7763.6
840.8	926.4	1346.8
116.8	754.0	1491.8
8396.9	9798.5	11186.8
4183.5	4721.9	6152.0
8935.5	9484.9	10516.0
3140.4	2727.0	4225.1
3603.5	4505.4	5059.7
2803.1	3520.1	5168.6
4682.0	5852.0	6947.1
4851.4	6053.4	7715.5
3305.6	2327.0	6450.4
8996.5	11142.3	10015.6
532.1	1538.6	3180.7
3697.2	4229.2	4014.9
182.1	145.9	655.9
3990.2	4762.8	7153.5
1917.8	3704.9	4522.8
854.9	1285.7	1946.2
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4716.8	5771.6	7775.9
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4726.9	4320.1	8163.1
182.3	468.5	304.7
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5901.7	6537.3	8481.8

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EF018439.1 gg_id:212726 aspen rhizosphere clone Amb_16S_1060 EF0184
AF013534.2 gg_id:1828 soil clone C112 AF0135
DQ660878.1 gg_id:251359 DongChuan copper pyrites PRC determined acid mine drainage (AMD) clone DCK-I-1 DQ660
GQ500739.1 gg_id:538176 Surveys Biofilms and Sediments Mammoth Cave Karst Aquifers Bio-Sep beads conta GQ500
AJ581628.1 gg_id:100705 soil near uranium mill tailings clone KCM-C-25 AJ5816
AY922137.1 gg_id:113301 farm soil clone AKYH551 AY9221
FM872961.1 gg_id:361264 occupant source house floor dust clone FB02B12 FM872
AF234701.1 gg_id:28670 sludge clone A22 AF2347
EU193040.1 gg_id:334337 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo EU193
EU700181.1 gg_id:297788 Study on Shantou Bay Marine Sediments Microorganisms sediment clone STU39 EU7001
AY963351.1 gg_id:154229 structures and correlated ecological factors soils two evergreen broad-leaved forests AY9633
EF597706.1 gg_id:238131 Metagenomics deep mediterranean warm bathypelagic habitat 3010m depth Ionian EF5977
EU050884.1 gg_id:250701 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_04_20 EU0508
AY921956.1 gg_id:113944 farm soil clone AKYG1148 AY9219
EU589288.1 gg_id:270648 China Ningxia rice paddy field soil clone 2_B10 EU5892
EU132175.1 gg_id:256235 tallgrass prarie soil clone FFCH11537 EU1321
DQ017915.1 gg_id:129839 upland stream clone S-Btb7_44 DQ017
EF612353.1 gg_id:243634 historic semiarid lead-zinc site mine tailings clone K6-C86 EF6123
EU449736.1 gg_id:551546 Soil are Changed Agricultural Practices agricultural soil clone Plot4-H05 EU4497
EU449671.1 gg_id:545542 Soil are Changed Agricultural Practices agricultural soil clone Plot4-2E07 EU4496
EU276508.1 gg_id:359433 -DGGE and Approaches Analyze Effect Agricultural Practices on Soil agricultural soil c EU2765
DQ289915.1 gg_id:172055 Microbial Carbon and Nitrogen Cycling Sediments South Atlantic Bight Permeable Sh DQ289
EF019507.1 gg_id:216553 aspen rhizosphere clone Elev_16S_1009 EF0195
AJ863210.1 gg_id:124071 poplar tree microcosm bulk soil unflooded clone 20BSU7 AJ8632
GU118680.1 gg_id:539508 Threatened Corals Provide Microbial Habitats clone Mfav_G07 GU118
EU881185.1 gg_id:310755 Karst region natural restoration land soil clone KNR200711-117 EU8811
EU202779.1 gg_id:319420 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo EU2027
EU440593.1 gg_id:553987 Soil are Changed Agricultural Practices agricultural soil clone Plot17-2H08 EU4405
EF061945.1 gg_id:180033 Xiamen China mangrove sediment clone XME61 EF0619
DQ811916.1 gg_id:169706 mangrove soil clone MSB-3H10 DQ811
AF280856.1 gg_id:71241 bioreactor clone mle1-25 AF2808
AJ536875.1 gg_id:78582 uranium mining waste pile soil sample clone JG30a-KF-145 sp. AJ5368
EF208702.1 gg_id:202031 Vertical and horizontal structure microbial sandy carbonate sediment clone CI75cm.2 EF2087
EF019194.1 gg_id:213048 aspen rhizosphere clone Amb_16S_1868 EF0191
AY963461.1 gg_id:155408 structures and correlated ecological factors soils two evergreen broad-leaved forests AY9634
EU449729.1 gg_id:571898 Soil are Changed Agricultural Practices agricultural soil clone Plot4-G06 EU4497
AY963360.1 gg_id:154596 structures and correlated ecological factors soils two evergreen broad-leaved forests AY9633
EF494338.1 gg_id:226552 Nunnock River granitic landscape clone NR.1.045 EF4943
EF516272.1 gg_id:224515 grassland soil clone FCPN628 EF5162
DQ833470.1 gg_id:162661 detected analyses depth sediment Guanting Reservoir clone 5-35 DQ833
AY289378.1 gg_id:88876 soil clone DS-231 AY2893

58.6	983.0	589.3	545.9	2361.3	1752.3	855.5	390.6	224.6	82.2	347.7
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38.0	50.2	63.3	57.5	34.2	39.4	36.6	42.3	37.8	20.2	35.2
152.2	2198.3	1580.0	3076.3	6420.9	2420.1	4837.9	4656.5	1359.4	1395.0	1101.7
27434.7	8618.8	7045.3	7079.6	10167.5	7679.1	8472.3	8281.2	10322.6	7137.4	10652.5
256.5	3018.1	3142.6	3720.9	5295.8	3079.3	4923.8	4028.1	4960.8	3241.2	2341.8
1696.8	7730.5	6555.4	7493.3	9142.7	6741.6	8554.7	6246.8	6424.6	5660.6	6719.3
59.2	1922.7	1642.0	2032.2	4252.3	1716.2	3644.2	2049.0	525.1	380.2	925.8
12526.6	9402.3	9822.8	11292.7	11192.7	9651.8	12118.3	9599.3	10043.8	13018.1	11607.6
1643.4	6869.3	7050.0	7315.4	8854.6	6913.9	9336.9	6336.6	5522.2	5206.7	5396.2
1615.8	1762.4	1966.6	1800.2	3061.8	2373.7	2570.8	1412.2	1323.7	1737.9	1229.7
5444.8	3663.2	3083.6	3574.7	4639.0	3107.2	4873.9	2652.9	2180.2	1225.8	2430.6
61.3	5149.5	4780.7	5791.1	8117.3	5174.0	8226.6	5274.5	1404.5	1458.5	2660.7
4788.2	7296.5	6444.0	8023.2	10416.2	6739.2	10132.1	6215.1	4262.6	2557.4	5786.8
1914.9	7473.6	7382.8	8912.2	7550.5	7100.7	7649.2	7598.9	8991.2	5956.2	9037.2
14448.2	4984.3	4071.7	4867.0	5644.9	4697.9	5745.2	4513.3	3668.5	3161.6	5243.3
34.6	84.2	35.1	54.3	992.9	32.8	32.6	33.7	23.1	17.4	22.6
76.7	1467.7	1413.9	1576.5	2533.5	1414.4	2105.0	1305.6	917.8	465.2	1212.0
550.9	4077.6	3940.2	3573.5	5063.3	3720.3	4724.6	2896.7	3193.6	2089.2	3757.4
10707.4	8864.5	6982.7	7746.8	11543.0	7799.2	9522.4	7324.9	6700.9	6538.0	8304.6
6775.7	4533.6	5232.5	5659.1	7944.0	4732.5	7228.0	4864.6	3651.2	4929.3	5231.2
2752.2	1630.0	1713.1	2744.7	2683.7	1571.1	3373.7	2094.0	1146.9	554.7	1308.0
215.7	501.9	1030.2	601.2	1961.2	710.0	962.6	461.1	266.3	141.7	459.5
44.5	457.4	320.4	406.1	556.3	491.0	697.5	286.7	120.9	64.6	92.4
1612.1	6559.4	6727.4	7609.2	8010.7	7185.0	8038.4	6975.4	8585.0	7981.3	8902.1
52.4	2367.4	1851.4	2486.9	5887.4	2419.9	3553.2	1263.0	675.6	390.3	847.7
47.7	1360.3	1013.4	900.0	2092.1	1482.3	1886.7	1076.0	370.0	293.8	533.8
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46.5	423.0	426.2	295.9	513.5	447.7	440.7	361.5	98.0	77.6	178.8
54.5	453.2	586.3	660.2	743.0	810.2	433.3	249.7	119.2	71.4	207.8
348.3	3508.1	3743.8	4506.9	7289.1	3498.0	5603.4	3739.0	1503.0	1063.3	1853.6
41.9	99.8	41.6	63.7	222.7	161.5	94.8	70.0	38.9	27.0	49.7
38.2	33.1	52.8	51.3	56.6	29.3	85.2	42.3	16.2	16.4	28.0
48.0	152.5	164.7	225.5	386.1	176.4	415.4	162.9	67.2	24.1	184.5
29.0	142.9	208.0	177.0	262.1	247.6	204.6	69.6	33.4	18.8	113.9
5929.5	9343.0	7637.7	9921.2	11634.8	9576.6	12038.9	9220.1	8264.9	6754.3	9564.2
288.1	2342.3	2932.1	2856.8	4491.5	2714.7	3896.8	3143.0	5322.3	3133.1	1222.1
42.2	252.5	269.6	165.8	673.9	414.1	361.7	166.4	44.8	42.7	200.1
48.5	130.5	147.4	140.3	218.9	131.6	172.9	171.9	96.8	42.3	62.1
39.5	327.0	249.7	315.7	756.7	256.3	484.1	223.5	58.3	53.1	115.0
77.9	1700.7	1312.3	1614.1	1840.5	1510.6	2084.6	1339.6	937.1	532.6	1054.8

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27.9	45.8	45.4
5595.6	1816.0	2291.2
7178.6	8781.5	8846.6
3294.8	4201.2	4750.9
6913.5	7694.7	10266.6
1729.2	1603.3	2922.8
9499.4	11352.1	10690.4
5714.0	6721.7	8781.2
1164.3	1832.9	3791.8
2919.5	3332.9	5950.7
6831.5	4500.0	8265.5
7187.0	6418.4	9822.1
6743.0	7089.1	7935.0
4631.8	4011.0	6130.1
23.8	27.0	53.6
1372.2	1437.8	2487.2
3103.6	4301.8	7775.5
7429.0	8536.6	10251.3
4904.9	4422.1	5691.0
2097.9	1890.1	2303.3
403.7	1087.4	2379.0
344.3	441.3	1006.0
7215.3	7824.6	9656.3
1642.1	2091.1	4699.0
1020.2	1701.0	3398.4
5844.9	6863.9	6664.4
388.0	489.0	774.7
310.8	895.8	2043.0
4243.3	3492.0	4904.1
90.8	120.8	575.8
24.1	38.1	45.7
169.6	216.1	696.6
63.3	160.3	776.1
7748.3	10070.2	12083.7
1280.4	3167.7	4440.9
214.8	479.4	1128.9
158.9	213.1	260.0
166.8	470.9	721.3
1215.7	1774.1	2726.1

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EU035924.2 gg_id:338434 Insight microbial structure Norwegian deep-water Desmacidon sponge deep-sea cor EU035
EU335210.1 gg_id:256500 Changes microbial metabolic and along hydrogeochemically variable profile saturate EU335
EF492967.1 gg_id:251273 Iron-manganese Nodule and Its Surrounding Soil soil around iron-manganese nodule EF4929
EU491617.1 gg_id:258921 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU491
EF020018.1 gg_id:211775 aspen rhizosphere clone Elev_16S_1409 EF0200
AJ519379.1 gg_id:75044 uranium mining waste pile clone JG37-AG-73 sp. AJ5193
EU276472.1 gg_id:359394 -DGGE and Approaches Analyze Effect Agricultural Practices on Soil agricultural soil c EU276
EF018874.1 gg_id:212877 aspen rhizosphere clone Amb_16S_1358 EF0188
DQ837260.1 gg_id:256297 Archaeal and pristine National Park Spain Donana coastal aquifer clone 49S1_2B_67 DQ837
EU202778.1 gg_id:316315 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo EU202
AY913238.1 gg_id:112964 forest soil clone DUNssu017 (+1B) (OTU#052) AY913
EU680459.1 gg_id:280233 unculturable forest Gaoligong Mountains Yunnan soil clone S13-37 EU680
DQ984553.1 gg_id:240236 Mt. Nan-Jen soil clone IFD_41 DQ984
FJ466387.1 gg_id:553417 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea FJ4663
EF018503.1 gg_id:204592 aspen rhizosphere clone Amb_16S_1139 EF0185
FJ466241.1 gg_id:512006 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea FJ4662
DQ202227.1 gg_id:140433 Enrichment s Type II Methane-Oxidizing Inhabiting Northern Peatlands peatland clo DQ202
EF042585.2 gg_id:232738 Microbial and geochemical dynamics extremely acidic metal-rich stream massive sulf EF0425
AY289385.1 gg_id:90452 soil clone DS-87 AY289
EF018868.1 gg_id:215513 aspen rhizosphere clone Amb_16S_1351 EF0188
AY963368.1 gg_id:155297 structures and correlated ecological factors soils two evergreen broad-leaved forests AY963
AJ581608.1 gg_id:93865 soil near uranium mill tailings clone KCM-B-77 AJ5816
EU050885.1 gg_id:256652 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_02_91 EU0508
EF999370.1 gg_id:252534 Vertical and Methanotrophs Estuarine Sediments Pearl River Estuary sediments 22cn EF9993
EU202826.1 gg_id:314799 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo EU2028
FJ465984.1 gg_id:553387 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea FJ4659
EF061943.1 gg_id:194730 Xiamen China mangrove sediment clone XME2 EF0619
FJ466047.1 gg_id:559379 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea FJ4660
AY922048.1 gg_id:112734 farm soil clone AKYG647 AY922
EF516699.1 gg_id:224638 grassland soil clone FCPN431 EF5166
GQ402710.1 gg_id:566158 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
DQ917891.1 gg_id:226056 Microbial profiles bleached and wild-type Muricea elongata Acidobacteria clone ME DQ917
EU881286.1 gg_id:331724 (long-term grazing and burned annual) Karst region serious disturbance field soil clo EU881
AF524859.1 gg_id:77390 sphagnum peat bog clone K-5b10 AF5248
AY963390.1 gg_id:154565 structures and correlated ecological factors soils two evergreen broad-leaved forests AY963
EF600574.1 gg_id:302530 soil clone E5-34 EF6005
EF018170.1 gg_id:211684 aspen rhizosphere clone Amb_16S_507 EF0181
AY765992.1 gg_id:108645 Acidobacteriaceae KP3 AY765
DQ984543.1 gg_id:256036 Mt. Nan-Jen soil clone IFD_19 DQ984
EF019556.1 gg_id:213076 aspen rhizosphere clone Elev_16S_1065 EF0195
EF600563.1 gg_id:291339 soil clone E5-8 EF6005

3513.0	4805.7	5106.2	5826.8	6432.0	4499.4	6244.9	4406.2	3401.1	2033.3	4660.3
5516.3	6158.9	5669.5	7008.0	8967.2	6386.6	8031.0	4943.6	3105.0	1983.1	3484.7
54.5	1113.3	1105.8	540.3	1759.7	1259.6	1001.0	672.1	365.2	326.9	758.8
324.4	3682.8	3590.1	4031.0	5364.6	3313.5	5382.0	2832.1	1172.1	583.9	2194.8
42.6	514.9	831.5	229.5	2394.8	843.4	902.4	129.6	90.8	35.5	673.2
47.0	850.1	891.3	695.2	1363.8	688.3	1011.6	745.5	137.1	398.2	245.7
135.7	3870.7	2754.7	4437.4	7356.4	3902.5	5636.8	3261.3	1291.6	904.7	1913.8
4651.8	3835.4	3269.1	3762.9	6159.9	3533.9	5006.5	3223.6	1501.0	1072.9	2107.4
15375.2	7981.6	7154.8	8743.8	11506.2	8318.3	10137.4	8687.0	6708.9	5807.2	8791.3
42.2	1969.3	1360.5	1301.5	4636.1	3764.5	1969.9	931.3	379.4	128.9	788.7
87.2	123.3	160.7	132.6	380.7	128.6	193.4	108.3	66.8	35.7	83.7
45.9	313.0	479.3	222.5	1084.5	387.0	304.6	67.5	37.0	32.5	285.1
655.0	3570.7	3585.6	4520.9	5748.0	4036.3	5047.9	4447.2	2706.5	3198.4	3123.2
6576.2	4022.4	4831.9	4622.5	5441.0	4222.6	5398.1	4477.1	4343.5	4623.7	4997.6
55.7	112.4	215.2	213.3	240.9	146.1	303.2	145.5	45.7	29.8	73.4
2448.1	3550.5	3672.3	3476.3	3385.1	3333.1	3129.1	2750.0	1739.1	1205.2	3381.0
3196.0	3058.2	3520.1	3724.2	3798.1	3132.9	3070.1	3360.0	3290.7	1428.2	3914.0
49.0	256.6	426.1	272.6	462.5	247.7	364.7	235.9	62.1	80.5	112.4
56.1	477.5	437.3	526.1	996.1	448.6	890.9	437.4	141.5	118.7	220.7
2321.5	2535.5	2804.7	3331.9	4841.6	2987.5	3928.2	2710.1	2103.7	909.4	1711.7
31.8	21.4	20.0	11.7	22.0	13.4	21.9	13.3	10.3	12.3	14.0
337.1	4085.2	3227.1	3677.1	5882.0	3294.2	4590.9	3001.9	1499.1	722.2	1518.4
309.0	3950.2	4807.3	5287.1	5230.4	4307.5	6344.7	4708.2	2121.1	1591.4	3599.2
406.6	5103.4	4494.9	5885.2	8038.8	4832.1	7390.6	4429.9	1599.8	1091.1	3058.0
108.0	4247.9	3045.1	4104.2	7047.9	4416.1	6230.7	2083.6	1052.4	583.7	1549.8
4734.6	2446.9	3178.7	3062.3	4080.4	2489.1	3945.0	2904.7	3118.9	1062.1	2569.6
3486.1	4867.0	4682.6	4785.5	7050.6	4635.4	6296.2	3763.4	3351.5	2160.6	3865.7
152.7	2607.1	3086.5	3254.4	3473.7	2663.7	3536.2	2609.7	1423.5	829.8	2129.6
15698.4	5248.2	3259.5	5853.7	6960.4	4923.8	6174.6	4125.9	7865.9	5846.5	7615.2
73.8	335.8	621.7	419.4	281.2	212.1	405.3	246.7	106.7	44.7	311.6
251.2	2503.4	3612.0	2905.0	3511.9	2354.4	3769.3	2442.8	799.2	546.8	1990.6
46.2	261.9	347.8	455.3	982.5	297.5	597.8	435.9	199.5	133.3	204.1
1847.5	3192.9	4314.8	4785.0	5248.0	4083.9	6066.3	4339.4	3398.5	3952.1	3950.3
366.4	2608.8	2874.6	3126.6	3350.3	2696.1	5108.8	2548.7	1878.1	2256.5	2274.1
4508.2	2622.5	3079.4	2962.4	2754.4	2670.6	3170.7	2645.6	3820.8	3845.1	3642.1
12130.1	5665.4	4369.7	6718.3	6136.0	5498.2	6576.6	5452.8	5851.5	4882.6	5953.7
3843.8	2949.2	3265.7	4210.3	5466.0	3138.7	5791.7	3107.9	1686.3	1665.1	2148.6
83.1	1737.6	2275.1	2620.2	3754.5	2195.3	3473.2	2914.7	796.3	187.0	1373.4
711.3	1352.1	1322.6	1605.0	2651.2	1654.5	2261.7	1403.6	583.4	395.2	1188.2
56.6	225.9	263.4	304.2	493.2	294.3	523.8	345.7	73.3	76.9	136.6
11360.7	5540.4	5331.5	6553.4	6100.0	5779.6	6207.2	5879.6	6182.7	3066.6	6308.4

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279.8	765.9	2278.8
824.9	551.9	1110.9
4114.9	3112.3	5744.4
3437.8	3376.9	5607.7
8603.8	8793.8	10960.1
870.9	4381.3	6595.7
184.4	224.6	267.1
83.2	386.5	1123.9
3621.0	3985.8	3899.4
4849.5	6177.5	5664.8
219.5	253.1	224.1
2635.0	3767.1	4289.9
3195.9	3952.7	3439.6
241.0	339.5	538.3
540.5	431.7	713.6
3014.0	3648.2	5847.5
11.3	15.4	23.0
3292.5	3893.4	6321.3
3779.6	4378.9	6416.7
4939.2	4291.8	8014.8
2769.2	3929.6	7374.1
2948.3	3064.6	3768.7
3873.2	5223.0	5879.8
2132.0	2589.2	2444.7
4666.9	5291.5	5506.7
113.3	155.5	289.2
1636.3	2362.6	2966.4
420.7	411.2	455.8
3467.9	4372.5	6284.7
1745.2	3141.5	3453.0
2549.0	3346.6	3256.8
5159.9	6040.6	7029.7
2364.4	2863.9	3928.7
2803.5	2267.2	3433.3
1363.9	2036.0	4008.4
462.4	356.9	640.4
5460.2	5963.6	7673.7

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AY922010.1 gg_id:113782 farm soil clone AKYG420 AY922
AY922151.1 gg_id:114240 farm soil clone AKYH715 AY922
DQ450715.1 gg_id:160091 Microbial Alpine Tundra Wet Meadow Soil: Chloroflexi Cold Water-Saturated satura DQ450
DQ058684.1 gg_id:138816 Identification biofilm and bulk s nonchlorinated model system: detection large nitrit DQ058
EF018355.1 gg_id:215113 aspen rhizosphere clone Amb_16S_728 EF0183
AY963471.1 gg_id:154234 structures and correlated ecological factors soils two evergreen broad-leaved forests AY9634
AY234636.1 gg_id:111882 soil isolate Ellin5285 AY2346
EF580946.1 gg_id:278766 Survey Microbial Freshwater Calcareous Mats freshwater calcareous mat clone CM6 EF5809
EU150213.1 gg_id:278429 acidobacteria and soil Niwot Ridge LTER; spruce fir forest clone NiA_SF_24 EU150
FJ478852.1 gg_id:545536 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4788
EU491650.1 gg_id:265935 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU491
FM877546.1 gg_id:357743 Microbial several mining wastes Bulgaria uranium mill tailings clone BuhD-119 FM877
FJ466293.1 gg_id:541280 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea FJ4662
EU132210.1 gg_id:247003 tallgrass prarie soil clone FFCH13193 EU132
EF516049.1 gg_id:217420 grassland soil clone FCPS633 EF5160
GQ120646.1 gg_id:375577 rhizosphere pioneer plants (Bahia xylopoda and Viguiera linearis) growing on heavy GQ120
FJ479234.1 gg_id:582150 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4792
AF234142.1 gg_id:28512 Sturt arid-zone soil clone #0319-7F19 AF2341
FJ478926.1 gg_id:578528 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4789
FM877548.1 gg_id:369088 Microbial several mining wastes Bulgaria uranium mill tailings clone BuhD-130 FM877
AY289399.1 gg_id:90674 soil clone ABS-10 AY2893
DQ906060.1 gg_id:220544 nickel resistance genes metagenome Tinto River rhizosphere clone ERF-1H3 DQ906
FJ152605.1 gg_id:311752 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX1A_ FJ1526
EU335268.1 gg_id:257461 Changes microbial metabolic and along hydrogeochemically variable profile unsatura EU335
EU449702.1 gg_id:567134 Soil are Changed Agricultural Practices agricultural soil clone Plot4-C01 EU449
FJ205234.1 gg_id:570312 Prokaryotic deep-sea region East Lau Spreading Centre inactive hydrothermal field se FJ2052
AY963500.1 gg_id:152510 structures and correlated ecological factors soils two evergreen broad-leaved forests AY9635
EF597694.1 gg_id:248253 Metagenomics deep mediterranean warm bathypelagic habitat 3010m depth Ionian EF5976
FJ466210.1 gg_id:544431 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea FJ4662
AJ292578.1 gg_id:45591 PCB-polluted soil clone WD228 AJ2925
DQ829645.1 gg_id:249932 Acidobacteria (Spain) Donana National Park clone DON6 DQ829
GQ402674.1 gg_id:567036 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
FJ466400.1 gg_id:571342 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea FJ4664
EU202738.1 gg_id:327251 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo EU202
FJ466332.1 gg_id:544403 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea FJ4663
EU370269.1 gg_id:363971 structure photosynthetic complex biofilm acidophilic streams Rio Tinto (SW Spain) e EU370
EU202782.1 gg_id:309400 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo EU202
FJ466085.1 gg_id:548939 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea FJ4660
AJ850100.1 gg_id:198267 Sponge Italy:Lingurian Sea clone SLIIK0 AJ8501
FJ466166.1 gg_id:552854 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea FJ4661
FJ466014.1 gg_id:575126 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea FJ4660

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51.8	1730.2	1141.4	1190.9	3195.8	2488.8	1837.2	788.9	284.6	122.5	668.8
670.9	1564.6	1830.7	1664.5	2315.2	1700.4	2293.5	4758.9	1048.4	535.6	4269.4
51.5	1520.7	658.2	871.3	4729.4	1133.3	1205.8	285.1	345.9	78.7	329.3
47.2	90.9	60.4	46.9	239.3	77.0	91.7	36.1	37.7	20.5	83.7
73.6	474.9	450.2	449.0	730.5	529.2	828.5	625.9	159.6	125.4	242.3
4985.3	3975.4	3586.8	3311.9	3691.0	3528.7	3482.0	3101.2	3089.0	3491.4	2978.7
6004.9	3156.9	2182.5	2683.7	2646.9	2232.5	3559.4	2496.6	3332.5	2994.9	3634.5
8078.1	3492.0	3666.2	3478.1	4079.7	3399.8	3821.8	3289.0	5162.4	3779.1	4898.0
211.6	2186.1	2406.7	2755.9	4473.4	2995.8	4286.9	3022.2	1501.9	1258.4	2197.4
12191.4	4746.3	3583.0	4465.5	6672.9	3900.9	5740.6	4353.2	2261.4	2465.6	2692.2
116.6	4160.6	4774.2	6178.2	8935.5	3833.1	8442.4	3770.8	855.9	1307.8	2852.1
82.1	922.5	1224.2	826.9	1513.1	898.8	1332.4	714.6	268.9	130.9	514.4
1501.3	7097.4	6067.6	7115.1	9327.6	6000.9	8326.7	5694.1	5487.9	2369.0	5269.0
1116.5	3185.6	2427.2	2706.2	5056.0	3299.1	3385.6	2173.2	2295.3	1217.4	1279.8
33.4	132.6	178.3	83.5	341.5	165.4	112.7	56.1	27.9	18.8	75.0
8937.3	4491.0	3767.0	4055.1	4181.7	3689.5	4694.6	3299.2	4486.2	3234.6	4813.0
51.7	504.6	462.0	592.3	1266.8	508.0	1040.9	377.1	151.0	197.3	206.9
8232.7	7254.7	7311.1	8726.7	10080.9	7329.9	9557.0	6691.0	4972.3	5328.3	7030.2
9913.6	5905.9	4993.4	6365.3	8386.9	5362.2	7726.2	5020.6	4690.6	4148.0	4442.0
8340.9	7422.9	7212.2	8077.1	9882.0	7708.3	9283.4	6440.8	5737.8	5555.7	7497.3
1074.2	1362.0	1999.9	1562.6	2326.4	1580.5	1906.9	1611.4	1098.2	732.4	1223.6
6554.6	5358.2	4823.1	5688.0	6825.5	4839.0	6507.6	4395.1	3086.4	3306.4	4254.2
60.7	918.5	458.8	769.5	694.1	545.6	962.8	536.5	190.2	50.2	371.5
15179.1	5067.4	3420.9	4074.6	5223.8	4381.4	4162.1	4035.3	5156.9	4322.6	5443.0
5582.0	7814.5	8406.9	8645.3	10629.1	7634.4	10507.0	7445.9	6460.9	4186.6	8005.4
39.5	490.9	668.7	350.8	1515.5	793.1	923.1	558.8	358.1	104.2	395.2
363.8	5308.8	5252.6	5935.7	7250.2	5614.8	7448.8	4591.1	3222.4	3527.7	5098.5
35.8	225.1	741.4	338.4	529.2	374.7	289.5	374.4	128.3	96.9	203.0
44.9	98.3	355.6	84.2	86.8	171.9	38.9	93.7	35.7	26.3	47.6
451.8	3612.9	3623.2	3817.1	4094.3	3664.5	3930.6	3427.7	4276.2	3170.4	3757.3
86.9	786.1	1089.3	1149.3	1552.3	996.1	1295.5	1180.7	422.2	148.1	562.7
3780.9	4794.7	5876.3	6131.3	6894.0	4522.6	7438.5	4489.3	2828.7	1566.5	4331.5
112.5	1598.9	2537.5	3073.2	2639.7	1625.6	2143.3	1494.8	676.3	361.7	1341.4
5410.1	3705.4	3960.9	3618.3	4904.6	3593.2	4314.4	3396.2	4444.8	1918.7	2725.4
7141.9	3861.8	4729.8	5167.5	6082.8	4998.5	6162.4	6816.5	3871.5	2354.8	5269.9
3880.8	3275.3	3006.9	3278.1	5918.1	3275.5	5689.4	2833.8	1041.7	748.5	1961.3
3919.0	3381.3	3787.3	3724.4	4490.5	3446.3	4409.7	4326.1	3811.5	1854.7	2771.2
68.3	1012.2	1080.9	1229.9	1568.2	1134.1	1464.0	1150.2	218.5	174.5	644.4
970.1	2552.8	3415.2	3553.0	3841.3	4005.4	3972.7	3767.5	2511.9	4371.5	3386.2
15908.8	8241.9	6664.1	6388.1	7230.5	7268.5	7182.2	6096.2	7810.1	7652.3	7687.7

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1163.5	483.7	1357.5
35.5	79.8	196.2
657.5	401.2	881.0
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2069.7	2285.5	2540.3
2883.1	4762.5	3492.5
2663.3	3450.9	5179.5
4950.1	4710.6	5441.3
4520.4	1525.1	4082.0
523.5	866.7	1035.7
6759.2	6901.3	11275.6
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64.7	286.8	604.6
3477.0	4891.2	5719.9
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5820.3	4968.9	6593.1
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1334.5	2600.7	2317.2
4521.7	4879.8	6608.2
584.3	925.0	2385.7
3718.3	5166.4	7806.1
7313.6	7760.0	8822.1
388.7	741.6	1266.6
4088.8	5763.5	8053.4
624.0	489.4	609.2
95.0	90.3	123.8
3461.4	3767.6	5393.3
892.4	1485.6	1784.5
4749.8	5211.5	5111.0
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2733.6	3953.4	4486.9
5527.4	5977.0	5897.3
3366.8	3164.0	5546.6
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DQ404735.1 gg_id:151798 contaminated sediment clone 655075 DQ404
DQ906783.1 gg_id:241820 Oman subsurface soil clone 2B-4 DQ906
EF516149.1 gg_id:223221 grassland soil clone FCPU726 EF5161
AY922112.1 gg_id:114322 farm soil clone AKYH1441 AY9221
EU276532.1 gg_id:370090 -DGGE and Approaches Analyze Effect Agricultural Practices on Soil agricultural soil c EU2765
DQ451491.1 gg_id:156804 forest soil clone FAC52 DQ451
EU335330.1 gg_id:254143 Changes microbial metabolic and along hydrogeochemically variable profile unsatura EU3353
FJ529274.1 gg_id:554828 Evidence vertical transmission symbionts adult embryo Caribbean sponge Svenzea ze FJ5292
EU491480.1 gg_id:260260 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X4 clone EU4914
AY395324.1 gg_id:104834 pasture soil clone EB1005 AY3953
FM873305.1 gg_id:363171 occupant source house floor dust clone FD01D10 FM873
DQ451496.1 gg_id:156857 forest soil clone FAC57 DQ451
AM162414.1 gg_id:151114 and situ identification acidic sphagnum peat bog clone B59 AM162
EF999388.1 gg_id:252185 Vertical and Methanotrophs Estuarine Sediments Pearl River Estuary sediments 22cn EF9993
EU150228.1 gg_id:279590 acidobacteria and dry meadow soil Niwot Ridge LTER clone NiA_DM_1 EU1502
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EU193005.1 gg_id:321058 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo EU1930
AJ292581.1 gg_id:25003 PCB-polluted soil clone WD247 AJ2925
GU208393.1 gg_id:582704 Study on Sediment Dongping Lake sediment clone Fh1-6 GU208
AY963503.1 gg_id:154268 structures and correlated ecological factors soils two evergreen broad-leaved forests AY9635
AM162415.1 gg_id:152327 and situ identification acidic sphagnum peat bog clone B62 AM162
EF688384.1 gg_id:241619 soil clone F6-100 EF6883
EU373956.1 gg_id:261742 southern Cretan margin (eastern Mediterranean Sea) canyon and slope sediment clc EU3739
EU276529.1 gg_id:362467 -DGGE and Approaches Analyze Effect Agricultural Practices on Soil agricultural soil c EU2765
Z95710.1 gg_id:22391 Holophaga/Acidobacterium phylum clone 32-10 Z95710
EU117175.1 gg_id:238372 Scratching surface rare biosphere tag primers recent progress made toward microbi EU1171
AY493928.1 gg_id:136996 Fingerprinting aggregates soil clone 537 AY4939
AY922148.1 gg_id:113191 farm soil clone AKYH694 AY9221
FJ479477.1 gg_id:577222 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4794
AY289380.1 gg_id:89699 soil clone ABS-150 AY2893
EF494364.1 gg_id:220562 Nunnock River granitic landscape clone NR.1.008 EF4943
FJ478491.1 gg_id:553968 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4784
EU449733.1 gg_id:548647 Soil are Changed Agricultural Practices agricultural soil clone Plot4-G12 EU4497
DQ829644.1 gg_id:236775 Acidobacteria (Spain) Donana National Park clone DON5 DQ829
GU061236.1 gg_id:584106 Evaluation culturing methods cultivate previously Yel Sea intertidal beach seawater GU061
EF018559.1 gg_id:211201 aspen rhizosphere clone Amb_16S_822 EF0185
AY289382.1 gg_id:89580 soil clone DS-130 AY2893
FJ004671.1 gg_id:566891 Acidobacteria former agricultural soil rhizosphere clone 246 FJ0046
EU373917.1 gg_id:264000 southern Cretan margin (eastern Mediterranean Sea) canyon and slope sediment clc EU3739

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1091.4	5559.3	4678.7	5290.0	6237.3	5303.9	6480.2	4660.9	5370.5	5016.9	5499.5
60.7	90.7	93.9	82.0	134.5	215.5	159.2	72.5	49.8	61.2	131.2
1938.9	5828.2	5099.0	6455.5	8342.8	5477.2	7605.0	5012.3	4262.0	4384.3	5184.2
30.2	130.7	109.2	105.2	278.8	233.9	474.0	63.1	31.0	19.0	73.1
74.4	4791.5	3775.9	5011.3	8113.7	4409.4	7156.6	3933.5	1545.9	678.4	1965.7
59.8	1287.9	589.3	989.0	1045.0	1089.2	1501.8	466.6	307.1	250.6	369.1
1054.0	3058.4	3171.9	3627.1	6230.9	3936.7	4628.2	2802.8	767.5	310.4	2326.4
318.6	2391.7	2602.5	3018.1	3162.4	2348.3	3245.1	2498.8	851.6	444.5	1501.3
2193.4	6459.7	6221.9	7293.3	7818.8	6135.5	8647.4	5257.0	5370.5	3032.1	6640.3
1794.3	4497.8	4982.3	4955.1	6534.1	4333.7	6368.1	5304.2	4431.7	2704.8	3381.3
16433.8	8781.5	8595.6	10587.6	8891.0	8337.1	9940.3	7922.9	11863.5	8992.7	12026.8
571.5	2214.4	2519.2	2796.5	2965.9	2303.4	3135.9	2913.5	1226.0	494.8	1789.6
639.1	4078.2	4626.8	5084.9	8044.9	3998.8	7245.8	3967.1	2891.3	2347.9	3215.0
441.0	1661.3	2198.5	1972.4	2976.4	2115.9	2045.5	1682.5	2005.2	2485.5	3110.6
1644.2	8160.4	8760.6	8630.8	10301.6	7628.3	10578.7	7652.9	6298.2	3732.3	7934.9
25655.1	6577.1	6381.9	7513.9	7132.3	6853.2	6843.5	6842.3	8861.7	7776.3	8439.8
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41.6	82.9	247.7	103.1	334.5	126.9	115.3	101.7	34.7	36.1	62.1
698.8	5040.4	5092.2	7281.8	6742.6	2969.9	6081.5	2969.3	546.7	1085.2	1723.7
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4925.0	2276.4	1950.8	2181.6	2840.5	1873.3	3220.2	1718.9	2016.1	1761.3	2781.7
3428.3	9562.3	8885.2	10444.2	13221.7	9553.1	12493.0	8445.2	6682.4	5388.2	7167.1
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EU335387.1 gg_id:244133 Changes microbial metabolic and along hydrogeochemically variable profile unsatura EU3353
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FN396687.1 gg_id:543863 constant flux thermophilic cold seabed Arctic marine surface sediment clone s5_0_V FN3966
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FM872485.1 gg_id:362116 occupant source house floor dust clone FA01A05 FM872
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GU205312.1 gg_id:531776 unusual Microbial Venezuelan Tepui (Orthoquartzite) Cave: Dominance Chloroflexal GU205
GQ402599.1 gg_id:508855 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
AY963463.1 gg_id:150792 structures and correlated ecological factors soils two evergreen broad-leaved forests AY9634
FJ152824.1 gg_id:331686 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX5A_ FJ1528
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AF317741.1 gg_id:136924 Nullarbor cave clone wb1_A08 AF3177
AB486755.1 gg_id:565220 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCOR(AB4867
EF492944.1 gg_id:245527 Iron-manganese Nodule and Its Surrounding Soil soil around iron-manganese nodule EF4929
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EU276463.1 gg_id:361472 -DGGE and Approaches Analyze Effect Agricultural Practices on Soil agricultural soil c EU2764
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FJ479104.1 gg_id:538113 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4791
GQ500793.1 gg_id:540282 Surveys Biofilms and Sediments Mammoth Cave Karst Aquifers Bio-Sep beads conta GQ500
X97098.1 gg_id:3730 peat bog clone TM2 X97098
EF597699.1 gg_id:240765 Metagenomics deep mediterranean warm bathypelagic habitat 3010m depth Ionian EF5976

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65.4	551.5	658.7	521.4	1482.5	675.0	736.1	410.6	149.6	50.9	418.3
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50.4	1417.4	1846.8	1450.6	3607.7	1917.1	3554.8	1541.9	251.2	166.6	898.0
154.6	307.5	247.5	203.9	226.0	368.3	126.4	166.4	199.0	122.3	93.4
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1351.3	6961.9	6730.0	7557.4	9299.5	6822.7	9677.0	7121.1	4981.5	3419.3	6270.1
1146.3	5784.0	5047.3	5571.7	5994.9	4425.9	6169.7	4720.5	4724.1	3701.4	4608.8
3038.6	3067.3	2915.5	2517.2	3626.3	2927.1	2873.5	2508.1	2865.3	1672.7	2882.3
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3388.3	4874.0	4799.4	5279.3	8346.2	6305.5	6580.7	4264.9	3940.7	2533.3	3362.8
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42.1	397.5	650.9	598.4	1165.3	341.3	808.1	394.0	323.5	86.4	184.7
5506.0	8688.5	8678.1	9775.0	10762.0	8870.6	10630.7	8454.4	8200.8	5447.9	9050.6
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59.5	690.2	912.7	1026.7	1476.7	694.0	1447.0	732.4	179.8	136.0	323.6
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EF125431.1 gg_id:195246 mangrove soil clone MSB-2D12 EF1254
AY850302.1 gg_id:136684 depending on what microbial treatment present soil clone cw7 AY8503
DQ906775.1 gg_id:236062 Oman subsurface soil clone 2A-3 DQ906
EU676420.1 gg_id:302540 rhizosphere pioneer plants (Bahia xylopoda and Viguiera linearis) growing on metals EU676
EF018157.1 gg_id:212760 aspen rhizosphere clone Amb_16S_492 EF0181
EF173346.1 gg_id:182111 Options situ remediation contaminated mixture chlorinated hydrocarbons hydrocarb EF1733
GU172193.1 gg_id:582540 Microbial Eucalyptus plantation soil clone DSM-R21 GU172
DQ451525.1 gg_id:156611 forest soil clone FAC86 DQ451
FJ465992.1 gg_id:546843 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea FJ4659
EF516950.1 gg_id:221187 grassland soil clone FCPP719 EF5169
FJ152801.1 gg_id:346446 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX5A_ FJ1528
EU132094.1 gg_id:253652 tallgrass prarie soil clone FFCH4380 EU132
EU734939.1 gg_id:322030 assemblages sediment station DBSE Northern Bering Sea clone 030C26 EU7349
EF600570.1 gg_id:291945 soil clone E5-24 EF6005
EF494374.1 gg_id:217344 Nunnock River granitic landscape clone NR.1.127 EF4943
GQ402697.1 gg_id:538729 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
AY963323.1 gg_id:155327 structures and correlated ecological factors soils two evergreen broad-leaved forests AY9633
AB262723.1 gg_id:243925 microorganisms shal subsurface Sarobetsu mire peat soil clone HSM050P-B-12 AB2627
EU421852.1 gg_id:271460 Un-culturable Indian Himalayas soil under glacier Lahaul-Spiti Valley clone KC-27 EU4218
FJ517001.1 gg_id:551640 semiarid 'Tablas de Daimiel National Park' wetland (Central Spain) unravelled water c FJ5170
EF019493.1 gg_id:206727 aspen rhizosphere clone Elev_16S_761 EF0194
AB300068.1 gg_id:220849 Wide ancient microbial DNAs Quaternary sediments holocene mud sediment clone S AB300
AB300075.1 gg_id:218783 Wide ancient microbial DNAs Quaternary sediments holocene mud sediment clone S AB300
GQ246334.1 gg_id:590912 Temporal and spatial China North Yel Sea sediments clone Sd1-53 GQ246
AY225646.1 gg_id:97685 Mid-Atlantic Ridge hydrothermal sediment clone AT-s3-28 AY2256
EU385737.1 gg_id:276636 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S EU3857
AB177178.1 gg_id:133702 seafloor methane hydrate clone ODP1230B23.02 AB177
EU925844.1 gg_id:347415 sediments sediment station DBS1 northern Bering Sea clone 035E60 EU9258
GQ246376.1 gg_id:587607 Temporal and spatial China North Yel Sea sediments clone Cm1-39 GQ246
EU386023.1 gg_id:267584 Biogeographical and microbes sediments on subseafloor sediment South China Sea c EU3860
EU925841.1 gg_id:323947 sediments sediment station DBS1 northern Bering Sea clone 022E38 EU9258
EU287157.1 gg_id:236701 Pacific arctic surface sediment clone P13-64 EU287
GQ246383.1 gg_id:558182 Temporal and spatial China North Yel Sea sediments clone Cm1-46 GQ246
EU734964.1 gg_id:342871 assemblages sediment station DBSE Northern Bering Sea clone 058D16 EU7349
AM176872.1 gg_id:160549 Recovery mangrove sediment clone SZB79 AM176
EU246285.1 gg_id:242979 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-P6-C11 EU2462

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38.7	740.9	660.2	743.7	1289.7	848.1	1073.3	820.5	161.1	267.4	333.3
193.7	6243.2	4856.3	5691.7	8605.2	6163.4	8050.7	4734.2	2952.8	2847.4	4160.9
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628.6	4759.9	4070.4	4841.9	8191.7	4917.5	7164.8	4160.6	2075.2	1603.1	2725.2
223.5	1583.6	1858.9	1823.7	2834.2	1688.3	3009.6	2301.6	926.4	1755.9	1051.9
1922.6	1761.7	1993.1	2260.7	1805.7	1854.7	1975.5	2509.9	1556.9	1216.3	2239.8
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1160.6	6148.8	7913.3	6449.6	7361.2	6681.4	7947.1	6412.1	5150.2	4740.0	6383.2
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41.9	36.4	44.9	46.8	511.3	62.2	73.9	31.7	26.1	24.7	34.6
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46.9	2552.3	1431.1	2159.1	3795.0	2030.8	3310.6	1403.6	764.7	231.0	831.6
958.0	6207.0	6018.7	7262.3	9889.7	6497.7	10371.3	5772.9	4630.8	4267.4	5998.8
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93.7	2113.4	2596.1	2769.8	4940.0	2784.4	3599.9	2829.5	783.7	826.2	1560.0
34.4	48.6	57.8	62.7	93.4	99.5	82.9	47.6	26.8	33.7	40.2
100.5	5315.1	6126.0	7070.8	5966.7	5635.8	7166.2	6150.6	4369.9	4363.7	5472.1
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44.9	64.4	93.8	62.8	141.7	74.7	94.9	71.1	38.0	22.6	44.3
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4057.7	4166.0	4423.8
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3816.9	4206.2	5914.5
142.9	356.7	1229.0
6827.4	8326.7	8165.0
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1995.5	1403.5	4661.6
5408.3	5781.5	8430.6
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GQ259273.1 gg_id:565350 Microbial activities coastal marine sediments and water column Svalbard deep sedir GQ259
EU491345.1 gg_id:270093 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X3 clone EU491
FJ205355.1 gg_id:555830 Prokaryotic deep-sea hydrothermal region East Lau Spreading Centre deep marine se FJ2053
EU373945.1 gg_id:259584 southern Cretan margin (eastern Mediterranean Sea) canyon and slope sediment clc EU373
EU328055.1 gg_id:279230 dynamics during bioremediation crude oil contaminated moderate saline soil clone B EU328
FJ748804.1 gg_id:512374 Vertical and sulfate-reducing prokaryotes estuarine Southern China Pearl River Estuar FJ7488
FJ269346.1 gg_id:587166 Microbes marine sponges sponge tissue clone XE1A06 FJ2693
DQ297966.1 gg_id:144752 Microbial hydrocarbon contaminated soil clone UD7 DQ297
EF127615.1 gg_id:208380 Fossil Genes and Microbes Entombed Oldest Ice on Earth ice clone DLE014 EF1276
EF492965.1 gg_id:256992 Iron-manganese Nodule and Its Surrounding Soil soil around iron-manganese nodule EF4929
AB240484.1 gg_id:141861 microbial structure rhizosphere biofilm Sapporo root-tip (0 40 mm) Phragmites Sosei AB240
EF516139.1 gg_id:221008 grassland soil clone FCPU691 EF5161
AY250867.1 gg_id:86097 lichen-dominated Antarctic cryptoendolithic community clone FBP241 AY2508
EU150230.1 gg_id:279384 acidobacteria and dry meadow soil Niwot Ridge LTER clone NiA_DM_4 EU150
FJ592765.1 gg_id:511315 Fumarole-supported islands biodiversity within hyperarid -elevation landscape on Pur FJ5927
AM116734.1 gg_id:142650 Interactions U(VI) added natural dependance on various incubation conditions soil u AM116
EF584528.1 gg_id:234366 mixed granule anammox reactor clone KIST-JJY008 EF5845
AF173822.1 gg_id:1768 Antarctic clone LB3-30 AF1738
EU132395.1 gg_id:253431 tallgrass prarie soil clone FFCH1720 EU1323
GU459003.1 gg_id:563320 microbiota human male female forehead forearm and influence make-up skin clone GU459
EU223961.1 gg_id:247010 -RFLP microbes Qinghai-Tin rail soil clone 149 EU2239
AY289362.1 gg_id:88737 soil clone DS-249 AY2893
AY921973.1 gg_id:113400 farm soil clone AKYG1698 AY9219
EF018286.1 gg_id:209520 aspen rhizosphere clone Amb_16S_647 EF0182
AY289372.1 gg_id:112292 soil clone DS-13 AY2893
EF516486.1 gg_id:221484 grassland soil clone FCPP426 EF5164
EU669595.1 gg_id:351338 soil clone S11-2 EU6695
EU786139.1 gg_id:564389 cotton rhizosphere soil clone 3Y-6 EU7861
EF019956.1 gg_id:209832 aspen rhizosphere clone Elev_16S_1335 EF0199
EU335391.1 gg_id:239226 Changes microbial metabolic and along hydrogeochemically variable profile unsatura EU3353
AF368181.1 gg_id:55946 non-EBPR sludge clone SBRT166 AF3681
FJ478811.1 gg_id:578620 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4788
EF516663.1 gg_id:223948 grassland soil clone FCPU688 EF5166
AY211077.1 gg_id:81698 anaerobic VC-degrading enrichment clone VC47 bacterium AY2110
AM777958.1 gg_id:246222 nonsaline . Influence pore-size filters determination structure alkaline groundwater AM777
EF516301.1 gg_id:223489 grassland soil clone FCPN505 EF5163
DQ648917.1 gg_id:185831 biodiversity and rhizosphere polluted site TGGE screening libraries PCB contaminate DQ648
EF127618.1 gg_id:204154 Fossil Genes and Microbes Entombed Oldest Ice on Earth ice clone DLE075 EF1276
FJ479148.1 gg_id:509991 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4791
DQ648922.1 gg_id:193986 biodiversity and rhizosphere polluted site TGGE screening libraries PCB contaminate DQ648
EU979109.1 gg_id:340198 Effects intercropping Rhizobium inoculation on microbial biomass and rhizosphere b EU979

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2038.5	7353.8	7609.3	8224.7	9882.4	7270.5	10119.2	6802.4	5005.0	4780.1	8616.7
1323.5	6555.5	7698.7	7862.7	9907.1	6447.3	9684.8	6573.9	3858.7	4752.8	6949.6
601.8	4245.9	5221.3	4289.5	4316.1	4494.6	5023.1	4359.4	3594.5	1556.2	3826.3
2025.4	5913.0	5952.8	6679.2	8535.6	5633.7	8741.1	5197.1	3270.1	2795.5	4031.9
489.4	3033.6	3171.0	3235.8	4149.4	3143.9	4354.4	2941.9	1815.0	2184.8	6787.4
948.0	6314.1	7382.5	6901.7	6770.6	5994.5	6804.6	5685.9	4111.0	2539.4	5594.8
295.8	3315.4	2483.0	2567.9	4678.4	2967.4	3091.5	2410.4	2489.6	1447.5	2160.5
40.8	211.7	267.6	277.2	758.1	252.0	465.7	164.1	58.1	10.7	98.9
7401.6	4525.1	4049.6	4413.2	9539.3	5204.9	5972.4	3685.2	4433.0	3429.9	5159.5
8137.2	3138.1	3706.6	4450.3	8210.3	4156.9	8664.9	3507.2	1694.3	976.4	2013.6
52.0	106.3	61.3	49.7	211.0	56.4	70.6	26.6	28.6	20.2	36.2
46.4	19.1	20.1	23.6	27.7	12.8	25.9	16.3	20.3	22.7	14.5
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1188.9	6868.2	6090.7	4474.2	6556.5	5482.2	5206.0	4470.6	9232.3	7434.9	5283.2
56.5	212.2	104.1	234.4	1166.1	129.3	208.7	32.2	41.9	27.9	183.6
50.1	150.9	167.3	160.1	649.5	242.6	323.9	80.8	54.5	45.3	35.5
798.6	4872.7	3522.8	3701.5	7316.9	4658.2	5238.1	3659.8	3332.8	2062.1	2086.8
88.0	1217.8	1267.5	1471.5	2034.6	1559.4	1926.4	1542.2	695.5	511.0	935.2
45.2	1858.4	1883.7	1932.0	5452.3	2030.9	2792.2	1556.1	1277.5	1034.1	1673.0
56.5	486.6	448.9	469.2	1035.3	507.5	606.1	431.7	249.3	91.5	314.4
2241.5	8330.7	7668.5	9148.6	16403.1	8449.3	14304.7	6523.0	6651.6	4857.1	9855.6
37.2	3056.1	3342.9	4476.6	5467.6	4135.1	5345.4	3425.6	944.3	1045.2	1136.9
15562.2	4717.4	4284.5	4641.4	7450.6	5274.1	8072.8	3831.7	5283.9	4296.2	6532.9
5522.6	3746.7	3652.9	3682.8	4306.3	3195.1	4043.7	3881.0	2938.2	4509.2	4152.2
51.0	986.1	621.9	600.5	2495.0	2890.7	558.4	42.2	135.4	66.7	918.8
221.1	3020.4	2719.3	2699.3	4762.5	3146.6	3753.2	2302.0	1743.1	687.4	2332.6
1609.7	4674.2	3902.0	4336.6	6324.8	4415.1	5245.4	4225.5	2983.0	984.6	4291.6
52.6	526.4	693.6	747.7	1570.7	659.3	654.6	1085.0	357.0	406.6	554.4
94.7	4029.9	4578.1	4994.4	9721.0	4841.3	8503.2	3627.1	1212.2	1150.8	1451.9
196.7	499.3	525.6	544.0	953.6	483.9	599.1	458.0	355.7	408.1	440.8
53.5	441.6	235.7	266.9	1950.9	318.6	367.3	138.5	125.7	42.2	348.9
5621.0	4312.0	3478.3	3658.0	4696.2	3945.7	3832.4	3879.4	3878.0	3990.6	4037.6
39.1	923.1	1566.2	2112.8	5764.1	1259.1	3342.4	1064.5	233.9	278.4	294.8
268.5	1890.6	2223.9	2191.9	3806.8	2149.2	3152.3	2562.1	1694.8	1065.3	1543.0
70.0	329.4	332.9	305.0	1212.9	421.6	855.0	236.9	108.4	78.6	111.7
26316.7	10360.3	9093.3	10461.2	11958.4	9424.1	10945.2	8004.7	13279.7	9982.7	12489.8
117.9	1706.6	1650.5	2031.2	4117.6	2134.9	3011.3	2454.4	984.6	430.8	699.2
63.3	1538.5	1070.1	1195.3	5205.4	1910.2	1983.5	972.4	511.8	184.4	926.1
6668.1	4747.0	4159.6	4856.5	6140.3	4795.4	5711.0	4601.5	4533.9	2903.5	5978.7
930.1	4000.1	3774.3	4314.3	6394.0	4219.1	5893.4	4340.1	3397.4	3126.4	3847.1

4115.9	5246.1	4969.2
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4377.2	5609.8	8467.6
2949.6	3088.9	3457.7
6372.0	6043.5	8224.4
2555.9	2910.6	5007.6
222.9	362.9	442.1
3299.6	4439.0	8570.6
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33.1	23.9	41.9
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28.9	156.6	365.8
126.3	145.5	485.2
4268.5	3498.6	5089.5
1796.2	1821.7	1798.0
2174.2	1975.6	2404.4
442.6	847.5	1423.1
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3329.1	2345.8	5295.6
3720.6	4492.6	4058.8
3915.4	4200.0	4360.2
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3929.2	4292.3	5840.3
470.8	912.3	1715.2
3156.8	2350.0	5659.3
447.2	680.7	555.9
95.8	267.7	928.8
3978.8	4521.5	4422.7
896.0	662.3	3722.1
1928.3	2564.6	2231.6
131.8	329.9	617.9
6714.4	8508.0	10029.1
1997.0	1861.9	2435.5
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4181.3	6329.1	7269.2
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Z95720.1 gg_id:3697 soil clone RB30 Z95720
EU669608.1 gg_id:322898 soil clone S11-33 EU669
DQ648925.1 gg_id:197697 biodiversity and rhizosphere polluted site TGGE screening libraries PCB contaminate DQ648
FJ004727.1 gg_id:573937 Acidobacteria former agricultural bulk soil clone 1L2B FJ0047
AF097766.1 gg_id:1776 activated sludge clone 2951 AF097
FJ790561.1 gg_id:549105 Chasmolithic microbial niches -altitude arid tuff Tibet desert clone VB43 FJ7905
AY493926.1 gg_id:136943 Fingerprinting aggregates soil clone 539 AY493
FJ479201.1 gg_id:513643 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4792
EF494321.1 gg_id:218151 Nunnock River granitic landscape clone NR.4.007 EF4943
DQ450705.1 gg_id:161241 Microbial Alpine Tundra Wet Meadow Soil: Chloroflexi Cold Water-Saturated satura DQ450
EF516128.1 gg_id:224218 grassland soil clone FCPT565 EF5161
FJ479029.1 gg_id:556814 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4790
GQ264352.1 gg_id:567627 Structure Simulated Level Waste Site simulated level waste site clone WW2_25 GQ264
DQ532357.2 gg_id:164562 Geographical Variation Microbial Burden and Spacecraft Assembly Kennedy Space C DQ532
FJ479240.1 gg_id:589151 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4792
FJ478618.1 gg_id:590565 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4786
EU979032.1 gg_id:340207 Effects intercropping Rhizobium inoculation on microbial biomass and rhizosphere b EU979
DQ648920.1 gg_id:191363 biodiversity and rhizosphere polluted site TGGE screening libraries PCB contaminate DQ648
DQ083266.1 gg_id:128164 Acidobacteria pasture soil clone EC1038 DQ083
AF173824.1 gg_id:1767 Antarctic clone LB3-92 AF1738
DQ532263.1 gg_id:171397 Geographical Variation Microbial Burden and Spacecraft Assembly Johnson Space C DQ532
EU150244.1 gg_id:277931 acidobacteria and dry meadow soil Niwot Ridge LTER clone NiA_DM_21 EU150
EU669596.1 gg_id:341165 soil clone S11-7 EU669
GQ029460.1 gg_id:401741 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw861f09 GQ029
CU921698.1 gg_id:565019 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU921
GQ275099.1 gg_id:586270 gut symbionts are tightly linked herbivory ants extract single ant clone #123 GQ275
EU131955.1 gg_id:242792 tallgrass prarie soil clone FFCH15207 EU1319
EF019535.1 gg_id:209516 aspen rhizosphere clone Elev_16S_1040 EF0195
FJ479597.1 gg_id:588240 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4795
EF018479.1 gg_id:216034 aspen rhizosphere clone Amb_16S_1107 EF0184
EF019534.1 gg_id:206841 aspen rhizosphere clone Elev_16S_1038 EF0195
EU276488.1 gg_id:367606 -DGGE and Approaches Analyze Effect Agricultural Practices on Soil agricultural soil c EU2764
EF492911.1 gg_id:247203 Iron-manganese Nodule and Its Surrounding Soil soil around iron-manganese nodule EF4929
FJ466180.1 gg_id:566535 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea FJ4661
EU132318.1 gg_id:257472 tallgrass prarie soil clone FFCH10172 EU1323
FJ152715.1 gg_id:315631 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX5A_ FJ1527
EU335388.1 gg_id:255794 Changes microbial metabolic and along hydrogeochemically variable profile unsatura EU3353
EU335275.1 gg_id:250547 Changes microbial metabolic and along hydrogeochemically variable profile unsatura EU3352
AY509523.1 gg_id:136325 cyanobacterial blooms four Swedish lakes freshwater clone LiUU-11-191 AY5095
EU202757.1 gg_id:340218 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo EU2027
EU131979.1 gg_id:236098 tallgrass prarie soil clone FFCH2893 EU1319

37.2	1008.3	886.4	609.0	3969.6	1459.6	854.5	276.3	345.0	92.6	494.3
2930.1	3310.5	3301.1	3313.9	3698.8	3340.7	3141.1	3631.1	2642.0	2021.0	2707.9
44.2	180.6	254.8	236.1	937.4	232.7	245.2	188.1	113.7	69.8	189.4
74.7	1503.1	1202.1	1254.0	3124.1	1680.7	1791.5	1112.4	376.7	292.8	873.6
509.0	1677.7	1892.9	2126.7	2139.8	1571.5	1930.1	1999.1	915.1	752.1	1679.9
197.1	4445.8	3994.3	4448.1	8613.5	4888.3	5745.9	3464.9	3597.1	2792.9	3060.2
84.1	1181.2	1233.4	1504.5	2771.6	1619.8	1872.0	1263.6	1556.3	235.3	692.8
4200.4	3399.8	3514.6	3723.3	6596.8	3557.9	4315.9	3023.8	3757.1	2492.5	3264.4
5357.2	2683.1	2226.4	2210.2	3027.9	2500.3	2365.1	2407.3	3973.8	998.5	3838.0
312.5	1157.4	952.6	645.8	3961.5	1785.7	448.1	579.3	371.7	159.2	639.9
31.2	260.5	260.9	416.7	1412.1	340.1	803.5	115.7	46.0	24.9	49.4
2645.3	3762.2	4112.6	4496.3	5165.0	4155.4	4576.3	4612.8	3579.0	2306.9	4951.0
31.7	1408.7	1138.5	1225.7	4664.9	1745.9	2982.2	737.2	374.6	277.8	306.2
71.3	1526.5	1372.7	1757.9	4076.0	1725.9	2408.1	1343.6	547.6	414.0	1025.1
5310.4	4150.1	3777.7	3575.2	5161.8	3757.2	4225.0	3309.7	3640.6	2183.1	4064.1
1063.4	1702.6	2056.2	2169.6	3118.6	1813.1	3228.7	2112.3	1453.2	618.3	1631.9
5487.4	4795.5	3217.7	3609.6	8345.1	5153.9	4491.5	3570.0	1470.5	1490.3	1530.4
5626.2	2688.2	2940.5	3454.6	3158.8	3051.7	3714.8	3501.3	3216.6	1445.4	3153.3
80.7	3003.1	2660.9	2940.4	9895.2	3742.0	5753.3	1275.3	948.2	396.9	692.9
116.9	3607.8	2760.3	2574.9	6017.2	3043.5	4720.2	2694.9	1379.1	2888.6	1583.9
48.6	342.2	317.3	444.8	877.0	402.2	381.5	382.5	137.8	241.8	164.7
30.7	1226.8	625.7	359.4	6009.8	1954.0	758.9	175.4	336.8	43.3	478.3
9904.6	6396.6	4310.2	4745.3	6485.0	5435.2	5900.5	4505.8	4757.5	3597.1	5762.7
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5003.2	2490.8	2971.0	3727.3	5846.6	3639.2	4591.4	2900.6	2755.0	1997.3	3035.2
5096.3	3731.1	3650.4	3659.9	4834.7	3723.0	3665.7	4337.7	4311.6	3613.1	4718.7
1460.8	2671.4	2136.7	2067.9	4742.9	2884.0	3744.4	1810.1	1345.3	849.5	2265.7
39.0	143.9	20.4	22.4	43.1	182.6	21.3	18.4	15.9	20.2	108.3
3481.2	3100.5	2147.2	2747.1	4405.5	2914.5	3550.4	2485.1	1453.8	640.4	1774.4
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13208.5	8987.6	7907.1	8891.5	9325.1	8458.4	9267.5	7636.9	9696.2	6680.3	9332.5
44.8	387.5	573.6	706.5	1169.1	764.3	868.9	632.7	155.1	75.9	251.8
3908.2	5697.3	6144.1	5831.9	8177.6	5850.3	8197.2	5456.5	4375.3	2011.9	5461.3
821.1	4081.7	3563.2	4026.1	5872.5	3591.7	5293.9	3929.4	4013.9	1283.5	2547.3
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123.2	2220.0	2606.5	2821.5	6995.8	2734.7	3487.4	2925.2	1927.5	802.9	1340.0
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717.1	2076.6	5219.5
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1117.6	1424.9	3187.7
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205.8	2652.7	3315.6
538.7	2314.1	6066.6
194.9	216.2	569.7
3754.9	4745.1	6694.5
720.7	1008.4	1462.5
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1486.1	2335.0	6560.6
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2323.4	2533.3	4888.0
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AM902631.1 gg_id:237774 Acidobacteria and Planctomycetes radioactive mineral Central Alps Austria subsurfa AM902
EU669607.1 gg_id:336301 soil clone S11-31 EU669
EU192989.1 gg_id:353698 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo EU192
EU131934.1 gg_id:249598 tallgrass prarie soil clone FFCH11145 EU131
FJ478812.1 gg_id:558300 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4788
EU881303.1 gg_id:307883 (maize-sweet cropping field) Karst region maize-sweet potato cropland soil clone KM EU8813
EU132097.1 gg_id:242038 tallgrass prarie soil clone FFCH1205 EU132
DQ532341.1 gg_id:166649 Geographical Variation Microbial Burden and Spacecraft Assembly Kennedy Space C DQ532
FJ790570.1 gg_id:568934 Chasmolithic microbial niches -altitude arid tuff Tibet desert clone VB74 FJ7905
EF205575.1 gg_id:210897 among geographically regions central Tibet geothermal spring mat clone TP32 EF2055
EF205532.1 gg_id:208981 among geographically regions central Tibet geothermal spring mat clone DTB48 EF2055
FJ478484.1 gg_id:543361 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4784
EU335287.1 gg_id:251244 Changes microbial metabolic and along hydrogeochemically variable profile unsatura EU335
FN396738.1 gg_id:575010 constant flux thermophilic cold seabed Arctic marine surface sediment clone s5_8_II FN396
AB303221.1 gg_id:289370 Acanthopleuribacter pedis str. NBRC 101209 AB303
U41563.1 gg_id:1736 "Geothrix fermentans" U4156
DQ660831.1 gg_id:237050 DongChuan copper pyrites PRC determined acid mine drainage (AMD) clone DCN-I- DQ660
GQ390238.1 gg_id:562850 oxic-anoxic interface meromictic crater lake Lac Pavin clone eub62A6 GQ390
DQ660849.1 gg_id:240444 DongChuan copper pyrites PRC determined acid mine drainage (AMD) clone DCN-I- DQ660
AB240350.1 gg_id:144899 microbial structure Phragmites rhizosphere biofilm reed bed reactor laboratory clon AB240
EU803304.1 gg_id:322696 It's all ranking aquatic Lake Gatun clone 5C230854 EU803
AB240249.1 gg_id:142414 microbial structure rhizosphere Phragmites bulk soil reed bed reactor laboratory clo AB240
FJ810540.1 gg_id:373070 Subsurface ecosystem resilience: Long-term attenuation subsurface contaminants su FJ8105
EU156148.1 gg_id:252532 thermal spring microbial and functional genes Coffee Pots Hot Spring clone pCOF_65 EU156
AM086131.1 gg_id:149184 Abundance and archaea mesotrophic Lake Kinneret lake profundal sediment clone AM086
AB192122.1 gg_id:142455 termite gut homogenate clone M1PL1-36 AB192
FJ810545.1 gg_id:433880 Subsurface ecosystem resilience: Long-term attenuation subsurface contaminants su FJ8105
GQ472456.1 gg_id:542134 Microbial Dongping Lake lake sediment clone 5F1-11 GQ472
AM180887.1 gg_id:149516 situ detection Acidobacteria mats chemoautotrophic cave (Lower Kane Cave WY US AM180
EU169840.1 gg_id:361234 Bio-reduction Trichloroethene Hydrogen-Based Membrane Biofilm Reactor membra EU169
X77215.1 gg_id:1732 Holophaga foetida X77215
EU340170.1 gg_id:235707 on Aquatic Macrophytes Geothermally Active Area Sedge Bay Yellowstone Lake WY EU340
AJ009478.1 gg_id:1733 anaerobic TCB-transforming consortium clone SJA-87 AJ0094
AB192121.1 gg_id:144303 termite gut homogenate clone M1NP1-62 AB192
DQ066997.1 gg_id:133176 Lake Washington sediment clone pLW-59 DQ066
FN554392.1 gg_id:554680 Isolation members group 8 Acidobacteria subdivision 1 Verrucomicrobia and other h FN5543
GQ487951.1 gg_id:553643 Microbial metal soil polluted heavy metals clone T7-99 GQ487
GU169059.1 gg_id:592179 Biofilms formed on substances: response f conditions and carbon concentrations sy GU169

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5970.3	9538.4	9387.7	9185.6	11648.2	10023.0	10393.0	9258.4	9063.4	6208.3	12048.3
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1513.6	6801.9	6771.6	6013.9	7360.1	6302.2	6845.2	6785.5	5609.1	4213.6	8994.9
2295.6	7141.1	7023.1	7561.7	10941.4	7265.0	10714.9	6320.5	6725.9	4713.9	6790.9
26139.1	11279.4	10902.0	11824.3	12286.9	10508.8	12023.5	10608.2	11910.2	11888.3	13115.4
1896.3	6306.5	5984.6	6752.8	9645.6	6378.1	8245.5	5952.7	4066.5	5176.6	4961.7
261.8	1477.1	1734.0	2125.3	3018.1	1595.9	2704.2	1518.9	952.3	750.9	1276.6
190.0	1826.0	1815.6	2370.1	3925.2	2196.5	3186.6	2061.4	1025.4	994.2	1456.0
70.7	627.9	648.1	842.9	951.4	635.5	825.2	812.3	323.6	187.2	324.6
46.6	424.1	1217.9	486.2	670.4	414.0	572.3	702.1	97.2	77.8	448.7
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1944.6	7171.9	7822.0	7993.5	10477.9	6852.3	10148.4	6527.9	6656.5	5355.5	6250.9
2215.5	2781.6	2089.7	2091.8	3502.3	2515.5	2638.4	2756.2	2598.1	1276.9	1433.5
135.2	1552.1	1759.0	1817.6	3699.7	2186.8	3439.2	1337.1	609.3	198.0	739.4
60.5	831.7	988.8	948.4	1164.9	981.1	1234.3	4378.7	695.4	196.3	820.3
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82.3	4129.5	5735.2	6901.0	9969.2	6262.1	10283.2	5615.6	836.9	205.0	4450.3
5044.4	8930.1	9897.5	10642.3	12506.7	9276.0	13243.0	8573.2	6985.9	8697.1	9292.5
55.7	3071.6	4039.3	3854.4	6810.3	4332.5	7090.5	2638.0	954.1	358.3	2450.7
7461.7	11389.5	10052.8	12391.6	11183.3	10398.0	12238.7	9949.6	11212.3	8243.4	12142.6
46.4	5199.7	6915.2	7640.6	11058.9	7325.5	12050.9	5741.5	1322.9	263.0	4806.5
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EU360308.1 gg_id:274047 microbial fuel cell enriched sediment clone FWS 726 EU3603
EF032758.1 gg_id:194029 cyanobacterial mat in lava cave clone HAVOmat71 EF0327
EU404024.1 gg_id:311763 Microbial septic tank effluent and soil biozone infiltrative surface clean water clone (EU404(
AY963514.1 gg_id:154909 structures and correlated ecological factors soils two evergreen broad-leaved forests AY9635
EF494334.1 gg_id:225918 Nunnock River granitic landscape clone NR.1.031 EF4943
AB240310.1 gg_id:144019 microbial structure Phragmites rhizosphere biofilm reed bed reactor laboratory clone AB2403
AB486063.1 gg_id:586133 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC AB486(
EF516537.1 gg_id:218957 grassland soil clone FCPT436 EF5165
EU132113.1 gg_id:251439 tallgrass prarie soil clone FFCH10391 EU1321
Z95713.1 gg_id:1728 soil clone 32-20 Z95713
AB486378.1 gg_id:588194 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC AB4863
DQ906890.1 gg_id:251805 Oman subsurface soil clone 11B-20 DQ906
AY395447.1 gg_id:103470 pasture soil clone EB1128 AY3954
AB488104.1 gg_id:578435 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSSUR0 AB4881
EF516616.1 gg_id:224372 grassland soil clone FCPN715 EF5166
DQ450820.1 gg_id:160986 Microbial Alpine Tundra Wet Meadow Soil: Chloroflexi Cold Water-Saturated saturat DQ450
EF515929.1 gg_id:218370 grassland soil clone FCPS615 EF5159
GQ397044.1 gg_id:586275 Functional unvegetated perhumid recently-deglaciated soils do not correlate shifts s GQ397
GQ302583.1 gg_id:542433 prokaryotic sediment Shawan methods cold spring clone sw-xj162 GQ302
AY921868.1 gg_id:113021 farm soil clone AKYG1139 AY9218
EF492961.1 gg_id:250693 Iron-manganese Nodule and Its Surrounding Soil soil around iron-manganese nodule EF4929
Z95729.1 gg_id:1718 soil clone iii1-8 Z95729
FJ545583.1 gg_id:565231 Diveristy Seawater and Sediment Northern North Yel Sea sediment clone S2-65 FJ5455
FJ479007.1 gg_id:509899 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4790
DQ378223.1 gg_id:151990 oil-polluted soil clone M01_Pitesti DQ378
EF632944.1 gg_id:237284 Unique microbial contrasting aquatic altitude Andean Altiplano (northern Chile) fresh EF6329
EF515913.1 gg_id:224501 grassland soil clone FCPP604 EF5159
EU925899.1 gg_id:324084 sediments sediment station DBS1 northern Bering Sea clone 124H8 EU9258
EF516669.1 gg_id:219348 grassland soil clone FCPN472 EF5166
AB488081.1 gg_id:592475 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSSUR0 AB4880
AY289394.1 gg_id:111806 soil clone DS-215 AY2893
FN424397.1 gg_id:565655 structure sediments Bizerte (Tunisia) southern Mediterranean coastal anthropized la FN4243
FJ479328.1 gg_id:511937 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4793
DQ228377.1 gg_id:143029 microbial compositions two subglacial possible role microbes chemical weathering p DQ228
FJ868852.1 gg_id:509795 Effects nitrogen form on excessive fertilization soil Earth-cumuli-orthic anthrosols clo FJ8688
AY493935.1 gg_id:136569 Fingerprinting aggregates soil clone 869 AY4939
DQ001620.1 gg_id:157110 Microbial seeps asphalt seep clone E91-12 DQ001
GQ016556.1 gg_id:493114 Topographical and Temporal Human Skin Microbiome skin interdigital web space clo GQ016
GQ302580.1 gg_id:563979 prokaryotic sediment Shawan methods cold spring clone sw-xj147 GQ302
AB128876.1 gg_id:103558 deep marine sediments Nankai Trough Japan; ODP Leg 190 clone 1174-1091-17 AB1288

85.8	5270.1	7219.1	8654.2	11741.4	7457.6	12458.9	7189.2	1639.1	522.9	5504.8
65.2	3183.6	4130.1	4322.2	6521.5	4404.3	5818.4	3427.6	1107.0	396.8	2375.9
43.5	615.9	356.3	261.8	1507.5	497.6	594.3	383.1	139.1	42.7	237.6
42.5	1444.2	815.0	1006.7	1818.6	1262.4	1361.6	1048.9	620.4	328.5	604.9
1684.6	3489.2	2276.2	2363.4	3495.3	2870.6	3221.1	2328.9	1969.3	4904.6	2341.1
216.9	2892.3	2356.6	2311.9	4811.1	2357.9	4265.9	2202.3	918.3	3578.2	809.6
31.7	236.7	42.4	26.8	2024.2	372.7	105.1	19.1	19.0	19.1	71.9
71.9	1925.4	1387.6	1507.7	2776.4	1254.2	2153.6	1025.2	330.1	226.9	1015.3
53.7	99.7	83.4	60.1	403.8	140.5	64.1	21.2	17.0	19.1	51.8
2711.8	5483.7	4791.2	5458.2	7538.6	5222.2	5335.8	5295.5	5353.3	3627.1	4736.8
2767.2	2856.0	2507.3	2495.4	3525.1	2237.2	3017.7	2927.5	1475.4	2671.0	1988.0
42.9	1569.1	533.8	609.5	1524.9	827.8	1102.0	683.7	1155.8	487.2	534.5
951.3	6616.3	5726.5	6403.8	9094.3	5629.8	8189.7	4954.6	2691.4	1497.4	4232.7
34.5	114.7	302.3	120.5	397.4	144.8	183.6	107.4	46.2	96.4	82.8
5633.4	7626.9	8865.0	8872.4	8569.7	7207.7	11434.2	7118.1	8497.5	6457.2	8872.1
1002.9	3711.8	3260.5	3666.0	4195.6	3630.9	4930.5	3395.3	1817.8	1083.2	1611.4
27349.2	7975.9	7366.9	8670.1	9042.1	8041.3	10128.3	6559.2	9601.0	7467.0	10339.7
28.2	94.2	212.6	178.7	836.8	242.1	92.1	96.9	34.3	23.0	129.3
96.5	2504.0	2571.9	2794.8	3651.4	2435.0	5155.4	2589.4	1514.7	1045.3	1620.7
326.0	4586.3	3929.1	4763.2	7948.1	3359.1	9668.0	2909.6	1287.5	1374.4	2248.3
33.9	165.9	206.9	431.6	520.5	432.3	225.8	154.8	52.0	36.8	113.1
4908.3	5190.0	5174.7	5202.1	8093.3	4763.1	7568.9	5064.3	2342.6	4079.9	3369.2
2392.3	5219.8	3916.6	4347.8	5728.5	3596.1	7591.9	3322.4	2619.0	1626.2	2634.1
1141.9	6440.6	6160.3	7130.1	7869.2	6005.2	9940.9	6461.1	4392.8	3928.0	5445.5
223.7	1218.9	1713.2	1977.8	2290.1	1105.0	2592.6	1238.0	854.4	606.3	1275.9
93.7	192.4	119.7	179.9	545.5	134.4	333.7	110.6	121.4	41.7	99.8
808.8	3600.6	3890.3	3937.9	4638.6	3548.9	8277.1	3702.7	5252.8	3061.8	3946.3
27403.0	8163.5	8218.1	8635.7	8563.3	8934.6	9375.1	8701.0	12407.2	10154.9	10893.3
418.9	5495.0	5462.1	7057.9	7453.2	5036.5	9873.6	5333.2	2281.0	4022.3	3352.5
43.7	85.3	198.1	115.0	275.7	166.0	132.4	77.9	115.6	36.4	142.1
37191.6	9442.6	9491.5	9453.3	10261.8	8426.6	10742.5	8689.4	13588.7	11048.8	13332.0
34.3	87.4	83.1	125.7	108.8	66.8	163.1	53.7	45.6	28.3	61.6
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37.4	3511.9	2598.2	2730.5	2865.6	1412.3	3253.1	1307.2	603.8	488.2	919.4
27.4	1558.3	796.1	1789.0	1209.8	335.2	3709.4	835.9	76.7	126.0	273.2
6524.5	6822.2	6149.5	6760.0	6309.1	6554.7	7709.7	6298.7	5265.2	5738.1	5427.8
48.3	48.2	94.2	111.5	77.9	82.1	239.1	76.3	34.8	28.9	61.4
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23920.0	8539.1	9720.9	9403.8	10544.7	7943.6	10923.2	7769.8	10521.7	7499.9	9743.8
10325.8	7477.2	7807.2	7420.4	7808.9	7534.2	9141.6	7178.6	10953.7	6612.6	9187.6
242.1	2508.7	2703.5	2838.7	3572.1	2570.6	4099.8	2960.3	1433.4	1682.5	2078.6

5997.0	4611.9	8194.7
2870.5	2918.7	3952.8
231.3	453.5	1056.8
873.7	983.4	1617.3
1549.6	2335.9	3096.3
1463.3	2140.2	2794.2
17.5	93.9	624.1
887.4	1347.6	2775.5
23.2	258.6	1197.9
4831.4	4297.6	7403.8
2190.1	2659.5	3450.2
548.1	712.6	1105.6
4120.2	5313.4	7810.5
83.7	112.6	425.4
6359.7	9950.6	7846.8
3165.6	3413.1	5782.1
7018.9	7933.6	9732.7
35.0	145.0	673.9
2298.7	3029.8	5012.1
2107.2	2316.5	6779.6
59.0	244.1	1283.1
3865.6	3891.4	7899.9
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7464.7	5276.3	7743.3
1674.9	1187.1	1701.4
180.2	175.9	279.7
3351.4	3888.7	4015.9
8091.1	9297.0	9676.5
4640.4	5637.1	6400.5
70.3	165.6	303.7
6727.5	10072.2	9417.8
43.3	86.7	262.9
3657.2	3485.4	3938.5
674.4	898.4	2728.1
130.5	178.1	586.4
5528.6	6454.7	7928.8
68.7	83.2	149.6
1214.8	1610.5	2940.6
7807.5	7925.3	9553.9
6877.8	8741.7	7677.5
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EU132022.1 gg_id:244993 tallgrass prarie soil clone FFCH16206 EU132
EF516758.1 gg_id:217242 grassland soil clone FCPN518 EF5167
AB240376.1 gg_id:141305 microbial structure Phragmites rhizosphere biofilm reed bed reactor laboratory clon AB240
DQ415770.1 gg_id:158462 Dominant microbial limestone-corroding biofilms frasassi system Italy Frasassi sulfid DQ415
AB426221.1 gg_id:272259 -situ identification study benzene-degrading s under methanogenic condition anaerc AB426
AB426190.1 gg_id:263608 -situ identification study benzene-degrading s under methanogenic condition anaerc AB426
AY177760.1 gg_id:78424 subsurface soil beneath grassland clone AY177
GQ402795.1 gg_id:584529 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
AB240315.1 gg_id:142591 microbial structure Phragmites rhizosphere biofilm reed bed reactor laboratory clon AB240
FJ825470.1 gg_id:532951 Microbial during start-up mesophilic biogas plant clone 150b_BE4_38 FJ8254
AM902640.1 gg_id:252937 Acidobacteria and Planctomycetes radioactive mineral Central Alps Austria subsurfa AM902
AB426230.1 gg_id:263257 -situ identification study benzene-degrading s under methanogenic condition anaerc AB426
FJ478644.1 gg_id:543083 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4786
AF523992.1 gg_id:63234 forested wetland clone FW32 AF523
EU132238.1 gg_id:237679 tallgrass prarie soil clone FFCH15579 EU132
AY222310.1 gg_id:113738 host hindgut caecum clone Aci 1 AY222
AB300113.1 gg_id:226421 Wide ancient microbial DNAs Quaternary sediments holocene mud sediment clone K AB300
EF688201.1 gg_id:333448 Detection microbial sludge anaerobic wastewater treatment system clone 4F4_cons EF6882
DQ811915.1 gg_id:170193 mangrove soil clone MSB-3G5 DQ811
GU208397.1 gg_id:583865 Study on Sediment Dongping Lake sediment clone Fh1-16 GU208
DQ676398.1 gg_id:222747 Archaeal and plankton freshwater pond suboxic freshwater-pond sediment clone M DQ676
AJ240998.1 gg_id:1724 marine sediment clone Sva0450 AJ2409
EU617730.1 gg_id:310379 Seasonal variation microbial Yel Sea sediment clone C13S-4 EU617
FJ416122.1 gg_id:361045 sediments sediment station NEC5 Northern Bering Sea clone 111N77 FJ4161
EF125429.1 gg_id:178099 mangrove soil clone MSB-2C8 EF1254
DQ154825.1 gg_id:138946 Diel Migration Restructures Hypersaline Microbial Mat hypersaline microbial mat cl DQ154
GQ472454.1 gg_id:556802 Microbial Dongping Lake lake sediment clone 5F4-8 GQ472
GQ249526.1 gg_id:556154 Microbial anaerobic sediments Bay Cadiz (Spain) marine sediment: 6-8 cm layer clor GQ249
EU925849.1 gg_id:333078 sediments sediment station DBS1 northern Bering Sea clone 041E69 EU9258
AB525453.1 gg_id:541520 Segregated ANME-1 and -2 cold-seep marine sediments deep-sea methane seep sed AB5254
FM242439.1 gg_id:318951 sequences sediment clone 20 T12d+oil FM242
GQ259274.1 gg_id:576470 Microbial activities coastal marine sediments and water column Svalbard deep sedir GQ259
GU180169.1 gg_id:583825 Impact coplanar PCBs on microbial activity anaerobic estuarine sediments sediment GU180
EU617731.1 gg_id:309253 Seasonal variation microbial Yel Sea sediment clone C13S-111 EU617
GQ356996.1 gg_id:584697 Metal Dependent Marine Methane Oxidation methane seep sediment clone FeLive GQ356
AB426217.1 gg_id:261015 -situ identification study benzene-degrading s under methanogenic condition anaerc AB426
EF597692.1 gg_id:257405 Metagenomics deep mediterranean warm bathypelagic habitat 3010m depth Ionian EF5976
FJ902087.1 gg_id:555433 phreatic limestone sinkholes northeastern Mexico orange biomat 8m deep cenote Ca FJ9020
EU132182.1 gg_id:236707 tallgrass prarie soil clone FFCH11809 EU132
FJ269274.1 gg_id:580045 Microbes marine sponges sponge tissue clone XA2D09F FJ2692
FJ535081.1 gg_id:539336 microbial colonizing walls Karstic Slovenia cave wall biofilm clone 2PJM22 FJ5350

1138.9	6438.8	5394.3	6122.7	7318.8	6786.7	6917.3	6828.7	6932.5	3648.7	5861.7
308.1	2869.0	2489.8	3296.5	7039.1	3043.3	4717.9	2267.8	2627.5	1186.1	2054.3
43.4	426.3	223.2	451.0	6201.5	1489.4	779.4	186.2	63.7	62.4	103.5
147.2	990.8	1523.9	3205.0	6434.3	1125.9	7087.6	891.3	228.2	467.6	493.2
1472.3	3487.2	3962.2	3998.9	4674.0	3311.7	4624.5	3184.6	1691.0	1011.4	2471.8
67.9	993.3	1414.0	1371.5	1441.9	1080.7	2058.1	1194.9	234.7	132.7	484.1
4284.9	3447.3	3446.5	3861.0	3789.9	3587.6	5314.3	3355.0	3661.7	1529.9	2821.7
34.1	830.7	1420.7	1544.6	2290.2	851.1	3274.6	552.6	195.3	31.5	177.5
208.4	1827.2	2233.6	1955.8	2074.1	2371.7	2486.7	2206.6	568.2	329.9	1375.8
112.9	2579.4	2755.7	2575.1	2665.3	2459.2	3159.4	2899.1	901.8	390.3	2195.9
3419.8	5370.8	5347.5	5998.8	5988.3	5633.9	8119.5	4891.3	4849.9	4116.6	4802.1
348.7	2897.3	3432.0	3485.8	4160.9	2774.6	5955.6	2586.6	845.5	217.9	1289.0
5835.1	4227.4	3924.0	4375.0	4231.2	3855.7	4422.3	5930.5	2445.3	913.2	3582.2
79.9	928.4	1500.4	1773.4	1425.2	1276.9	2073.4	896.6	260.1	195.0	344.3
3316.7	7080.6	7010.5	7864.0	7294.1	7561.5	7543.1	6736.8	8265.9	6153.0	7266.3
509.9	4022.4	4201.6	5647.5	6652.8	4542.1	4387.1	4422.4	2711.6	2118.9	5234.2
10714.5	10333.0	11115.3	11177.5	12068.1	10165.4	12737.6	9915.0	11142.9	12226.4	12285.7
4180.1	7781.1	7589.8	9177.3	8989.7	7346.0	9868.9	6587.7	7452.2	3902.7	7956.2
45.7	1036.2	983.6	961.4	1559.6	1045.0	1443.2	1428.9	241.4	130.5	966.4
4122.2	9200.1	9512.1	9572.0	10868.4	8773.7	11486.1	8409.8	8689.2	6593.8	8966.1
45.8	443.5	73.0	322.4	532.8	277.7	1484.8	358.2	104.3	29.8	141.5
69.1	472.4	466.8	396.7	600.1	479.2	596.7	419.0	107.1	72.1	142.6
11201.7	6742.6	5786.2	5945.4	6938.0	6297.9	7213.6	5136.6	8468.5	6790.3	7099.8
1485.4	2079.4	2773.2	4440.7	6109.3	4382.4	6665.7	4786.6	5566.9	2610.5	5668.8
7602.1	4393.8	3934.3	4278.6	4540.3	4274.6	4630.1	4265.8	4263.1	4112.3	3044.4
47.1	46.7	63.5	70.1	68.3	49.0	77.0	54.0	39.7	24.1	55.5
1447.3	5715.6	6151.5	7047.0	7633.6	5426.1	9071.2	5919.4	4000.6	2878.2	4691.6
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2512.7	2130.6	2857.4
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EU734973.1 gg_id:316232 assemblages sediment station DBSE Northern Bering Sea clone 067C77 EU7349
GU363017.1 gg_id:559646 and archaeal biogeochemical cycling genes within Qiongdongnan basin Sea: pilot stu GU363
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AY225648.1 gg_id:96645 Mid-Atlantic Ridge hydrothermal sediment clone AT-s3-42 AY2256
EU617725.1 gg_id:319376 Seasonal variation microbial Yel Sea sediment clone C13S-2 EU6177
EU542527.1 gg_id:266442 Effects chemical structure concentration on pathways microbial during dechlorinatio EU5425
DQ017924.1 gg_id:130184 upland stream clone S-Rwb_44 DQ017
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EF687475.1 gg_id:283700 Biogeochemistry iron- and sulfur-precipitating microbial mats (Nile Mediterranean) s EF6874
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FJ205358.1 gg_id:508870 Prokaryotic deep-sea hydrothermal region East Lau Spreading Centre deep marine se FJ2053
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EU043622.1 gg_id:240534 luences structure fosters richness subtropical Altamaha Ohopee River Valley inland c EU0436

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2206.8	6485.2	6790.1	7093.8	8519.9	6626.8	7905.5	8085.7	6681.6	4209.5	5408.8
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288.5	5274.1	4883.5	4992.3	6886.1	4675.7	7057.9	4188.4	2247.1	1031.0	3448.7
4044.6	6553.9	6658.9	8177.1	8014.7	6169.7	9457.9	6324.8	5150.3	3658.7	6840.3
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402.9	4231.3	4815.9	4531.4	6112.7	4069.8	5972.6	3780.1	2930.8	2898.5	2897.3
1351.9	8561.8	9522.5	9342.6	11566.8	8591.4	12101.6	8132.3	8096.1	5297.4	8057.8
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56.5	220.5	200.5	234.2	436.3	167.8	342.1	217.3	95.5	75.7	105.3
114.6	257.7	381.2	447.9	511.1	435.6	580.4	308.8	181.5	312.6	220.3
2556.9	6263.8	5762.7	6160.4	6561.8	6275.9	7730.6	6307.4	8384.7	8541.8	8510.8
161.7	3621.7	3515.3	3283.4	3763.9	3343.5	4195.8	3638.8	1669.2	1556.6	2352.4
1705.4	8418.9	7945.6	8006.9	8766.1	8080.7	9703.0	7471.0	6590.8	7850.8	8154.6
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2254.0	2685.3	5742.0
723.4	627.3	1109.0
6903.5	9532.3	10645.6
74.8	153.4	105.9
4988.9	5079.2	7514.9
3549.2	4722.4	6705.0
5426.8	6134.3	8868.2
6070.4	6622.0	9039.5
2301.1	2065.3	3806.2

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EU132197.1 gg_id:252933 tallgrass prarie soil clone FFCH12594 EU132
AJ966601.1 gg_id:138615 and screening metagenomic library 5274m depth Pacific nodule province deep sea se AJ9666
EU386096.1 gg_id:259105 Biogeographical and microbes sediments on subseafloor sediment South China Sea c EU386
EU202817.1 gg_id:329074 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo EU2028
EU287123.1 gg_id:256935 Pacific arctic surface sediment clone P13-30 EU287
AY225649.1 gg_id:95646 Mid-Atlantic Ridge hydrothermal sediment clone AT-s54 AY2256
EF492943.1 gg_id:244081 Iron-manganese Nodule and Its Surrounding Soil soil around iron-manganese nodule EF4929
AM935858.1 gg_id:574623 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM935
FJ484816.1 gg_id:513563 microbial autonomous rover world's deepest phreatic sinkhole wall biomat El Zacator FJ4848
GQ487923.1 gg_id:581733 Microbial metal soil polluted heavy metals clone T1-98 GQ487
EU652507.1 gg_id:278012 Seasonal variation microbial Yel Sea sediment clone B8S-56 EU6525
EU050878.1 gg_id:249658 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_05_33 EU0508
DQ431890.1 gg_id:204817 microorganisms catalyzing nitrogen removal and organic matter metabolism perme DQ431
EU617729.1 gg_id:321065 Seasonal variation microbial Yel Sea sediment clone D13S-22 EU617
EU335214.1 gg_id:255335 Changes microbial metabolic and along hydrogeochemically variable profile saturate EU335
CP000473.1 gg_id:187098 Solibacter usitatus str. Ellin6076 CP000
AF407714.1 gg_id:60585 Great Artesian Basin clone B11 AF407
FJ466444.1 gg_id:547632 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea FJ4664
EU192982.1 gg_id:327098 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo EU192
AY963381.1 gg_id:154988 structures and correlated ecological factors soils two evergreen broad-leaved forests AY9633
GQ402590.1 gg_id:537224 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
FJ516981.1 gg_id:567172 semiarid 'Tablas de Daimiel National Park' wetland (Central Spain) unravelled upper s FJ5169
GQ402745.1 gg_id:582351 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
EF018429.1 gg_id:210152 aspen rhizosphere clone Amb_16S_1048 EF0184
AB486803.1 gg_id:579143 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCOR AB4868
EF205576.1 gg_id:211735 among geographically regions central Tibet geothermal spring mat clone TP146 EF2055
FJ466104.1 gg_id:557785 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea FJ4661
FJ004654.1 gg_id:540110 Acidobacteria former agricultural rhizosphere soil clone 6C2R FJ0046
GU208327.1 gg_id:575999 Study on Sediment Dongping Lake sediment clone Se2-22 GU208
AJ617852.1 gg_id:110461 oxic-anoxic interphase flooded paddy soil clone D28218 AJ6178
EF589996.2 gg_id:233946 changes structure sediments Songhua River contaminated nitrobenzene -DGGE clon EF5899
FJ465983.1 gg_id:561042 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea FJ4659
EU373937.1 gg_id:268134 southern Cretan margin (eastern Mediterranean Sea) canyon and slope sediment cl EU3739
DQ450709.1 gg_id:160412 Microbial Alpine Tundra Wet Meadow Soil: Chloroflexi Cold Water-Saturated satura DQ450
AB300108.1 gg_id:220379 Wide ancient microbial DNAs Quaternary sediments holocene mud sediment clone AB300
AJ292589.1 gg_id:31570 PCB-polluted soil clone WD292 AJ2925
GQ264513.1 gg_id:590045 Structure Simulated Level Waste Site simulated level waste site clone WW3_65 GQ264
EU150240.1 gg_id:278511 acidobacteria and dry meadow soil Niwot Ridge LTER clone NiA_DM_17 EU150
AF186410.1 gg_id:3678 sponge symbiont clone PAUC26f AF1864
GU208471.1 gg_id:540593 Study on Sediment Dongping Lake sediment clone Shr2-7 GU208

19.3	438.4	703.8	756.5	656.8	452.6	705.1	615.6	182.6	400.2	284.5
2604.3	7369.3	7452.3	8737.7	6977.0	7420.6	8958.5	7535.8	8505.9	5970.2	7824.0
45.9	303.5	390.1	456.0	238.0	291.9	403.7	329.0	66.3	47.5	199.9
4073.8	6236.2	5795.1	7305.3	7870.3	6346.5	8358.6	7375.0	6144.2	3674.2	6979.8
5240.5	7592.5	7757.6	8636.2	8783.2	7319.8	9514.2	7876.9	7856.1	6647.9	7476.4
6302.6	9335.3	7604.2	9176.8	9164.2	7904.9	10014.0	8151.1	11508.8	9413.6	9678.1
33.4	109.6	132.2	114.7	167.2	124.7	113.3	86.4	77.8	35.8	63.4
4833.9	8031.7	8391.9	8929.5	11032.5	8881.5	10968.0	8099.7	9123.8	5183.7	7345.3
10135.6	6597.0	7266.0	8263.5	9565.2	6980.3	9831.5	6550.9	5473.9	3325.2	7783.1
1457.3	8362.8	8219.6	8239.7	9773.0	8483.9	10263.5	7464.6	5688.7	5527.7	15188.7
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2555.9	6856.2	6704.3	7568.0	7112.9	6005.9	7475.3	7537.9	5474.7	4622.7	7055.6
10366.9	10570.3	10614.7	11724.5	12963.9	10973.2	12920.9	11713.1	11350.8	9119.7	11774.6
55.3	185.8	157.5	206.3	194.2	145.6	256.3	183.4	69.0	38.5	91.3
1809.5	6221.0	5961.7	6382.8	8440.6	5381.5	9737.1	4899.6	4279.7	2642.5	5950.8
1403.6	5528.9	6715.2	7172.6	8769.3	5843.8	9378.5	6029.5	3773.8	2728.1	4929.2
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37.6	996.6	2132.5	1715.4	5223.1	1561.2	6170.8	611.5	139.5	132.1	454.2
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7082.2	11444.7	11171.1	11430.0	14269.1	11557.9	14535.6	10431.5	13167.3	8934.5	13327.5
145.5	5603.7	5209.0	5121.6	7311.4	5861.9	7078.6	5643.3	4570.3	4152.6	4028.2
417.6	6236.7	6001.1	6931.0	9157.0	6740.5	8665.0	6172.3	4617.0	2208.8	5440.1
1751.5	5294.4	5666.7	5715.2	4435.3	5859.9	4196.9	5859.0	7697.1	4420.1	5518.3
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55.4	196.3	298.2	209.6	457.5	222.4	419.3	228.3	81.9	64.4	212.5
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57.4	1252.4	1260.7	842.1	2065.2	1426.0	2077.3	842.0	370.1	143.9	473.5
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53.4	1226.4	1862.0	1279.9	2925.4	1473.3	2133.9	1833.4	485.5	355.3	554.3
8058.2	6919.6	7271.7	8666.7	9828.2	7265.4	10242.8	6957.0	5593.1	2786.9	6691.2
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79.2	429.7	454.9	838.1	606.9	437.9	366.1	596.4	204.8	148.6	351.7
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DQ404599.1 gg_id:154141 contaminated sediment clone 656043 DQ404
GQ402596.1 gg_id:559586 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
EU335355.1 gg_id:257039 Changes microbial metabolic and along hydrogeochemically variable profile unsatura EU3353
EF018600.1 gg_id:213933 aspen rhizosphere clone Amb_16S_874 EF0186
AY963431.1 gg_id:154089 structures and correlated ecological factors soils two evergreen broad-leaved forests AY9634
AY963354.1 gg_id:154309 structures and correlated ecological factors soils two evergreen broad-leaved forests AY9633
EF520625.1 gg_id:231211 structure lakes: what controls ? acid-impacted lake clone ADK-SGh02-62 EF5206
AB262728.1 gg_id:245506 microorganisms shal subsurface Sarobetsu mire peat soil clone HSM050P-B-17 AB2627
EF515945.1 gg_id:217695 grassland soil clone FCPN757 EF5159
AB486891.1 gg_id:580183 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCOR AB4868
DQ451519.1 gg_id:156650 forest soil clone FAC80 DQ451
EF019301.1 gg_id:203801 aspen rhizosphere clone Elev_16S_492 EF0193
AY913513.1 gg_id:113638 forest soil clone DUNssu336 (+7B) (OTU#091) AY9135
EU399672.1 gg_id:272782 and localization microbial consortium full-scale granular activated carbon anaerobic EU3996
EU445204.1 gg_id:532631 Isolation Weight Forest Topsoil Metagenomic tropical forest topsoil clone R17 EU4452
AY395354.1 gg_id:102185 pasture soil clone EB1035 AY3953
EF492952.1 gg_id:245898 Iron-manganese Nodule and Its Surrounding Soil soil around iron-manganese nodule EF4929
AY234723.1 gg_id:111405 soil isolate Ellin6071 AY2347
FN594692.1 gg_id:581422 and arsenic mobilization rock biofilms ancient biofilom gold mine Zloty Stok clone a8 FN5946
FJ461997.1 gg_id:581847 Microbial ecology industrial digestor mesophilic anaerobic reactor fed effluent chemi FJ4619
AM162425.1 gg_id:156359 and situ identification acidic sphagnum peat bog clone B119 AM162
GQ340081.1 gg_id:588765 Prokaryotic Marathonas Reservoir Greece water column clone A07-42-BAC GQ340
GQ263798.1 gg_id:540293 Structure Simulated Level Waste Site simulated level waste site clone WC1_b37 GQ263
EU861915.1 gg_id:332934 effects chronic fertilization on alpine tundra microbial implications carbon and cyclin EU8619
GQ402586.1 gg_id:556383 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
EF018723.1 gg_id:207760 aspen rhizosphere clone Amb_16S_1178 EF0187
EU202741.1 gg_id:347427 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo EU2027
AM749736.1 gg_id:256750 Isolation ing candidate division soils New Zealand steam-affected geothermal soil cl AM749
AM935398.1 gg_id:534931 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM935
AY963366.1 gg_id:154125 structures and correlated ecological factors soils two evergreen broad-leaved forests AY9633
EF018819.1 gg_id:210872 aspen rhizosphere clone Amb_16S_1297 EF0188
AY963393.1 gg_id:152086 structures and correlated ecological factors soils two evergreen broad-leaved forests AY9633
DQ451511.1 gg_id:156603 forest soil clone FAC72 DQ451
GQ402695.1 gg_id:574269 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
AJ536873.1 gg_id:79020 uranium mining waste pile soil sample clone JG30a-KF-40 sp. AJ5368
GQ402805.1 gg_id:513782 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
DQ066995.1 gg_id:131970 Lake Washington sediment clone pLW-63 DQ066
AY963443.1 gg_id:152545 structures and correlated ecological factors soils two evergreen broad-leaved forests AY9634
AY963420.1 gg_id:156507 structures and correlated ecological factors soils two evergreen broad-leaved forests AY9634
EF126260.1 gg_id:263285 Phototrophic microbial build laminated Fe-formations on Sulawesi Indonesia mesoph EF1262
AY493924.1 gg_id:136281 Fingerprinting aggregates soil clone 355 AY4939

4747.4	3229.2	4198.4	4444.4	7898.6	4257.4	8150.8	3491.4	2724.2	1542.4	2821.0
191.5	2463.1	2627.0	2811.9	5199.3	3731.8	3892.3	2911.3	1577.9	2570.9	1777.1
10943.8	1737.2	1673.5	1545.7	1805.1	1662.0	2034.8	1599.2	2620.0	2301.0	2990.1
95.8	3056.6	3125.1	3722.7	3898.7	2550.8	3421.9	2312.8	1742.4	539.0	2034.6
1584.2	4236.2	3250.4	3405.4	4492.1	4231.0	5104.9	2686.5	3142.3	2582.7	3894.9
56.5	804.8	826.0	766.7	1958.8	968.8	1646.3	1055.4	437.4	47.6	596.7
35.4	174.9	109.8	119.0	413.8	212.1	232.5	173.3	60.9	42.5	108.0
275.6	2011.0	3215.0	1781.5	5418.2	2493.2	4720.2	1867.8	848.1	306.0	978.1
34.6	359.8	491.1	503.8	681.1	564.5	496.6	485.4	300.0	83.0	259.4
1831.9	4564.4	4425.3	4337.0	7415.1	4428.1	6938.5	3731.9	3397.4	1833.3	3416.7
45.1	231.0	241.1	264.4	489.8	333.6	474.1	117.5	52.1	41.7	161.2
98.9	969.7	1019.0	1211.4	2095.3	1246.7	1457.7	1074.2	500.6	391.4	454.2
48.3	323.7	390.9	444.7	600.9	289.9	662.4	357.9	130.5	88.1	206.5
1635.8	4209.1	5105.7	4539.9	6633.2	5471.6	7001.7	4483.9	3690.6	2830.7	2445.6
59.3	419.7	425.3	349.8	1443.3	553.5	680.6	333.4	102.5	57.8	209.3
572.8	2609.1	2757.2	2671.2	3310.5	3013.5	3534.7	4398.8	2313.8	828.7	2381.3
35.9	464.7	369.6	435.3	420.6	682.2	722.2	244.0	25.3	29.8	500.6
59.4	2043.3	3427.1	1991.6	5903.6	2799.1	5928.0	2243.4	1109.5	476.9	3957.4
1864.2	1345.9	2142.9	1515.8	2465.8	1496.0	2596.9	1352.0	921.1	460.8	1155.1
1522.5	2939.7	3861.1	3401.6	6248.1	3661.7	6958.3	2908.3	1931.1	1036.9	2408.5
31.1	133.6	211.7	192.8	196.6	249.8	155.7	110.4	61.0	35.4	135.9
21601.0	6194.9	6247.4	5979.6	5248.0	5925.4	5605.1	6013.9	8184.8	7794.4	9080.4
1895.7	4652.5	5627.8	5521.2	8593.8	5469.4	8201.2	5539.3	3463.2	2010.3	3690.2
720.2	1408.4	1554.5	2966.4	4357.2	2930.9	4043.0	2665.5	1010.0	321.9	3745.9
275.6	2578.5	2310.6	2639.6	4014.7	3177.8	3174.0	2552.1	2996.1	1499.9	2004.6
1943.4	1891.9	2082.4	2028.5	3930.6	2149.5	4264.6	2962.9	2250.9	565.3	1209.2
458.3	2048.9	2654.4	2313.8	3879.4	2578.7	4293.4	2536.0	1375.3	656.8	1791.4
704.3	4079.9	4365.6	4861.8	6577.2	3842.3	6218.9	3185.0	2027.4	1639.4	3142.0
695.5	1971.8	2475.3	2377.8	3053.1	2063.4	3216.6	2198.6	858.8	771.5	1414.6
46.6	22.2	25.0	18.5	25.1	18.7	23.1	21.3	16.1	13.6	13.7
792.5	1855.2	1608.0	2053.3	4157.0	2026.5	2595.7	2123.2	732.5	656.2	1840.9
3876.8	5071.2	6092.0	5048.2	7535.9	5027.4	8387.5	4456.1	3862.7	2577.7	5031.6
40.8	316.9	338.5	342.5	2507.6	1331.3	773.7	93.6	23.4	24.5	409.3
76.3	1122.7	1182.6	1281.6	2804.9	1434.1	1868.6	741.7	600.0	215.1	756.9
65.1	2206.8	2484.8	2499.4	3437.5	2881.3	3405.8	2767.7	1260.4	441.7	1555.4
111.9	2764.8	3435.9	3136.8	5932.0	3617.5	5413.3	3931.6	2311.0	1059.2	2123.0
37.3	1486.0	1305.0	1470.4	2678.4	1769.1	2197.5	1215.4	614.4	214.8	667.6
62.5	955.8	1468.1	912.2	3685.3	1524.8	2862.4	949.5	356.2	106.6	556.5
1623.1	428.1	290.6	292.6	593.7	279.1	212.7	40.9	301.1	455.0	286.6
106.8	1742.6	2457.1	1641.8	3635.0	2527.9	3243.1	2173.6	1481.8	492.2	868.9
50.8	303.5	611.6	307.4	833.6	512.5	880.4	253.8	117.5	38.0	136.9

3583.2	3454.4	4563.4
2051.7	4186.1	4885.3
1239.7	1840.2	2122.7
2312.4	3179.9	4121.7
3138.1	3771.0	5960.8
528.8	1066.3	3205.4
174.1	197.8	565.1
1514.9	1820.2	4726.8
887.5	515.0	895.5
3930.2	3583.8	7395.1
83.4	325.2	1015.7
1141.8	1534.6	3166.4
293.3	406.7	521.6
4753.4	5220.3	5981.6
389.0	389.9	2733.3
2862.5	3438.8	4302.5
57.3	358.1	1737.0
1733.7	1978.5	4348.8
1290.1	1735.9	3001.0
3272.2	3059.3	4335.2
114.8	332.9	228.2
5393.2	5261.1	5534.1
4453.9	4889.4	6375.0
2731.5	3464.8	4153.8
1556.9	2740.8	5547.5
2889.9	2427.8	4629.6
2312.6	2564.9	4255.6
2933.9	4070.6	6309.7
1681.9	2448.4	4684.3
26.9	27.9	20.9
1524.0	2200.3	3463.6
4187.3	4963.3	7037.9
110.5	771.6	3864.8
714.1	1165.6	2552.1
2431.7	2781.7	5865.1
4303.4	2945.9	5234.5
1183.0	1350.5	3780.6
1253.7	1411.6	4291.7
194.8	748.9	522.5
1836.3	1355.7	2685.6
227.8	596.5	1161.3

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FJ466389.1 gg_id:539027 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea FJ4663
EF600568.1 gg_id:297775 soil clone E5-18 EF6005
FJ478620.1 gg_id:589802 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4786
EU676415.1 gg_id:287625 rhizosphere pioneer plants (Bahia xylopoda and Viguiera linearis) growing on metals- EU6764
EU044116.1 gg_id:237652 luences structure fosters richness subtropical Altamaha Ohopee River Valley inland c EU0441
AB254784.1 gg_id:161597 Biogenic Fe-oxyhydroxides nodules (takashikozo) encrusted iron-oxide reducing sedi AB2547
FJ466097.1 gg_id:557180 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea FJ4660
GU205285.1 gg_id:525931 unusual Microbial Venezuelan Tepui (Orthoquartzite) Cave: Dominance Chloroflexal GU205
EU335301.1 gg_id:242467 Changes microbial metabolic and along hydrogeochemically variable profile unsatura EU3353
AY212581.1 gg_id:103580 water 10 m downstream manure clone 130ds10 AY2125
AJ306764.1 gg_id:66935 DCP-dechlorinating consortium clone SHA-261 AJ3067
AM712324.1 gg_id:241307 detection and ly microbial Brothers Seamount Kermadec Arc New Zealand biofilm h AM712
EF019821.1 gg_id:209523 aspen rhizosphere clone Elev_16S_1166 EF0198
AM162421.1 gg_id:155041 and situ identification acidic sphagnum peat bog clone B18 AM162
AY963378.1 gg_id:155208 structures and correlated ecological factors soils two evergreen broad-leaved forests AY9633
FM877544.1 gg_id:369392 Microbial several mining wastes Bulgaria uranium mill tailings clone BuhD-110 FM877
AY326548.1 gg_id:136292 Amazon soil clone 157-2 AY3265
EU132409.1 gg_id:237818 tallgrass prarie soil clone FFCH2202 EU1324
AJ536863.1 gg_id:78832 uranium mining waste pile soil sample clone JG30-KF-C5 sp. AJ5368
AM162419.1 gg_id:152963 and situ identification acidic sphagnum peat bog clone B15 AM162
AY963364.1 gg_id:153346 structures and correlated ecological factors soils two evergreen broad-leaved forests AY9633
FJ479149.1 gg_id:572184 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4791
AB179516.1 gg_id:101119 sedimentary rock clone MIZ25 AB1795
FJ535085.1 gg_id:593912 microbial colonizing walls Karstic Slovenia cave wall biofilm clone 3PJM113 FJ5350
FJ462107.1 gg_id:592473 Microbial ecology industrial digestor mesophilic anaerobic reactor fed effluent chemi FJ4621
AY493921.1 gg_id:136304 Fingerprinting aggregates soil clone 351 AY4939
AM935004.1 gg_id:545992 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM935
FJ466071.1 gg_id:564195 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea FJ4660
AB179509.1 gg_id:105453 sedimentary rock clone MIZ18 AB1795
GQ263793.1 gg_id:566933 Structure Simulated Level Waste Site simulated level waste site clone WC1_b31 GQ263
DQ906868.1 gg_id:256303 Oman subsurface soil clone 11A-3 DQ906
EF018657.1 gg_id:204324 aspen rhizosphere clone Amb_16S_943 EF0186
GQ402789.1 gg_id:582679 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
AB486182.1 gg_id:584693 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC AB486
FJ466148.1 gg_id:544575 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea FJ4661
AY963331.1 gg_id:154822 structures and correlated ecological factors soils two evergreen broad-leaved forests AY9633
FJ466083.1 gg_id:533572 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea FJ4660
EU676414.1 gg_id:299684 rhizosphere pioneer plants (Bahia xylopoda and Viguiera linearis) growing on metals- EU6764
FJ466197.1 gg_id:513591 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea FJ4661
EF018283.1 gg_id:210615 aspen rhizosphere clone Amb_16S_644 EF0182
EU335379.1 gg_id:240295 Changes microbial metabolic and along hydrogeochemically variable profile unsatura EU3353

206.7	846.4	407.7	502.7	1559.9	1829.2	746.9	509.4	105.8	63.9	233.6
2898.5	6298.9	6386.5	6193.4	10245.1	6617.4	8371.7	6090.4	4807.3	2444.7	4157.5
86.3	1742.6	1858.4	1970.7	3392.4	2088.2	3022.2	1552.4	2041.6	267.8	1112.8
8653.5	5071.2	6484.9	6441.7	8112.3	5850.1	8353.8	6174.1	6482.4	5204.2	5691.6
2434.2	3621.9	3345.3	3838.5	4079.2	4137.3	3979.8	3600.6	4618.5	3102.6	3918.3
56.7	62.2	78.8	67.3	99.0	160.5	72.7	44.0	38.0	30.1	72.3
403.1	2865.2	2906.8	2680.6	4765.3	3203.0	4520.2	2879.7	1964.4	1029.6	1491.1
10459.1	4381.3	4824.8	4992.7	6483.8	4624.8	6894.1	4686.0	5129.8	3871.1	4648.3
2730.3	3291.8	3356.7	3698.0	4530.3	3869.0	3546.8	3424.8	4355.0	4364.0	3378.1
82.0	482.0	860.0	735.7	1072.4	272.4	1057.2	1096.3	479.3	173.1	556.2
187.2	740.4	1338.2	1234.9	1436.1	833.5	1881.5	1100.2	236.1	160.5	560.3
56.9	2550.6	2996.8	2670.1	5150.9	3588.9	4660.9	3211.9	2154.6	341.2	1665.5
92.6	1994.1	2834.2	2247.4	4333.0	2724.2	5131.9	1992.8	1472.6	447.0	1101.7
4967.0	4992.2	5890.1	5462.0	8335.4	5962.9	8176.4	5058.5	4414.8	2816.7	5346.9
104.5	2238.2	4460.4	2117.9	6942.7	3030.1	7507.6	2203.9	1157.5	585.8	1515.3
2966.3	3646.8	4276.8	3788.5	4970.7	4159.5	5348.1	4199.2	2869.3	2208.6	3285.8
2776.6	1600.1	1927.1	1836.8	3280.7	1822.9	3043.8	1779.9	1757.4	560.0	1228.3
1873.1	7162.2	7421.6	7257.2	9414.5	7736.5	9842.7	6690.9	6235.1	5634.7	6597.2
38.4	211.7	360.2	255.2	547.8	342.6	456.3	565.9	66.8	49.2	98.7
56.8	1304.4	2428.0	1049.7	3185.9	1665.0	3270.4	1008.8	385.7	175.8	697.0
860.9	2370.0	3588.7	2134.1	4958.9	2600.3	4717.8	2157.5	1712.3	1162.2	1350.0
213.4	3822.4	5058.9	4761.5	6504.7	4328.5	6522.6	4618.4	2940.5	1418.1	3254.0
34.4	574.1	672.2	228.5	1760.5	724.1	1501.6	210.6	51.1	19.7	257.9
1762.4	3399.7	3268.9	3842.8	6042.9	3387.5	5330.0	3538.5	2653.1	1866.9	2026.3
1197.3	4588.9	6102.8	5092.4	9582.9	5686.0	10537.5	3671.6	2754.7	1269.8	3459.6
73.0	55.3	139.6	93.8	251.1	97.3	213.1	106.6	58.0	34.8	50.1
7794.0	3476.1	5216.2	3584.6	7764.6	4525.4	8054.2	3974.3	2738.1	1738.7	2260.6
451.5	5275.0	5197.8	6000.5	8535.4	5603.9	8852.3	5835.8	4657.0	3066.8	4564.6
41.7	945.5	1530.6	1304.9	2669.1	1390.9	2468.8	1819.5	663.8	304.9	604.0
6395.6	10462.8	11255.4	11501.9	15086.5	10801.1	15825.6	9986.7	10571.7	7219.3	11791.8
5309.4	5740.1	6386.0	7121.9	9450.8	6674.6	10140.0	5735.3	6630.2	5211.4	7139.9
82.3	246.5	404.9	177.1	798.7	417.2	612.8	145.2	103.5	51.2	212.3
2109.1	3769.5	3719.0	3555.4	4325.0	4413.2	3951.1	2962.7	3813.9	3141.6	4496.7
964.7	3358.2	4546.4	3829.4	5731.5	3747.8	6398.9	3773.7	2664.3	1772.0	3488.2
303.4	2661.2	2703.8	3159.4	4708.4	3584.6	4240.8	2967.1	1422.6	544.6	2176.8
1104.9	1548.0	2258.1	1667.8	2368.7	1962.3	1674.4	2169.8	1126.3	2378.3	1558.9
75.3	535.9	563.6	512.3	826.4	760.6	733.8	650.3	161.7	189.0	477.6
11650.1	5749.3	6509.4	6564.1	7832.5	6182.1	8044.5	6188.4	5380.4	4047.6	5946.1
40.0	1443.8	1801.0	1595.7	2922.0	1553.7	2502.1	1288.1	886.8	288.4	696.8
61.0	1193.8	2972.5	1162.7	3533.8	1733.7	3705.0	1521.6	782.3	122.2	947.9
84.0	925.4	559.6	474.1	1019.9	903.9	757.0	589.2	52.0	47.9	429.2

430.1	660.6	1691.3
6124.9	6586.9	9681.7
1221.7	2193.7	2777.1
6003.8	7155.3	6795.7
3335.7	4776.1	5661.0
53.4	146.2	226.1
2872.3	2517.2	5514.0
4690.8	5294.8	5648.2
3293.7	4700.2	4628.6
1552.3	1126.9	1061.8
587.6	837.2	1824.8
2976.3	1985.2	4089.0
2624.4	2102.7	4156.4
4529.8	4928.1	7183.8
2389.2	1906.7	5830.5
3580.4	5041.8	6263.7
2243.2	2420.5	3472.2
6892.3	6853.9	10395.6
316.3	442.0	1177.5
918.2	1323.0	3144.3
2562.4	2753.4	4927.3
4050.0	4238.1	6731.1
188.6	450.1	2448.9
3773.9	3257.7	4215.8
4756.7	4127.0	6775.6
107.3	140.9	118.6
3930.2	3374.0	6458.9
5561.4	5299.0	8829.9
1425.2	1762.1	3523.0
10258.8	9666.5	14260.4
5737.6	6594.6	8943.6
117.9	568.3	1827.8
2914.0	3988.3	6980.7
4616.6	4251.0	5748.8
2441.9	3202.1	5183.4
1594.2	2431.4	2375.7
518.1	1521.2	2378.4
5462.0	7101.2	7799.0
1479.3	1518.3	2927.1
1382.9	1749.6	3822.4
468.4	743.6	1790.5

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EU132045.1 gg_id:240983 tallgrass prarie soil clone FFCH9825 EU132
EF516126.1 gg_id:226281 grassland soil clone FCPT514 EF5161
DQ129637.1 gg_id:138184 microarray level air two cities Texas urban aerosol clone AKIW659 DQ129
EF019147.1 gg_id:208718 aspen rhizosphere clone Amb_16S_1790 EF0191
GQ263218.1 gg_id:592008 Structure Simulated Level Waste Site simulated level waste site clone F3_25X GQ263
FJ152859.1 gg_id:350446 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX5A_ FJ1528
EF018719.1 gg_id:210677 aspen rhizosphere clone Amb_16S_1170 EF0187
GQ264287.1 gg_id:544353 Structure Simulated Level Waste Site simulated level waste site clone WW2_101 GQ264
EU881125.1 gg_id:322588 Karst region primary forest soil clone KPF200711-143 EU881
EF018078.1 gg_id:204993 aspen rhizosphere clone Amb_16S_404 EF0180
GQ402709.1 gg_id:587893 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
EF020033.1 gg_id:215120 aspen rhizosphere clone Elev_16S_1428 EF0200
EF516689.1 gg_id:226313 grassland soil clone FCPN758 EF5166
EU150203.1 gg_id:278495 acidobacteria and soil Niwot Ridge LTER; spruce fir forest clone NiA_SF_14 EU150
FJ901511.1 gg_id:568755 phreatic limestone sinkholes northeastern Mexico biomat 80m deep cenote La Palita FJ9015
DQ833485.1 gg_id:161914 detected analyses depth sediment Guanting Reservoir clone 35-19 DQ833
FJ004679.1 gg_id:553090 Acidobacteria former agricultural soil rhizosphere clone 89 FJ0046
DQ404851.1 gg_id:153227 contaminated sediment clone 655981 DQ404
EU044114.1 gg_id:249968 luences structure fosters richness subtropical Altamaha Ohopee River Valley inland c EU044
GQ402578.1 gg_id:545323 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
EU132362.1 gg_id:242626 tallgrass prarie soil clone FFCH13873 EU132
EF516577.1 gg_id:221845 grassland soil clone FCPT524 EF5165
EF019667.1 gg_id:205391 aspen rhizosphere clone Elev_16S_822 EF0196
FJ466067.1 gg_id:575896 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea FJ4660
EF516304.1 gg_id:222573 grassland soil clone FCPT689 EF5163
DQ017939.1 gg_id:134417 upland stream clone S-Jos_51 DQ017
DQ001647.1 gg_id:158148 Microbial seeps asphalt seep clone E101-54 DQ001
AM749754.1 gg_id:246440 Isolation ing candidate division soils New Zealand steam-affected geothermal soil cl AM749
AY963377.1 gg_id:150731 structures and correlated ecological factors soils two evergreen broad-leaved forests AY9633
FJ004775.1 gg_id:554827 Acidobacteria former agricultural bulk soil clone 31L2B FJ0047
DQ984552.1 gg_id:241889 Mt. Nan-Jen soil clone IFD_30 DQ984
EF516032.1 gg_id:219884 grassland soil clone FCPP523 EF5160
AY963418.1 gg_id:154876 structures and correlated ecological factors soils two evergreen broad-leaved forests AY9634
EU150229.1 gg_id:278164 acidobacteria and dry meadow soil Niwot Ridge LTER clone NiA_DM_2 EU150
FJ465995.1 gg_id:544523 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea FJ4659
EU331380.1 gg_id:250740 Influence Nitrate on Microbial Reduction Pertechnetate microcosm sediment contan EU3313
EF516947.1 gg_id:227230 grassland soil clone FCPS681 EF5169
AJ009495.1 gg_id:3677 chlorobenzene-degrading consortium clone SJA-149 AJ0094
EF019981.1 gg_id:206392 aspen rhizosphere clone Elev_16S_1368 EF0199
AM935451.1 gg_id:557468 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM935
EF494337.1 gg_id:222398 Nunnock River granitic landscape clone NR.1.044 EF4943

1506.4	2794.3	2808.4	2862.6	4174.9	3074.2	3620.8	3139.8	1090.1	920.0	1485.5
58.8	490.1	627.8	420.3	1255.9	668.6	989.0	305.7	138.0	61.7	230.8
44.6	936.4	750.3	330.2	1176.2	609.1	1276.7	237.9	347.2	228.1	225.1
2710.4	3013.6	3054.5	3099.0	3210.3	3113.3	3778.1	2685.5	3710.3	4080.9	3921.8
4809.0	4866.8	5321.2	5405.2	6082.9	4705.0	6198.3	4396.0	4681.0	5228.4	6362.5
58.7	2029.2	2636.0	1329.9	3172.7	2032.5	3448.5	1594.9	661.8	387.8	987.6
124.0	2010.9	2265.7	2073.5	3101.6	2613.6	2952.6	1593.7	664.0	237.7	1208.8
3272.8	3917.0	4051.4	3935.7	4888.9	3611.8	5364.4	4317.6	3853.9	1983.7	4824.7
538.2	4798.6	5620.9	5553.6	9237.9	5763.4	8909.5	5254.7	4777.8	3550.0	4346.6
45.7	274.5	290.7	255.4	529.5	418.1	460.5	264.1	80.3	51.5	138.4
18046.3	5043.2	4442.7	5150.2	4963.3	4631.1	5912.1	5145.1	3987.5	4850.1	7603.9
76.2	1208.9	2422.8	1095.9	2799.7	1547.5	2265.1	1146.3	1021.1	687.6	983.6
1673.2	4717.8	5607.9	5244.8	8830.6	5311.1	9049.9	4251.8	2666.2	1682.1	3301.4
62.9	2300.3	3263.3	1832.2	4729.7	2394.5	5560.1	1712.0	1129.0	214.7	818.3
75.7	891.6	1343.4	1211.3	1475.9	1337.8	1569.3	1032.1	397.3	181.6	609.4
33.6	744.9	705.3	533.4	1951.7	776.1	1077.4	877.3	115.3	112.3	342.8
65.4	1186.8	1288.3	1119.1	2811.5	1547.8	2108.7	1073.5	576.6	210.8	653.1
697.4	1194.4	1523.9	1368.6	2611.9	1546.8	2515.6	1467.0	679.4	499.4	740.3
7651.6	5393.7	5498.0	5789.7	5725.1	6824.3	5748.3	5220.6	7302.7	5085.8	7543.0
13658.6	4626.1	5778.3	4350.9	7468.9	5086.4	7999.6	4037.6	4263.4	3127.4	5392.3
712.8	1736.0	2058.9	2012.4	3762.4	2038.5	3674.1	1974.6	1826.4	1511.9	1387.7
154.3	2461.1	3701.2	2251.0	6394.3	3187.8	6437.0	1938.3	1143.0	408.6	1603.1
49.3	407.3	53.6	83.2	131.1	149.7	239.5	53.9	45.7	40.0	50.4
3604.0	6340.7	6271.5	7431.5	9013.8	6856.0	8901.9	7166.4	4789.1	5072.8	5327.3
40.3	213.6	683.2	192.1	746.1	314.1	995.0	187.6	84.3	35.9	144.2
3867.0	6329.9	7605.9	6382.7	9700.0	6818.4	10229.4	5804.9	5822.8	3471.2	6076.4
593.6	2925.7	4253.7	3346.9	5800.5	4151.8	6185.0	3890.2	2514.3	1588.5	2568.6
11276.6	11550.2	10682.6	12858.3	15240.3	11758.8	14847.2	9952.5	9698.3	5590.0	11400.5
20250.2	7128.8	6597.0	6315.9	7128.2	6972.1	6865.7	5812.4	8273.2	8819.4	8487.7
58.7	709.5	830.1	597.5	1599.1	858.5	751.9	776.6	137.4	93.7	302.1
107.0	2409.9	3822.3	3613.6	7537.9	3220.2	4842.0	2856.4	1164.9	547.8	1370.6
582.2	2918.4	3708.0	2945.6	5022.4	2944.1	4875.2	2502.5	2146.2	1860.8	2374.5
53.2	274.6	307.5	288.7	778.4	932.6	684.9	250.3	103.5	47.9	170.1
1057.1	3979.4	4707.7	3690.1	6210.6	4346.0	6682.1	3465.6	3397.1	2147.8	3108.9
36.1	356.5	495.9	452.1	913.9	344.3	591.5	661.0	223.3	117.2	170.0
79.3	1300.4	1947.2	1154.7	2520.2	1308.2	2717.7	797.7	465.1	194.6	678.8
222.6	2474.5	3277.0	1985.9	4558.5	2480.0	4348.4	1691.4	1069.0	688.7	1691.5
53.1	689.4	1318.5	1184.3	3322.8	1114.9	1998.9	737.6	301.7	76.1	251.9
4793.8	8304.6	6866.4	8454.3	9307.8	7689.2	9646.9	8063.7	8649.7	6688.7	7437.2
1395.9	4736.7	4568.1	4853.0	6886.8	4984.9	6531.6	5016.7	3371.7	2383.5	4728.8
692.4	2573.1	2618.2	3222.6	2261.1	3747.8	1941.1	2267.9	1277.4	623.7	2481.2

3396.5	2945.2	3920.5
234.8	712.2	2825.1
205.8	467.8	620.4
2336.2	3646.3	3602.9
4668.7	5662.0	6175.9
1303.8	1646.4	3502.9
1160.4	2348.9	4707.7
4025.5	4564.2	5441.5
5512.1	4844.4	7963.2
207.7	353.6	1688.1
3717.1	5261.0	5514.7
1101.5	1354.1	3483.3
4359.7	4369.5	7726.3
1714.7	1685.1	4956.6
817.1	1064.3	1998.7
465.5	595.8	1788.1
848.8	1329.4	2850.4
1456.7	1995.5	2163.3
5098.2	5970.9	6614.8
4093.6	4511.4	7896.1
2240.7	2020.5	3155.6
1755.2	2365.1	6446.4
125.1	326.6	3376.8
7094.3	7262.0	10092.0
124.3	339.8	508.9
6041.6	7002.3	10229.1
3901.4	3475.5	4684.6
10984.2	11571.5	15863.9
5558.7	8481.4	7674.8
1013.5	1221.7	2835.2
3439.5	2795.4	6970.5
2413.7	2588.9	4444.3
244.9	575.5	1232.8
2754.4	3761.6	5868.0
754.6	396.2	903.7
796.1	1131.0	2804.8
1461.8	2045.6	4409.4
472.6	665.5	989.1
8616.2	8355.3	9493.6
4324.0	5161.4	7527.1
1978.7	3240.2	4202.3

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AY913265.1 gg_id:114356 forest soil clone DUNssu045 (-2B) (OTU#121) AY913
FJ478535.1 gg_id:583760 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4785
FJ205213.1 gg_id:549259 Prokaryotic deep-sea region East Lau Spreading Centre inactive hydrothermal field se FJ2052
EF492968.1 gg_id:247708 Iron-manganese Nodule and Its Surrounding Soil soil around iron-manganese nodule EF4929
AY922037.1 gg_id:112776 farm soil clone AKYG600 AY922
AF465650.1 gg_id:17775 thermal soil clone YNPRH2B AF465
GU172173.1 gg_id:536567 Microbial Eucalyptus plantation soil clone DSM-R1 GU172
EU445207.1 gg_id:541749 Isolation Weight Forest Topsoil Metagenomic tropical forest topsoil clone R20 EU445
EF492956.1 gg_id:241718 Iron-manganese Nodule and Its Surrounding Soil soil around iron-manganese nodule EF4929
EF515983.1 gg_id:226166 grassland soil clone FCPS403 EF5159
FJ479535.1 gg_id:553939 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4795
DQ450706.1 gg_id:161275 Microbial Alpine Tundra Wet Meadow Soil: Chloroflexi Cold Water-Saturated satura DQ450
EU150248.1 gg_id:278253 acidobacteria and dry meadow soil Niwot Ridge LTER clone NiA_DM_26 EU150
FJ793181.1 gg_id:526228 Archaea and Hot Spring Thailand Tao Dam hot spring clone TDB66 FJ7931
AY963425.1 gg_id:151183 structures and correlated ecological factors soils two evergreen broad-leaved forests AY963
FJ004745.1 gg_id:575745 Acidobacteria former agricultural bulk soil clone 26L2B FJ0047
EF157254.1 gg_id:241324 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon EF1572
EF032754.1 gg_id:190912 cyanobacterial mat in lava cave clone HAVOmat42 EF0327
FJ466195.1 gg_id:543818 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea FJ4661
EU202739.1 gg_id:343210 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo EU202
GU444079.1 gg_id:519245 Effects amendments on fertility and microbial structure cucumber Cucumis sativus L GU444
FJ624931.1 gg_id:566511 Influence lead contamination on boreal pine forest soil clone HF_C_58 FJ6249
FJ710779.1 gg_id:510168 Abundance and microbial long-term operated anammox biofilm reactors initiated ino FJ7107
EF018396.1 gg_id:205033 aspen rhizosphere clone Amb_16S_1009 EF0183
GQ264426.1 gg_id:589387 Structure Simulated Level Waste Site simulated level waste site clone WW3_116 GQ264
FJ479270.1 gg_id:594169 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4792
AB186882.1 gg_id:105319 polychlorinated dioxin dechlorinating microcosm clone TSBb06 AB186
EF019361.1 gg_id:216341 aspen rhizosphere clone Elev_16S_581 EF0193
GU118588.1 gg_id:588882 Threatened Corals Provide Microbial Habitats clone Mfav_P18 GU118
AB240298.1 gg_id:141801 microbial structure Phragmites rhizosphere biofilm reed bed reactor laboratory clon AB240
FJ592762.1 gg_id:562807 Fumarole-supported islands biodiversity within hyperarid -elevation landscape on Pu FJ5927
AM935189.1 gg_id:558353 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM935
AY703464.1 gg_id:139346 Detection and ly acidobacterial analyses Altamira Cave clone ALT40 AY7034
GU187034.1 gg_id:578443 Isolation -yet Acidobacteria on solid dilute media surface soil clone IGE-015 GU187
EF018402.1 gg_id:210745 aspen rhizosphere clone Amb_16S_1015 EF0184
EU132316.1 gg_id:240950 tallgrass prarie soil clone FFCH1016 EU132
EF516154.1 gg_id:221233 grassland soil clone FCPO684 EF5161
EF494368.1 gg_id:225293 Nunnock River granitic landscape clone NR.1.042 EF4943
EF018351.1 gg_id:209415 aspen rhizosphere clone Amb_16S_723 EF0183
EF494344.1 gg_id:220327 Nunnock River granitic landscape clone NR.1.077 EF4943
DQ066994.1 gg_id:136128 Lake Washington sediment clone pLW-64 DQ066

43.5	146.7	305.7	228.4	813.5	1129.2	139.7	107.2	26.1	21.1	294.1
1758.5	4314.7	4850.2	3827.2	6667.9	4509.5	7014.1	3618.5	4211.0	1666.0	3429.8
148.7	2946.8	3322.3	3379.2	4883.0	2909.5	5467.8	2873.2	1166.4	968.3	1897.1
15230.1	8425.3	9159.9	10374.4	10689.8	8966.6	11517.1	9156.6	9199.6	7186.5	8825.8
45.8	118.8	299.6	164.9	382.0	148.7	237.3	126.2	56.1	35.8	95.2
130.9	4444.4	4051.9	5297.2	7200.3	4457.1	7151.3	4389.4	4095.3	1696.3	3110.5
4549.9	5709.7	6675.4	5766.4	8079.4	5479.8	8672.3	5007.8	5141.3	3576.7	6285.5
3068.5	1781.4	1677.2	2509.4	3004.4	2080.5	3053.9	1588.8	1483.5	337.6	1024.5
2620.1	985.0	1406.7	1188.5	2020.4	1443.0	2740.4	1153.4	711.5	286.4	608.1
65.6	1617.3	2816.0	1954.9	3908.2	1675.3	4211.0	1826.0	924.9	358.4	983.6
1607.2	4257.3	4872.3	4603.3	5784.1	4423.8	6658.4	4488.7	3781.9	1747.6	3296.1
44.4	3283.4	5143.8	3428.7	7142.2	3993.3	7717.4	3178.5	1688.9	652.9	2143.9
1926.8	2973.1	3755.4	2912.3	5322.5	3198.6	6038.3	3199.8	1743.0	1972.2	2448.5
110.0	2227.0	3629.8	3231.8	4866.5	3094.3	5401.8	3670.9	1763.7	1123.0	1804.5
753.6	2537.8	2912.2	2932.1	3564.9	2846.3	3886.2	2722.9	1951.1	566.1	1954.0
352.3	1080.6	855.1	1099.2	1817.9	1135.9	1229.5	1257.7	415.2	111.4	701.6
177.5	3946.8	5792.7	4719.6	7156.5	6003.0	7103.6	4644.1	3117.0	8546.4	3138.0
60.1	105.9	135.0	109.6	257.1	203.0	87.7	63.1	49.2	36.2	118.0
239.4	1899.9	3271.0	1918.2	3826.9	1870.2	4082.3	1216.8	731.4	216.9	1212.8
514.7	4084.2	5531.3	3304.1	8439.5	4305.7	9004.5	3219.6	2087.4	946.3	2678.5
619.5	2374.2	2479.0	2253.5	3740.8	3089.6	2967.3	2172.9	2221.2	987.9	2149.5
37.0	257.5	622.7	205.4	684.5	344.4	1059.0	123.1	88.8	32.9	115.9
97.6	2831.0	3589.1	3500.0	5055.5	3122.7	4834.2	2939.2	1827.7	733.6	2328.6
259.8	2779.4	2554.0	2925.4	4595.6	2911.9	3474.9	2951.8	3756.8	613.1	1814.9
4746.1	6955.6	7322.1	8632.7	8614.3	7506.6	8728.8	6999.2	7136.8	8620.2	8306.3
3148.9	5398.1	5744.8	6116.9	8991.1	6175.0	9409.4	5623.3	5361.2	3404.4	5655.3
26.7	176.9	287.7	246.4	421.7	235.3	455.1	153.0	72.3	34.6	162.8
165.9	1161.3	1695.6	1529.6	2724.0	1412.4	2929.3	1469.6	1225.8	242.1	671.7
205.6	1917.6	2034.4	2164.4	2844.3	1797.3	2822.4	1996.1	1851.7	755.0	1529.8
1108.3	4446.8	6524.3	4366.0	6222.0	4150.9	7678.1	3910.1	1295.0	1882.9	2895.9
57.4	602.1	1262.1	375.7	2844.3	823.7	2127.5	635.5	148.7	104.3	368.8
3786.1	6812.5	5967.2	5599.1	7717.6	6430.5	7630.4	5504.4	5066.3	3292.8	4972.2
77.1	1348.1	1260.7	1307.7	1157.8	1163.0	1564.1	1328.4	874.6	231.5	530.2
115.3	1302.1	1639.5	1353.8	3837.4	1892.6	2868.8	1332.4	624.3	553.6	861.4
57.0	502.1	518.6	586.0	985.0	652.0	1503.6	600.4	202.9	57.2	163.3
44.5	608.4	689.1	691.1	2492.7	951.0	1938.7	921.1	570.1	356.2	333.7
217.7	1635.3	2607.1	1608.1	3316.3	1738.2	3556.6	1737.3	650.8	826.5	930.4
999.7	5030.5	4436.0	5113.3	5887.4	5621.8	7145.7	4198.8	4065.3	3606.9	4833.6
163.5	878.2	1343.6	1015.6	1804.9	1051.7	2164.4	858.7	288.1	86.7	501.7
1169.4	3238.7	4578.3	2334.5	6974.9	3862.2	6834.4	2623.7	2659.7	942.1	3393.7
163.8	3492.9	4318.2	5677.0	6803.7	3765.1	6574.2	4149.7	1406.0	568.0	2205.0

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3552.2	4057.2	6552.3
2213.6	3100.7	4894.9
8725.3	10147.7	12616.8
111.8	201.2	239.9
4628.1	4914.3	5625.4
4884.1	5977.2	7493.2
1884.5	2522.0	3652.1
839.1	1766.2	2731.2
1516.3	2102.0	3048.6
4241.9	4854.7	6273.9
3181.3	3033.8	6533.7
3222.6	4265.9	4891.4
3514.5	2584.5	3616.5
2629.9	2596.3	3702.4
897.8	1441.5	2459.5
6110.8	5302.6	6795.8
74.7	242.6	844.2
933.1	1642.5	3390.0
2552.1	3758.1	7445.1
1837.6	2257.1	3639.3
79.4	177.7	876.3
3771.8	2800.6	5496.9
2335.1	3579.1	5094.4
6953.3	8451.6	9031.4
5611.4	5404.7	6410.5
60.2	144.2	622.4
2307.9	1295.2	2670.7
1812.8	2117.6	2307.9
2860.0	3615.1	5397.1
521.4	946.2	2904.5
6158.1	6272.6	8818.0
1267.0	1765.8	2116.7
1398.7	1437.0	2772.9
569.6	761.3	1652.5
965.9	738.9	1632.0
1491.7	1656.2	2664.2
4032.3	5274.0	8582.8
585.7	1223.7	1977.6
3181.6	3547.5	5429.9
3584.6	3360.2	5805.2

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AY963419.1 gg_id:156406 structures and correlated ecological factors soils two evergreen broad-leaved forests AY9634
AY963359.1 gg_id:151094 structures and correlated ecological factors soils two evergreen broad-leaved forests AY9633
EU491161.1 gg_id:272414 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak EU491
GQ263191.1 gg_id:577141 Structure Simulated Level Waste Site simulated level waste site clone F3_152X GQ263
EF018769.1 gg_id:211221 aspen rhizosphere clone Amb_16S_1230 EF0187
AY913237.1 gg_id:113212 forest soil clone DUNssu016 (+1B) (OTU#120) AY9132
EU665077.1 gg_id:545745 Soil are Changed Agricultural Practices agricultural soil clone Plot22-H02 EU6650
EU132291.1 gg_id:254271 tallgrass prarie soil clone FFCH4169 EU1322
EF020317.1 gg_id:204462 aspen rhizosphere clone Elev_16S_1890 EF0203
EF688388.1 gg_id:245809 soil clone F6-128 EF6883
AY963374.1 gg_id:151872 structures and correlated ecological factors soils two evergreen broad-leaved forests AY9633
EU335292.1 gg_id:250451 Changes microbial metabolic and along hydrogeochemically variable profile unsatura EU3352
EU881304.1 gg_id:305083 (maize-sweet cropping field) Karst region maize-sweet potato cropland soil clone KM EU8813
AY913231.1 gg_id:113763 forest soil clone DUNssu010 (+1B) (OTU#116) AY9132
EF492904.1 gg_id:254383 Iron-manganese Nodule and Its Surrounding Soil soil around iron-manganese nodule EF4929
AY118153.1 gg_id:60816 anaerobic benzene-degrading clone Cart-N4 AY1181
EF516655.1 gg_id:221341 grassland soil clone FCPU664 EF5166
AM162427.1 gg_id:151955 and situ identification acidic sphagnum peat bog clone B22 AM162
AB234235.1 gg_id:145554 Biotransformation Polychlorinated Dioxins Microbial Dynamics Sediment Microcosm AB2342
AB426196.1 gg_id:274878 -situ identification study benzene-degrading s under methanogenic condition anaerc AB4261
EU132276.1 gg_id:253770 tallgrass prarie soil clone FFCH2719 EU1322
AY963303.1 gg_id:153327 structures and correlated ecological factors soils two evergreen broad-leaved forests AY9633
EU881313.1 gg_id:339795 (maize-sweet cropping field) Karst region maize-sweet potato cropland soil clone KM EU8813
AY555784.1 gg_id:101141 Bor Khlueng hot spring clone PK34 AY5557
AJ519364.1 gg_id:75894 uranium mining waste pile near Johanngeorgenstadt soil clone JG37-AG-5 AJ5193
AJ617858.1 gg_id:110291 oxic-anoxic interphase flooded paddy soil clone D282110 AJ6178
EU404033.1 gg_id:313796 Microbial septic tank effluent and soil biozone infiltrative surface clean water clone (EU4040
FJ197547.1 gg_id:310970 deep Pacific Ocean and Eastern Mediterranean Sea sediment clone ALVIN29a_4C_ FL FJ1975
DQ676411.1 gg_id:220290 Archaeal and plankton freshwater pond suboxic freshwater-pond sediment clone M DQ676
EF018300.1 gg_id:212449 aspen rhizosphere clone Amb_16S_662 EF0183
DQ328617.1 gg_id:145959 microorganisms populating site extreme acid mine drainage sediment clone H5 DQ328
AY963324.1 gg_id:156453 structures and correlated ecological factors soils two evergreen broad-leaved forests AY9633
EF516650.1 gg_id:222943 grassland soil clone FCPP504 EF5166
AB369160.1 gg_id:241567 Microbiological Assessment Circulation Mud Fluids During First Operation Drilling De AB3691
FJ625319.1 gg_id:570620 Influence lead contamination on boreal pine forest soil clone HF_M_16 FJ6253
DQ129640.1 gg_id:137789 microarray level air two cities Texas urban aerosol clone AKIW863 DQ129
EU780449.1 gg_id:316355 modern freshwater stromatolites Ruidera Pools Natural Park Spain dry stromatolite (EU7804
EF494361.1 gg_id:223616 Nunnock River granitic landscape clone NR.1.005 EF4943
GU183624.1 gg_id:557366 Structures Reduced and Oxidized Aquifer lower Aqueous Arsenic Titas Bangladesh a GU183
AM997648.1 gg_id:542627 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A AM997

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10932.2	3587.4	4148.6	4864.1	4818.2	4212.6	4270.7	3275.7	3047.4	1660.5	1906.5
370.2	1705.1	3250.3	1962.6	5281.1	2414.0	4994.0	2110.6	1157.3	484.3	1238.6
7417.8	7042.0	8193.5	9080.3	10533.0	7425.0	10088.8	7971.9	6001.8	5630.9	7584.6
4296.6	6577.5	6781.3	6854.3	8759.3	6303.9	8589.7	6334.3	6075.5	5698.8	7237.3
1322.5	3475.7	3718.7	3440.8	5355.3	4716.3	4941.3	3745.5	4733.4	1676.0	2229.1
46.3	418.3	455.1	581.9	727.1	378.5	515.8	395.0	69.8	53.9	278.5
117.8	3138.2	4508.6	3141.7	6632.9	3731.2	6287.7	2935.5	2004.5	579.2	2175.5
64.9	1075.8	1772.1	1316.7	5526.1	1475.1	5171.8	476.9	277.6	184.4	690.6
30.8	43.2	31.9	31.0	111.1	22.1	29.7	25.0	23.6	17.5	17.8
636.5	4085.6	5069.5	5098.5	7128.9	4838.4	7795.5	4169.6	2923.0	3337.6	3463.6
140.2	3127.7	4102.6	3177.4	7106.4	3798.4	6811.0	2862.1	2226.9	917.2	2110.0
46.8	1009.0	886.0	909.6	2714.3	1355.7	1364.7	756.7	218.9	98.5	536.9
2275.5	3408.3	4123.7	3291.7	4570.6	3229.0	4597.6	3107.8	2399.2	1492.3	3653.3
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91.9	144.2	400.8	160.9	503.3	200.3	681.8	99.1	67.2	27.3	75.9
37.7	236.1	402.2	339.6	615.2	239.6	579.1	177.8	83.6	50.5	120.6
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131.2	546.5	649.3	575.1	685.9	581.9	815.2	536.3	294.4	117.8	392.9
86.7	918.5	1092.2	952.7	2425.0	1332.3	2411.5	1131.9	520.1	277.7	416.3
181.2	2280.9	2884.2	2739.9	4760.7	2848.7	4817.0	2644.1	1028.8	507.2	1304.3
368.6	3466.5	3836.6	4121.8	3448.6	4136.6	4457.3	4006.8	4285.4	2116.4	3254.2
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DQ070820.1 gg_id:149756 Prokaryotic Structures Seafloor Basalts Varying Age East Pacific Rise and Ridge basal DQ070
GQ246348.1 gg_id:535475 Temporal and spatial China North Yel Sea sediments clone Cm1-11 GQ246
EU734999.1 gg_id:311554 assemblages sediment station DBSE Northern Bering Sea clone 093B48 EU7349
EU491394.1 gg_id:259756 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X3 clone EU4913
EU652606.1 gg_id:279002 Seasonal variation microbial Yel Sea sediment clone D8S-76 EU6526
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FJ358923.1 gg_id:550228 and redox-stratified sediments marine reef sandy sediment clone SO13 FJ3589
EF125465.1 gg_id:187788 mangrove soil clone MSB-2Y4 EF1254
AJ241003.1 gg_id:1702 Norway:(Svalbard)Hornsund clone Sva0725 AJ2410
EU287099.1 gg_id:251889 Pacific arctic surface sediment clone P13-6 EU2870
GQ984352.1 gg_id:590289 surface water Northern Bering Sea clone DBS1g27 GQ984
GU369908.1 gg_id:532228 and mats vents Arc white microbial film on pebble aphotic zone shal hydrothermal v GU369
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EU132194.1 gg_id:255963 tallgrass prarie soil clone FFCH12382 EU1321
EU881271.1 gg_id:313254 (long-term grazing and burned annual) Karst region serious disturbance field soil clor EU8812
AY703465.1 gg_id:139386 Detection and ly acidobacterial analyses Altamira Cave clone ALT41 AY7034
EF516971.1 gg_id:223577 grassland soil clone FCPU401 EF5169
FJ444736.1 gg_id:588064 Cotton Rhizosphere cotton rhizosphere clone 4h-60 FJ4447
EF516941.1 gg_id:223804 grassland soil clone FCPP416 EF5169
AY921811.1 gg_id:113092 farm soil clone AKYG1685 AY9218
EF516929.1 gg_id:224421 grassland soil clone FCPO720 EF5169
FJ269289.1 gg_id:568362 Microbes marine sponges sponge tissue clone XA3A05F FJ2692
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AJ347029.1 gg_id:60180 sponge clone TK29 AJ3470
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FJ269338.1 gg_id:576211 Microbes marine sponges sponge tissue clone XB3A12F FJ2693
DQ070804.1 gg_id:147802 Prokaryotic Structures Seafloor Basalts Varying Age and Juan de Fuca Ridge basalt gl DQ070
EU491423.1 gg_id:259892 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X4 clone EU4914
EU735006.1 gg_id:354311 assemblages sediment station DBSE Northern Bering Sea clone 100B74 EU7350
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DQ521809.1 gg_id:161180 Anaerobic Methane Oxidizing ANME-1b Archaea Hypersaline Sediments Gulf Mexic DQ521
GQ246332.1 gg_id:568581 Temporal and spatial China North Yel Sea sediments clone Sd1-51 GQ246
AB294958.1 gg_id:219459 -dependent & analyses hydrothermal system off Taketomi Island Japan microbial ma AB2949

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43.2	144.6	250.7	210.0	221.6	165.1	229.1	254.9	46.0	53.0	126.4
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3965.6	3838.6	3582.4	4120.8	5700.7	3718.0	5822.8	3442.2	2563.5	1903.2	3578.1
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6399.1	6774.9	9832.0
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EU491665.1 gg_id:259485 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU491
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FJ437927.1 gg_id:543301 Benthic okenone production Fayetteville New York Green Lake surface sediments 16. FJ4379
EU755076.1 gg_id:351025 and Dioxygenase Genes Coal Tar Contaminated Soils coal tar-contaminated soil clon EU755
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FJ425650.1 gg_id:363109 communnities healthy and diseased colonies Caribbean coral Montastrea faveolata g FJ4256
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FJ358922.1 gg_id:594049 and redox-stratified sediments marine reef sandy sediment clone AO15 FJ3589
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AM259858.1 gg_id:204709 Spatial sponge- Mediterranean Tethya aurantium sponge cortex clone TAA-10-23 AM259
AF385537.1 gg_id:73910 swab advanced noma lesion clone CA002 AF385
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EU528207.1 gg_id:286946 Seasonal Dynamics Mudflat Mouth Major Kentucky Lake Reservoir Tributary sedime EU528
DQ129284.1 gg_id:137747 microarray level air two cities Texas urban aerosol clone AKIW896 DQ129
EU133029.1 gg_id:249727 tallgrass prarie soil clone FFCH18764 EU133
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EU132829.1 gg_id:253573 tallgrass prarie soil clone FFCH13720 EU132
AY093463.1 gg_id:55589 deep marine sediment clone MB-A2-108 AY0934
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AB486164.1 gg_id:532857 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC AB486
DQ067014.1 gg_id:128299 Lake Washington sediment clone pLW-76 DQ067
FJ479558.1 gg_id:577549 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4795
EU133207.1 gg_id:236133 tallgrass prarie soil clone FFCH8340 EU133
FJ479097.1 gg_id:545487 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4790
FJ478871.1 gg_id:513347 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4788
EU132575.1 gg_id:238110 tallgrass prarie soil clone FFCH10523 EU132
GQ263065.1 gg_id:547749 Structure Simulated Level Waste Site simulated level waste site clone F2_188X GQ263