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EF179125.1 gg_id:275713 Yersinia aldovae str. CCUG 18770 EF1791
NZ_ABAT01000008.1 gg_id:260769 Yersinia pestis biovar Orientalis str. F1991016 NZ_AB
AJ232237.1 gg_id:10382 Yersinia pestis SS-Yp-115 AJ2322
AJ627597.1 gg_id:107378 Yersinia aleksici str. Y159 AJ6275
NR_027543.1 gg_id:535819 Yersinia bercovieri str. CNY 7506; ATCC 43970 NR_02
U63135.1 gg_id:10347 Yersinia enterocolitica German U63135
AF282308.1 gg_id:41539 Yersinia enterocolitica str. 8081 AF2823
Z49830.1 gg_id:10349 Yersinia enterocolitica str. ER-31406-92 serotype O:5 Z49830
GU596500.1 gg_id:527323 Yersinia enterocolitica str. GP2 GU596
EF179130.1 gg_id:272269 Yersinia enterocolitica str. CCUG 8239A EF1791
X68674.1 gg_id:10341 Yersinia enterocolitica serotype 0:3; strain 11472 Princess Alexandra Hospital Brisbane A X68674
EU523225.1 gg_id:269635 Yersinia enterocolitica str. KM1 EU523
DQ486901.1 gg_id:158291 Yersinia frederiksenii 49 DQ486
AF366384.1 gg_id:34461 Yersinia rohdei str. ATCC 43380 AF3663
EF179123.1 gg_id:265704 Yersinia intermedia str. CCUG 11292 EF1791
DQ917929.1 gg_id:163194 Yersinia intermedia str. H-27 DQ917
NR_027546.1 gg_id:557655 Yersinia mollaretii str. CNY 7263; ATCC 43969 NR_02
NZ_ACCA01000078.1 gg_id:382211 Yersinia kristensenii str. ATCC 33638 NZ_AC
FM955884.1 gg_id:546539 Yersinia kristensenii str. Asd MY-1 FM955
EU401667.1 gg_id:263404 Yersinia ruckeri EU401
X75275.1 gg_id:10363 Yersinia ruckeri X75275
FJ873802.1 gg_id:534783 Yersinia ruckeri str. LY0903 FJ8738
AY359283.1 gg_id:102805 Aquicella siphonis str. SGT-108 AY3592
EF688351.1 gg_id:245537 soil clone F4-96 EF6883
FJ542924.1 gg_id:526380 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone B FJ5429
EU801111.1 gg_id:320125 It's all ranking aquatic Delaware Bay NJ clone 2C229435 EU801
FM877663.1 gg_id:362619 Microbial several mining wastes Bulgaria vicinity uranium mine Sliven clone Sliv-27 FM877
EF019154.1 gg_id:212714 aspen rhizosphere clone Amb_16S_1801 EF0191
FJ382597.1 gg_id:542155 Potentially pathogenic and air stem cell transplant summer hospital shower water BN FJ3825
AY734242.1 gg_id:135830 dynamics aquifers indicates presence stable autochthonous microbial endokarst spri AY7342
AJ252651.1 gg_id:36918 agricultural soil clone SC-I-71 AJ2526
NR_025763.1 gg_id:552844 Aquicella lusitana str. SGT-39; CIP 107650 NR_02
GQ054582.1 gg_id:454783 Topographical and Temporal Human Skin Microbiome skin back clone nbw1092b02c GQ054
FJ793155.1 gg_id:529786 Archaea and Hot Spring Thailand Tao Dam hot spring clone TDB06 FJ7931
FJ542873.1 gg_id:529296 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone A FJ5428
DQ083104.1 gg_id:132329 Fnctnl and rspnss mcrbl cntr-old fld sl cln X174 DQ083
EF540406.1 gg_id:227017 oil-shale semi-coke solid waste clone 4_15MK EF5404
NC_011527.1 gg_id:356835 Coxiella burnetii str. CbuG_Q212 NC_01
EU881324.1 gg_id:314162 (maize-sweet cropping field) Karst region maize-sweet potato cropland soil clone KM EU8813
EU143669.1 gg_id:251151 Coxiella-like infection Psittacine birds liver clone 1358 EU1436

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AB001519.1 gg_id:8016 Haemaphysalis longicornis symbiont AB001
NZ_AAQJ02000001.1 gg_id:237975 Rickettsiella grylli NZ_AA
FJ542982.1 gg_id:524171 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone B FJ5429
FJ542909.1 gg_id:527108 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone A FJ5429
AY447040.1 gg_id:107683 hepatopancreatic symbiont clone 7 AY447
AF286124.1 gg_id:73506 eubacterium Cecidotrioza sozanica AF286
AF327558.1 gg_id:50747 Folsomia candida symbiont AF327
U97547.1 gg_id:8028 Rickettsiella grylli U9754
FJ437936.1 gg_id:574974 Benthic okenone production Fayetteville New York Green Lake surface sediments 16. FJ4379
EU134738.1 gg_id:235968 tallgrass prarie soil clone FFCH12405 EU134
DQ396123.1 gg_id:154082 deep-sea octacoral clone ctg_NISA227 DQ396
AF526927.2 gg_id:55626 Mars Odyssey Orbiter and encapsulation facility clone T5-3 AF526
GQ346963.1 gg_id:547615 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ346
EU491737.1 gg_id:265658 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU491
GQ402591.1 gg_id:587585 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
DQ450792.1 gg_id:160953 Microbial Alpine Tundra Wet Meadow Soil: Chloroflexi Cold Water-Saturated satura DQ450
EU134722.1 gg_id:251564 tallgrass prarie soil clone FFCH7120 EU134
AY326588.1 gg_id:136759 Amazon soil clone 776-1 AY326
GQ339152.1 gg_id:515598 Comprehensive Investigation on Iron Cycling Freshwater Seep ing Microscopy Cultiv GQ339
EU802753.1 gg_id:319778 It's all ranking aquatic Northeast Colon Panama clone 4C230126 EU802
EU050790.1 gg_id:256320 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_07_86 EU050
EU276556.1 gg_id:359663 -DGGE and Approaches Analyze Effect Agricultural Practices on Soil agricultural soil c EU276
EF515889.1 gg_id:218114 grassland soil clone FCPS672 EF5158
EU134752.1 gg_id:255441 tallgrass prarie soil clone FFCH15063 EU134
DQ083100.1 gg_id:137191 Functional and responses microbial century-old field soil clone X14 DQ083
EU881328.1 gg_id:353731 (maize-sweet cropping field) Karst region maize-sweet potato cropland soil clone KM EU881
EU735697.1 gg_id:340556 archaeal structures oil contaminated and soils China pristine soil Jidong Oilfield clone EU735
EF580986.1 gg_id:279663 Survey Microbial Freshwater Calcareous Mats freshwater calcareous mat clone CM6 EF5809
AF255638.1 gg_id:32355 EBPR sludge clone Ebpr13 AF255
FJ638597.1 gg_id:511763 Temperature dependent succession sulfate reducing muddy southwestern Taiwan hc FJ6385
AM746627.1 gg_id:244768 Proteinimicrobium ihbtica str. HMPB3 AM746
AB058914.1 gg_id:49724 Legionella sp. OY6 AB058
EU134756.1 gg_id:240701 tallgrass prarie soil clone FFCH15686 EU134
AB179493.1 gg_id:99390 sedimentary rock clone MIZ02 AB179
AJ536872.1 gg_id:78512 uranium mining waste pile soil sample clone JG30a-KF-94 proteobacterium AJ5368
EU134735.1 gg_id:257122 tallgrass prarie soil clone FFCH11666 EU134
FJ542953.1 gg_id:514449 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone B FJ5429
EU937889.1 gg_id:334207 Biogeochemistry Iron Oxidation Circumneutral Freshwater Habitat riparian iron oxidi EU937
EU328043.1 gg_id:278735 dynamics during bioremediation crude oil contaminated moderate saline soil clone B EU328
EU134784.1 gg_id:239870 tallgrass prarie soil clone FFCH2111 EU134

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DQ396109.1 gg_id:156557 deep-sea octacoral clone ctg_NISA135 DQ396
EU803079.1 gg_id:326446 It's all ranking aquatic Northeast Colon Panama clone 4C230497 EU803
AJ252619.1 gg_id:36221 agricultural soil clone SC-I-16 AJ2526
FJ444660.1 gg_id:578973 Cotton Rhizosphere cotton rhizosphere clone 2h-38 FJ4446
FJ444646.1 gg_id:587687 Cotton Rhizosphere cotton rhizosphere clone 2h-15 FJ4446
DQ431905.1 gg_id:207732 microorganisms catalyzing nitrogen removal and organic matter metabolism perme DQ431
GQ349429.1 gg_id:569326 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ349
EF515899.1 gg_id:225991 grassland soil clone FCPT587 EF5158
EU735661.1 gg_id:325840 archaeal structures oil contaminated and soils China pristine soil Jidong Oilfield clone EU735
CU466806.1 gg_id:317285 Evry wastewater treatment plant anoxic basin clone CU466
AB294332.1 gg_id:215917 Microbial structure deep coal seem groundwater stream clone SWB21 AB2943
EU202847.1 gg_id:347934 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo EU2028
FJ545549.1 gg_id:511371 Diveristy Seawater and Sediment Northern North Yel Sea sediment clone S2-5 FJ5455
GU305791.1 gg_id:534111 Research on changes structure during algae outbreak oligotrophic lakes (YangHe res GU305
FJ205343.1 gg_id:535383 Prokaryotic deep-sea hydrothermal region East Lau Spreading Centre deep marine se FJ2053
GQ350354.1 gg_id:587874 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ350
EU925916.1 gg_id:303457 sediments sediment station DBS1 northern Bering Sea clone 152H67 EU9259
AB015255.1 gg_id:8026 deepest cold-seep area Japan Trench clone JTB256 proteobacterium AB015
EF574681.1 gg_id:229650 site S25 near Coco's Island marine clone S25_1025 EF5746
EU644214.1 gg_id:282458 and Samoylov Island Lena active layer -centred polygon near surface horizon; Rim_T EU6442
AF235121.1 gg_id:74504 North Sea clone KTc0924 AF2351
EU134760.1 gg_id:238980 tallgrass prarie soil clone FFCH7560 EU1347
EU249954.1 gg_id:246142 Polyphasic description Pocillopora seawater adjacent Pacillopora meandrina coral co EU2499
EF575249.1 gg_id:232669 site S25 near Coco's Island marine clone S25_1593 EF5752
EU134712.1 gg_id:245968 tallgrass prarie soil clone FFCH5316 EU1347
FJ468390.1 gg_id:555059 Bioaugmentation Pseudomonas sp. strain MHP41 promotes attenuation and changes FJ4683
FJ236047.1 gg_id:334364 three Parisian treatment plants approaches drinking water clone Orly7 FJ2360
FJ437972.1 gg_id:539237 Benthic okenone production Fayetteville New York Green Lake surface sediments 16. FJ4379
EF575079.1 gg_id:237689 site S25 near Coco's Island marine clone S25_1423 EF5750
FJ205338.1 gg_id:555799 Prokaryotic deep-sea hydrothermal region East Lau Spreading Centre deep marine se FJ2053
AF255642.1 gg_id:22253 EBPR sludge clone Ebpr12 AF2556
EU386125.1 gg_id:272458 Biogeographical and microbes sediments on subseafloor sediment South China Sea c EU3861
EU134733.1 gg_id:237253 tallgrass prarie soil clone FFCH11328 EU1347
EU134753.1 gg_id:248221 tallgrass prarie soil clone FFCH15155 EU1347
EF019986.1 gg_id:216743 aspen rhizosphere clone Elev_16S_1373 EF0199
EU805209.1 gg_id:326155 It's all ranking aquatic 250 miles Panama City clone 6C233205 EU8052
EU834797.1 gg_id:541438 Microbiology Aerobic Phosphorus Removal Process aerobic phosphorus-removing se EU8347
FJ712415.1 gg_id:523629 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) K FJ7124
EU193049.1 gg_id:357896 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo EU1930
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AF129524.1 gg_id:51847 Legionella pneumophila str. E5C1; ATCC700713 AF1295
X97361.1 gg_id:7908 Legionella sp str. LLAP8 X97361
NC_006368.1 gg_id:129226 Legionella pneumophila str. Paris NC_00
AB233212.1 gg_id:140544 Legionella landfill str. OA1-4 AB233
FJ542889.1 gg_id:522337 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone A FJ5428
FJ612289.1 gg_id:592165 and Biogeochemistry Dongping Lake Ecosystems lake water clone DP7.5.15 FJ6122
NR_026522.1 gg_id:565488 Legionella tucsonensis str. 087-AZ-H; ATCC 49180 NR_02
EU250236.1 gg_id:246283 acid mine drainage clone GXDC-22 EU250
FJ230896.1 gg_id:315994 under Level Antibiotic Selection Pressures river water clone F20 FJ2308
EU134790.1 gg_id:244967 tallgrass prarie soil clone FFCH3904 EU134
GQ002634.1 gg_id:507027 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbu GQ002
GQ264139.1 gg_id:564434 Structure Simulated Level Waste Site simulated level waste site clone WC3_79 GQ264
DQ814490.1 gg_id:168390 zebrafish digestive tract clone aaa29e09 DQ814
Z49722.1 gg_id:7972 Legionella fairfieldensis Z49722
DQ413099.1 gg_id:154202 Microbial -dependent and Approaches Anaerobic/Aerobic SBR Reactor EBPR sludge DQ413
Z49724.1 gg_id:7994 "Legionella donaldsonii" Z49724
DQ337039.1 gg_id:145455 subsurface water clone EV818EB5CPSAJJ36 DQ337
AY792279.1 gg_id:123281 Humic Lake clone CrystalBog1D4 AY792
FJ744881.1 gg_id:549676 Transporter genes expressed coastal response dissolved organic carbon surface wate FJ7448
AY662002.1 gg_id:137028 uranium-contaminated groundwater clone 300G-C11 AY662
DQ667196.1 gg_id:171418 Legionella taurinensis str. ATCC 700508 DQ667
X97363.1 gg_id:7946 Legionella sp str. LLAP10 X97363
FM877662.1 gg_id:359700 Microbial several mining wastes Bulgaria vicinity uranium mine Sliven clone Sliv-17 FM877
DQ327699.1 gg_id:166988 Biological filtration limits carbon availability affects downstream biofilm formation a DQ327
FJ542894.1 gg_id:518474 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone A FJ5428
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AF467296.1 gg_id:64661 Xanthomonas sp. clone 88_5_2 AF467
AY598719.2 gg_id:99452 Amoeba proteus symbiotic AY598
AY957913.1 gg_id:114944 drinking water biofilm clone B3NR56D11 AY957
GU062706.1 gg_id:590087 Legionella sp. str. NML 93L054 GU062
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Z49739.1 gg_id:7955 Legionella worsliensis Z49739
EU937840.1 gg_id:331322 Biogeochemistry Iron Oxidation Circumneutral Freshwater Habitat riparian iron oxidi EU937
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EU800944.1 gg_id:306074 It's all ranking aquatic Delaware Bay NJ clone 2C229203 EU800
Z49719.1 gg_id:7922 Legionella bozemanii Z49719
AJ969023.1 gg_id:120376 Legionella anisa UCSC 25 AJ969
FJ479065.1 gg_id:590656 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4790

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GQ347573.1 gg_id:555343 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ347
DQ327700.1 gg_id:163406 Biological filtration limits carbon availability affects downstream biofilm formation a DQ327
EU835422.1 gg_id:318862 structure and quorum sensing reverse osmosis RO membrane biofilm clone 1B17 EU8354
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Z32640.1 gg_id:7984 Legionella israelensis Z32640
EU236319.1 gg_id:298170 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg1bF3 EU2363
GQ054315.1 gg_id:463932 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw1108 GQ054
EU134769.1 gg_id:243485 tallgrass prarie soil clone FFCH9178 EU1347
Z49729.1 gg_id:7954 Legionella moravica Z49729
Z49728.3 gg_id:7971 Legionella londiniensis Z49728
AB255083.1 gg_id:173398 corroded concrete clone IC-85 AB2550
Z49736.1 gg_id:7956 Legionella shakespearei Z49736
Z49725.1 gg_id:7929 Legionella gratiana Z49725
Z49735.1 gg_id:7931 Legionella santicrucis Z49735
DQ413067.1 gg_id:153948 Microbial -dependent and Approaches Anaerobic/Aerobic SBR Reactor EBPR sludge DQ413
EU800974.1 gg_id:311942 It's all ranking aquatic Delaware Bay NJ clone 2C229243 EU8009
FJ382013.1 gg_id:543450 Potentially pathogenic and air stem cell transplant winter hospital shower water BMT FJ3820
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AM747393.1 gg_id:236913 Legionella dresdeniensis str. W03-356 AM747
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EU835445.1 gg_id:340760 structure and quorum sensing reverse osmosis RO membrane biofilm clone 2B20 EU8354
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AF227162.1 gg_id:52462 Tatlockia micdadei str. ATCC33218 AF2271
Z32642.1 gg_id:7981 Legionella oakridgenesis Z32642
AJ919271.1 gg_id:114678 Legionella nautarum AJ9192
GQ388900.1 gg_id:551369 quality deterioration drinking system during serious red water outbreak clone Z61 GQ388
FJ236838.1 gg_id:328884 Legionella sp. str. CDC-3041-AUS-E FJ2368
EU134750.1 gg_id:238279 tallgrass prarie soil clone FFCH14647 EU1347
Z49730.3 gg_id:7982 Legionella nautarum Z49730
NR_025196.1 gg_id:556395 Legionella busanensis str. K9951; KCTC 12084 NR_025
AF122884.2 gg_id:8008 Legionella beliardensis str. Montbeliard A1 AF1228
GQ009403.1 gg_id:500261 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw77 GQ009
EF612978.1 gg_id:233794 acid mine drainage clone YSK16S-15 EF6129
EF036512.1 gg_id:191570 Legionella jordanis NML 060502 EF0365
EF471571.1 gg_id:270320 Fast Screening and Estuarine Operon Libraries whole surface water Chesapeake Bay EF4715
EF520577.1 gg_id:229517 structure lakes: what controls ? acid-impacted lake clone ADK-RXe02-02 EF5205
DQ458002.1 gg_id:158776 acid mine drainage clone DX32 DQ458
EU491749.1 gg_id:263538 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU4917

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EU386109.1 gg_id:264331 Biogeographical and microbes sediments on subseafloor sediment South China Sea c EU386
GQ850579.1 gg_id:559606 bottom water northern Bering Sea clone d131 GQ850
AY050590.1 gg_id:52016 MCB-contaminated groundwater-treating reactor clone GOUTB2 AY0505
GQ261748.1 gg_id:550690 shifts taxa and response localized organic loading deep sea sediment whale falls clo GQ261
EU491526.1 gg_id:268607 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR4C EU491
EU491716.1 gg_id:267408 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU491
GQ472814.1 gg_id:574241 Biodiversity planktonic Northern surface water northern Bering Sea clone b45 GQ472
EU735642.1 gg_id:312981 archaeal structures and pristine soils China oil contaminated soil Jidong Oilfield clone EU735
EF520571.1 gg_id:230249 structure lakes: what controls ? acid-impacted lake clone ADK-HDe02-30 EF5205
EF516119.1 gg_id:221947 grassland soil clone FCPU740 EF5161
GU118075.1 gg_id:554366 Threatened Corals Provide Microbial Habitats clone Apal_M08 GU118
EU236332.1 gg_id:297516 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg5a2A5 EU236
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AY536226.1 gg_id:101534 host gut clone LAgut--P14 AY536
DQ295893.1 gg_id:145412 Cohn's Crenothrix filamentous oxidizer unusual methane monooxygenase physical e DQ295
GQ390223.1 gg_id:548160 oxic-anoxic interface meromictic crater lake Lac Pavin clone eub62A8 GQ390
AB504955.1 gg_id:565012 structure microorganisms reddish-brown iron-rich snow clone oze05B47 AB504
DQ837251.1 gg_id:247086 Archaeal and pristine National Park Spain Donana coastal aquifer clone 49S1_2B_45 DQ837
FJ502272.1 gg_id:509929 Co-occurrence denitrification and nitrogen fixation meromictic lake (Switzerland) Lak FJ5022
AF152597.1 gg_id:8098 Methylobacter psychrophilus str. Z-0021 AF1525
AJ583183.1 gg_id:94840 radioactive site ground water clone S15B-MN136 AJ5831
AB240527.1 gg_id:141423 microbial structure rhizosphere biofilm Sapporo root-base (80 160 mm) Phragmites S AB2405
DQ984190.1 gg_id:205851 Clonothrix fusca str. AW-b DQ984
AF351235.1 gg_id:48494 coal tar waste-contaminated groundwater clone 8-4 proteobacterium AF3512
DQ367735.1 gg_id:150338 Fluorescence Situ Hybridization-F Cytometry-Cell Sorting-Based Method Enrichment DQ367
AB240465.1 gg_id:141872 microbial structure rhizosphere biofilm Sapporo root-tip (0 40 mm) Phragmites Sosei AB2404
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AB240522.1 gg_id:140993 microbial structure rhizosphere biofilm Sapporo root-base (80 160 mm) Phragmites S AB2405
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M95657.1 gg_id:8104 Methylobacter luteus str. 11914 M9565
AF304195.1 gg_id:40043 Methylobacter luteus str. NCIMB 11914 AF3041
AF304197.1 gg_id:37065 Methylobacter marinus str. A45 AF3041
DQ270621.1 gg_id:142869 hydrothermal carbonate chimney clone LC1133B-99 DQ270
AJ704662.1 gg_id:109268 marine sediment clone HMMVBeg-7 AJ7046
DQ521819.1 gg_id:160617 Anaerobic Methane Oxidizing ANME-1b Archaea Hypersaline Sediments Gulf Mexic DQ521

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AB294954.1 gg_id:223386 -dependent & analyses hydrothermal system off Taketomi Island Japan microbial ma AB2949
FJ712420.1 gg_id:525836 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) K FJ7124
GQ346825.1 gg_id:533281 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ346
EU491680.1 gg_id:269280 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU4916
AB294957.1 gg_id:224998 -dependent & analyses hydrothermal system off Taketomi Island Japan microbial ma AB2949
FJ712568.1 gg_id:525302 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) K FJ7125
FJ712444.1 gg_id:516890 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) K FJ7124
AB294960.1 gg_id:218525 -dependent & analyses hydrothermal system off Taketomi Island Japan microbial ma AB2949
EU700156.1 gg_id:294790 Study on Shantou Bay Marine Sediments Microorganisms sediment clone STU14 EU700
GQ350283.1 gg_id:578592 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ350
AB188770.1 gg_id:113920 Maorithyas hadalis gill thioautotrophic symbiont II AB188
FJ717255.1 gg_id:511065 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United Kingc FJ7172
AB188776.1 gg_id:112716 Maorithyas hadalis gill thioautotrophic symbiont II AB188
AB476280.1 gg_id:549573 Compositional and functional transition epibiotic microbial hydrothermal vent galath AB476
FJ264669.1 gg_id:339219 Manganese and Iron Dependent Anaerobic Oxidation Methane methane seep sedime FJ2646
FJ717256.1 gg_id:555227 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United Kingc FJ7172
DQ070797.1 gg_id:145621 Prokaryotic Structures Seafloor Basalts Varying Age and Juan de Fuca Ridge basalt gl DQ070
DQ270620.1 gg_id:144477 hydrothermal carbonate chimney clone LC1133B-86 DQ270
GU302420.1 gg_id:555130 Spatial structure and activity sedimentary microbial underlying Beggiatoa spp. mat h GU302
AB042414.1 gg_id:24022 Maorithyas hadalis gill thioautotrophic symbiont II gill AB0424
DQ513099.1 gg_id:161529 Microbial life fluids ridge flank crustal fluid clone FS274-37B-03 DQ513
AB245479.1 gg_id:146843 Sulfurivirga caldicularium str. MM1 AB2454
EU528230.1 gg_id:286126 Seasonal Dynamics Mudflat Mouth Major Kentucky Lake Reservoir Tributary sedime EU528
DQ270629.1 gg_id:141697 hydrothermal carbonate chimney clone LC1446B-37 DQ270
GQ350218.1 gg_id:535569 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ350
DQ270612.1 gg_id:142835 hydrothermal carbonate chimney clone LC1133B-5 DQ270
U05595.1 gg_id:8100 methanotrophic symbiont of Louisiana Slope mussel gill U05595
NR_026064.1 gg_id:576044 Methylocaldum szegediense str. OR2 NR_02
AF215632.1 gg_id:71299 Methylocaldum sp. str. dr65 AF2156
EF203191.1 gg_id:208702 phylotypes sediments Lake Kastoria Greece sediment clone Kas146B EF2031
AJ617834.1 gg_id:110041 oxic-anoxic interphase flooded paddy soil clone D14307 AJ6178
U89297.1 gg_id:8046 Methylocaldum tepidum str. LK6 U89297
AF215633.1 gg_id:73918 Methylocaldum sp. str. r6f AF2156
FJ810597.1 gg_id:380204 Subsurface ecosystem resilience: Long-term attenuation subsurface contaminants su FJ8105
NR_026063.1 gg_id:572916 Methylocaldum gracile str. VKM 14L NR_02
NC_002977.6 gg_id:128429 Methylococcus capsulatus str. Bath NC_00
NR_029251.1 gg_id:540868 Methylococcus thermophilus str. IMV-B-3037; ACM 3585 NR_02
X72771.1 gg_id:8036 Methylococcus capsulatus Bath str. ACM 3302 ATCC 33009 NCIBM 1113 X72771
X72769.1 gg_id:8040 Methylococcus sp str. JB140 X72769
AB354618.1 gg_id:273571 Laminated iron texture iron-oxidizing calcite travertine iron-rich deposit clone FD09 AB3546

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AF307138.1 gg_id:39461 Methylomicrobium buryatense str. 5B AF307
U05570.1 gg_id:8080 Methylomicrobium pelagicum U0557
AF096091.1 gg_id:8060 Methylobacter alcaliphilus str. 5z AF096
EF495157.1 gg_id:222556 Methylobacter alcaliphilus str. 20Z EF4951
AF304194.1 gg_id:38046 Methylomonas rubra str. NCIMB 11913 AF304
AF150807.1 gg_id:8055 Methylomonas rubra AF150
AY995198.1 gg_id:119789 Methylomonas rubra str. UCM B-3075; NCIMB 11913; ACM3303; VKM-15m AY995
X72776.1 gg_id:8084 Methylomonas aurantiaca str. JB103 (phenon3) X7277
X72778.1 gg_id:8090 Methylomonas fodinarum str. ACM 3268 JB13 (phenon2) X7277
DQ837263.1 gg_id:245267 Archaeal and pristine National Park Spain Donana coastal aquifer clone 56S_1B_6 DQ837
GQ340208.1 gg_id:544467 Prokaryotic Marathonas Reservoir Greece water column clone VE07-15-BAC GQ340
NR_025040.1 gg_id:550440 Methylosarcina quisquiliarum str. AML-D4; ATCC 700908 NR_02
AF177296.1 gg_id:8051 Methylosarcina fibrata AML-C10 AF177
U67929.1 gg_id:8101 Methylosphaera hansonii str. AM6 U6792
DQ337085.1 gg_id:145089 subsurface water clone EV818SWSAP61 DQ337
DQ001669.1 gg_id:157473 Microbial seeps asphalt seep clone B91-30 DQ001
AM935153.1 gg_id:534315 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM935
AB486440.1 gg_id:585666 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC AB486
EU144025.1 gg_id:235630 Methylomicrobium album str. BG8 EU144
AM936189.1 gg_id:537819 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM936
X72775.1 gg_id:8059 Methylomicrobium pelagicum str. ACM 3505 NCIMB 2265 X7277
X72773.1 gg_id:8091 Methylobacter whittenburyi str. 3310 NCIMB 11128 ACM 3306 X7277
EU328101.1 gg_id:278818 dynamics during bioremediation crude oil contaminated moderate saline soil clone Y EU328
FM242408.1 gg_id:308594 sequences sediment clone 65 T12d-oil FM242
X72772.1 gg_id:8086 Methylobacter luteus str. ACM 3304 NCIMB 11914 X7277
AM936083.1 gg_id:539835 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM936
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NR_029240.1 gg_id:594166 Methylomicrobium agile str. A30; ATCC 35068 NR_02
EU144026.1 gg_id:252662 Methylomicrobium agile str. ATCC 35068 EU144
AM936065.1 gg_id:564002 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM936
EF648094.1 gg_id:254304 dynamics during produced water treatment aerobic activated sludge clone HB102 EF648
EU735633.1 gg_id:353064 archaeal structures and pristine soils China oil contaminated soil Jidong Oilfield clone EU735
AY007295.1 gg_id:22040 Methylobacter sp. str. LW12 AY007
NR_025955.1 gg_id:555220 Cycloclasticus pugetii str. PS-1; ATCC 51542 NR_02
AF148215.1 gg_id:7712 Cycloclasticus oligotrophus AF148
AF126548.1 gg_id:7703 Thialkalimicrobium aerophilum str. AL3 AF126
AF126549.1 gg_id:7704 Thialkalimicrobium sibericum str. AL7 AF126
CP000109.2 gg_id:141093 Thiomicrospira crunogena str. XCL-2 CP000
AB166731.1 gg_id:99742 Thiomicrospira thermophila str. I78 AB166
FJ792079.1 gg_id:548362 Unexpectedly archaeal species shift between rare and dominant over thousand year FJ7920

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NR_029135.1 gg_id:555362 Hydrogenovibrio marinus str. MH-110; JCM7688 NR_02
AF013978.1 gg_id:7695 Thiomicrospira kuenenii str. JB-A1 AF013
EU196336.1 gg_id:252812 Thiomicrospira sp. NP20 EU196
FJ791897.1 gg_id:557561 Unexpectedly archaeal species shift between rare and dominant over thousand year FJ7918
AJ294334.1 gg_id:75896 Thiomicrospira crunogena HY-62 AJ2943
DQ513094.1 gg_id:161678 Microbial life fluids ridge flank crustal fluid clone FS274-19B-03 DQ513
AY922201.1 gg_id:112990 whalefall clone 131635 AY922
FJ792061.1 gg_id:532975 Unexpectedly archaeal species shift between rare and dominant over thousand year FJ7920
AJ237758.1 gg_id:7698 Thiomicrospira sp. str. Milos-T2 AJ2377
DQ390450.1 gg_id:152006 Thiovibrio halophilus str. HL 5 DQ390
EF644790.1 gg_id:296669 genes and citrate lyase deep-sea microbial MAR Logatchev hydrothermal vent syster EF6447
AF013975.1 gg_id:7696 Thiomicrospira chilensis str. Ch-1 AF013
FJ792110.1 gg_id:564352 Unexpectedly archaeal species shift between rare and dominant over thousand year FJ7921
EU999014.1 gg_id:320018 Predominance Methanolobus and Methanoculleus spp. Archaeal Saline Gas Field Foı EU999
AB176166.1 gg_id:187293 Microbial Hydrothermal System Suiyo Seamount on Izu-Ogasawara Arc vent area wa AB176
FJ792063.1 gg_id:551499 Unexpectedly archaeal species shift between rare and dominant over thousand year FJ7920
FJ791999.1 gg_id:532862 Unexpectedly archaeal species shift between rare and dominant over thousand year FJ7919
DQ270630.1 gg_id:142939 hydrothermal carbonate chimney clone LC1446B-39 DQ270
FJ792260.1 gg_id:512284 Unexpectedly archaeal species shift between rare and dominant over thousand year FJ7922
FJ791896.1 gg_id:570053 Unexpectedly archaeal species shift between rare and dominant over thousand year FJ7918
EF687189.1 gg_id:286578 Biogeochemistry iron- and sulfur-precipitating microbial mats (Nile Mediterranean) ir EF6871
DQ513107.1 gg_id:160820 Microbial life fluids ridge flank crustal fluid clone FS275-74B-03 DQ513
AY575776.1 gg_id:106343 Thiomicrospira sp. str. AD03 AY5757
AM888291.1 gg_id:254539 Thiomicrospira sp. str. NV40C1 AM888
FJ792466.1 gg_id:539354 Unexpectedly archaeal species shift between rare and dominant over thousand year FJ7924
FJ792299.1 gg_id:511672 Unexpectedly archaeal species shift between rare and dominant over thousand year FJ7922
AF513949.1 gg_id:62496 Piscirickettsia group clone LA7-B48N AF513
FJ792295.1 gg_id:508761 Unexpectedly archaeal species shift between rare and dominant over thousand year FJ7922
DQ270607.1 gg_id:142087 hydrothermal carbonate chimney clone LC1408B-58 DQ270
AF069959.1 gg_id:7689 Thiomicrospira crunogena str. MA-3; ATCC700270 AF069
AF082327.1 gg_id:7682 Thiomicrospira sp. str. Milos T-1 AF082
FJ791989.1 gg_id:511184 Unexpectedly archaeal species shift between rare and dominant over thousand year FJ7919
AY575777.1 gg_id:106505 Thiomicrospira sp. str. AD07 AY5757
AF016046.1 gg_id:7702 Thiomicrospira thyasirae str. DSM 5322 AF016
EU050820.1 gg_id:245893 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_07_77 EU050
EU104341.1 gg_id:340969 Evidence Comamonadaceae determinants settling performance activated sludge clo EU104
EU104176.1 gg_id:311244 Evidence Comamonadaceae determinants settling performance activated sludge clo EU104
CU466829.1 gg_id:344621 Evry wastewater treatment plant anoxic basin clone CU466
DQ463205.1 gg_id:157299 Acid Drainage Tong Lushan Copper Mine China acid mine drainage clone tls3-10 DQ463
AY493942.1 gg_id:136796 Fingerprinting aggregates soil clone 105 AY493
EU134703.1 gg_id:243013 tallgrass prarie soil clone FFCH6306 EU134

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EF173354.1 gg_id:187488 Options situ remediation contaminated mixture chlorinated hydrocarbons hydrocarb EF1733
EU647558.1 gg_id:285678 Alcanivorax sp. str. PA2 EU6475
GQ153648.1 gg_id:581006 Alcanivorax dieselolei str. ANT-2400 S12 GQ153
EF647617.1 gg_id:270691 Alcanivorax dieselolei P40 EF6476
AB176073.1 gg_id:195877 Microbial Hydrothermal System Suiyo Seamount on Izu-Ogasawara Arc vent area wa AB1760
GU183681.1 gg_id:593585 Alcanivorax dieselolei str. H1673 GU183
DQ270698.1 gg_id:143401 Alcanivorax sp. B-3025 DQ270
DQ768648.1 gg_id:255548 Alcanivorax venustensis MARC4C DQ768
AJ244731.1 gg_id:73634 Smegmaraptor porcuscaenosi str. V4.BO.19 = MM_2368 AJ2447
GQ153640.1 gg_id:587714 Alcanivorax sp. str. ANT-2400 S4 GQ153
EU621895.1 gg_id:278807 Alcanivorax sp. str. LY2 EU6218
GQ153644.1 gg_id:589864 Alcanivorax dieselolei str. ANT-2400 S8 GQ153
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EF583624.1 gg_id:275378 Alcanivorax indicus str. B114 EF5836
EF648146.1 gg_id:244272 dynamics during produced water treatment aerobic activated sludge clone XJ93 EF6481
AY686709.1 gg_id:105070 Uruburuia balearica str. MACL04 AY6867
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FM242291.1 gg_id:314738 sequences sediment clone 12 T9d-oil FM242
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AB053125.1 gg_id:32122 Alcanivorax sp. str. I4 AB0531
EU369139.1 gg_id:340580 libraries oyster shell clone MBIOS-23 EU3691
NR_027574.1 gg_id:560452 Kangiella koreensis str. SW-125; DSM 16069 NR_027
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AY542567.1 gg_id:114206 Gulf Mexico seafloor sediment clone GoM GB425 02B-35 AY5425
AF382097.1 gg_id:79413 bacterioplankton clone ZA2202c AF3820
FJ905711.1 gg_id:551031 s Tonga-Kermadec iron oxide sediments Volcano 1 Tonga Arc clone V1F45b FJ9057
EF687362.1 gg_id:280438 Biogeochemistry iron- and sulfur-precipitating microbial mats (Nile Mediterranean) s EF6873
AY162089.1 gg_id:136096 Cultivating Sargasso Sea clone GMD38D11 AY1620
EU290714.1 gg_id:249481 microbial structure biogeochemical contrasting shelf sediments Namibian upwelling EU2907
FM242204.1 gg_id:313320 sequences sediment clone 317 T0h-oil FM242
EU652570.1 gg_id:278394 Seasonal variation microbial Yel Sea sediment clone B8S-19 EU6525
EU287139.1 gg_id:241890 Pacific arctic surface sediment clone P13-46 EU2871
EU050815.1 gg_id:240357 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_06_26 EU0508
FM242475.1 gg_id:321501 sequences sediment clone 29 T12d+oil FM242
EU037349.2 gg_id:259038 structure landfill sediments receiving long-term augmentations wastes chromium co EU0373
EU735618.1 gg_id:346955 archaeal structures and pristine soils China oil contaminated soil Jidong Oilfield clone EU7356

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GU061307.1 gg_id:582472 Evaluation culturing methods cultivate previously Yel Sea intertidal beach seawater GU061
AB015541.1 gg_id:8407 deep-sea sediment clone BD2-13 AB0155
FJ203036.1 gg_id:316869 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c FJ2030
FJ202771.1 gg_id:318714 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2027
EU491790.1 gg_id:275246 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU4917
DQ889922.1 gg_id:172811 natural product producing octocoral Erythropodium caribaeorum clone EC52 DQ889
AJ853538.1 gg_id:110075 landfill leachate clone GZKB44 AJ8535
AF006606.2 gg_id:8204 Candidatus Endobugula sertula str. BnSP AF0066
AY532642.1 gg_id:105318 Bugula simplex symbiont AY5326
EU287080.1 gg_id:246890 Pacific arctic surface sediment clone B78-116 EU2870
EU286987.1 gg_id:236857 Pacific arctic surface sediment clone B78-23 EU2869
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EF515971.1 gg_id:222753 grassland soil clone FCPS641 EF5159
AJ289161.1 gg_id:52677 Cellvibrio sp. str. R-4001 AJ2891
EU528236.1 gg_id:283599 Seasonal Dynamics Mudflat Mouth Major Kentucky Lake Reservoir Tributary sedime EU5282
AJ493583.1 gg_id:89552 Cellvibrio ostraviensis str. LMG 19434 AJ4935
GQ263640.1 gg_id:576714 Structure Simulated Level Waste Site simulated level waste site clone FW3_27C GQ263
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AM935949.1 gg_id:537030 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM935
AB186843.1 gg_id:103183 polychlorinated dioxin dechlorinating microcosm clone TSBX24 AB1868
EF648042.1 gg_id:257504 dynamics during produced water treatment aerobic activated sludge clone HB32 EF6480
EF420207.1 gg_id:213653 Mature fine processing harbour methanogenic oil sands tailings pond clone MLSB_30 EF4202
EU735695.1 gg_id:316525 archaeal structures oil contaminated and soils China pristine soil Jidong Oilfield clone EU7356
FM242423.1 gg_id:331444 sequences sediment clone 66 T12d-oil FM242
AM935832.1 gg_id:535164 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM935
AM935433.1 gg_id:532686 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM935
AY033301.1 gg_id:68989 marine bacterioplankton clone MB11B11 AY0333
EU005741.1 gg_id:277139 Major activity inside and outside natural iron-fertilized phytoplankton bloom 3 micro EU0057
EU544831.1 gg_id:267517 free-living particle- aggregate- archaeal and Laptev Sea 1.0-60 um size fraction (susp EU5448
AY697919.1 gg_id:103045 Antarctica clone F4C67 AY6979
GU230303.1 gg_id:585217 Multilevel approach along Rio de la Plata-South Atlantic Ocean coastal water clone A GU230
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EU874388.1 gg_id:321327 Marinimicrobium sp. str. ISL-43 EU8743

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GQ200189.1 gg_id:548606 Marinobacter hydrocarbonoclasticus str. DQHS-3 GQ200
FJ984522.1 gg_id:382828 Marinobacter hydrocarbonoclasticus str. NBSL04 FJ9845
NR_028841.1 gg_id:565301 Marinobacter litoralis str. SW-45; JCM 11547 NR_02
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DQ530479.1 gg_id:168080 Marinobacter sp. str. gap-e-81 DQ530
DQ521387.1 gg_id:164240 Marinobacter sp. str. ice-oil-325 DQ521
EF368018.1 gg_id:208660 Marinobacter taiwanensis str. 1645 EF368
AB513677.1 gg_id:582394 Marinobacter sp. str. PAD-2 AB513
GU183677.1 gg_id:548886 Marinobacter alkaliphilus str. H1711 GU183
EU603452.1 gg_id:275327 Marinobacter bryozoorum str. PTG4-16 EU603
FJ675262.1 gg_id:517038 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6752
DQ325514.1 gg_id:149482 Marinobacter koreensis str. DD-M3 DQ325
NR_025116.1 gg_id:573563 Marinobacter lutaoensis str. T5054; CCRC 17087; JCM 11179 NR_02
FJ675204.1 gg_id:528351 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6752
FJ675118.1 gg_id:527584 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6751
AY592402.1 gg_id:103215 deep-sea mud volcano clone Amsterdam-2B-44; BC20-2B-44 AY592
GQ131626.2 gg_id:581833 Marinobacter sp. str. YCSA7 GQ131
FJ674834.1 gg_id:518091 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6748
FJ746583.1 gg_id:547174 Marinobacter sp. str. H184B35 FJ7465
EF660754.1 gg_id:240909 Marinobacter goseongensis str. En6 EF6607
AB305311.1 gg_id:234441 Marinobacter sp. str. IW11-2CT AB305
EF667989.1 gg_id:244324 and biogeochemical influences active heterotrophic prokaryotes off Palmer Peninsul EF6679
FJ425903.1 gg_id:590148 Marinobacter zhanjiangensis str. JSM 078120 FJ4259
U14584.1 gg_id:8799 gas vacuolate str. S36-W<gv>1 U1458
AF468259.1 gg_id:80533 Arctic pack ice; northern Fram Strait; 80 31.1 N; 01 deg 59.7 min E clone ARKDMS-57 AF468
EU287196.1 gg_id:246628 Pacific arctic surface sediment clone S11-13 EU287
EU328041.1 gg_id:277828 dynamics during bioremediation crude oil contaminated moderate saline soil clone B EU328
AY180101.1 gg_id:78569 Marinobacter excellens str. KMM 3809 AY180
FJ196021.1 gg_id:351303 Marinobacter sp. str. ZS3-32 FJ1960
DQ015835.1 gg_id:139700 Antarctic lake water clone ELB19-223 DQ015
AM503093.1 gg_id:311877 Marinobacter guineae str. LMG 24048 = M3B AM503
AJ292527.1 gg_id:37115 Marinobacter sp. Trimyema-1 1 AJ2925
AJ439500.1 gg_id:59259 Marinobacter squalenivorans str. 2Asq64 AJ4395
GU223379.1 gg_id:557645 Marinobacter sp. str. EM492 GU223

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EU328057.1 gg_id:278624 dynamics during bioremediation crude oil contaminated moderate saline soil clone Y EU328
AJ871937.1 gg_id:163334 hydrocarbonoclastic Guanabara Bay Brazil mangrove sediments AJ8719
AB252057.1 gg_id:170550 Brassica napus str. SKA S2 AB252
EU440995.1 gg_id:340108 Marinobacter flavimaris str. 2PR54-4 EU440
EU293413.1 gg_id:242328 Marinobacter sp. str. cn74 EU293
NR_025799.1 gg_id:549391 Marinobacter flavimaris str. SW-145; KCTC 12185 NR_02
AB026946.1 gg_id:8806 Marinobacter sp. str. NK-1 AB026
FJ675374.1 gg_id:528098 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6753
FJ675429.1 gg_id:526155 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6754
NR_025671.1 gg_id:557510 Marinobacter lipolyticus str. SM-19; DSM 15157 NR_02
U85863.1 gg_id:8800 Marinobacter sp. str. IC022 U8586
EF428127.1 gg_id:277000 Marinobacter excellens str. LL406 EF4281
AF237685.1 gg_id:21327 Marinobacter sp AF237
FJ348439.1 gg_id:565377 Investigation microbial soil method saltern 15 cm be surface clone DGGE gel band ntu FJ3484
DQ097521.1 gg_id:129808 Marinobacter giovannonii str. IS17 DQ097
DQ530455.1 gg_id:170366 Marinobacter sp. str. gap-d-2 DQ530
EU718223.1 gg_id:337093 Microbial farmed prawn preservation methods Marinobacter clone HL13 EU718
EF632877.1 gg_id:238588 Unique microbial contrasting aquatic altitude Andean Altiplano (northern Chile) wate EF6328
DQ097526.1 gg_id:131161 Marinobacter koreensis str. KGB22 DQ097
NR_029028.1 gg_id:592275 Marinobacter sediminum str. R65; KMM 3657 NR_02
AY690675.1 gg_id:99388 Marinobacter sp. str. GC101 AY690
FJ973518.1 gg_id:454067 Marinobacter alkaliphilus str. NBSL07 FJ9735
FJ674980.1 gg_id:511539 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6749
AF173969.1 gg_id:21222 Marinobacter aquaeolei str. KT02ds19 AF173
EU440994.1 gg_id:353090 Marinobacter alkaliphilus str. 2PR56-13 EU440
GU223374.1 gg_id:554900 Marinobacter sp. str. EM491 GU223
EU196317.1 gg_id:255215 Marinobacter sp. NP38 EU196
EU907917.1 gg_id:326599 Marinobacter sp. str. SKUK MB1002 EU907
FJ897726.1 gg_id:547256 Marinobacter sp. str. Set74 FJ8977
DQ235263.1 gg_id:144953 Marinobacter vinulentus str. FB1 DQ235
GU370116.1 gg_id:517692 Marinobacter hydrocarbonoclasticus str. P721(1) GU370
AB166970.1 gg_id:104848 Marinobacter sp. str. NT N14 AB166
AJ557854.1 gg_id:84236 Arctic deep sea Isolation common chemoorganotrophic oxygen-respiring polar current AJ5578
EU432582.1 gg_id:262300 Marinobacter sp. str. 10050 EU432
FJ497670.1 gg_id:509005 Marinobacter sp. str. VS-43 FJ4976
AM990796.1 gg_id:278977 Marinobacter sp. MOLA 20 AM990
EU164778.1 gg_id:250476 Marinobacter szutsaonensis str. Halo30-39 EU164
AY771710.1 gg_id:108686 Marinobacter lipolyticus str. S2-44 AY7717
AB304799.1 gg_id:255218 Microbulbifer agarolyticus str. JAMM 0654 AB304
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AB167354.2 gg_id:108039 Pelagiobacter variabilis str. Ni2088 AB1673
AJ510266.1 gg_id:69355 Microbulbifer arenaceous str. RSBr-1 AJ5102
GQ262812.1 gg_id:558634 Microbulbifer sp. str. Y215 GQ262
FJ169190.1 gg_id:338941 microbial and polyketide biosynthetic potential palmerolide-producing tunicate Synoi FJ1691
AB500893.1 gg_id:555088 Microbulbifer sp. str. ABABA 23 AB5008
EF486352.1 gg_id:222510 Microbulbifer celer str. ISL-39 EF4863
DQ340189.1 gg_id:147845 Dominance Mycoplasma guts Long-Jawed Mudsucker Gillichthys mirabilis five Califo DQ340
EF674853.1 gg_id:257184 Microbulbifer halotolerans str. YIM 91118 EF6748
AY224196.1 gg_id:81821 Microbulbifer sp. str. Th/B/38 AY2241
AF479688.1 gg_id:51065 Microbulbifer salipaludis str. SM-1 AF4796
AM180745.1 gg_id:145463 Pseudomonas sp. UC14a AM180
AB500894.1 gg_id:573761 Microbulbifer sp. str. ABABA 212 AB5008
AB052969.1 gg_id:24308 Pseudomonas sp. PE2 AB0529
AY862188.1 gg_id:111195 Microbulbifer sp. str. MY05 AY8621
AB456139.1 gg_id:551285 Microorganisms involved anaerobic phenol degradation treatment synthetic coke-o\ AB4561
EU491487.1 gg_id:263181 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X4 clone EU4914
DQ334644.1 gg_id:194566 Impact metals on sediments heavy metal polluted marine sediment clone HB2-9-21 DQ334
AB456140.1 gg_id:572166 Microorganisms involved anaerobic phenol degradation treatment synthetic coke-o\ AB4561
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NC_007912.1 gg_id:153124 Saccharophagus degradans str. 2-40 NC_00
GQ872422.1 gg_id:569907 Simiduia sp. str. M2-5 GQ872
EF617350.1 gg_id:234841 Simidua agarivorans str. SA1 EF6173
FJ202639.1 gg_id:341703 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2026
FJ356668.1 gg_id:541691 Intra- Microheterogeneity Multiple Displacement Single-cells Marine Cyanobacteria L FJ3566
EF092194.1 gg_id:269778 Persistent Axinella corrugata clone Ax29_A1 EF0921
FJ203003.1 gg_id:317569 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2030
GU391220.1 gg_id:530532 Spongiibacter sp. str. JYr4 GU391
NR_027564.1 gg_id:565759 Teredinibacter turnerae T7901 str. T7902; ATCC 39867 NR_02
DQ269073.1 gg_id:198202 marine macro-alga surface clone DPC012 DQ269
DQ272313.1 gg_id:141068 Lyrodus pedicellatus symbiont RT18 DQ272
EF061962.1 gg_id:194319 Xiamen China mangrove sediment clone XME54 EF0619
AB467280.1 gg_id:534461 Umboniibacter marinipuniceus str. KMM 3892 AB4672
EU236385.1 gg_id:298139 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg92A4 EU2363
GQ920839.1 gg_id:550044 Marinimicrobium sp. str. SX15 GQ920
AY845232.1 gg_id:110380 sponge clone 34P38 AY8452
EU050817.1 gg_id:237439 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_05_77 EU0508
AY375151.1 gg_id:96709 deep sea sediment clone D78 AY3751
EU799127.1 gg_id:348578 It's all ranking aquatic Newport Harbour RI clone 1C226690 EU7991
FJ628337.1 gg_id:555614 transition and zone within near-shore basin: brackish water anoxic fjord Nitinat Lake (FJ6283
EU286983.1 gg_id:256729 Pacific arctic surface sediment clone B78-19 EU2869

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FJ347758.1 gg_id:370251 Endozoicomonas sp. str. CL-33 FJ3477
AM259915.1 gg_id:252743 Chondrilla nucula-specific sponge mesohyl clone CN34 AM259
AY700601.1 gg_id:109430 Australia: Great Barrier Reef clone PDA-OTU3 AY7006
AB205011.1 gg_id:113799 Spongiobacter nickelotolerans str. 00P-Ni033-1-1-2 AB2050
AM990755.1 gg_id:277802 Culturable along NW Mediterranean coast Petrosia ficiformis sponge AM990
FJ202634.1 gg_id:354436 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2026
EF516073.1 gg_id:223694 grassland soil clone FCPT525 EF5160
EU464803.1 gg_id:287677 Hartmann's mountain zebra feces clone AFZEB_aaj71b02 EU4648
EU104099.1 gg_id:351662 Evidence Comamonadaceae determinants settling performance activated sludge clo EU1040
EU464733.1 gg_id:301670 Hartmann's mountain zebra feces clone AFZEB_aaj69h03 EU4647
EU464904.1 gg_id:301529 Hartmann's mountain zebra feces clone AFZEB_aaj72h05 EU4649
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EU464879.1 gg_id:298205 Hartmann's mountain zebra feces clone AFZEB_aaj72d02 EU4648
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EU464760.1 gg_id:291795 Hartmann's mountain zebra feces clone AFZEB_aaj70c11 EU4647
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EU104152.1 gg_id:319880 Evidence Comamonadaceae determinants settling performance activated sludge clo EU1041
DQ824679.1 gg_id:181704 human fecal clone RL185_aaj71e11 DQ824
CU466815.1 gg_id:307591 Evry wastewater treatment plant anoxic basin clone CU4668
AF195410.1 gg_id:24515 Hahella chejuensis str. KCTC 2396 AF1954
EF495227.1 gg_id:217600 Hahella antarctica str. IMCC3113 EF4952
AY676463.1 gg_id:107320 Hahella ganghwensis str. FR1050 AY6764
AY130995.1 gg_id:70229 Zooshikella ganghwensis str. JC2045 AY1309
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AF400467.1 gg_id:46892 Primary endosymbiont Bemisia tabaci clone UG26 aleyrodidarum AF4004
Z11927.1 gg_id:8122 symbiont of Siphoninus phillyreae (ash whitefly) Z11927
AY266108.1 gg_id:99204 Neomaskellia andropogonis symbiont AY2661
AF286123.1 gg_id:51913 symbiont AF2861
AY266098.1 gg_id:103124 Aleuroparadoxus arctostaphylli symbiont AY2660
AF400469.1 gg_id:54022 Primary endosymbiont Bemisia tabaci clone UG25 AF4004
AY268081.1 gg_id:88180 Bemisia tabaci symbiont AY2680
AY266100.1 gg_id:106952 Aleuroplatus sp. symbiont AY2661
AY266107.1 gg_id:99043 Dialeurodes hongkongensis symbiont AY2661
AY266096.1 gg_id:102829 Aleurodicus dispersus symbiont AY2660
AY266095.1 gg_id:102674 symbiont AY2660
AF400462.1 gg_id:19222 Primary endosymbiont Bemisia tabaci clone MEX4 aleyrodidarum AF4004
DQ396070.1 gg_id:154863 deep-sea octacoral clone ctg_NISA053 DQ396
EU799800.1 gg_id:326262 It's all ranking aquatic Newport Harbour RI clone 1C227454 EU7998

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FJ826408.1 gg_id:510568 Succession during spring diatom bloom Sea filtered surface sea water contrasting nor FJ8264
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EU005838.1 gg_id:276035 Major activity inside and outside natural iron-fertilized phytoplankton bloom 3 micro EU005
AY033317.1 gg_id:55020 marine bacterioplankton clone MB12G11 AY033
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EU035854.2 gg_id:306650 Insight microbial structure Norwegian deep-water water deep-sea coral reef off Nor EU035
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GU119483.1 gg_id:592804 Threatened Corals Provide Microbial Habitats reef water clone Reef_M13 GU119
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AF211861.1 gg_id:43878 Chromohalobacter canadensis str. DSM6769 AF2118
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DQ789389.1 gg_id:163006 Chromohalobacter salexigens str. NJ2 DQ789
AM941743.1 gg_id:273506 Halomonas elongata str. ATCC 33173 AM941
EU652046.1 gg_id:276670 Chromohalobacter salexigens str. aa-27 EU6520
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AF211862.1 gg_id:43545 Chromohalobacter israelensis str. DSM6768 AF2118
AJ295146.1 gg_id:48786 Halomonas elongata str. DSM 3043 AJ2951
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AM110928.1 gg_id:140457 Bacillus subtilis B-1064 AM110
DQ270696.1 gg_id:142624 Halomonas sp. B-3020 DQ270
AJ427626.1 gg_id:42325 Chromohalobacter salinarum str. CG 4.1 AJ4276
DQ270679.1 gg_id:144129 Halomonas sp. B-1092 DQ270
EU937754.1 gg_id:324906 Haererehalobacter sp. str. JG 11 Iti 10 EU937
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EU175892.1 gg_id:261928 Drop-size lakes: transient microbial habitats soda lake on salt-secreting desert tree c EU1758
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X92137.1 gg_id:43696 Lake Magadi isolate 27M1 X92137
EF613111.1 gg_id:227593 Halomonas cerina str. 15CR EF6131
X67023.1 gg_id:8158 Halomonas elongata str. ATCC 33173 X67023
EU085034.1 gg_id:239476 Halomonas korla str. XK2 EU085
AJ320530.1 gg_id:70784 Halomonas muralis str. LMG 20969 AJ3205
AY962237.1 gg_id:115026 Halomonas sp. str. AIR-2 AY9622
AM490137.1 gg_id:203039 Halomonas sp. str. IB-O7-1 AM490
E15669.1 gg_id:46054 Deleya sp. ASE1315 E15669
X92144.1 gg_id:42889 Lake Nakuru isolate 28N1 X92144
X92147.1 gg_id:44380 Lake Elmenteita isolate 35E2 X92147
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DQ289069.1 gg_id:142310 Halomonas nitritophilus WST 6 DQ289
DQ289070.1 gg_id:143579 Halomonas nitritophilus WST 7 DQ289
X92146.1 gg_id:22591 Crater Lake isolate 75C4 X92146
X92417.1 gg_id:8131 Halomonas desiderata str. FB2 X92417
EF121854.1 gg_id:196601 Halomonas daqingensis str. DQD2-30T EF1218
X92149.1 gg_id:35481 Lake Nakuru isolate 19N1 X92149
L04942.1 gg_id:8170 Halomonas halodenitrificans L04942
AY121436.1 gg_id:63144 Halomonas sp. str. YIM-kkny11 AY1214
EF101990.1 gg_id:252290 Halomonas sp. EEZMo-14 EF1019
EU135707.1 gg_id:242748 Halomonas sp. str. YIM C248 EU1357
EU308354.1 gg_id:360286 Halomonas sp. str. SB136_1 EU3083
DQ642806.1 gg_id:159766 Halomonas sp. 3 DQ642
EU432570.1 gg_id:264242 Halomonas sp. str. 10112 EU4325
EU218533.1 gg_id:239013 Halomonas ilicicola str. SP8 EU2185
AJ564880.1 gg_id:100009 Halomonas alkantarctica str. CRSS AJ5648
EF554912.1 gg_id:219933 Halomonas sp. str. G-AMM1 EF5549
EU848479.1 gg_id:305095 Halomonas sp. str. SP1-3 EU8484
AF539764.1 gg_id:86698 Halomonas sp. str. R21 AF5397
AY204638.1 gg_id:81690 Halomonas variabilis str. HTG7 AY2046
FJ978734.1 gg_id:466034 feces clone CL_F_436 FJ9787
EF421176.1 gg_id:277105 Halomonas sp. ZB-2007 EF4211
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FJ153012.1 gg_id:328530 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX4CI FJ1530
U85873.1 gg_id:8145 Halomonas variabilis str. SW48 U85873
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EU432575.1 gg_id:259254 Halomonas sp. str. 10043 EU4325
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AF054286.1 gg_id:8133 Halomonas campisalis str. ATCC 700597 4A AF0542
GU001898.1 gg_id:589958 Halomonas shengliensis str. PL16 GU001
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AF173968.1 gg_id:71016 Halomonas variabilis str. KT1111 AF1739
FJ796247.1 gg_id:555230 Halomonas sp. str. JS46 FJ7962
EU822512.1 gg_id:317124 Halomonas xinjiangensis str. TRM 0175 EU8225
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NR_027219.1 gg_id:571751 Halomonas axialensis str. Althf1; ATCC BAA-802 NR_027
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AM110934.1 gg_id:139678 Bacillus subtilis B-1190 AM110
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AJ294348.1 gg_id:75905 Halomonas variabilis HY-61 AJ2943
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AJ876735.1 gg_id:157900 Halomonas sp. PH1226 AJ8767
EU308357.1 gg_id:363386 Halomonas sp. str. TB1612 EU3083
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DQ072719.1 gg_id:134569 Halospina denitrificans str. HGD 1-3 DQ072
D14555.1 gg_id:8114 Zymobacter palmae str. T109 D1455
AB021383.1 gg_id:8811 Pseudomonas halophila str. DSM 3050T AB021
EU305727.1 gg_id:340031 Pseudomonas sp. str. TBZ33 EU305
AY987840.1 gg_id:128215 Microbial Salterns Maras salterns clone 2B4 AY987
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EU308410.1 gg_id:368617 Halomonas sp. str. TB21_12 EU308
DQ641495.1 gg_id:215031 Chromohalobacter tunisiensis str. Lit 2 DQ641
GQ246216.1 gg_id:578822 Kushneria sp. str. YCWA18 GQ246
FJ463811.1 gg_id:580770 Chromohalobacter sp. str. ST307 FJ4638
FJ444986.1 gg_id:554249 Halomonas taeanensis str. whb40 FJ4449
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DQ421388.1 gg_id:156429 Halotalea alkalilenta str. AW-7 DQ421
EU487856.1 gg_id:568866 lucinid bivalve- symbiotic system: significance geochemical habitat on and gill symbi EU487
EU487858.1 gg_id:570303 lucinid bivalve- symbiotic system: significance geochemical habitat on and gill symbi EU487
EF508132.1 gg_id:241778 evidence unusual symbiont gills Acesta excavata bivalve gill specimen Ae1 320 m dep EF5081
AB054156.1 gg_id:48284 marine sponge clone HOC22 AB054
AB054159.1 gg_id:35099 marine sponge clone HOC25 AB054
FJ999614.1 gg_id:420931 sponge Haliclona simulans South China Sea clone B96 FJ9996
EF379881.1 gg_id:216695 sea water Victoria Harbor (Hong Kong) area clone PC-FL10-68 EF3798
EU799754.1 gg_id:306969 It's all ranking aquatic Newport Harbour RI clone 1C227399 EU799
AM259847.1 gg_id:210420 Spatial sponge- Mediterranean Tethya aurantium sponge cortex clone TAA-10-33 AM259
AY907757.1 gg_id:137084 identification picoplankton contrasting waters Arabian Sea water clone A314008 AY907
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DQ513029.1 gg_id:161219 Microbial life fluids ridge flank crustal fluid clone FS142-29B-02 DQ513
EU287155.1 gg_id:243868 Pacific arctic surface sediment clone P13-62 EU287
EF572288.1 gg_id:228537 Coco's Island site 23 marine clone S23_387 EF5722
DQ289914.1 gg_id:167947 Microbial Carbon and Nitrogen Cycling Sediments South Atlantic Bight Permeable Sh DQ289
EU979089.1 gg_id:329740 Effects intercropping Rhizobium inoculation on microbial biomass and rhizosphere b EU979
EF574537.1 gg_id:239885 site S25 near Coco's Island marine clone S25_881 EF5745
AM259920.1 gg_id:237509 Chondrilla nucula-specific sponge mesohyl clone CN46 AM259
AY386332.1 gg_id:98593 marine str. HTCC2089 AY3863
EF061958.1 gg_id:181469 Xiamen China mangrove sediment clone XME25 EF0619

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EU887784.1 gg_id:317155 and RFLP anaerobes Nisargruna biogas plant anaerobic digester clone 21IISN EU887
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DQ354722.1 gg_id:152853 subsurface water clone DR550SWSAEE23 DQ354
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DQ351750.1 gg_id:146687 Microbial Adherent Sediment Particles Heavy Metal Contaminated North Sea Surfac DQ351
EF157250.1 gg_id:235311 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon EF1572
AY344367.2 gg_id:91272 Lake Kauhako 30 m clone K2-30-25 AY3443
GU061024.1 gg_id:543804 Evaluation culturing methods cultivate previously Yel Sea intertidal beach clone SF2! GU061
GQ337269.1 gg_id:532913 Hydrography shapes biogeography deep Arctic Ocean water depth 428m clone CB18 GQ337
GQ349203.1 gg_id:544164 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ349
FM242421.1 gg_id:315848 sequences sediment clone 18 T12d-oil FM242
EU265950.1 gg_id:536666 transition and zone within near-shore anoxic basin: Nitinat Lake depth 20 m clone Ni EU2659
EU801454.1 gg_id:316013 It's all ranking aquatic Chesapeake Bay MD clone 3C002749 EU8014
AB262385.1 gg_id:160146 Microbial Ishigaki-jima Island Japan sea water Ishigaki Port clone IG-1-25 AB2623
GQ259231.1 gg_id:514087 Microbial activities coastal marine sediments and column Svalbard deep water clone GQ259
EU592358.1 gg_id:583231 Seasonal changes Salton Sea hypersaline water clone SSW83Ap EU5923
EU050827.1 gg_id:246352 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_06_91 EU0508
EU491768.1 gg_id:263897 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU4917
EU799676.1 gg_id:306629 It's all ranking aquatic Newport Harbour RI clone 1C227304 EU7996
GQ349449.1 gg_id:588121 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ349
AY907800.1 gg_id:137086 identification picoplankton contrasting waters Arabian Sea water clone A714013 AY9078
EU803061.1 gg_id:332281 It's all ranking aquatic Northeast Colon Panama clone 4C230470 EU8030
AY942761.1 gg_id:145162 but species richness marine sponge Cymbastela concentrica clone Cc044 AY9427
EU544859.1 gg_id:264271 free-living particle- aggregate- archaeal and Laptev Sea >60 um size fraction (aggreg EU5448
EU799735.1 gg_id:324875 It's all ranking aquatic Newport Harbour RI clone 1C227378 EU7997
AB526337.1 gg_id:546239 Spongiibacter sp. str. JAM-GA14 AB5263
AM990674.1 gg_id:278054 culturable oligotrophic ocean (South Pacific Gyre) sea water AM990
FJ889619.1 gg_id:559242 Melitea sp. str. ZS5-23 FJ8896
EF176580.1 gg_id:181920 Litincola lipolitica str. IMCC1097 EF1765
FJ745130.1 gg_id:565326 Transporter genes expressed coastal response dissolved organic carbon surface wate FJ7451
EU652550.1 gg_id:278194 Seasonal variation microbial Yel Sea sediment clone A8S-109 EU6525
AM930471.1 gg_id:275885 involved Tripneustes gratilla (Echinoidea) cloning and FISH host body wall lesions clc AM930
AB006765.1 gg_id:8206 Marinobacterium jannaschii str. IFO15466 AB0067
FN556570.1 gg_id:514502 Marinobacterium sp. str. JW3.2b FN5565
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AY563030.1 gg_id:100162 Marinobacterium halophilum str. Mano11 AY5630
AJ843079.1 gg_id:114569 Marinomonas aquimarina str. 11OM3 = CECT 5078 AJ8430
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NR_028636.1 gg_id:582426 Marinomonas primoryensis str. KMM 3633 NR_02
DQ403809.1 gg_id:150764 Marinomonas blandensis str. MED 121 DQ403
EU195937.1 gg_id:248961 Marinomonas sp. str. P111 EU195
AJ238597.1 gg_id:8210 Marinomonas protea AJ2385
EU722311.1 gg_id:354249 Marinomonas sp. str. S3-34 EU722
EF382680.1 gg_id:209816 Marinomonas sp. BSi20579 str. Bsi20579 EF3826
DQ311094.1 gg_id:144989 Marinomonas sp. str. NJ548 DQ311
DQ517862.1 gg_id:160848 Marinomonas sp. str. BSi20385 DQ517
AB074194.1 gg_id:52278 Marinomonas primoryensis str. KMM 3634 AB074
DQ421580.2 gg_id:208776 Salt Marsh Prokaryotes salt marsh clone SIMO-4215 DQ421
AJ627909.1 gg_id:103719 Marinomonas ushuaiensis str. U1 AJ6279
AY539835.1 gg_id:101289 Marinomonas pontica str. 46-16 AY5398
DQ011528.1 gg_id:120729 Marinomonas communis str. LMG 2864 DQ011
DQ923437.1 gg_id:174575 Marinomonas sp. W-3 DQ923
AB242868.1 gg_id:142302 Marinomonas sanya str. F128 AB2428
AY730245.1 gg_id:101261 Marinomonas sp. M6-20A AY730
AF321017.2 gg_id:30213 Marinomonas sp. GOBB3-320 AF321
EU188447.1 gg_id:362695 Marinomonas sp. str. IVIA-Po-159 EU188
AJ717294.1 gg_id:105555 Marinomonas sp. str. BJK13 AJ7172
NR_029228.1 gg_id:554750 Marinomonas vaga str. 40; ATCC 27119 NR_02
DQ676859.1 gg_id:172752 Marinomonas sp. str. ASs2032 DQ676
DQ007439.1 gg_id:124798 Marinomonas sp. str. BSi20101 DQ007
EU427306.1 gg_id:274342 Marinomonas sp. MSI03 EU427
EU188443.1 gg_id:359821 Marinomonas sp. str. IVIA-Po-145 EU188
EU188441.1 gg_id:362238 Marinomonas sp. str. IVIA-Po-185 EU188
DQ520888.1 gg_id:161293 Marinomonas sp. str. BSi20461 DQ520
DQ517876.1 gg_id:160773 Marinomonas sp. str. BSi20548 DQ517
DQ537501.1 gg_id:160057 Marinomonas sp. str. BSi20388 DQ537
AB098513.1 gg_id:75039 Marinospirillum insulare str. NB11 AB098
AB006769.1 gg_id:8111 Marinospirillum minutulum str. ATCC19193 AB006
AB006770.1 gg_id:8112 Marinospirillum megaterium AB006
AB291228.1 gg_id:246798 Neptunomonas japonica str. JAMM 1610 AB291
FJ889618.1 gg_id:544882 Neptunomonas sp. str. NF4-29 FJ8896
AB288092.1 gg_id:239047 Neptunomonas japonica str. JAMM 0745 AB288
AF053734.1 gg_id:8190 Neptunomonas naphthovorans str. NAG-2N-126 AF053
FJ764762.1 gg_id:570916 Nitrincola sp. str. E-048 FJ7647
FJ973520.1 gg_id:440184 Nitrincola lacisaponensis str. NBSL11 FJ9735
AB006763.1 gg_id:8178 Oceanospirillum maris subsp. williamsae str. IFO15468 AB006
AB006764.1 gg_id:8176 Oceanospirillum multiglobuliferum str. IFO13614 AB006
AB006761.1 gg_id:8184 Oceanospirillum beijerinckii subsp. pelagicum str. IFO13612 AB006
FJ403091.1 gg_id:367944 Disease- changes healthy and diseased colonies Caribbean coral Montastrea faveolat FJ4030

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AB006767.1 gg_id:8201 Oceanobacter kriegii str. IFO15467 AB006
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DQ071156.1 gg_id:134464 marine surface water clone Surf1.32 DQ071
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EF648167.1 gg_id:254655 dynamics during produced water treatment aerobic activated sludge clone XJ137 EF6481
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EU980447.1 gg_id:326525 Oleispira sp. str. DFH11 EU980
EU236351.1 gg_id:298239 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg91A7 EU2363
EU050832.1 gg_id:244721 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_09_46 EU0508
AJ426421.1 gg_id:47332 Oleispira antarctica str. RB-9 AJ4264
AY577900.1 gg_id:105462 roots new deep sea polychaete (Osedax frankpressi gen n. sp. novum) clone BoneC3 AY5779
DQ906761.1 gg_id:161773 and marine microorganisms Antarctic sea ice lower 10 cm clone AntCL3E3 DQ906
EU050834.1 gg_id:236381 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_02_57 EU0508
GQ349742.1 gg_id:587033 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ349
AY697896.1 gg_id:101312 Antarctica clone F3C18 AY6978
AY922202.1 gg_id:114064 whalefall clone 131636 AY9222
GU391221.1 gg_id:516971 Thalassolituus sp. str. JYr12 GU391
EF468717.1 gg_id:221209 Marinobacterium marisflavum str. IMCC4074 EF4687
DQ206422.1 gg_id:140325 microbial mediates arsenate reduction soda lake water clone ML-S-4 DQ206
DQ279852.1 gg_id:142469 Marinomonas sp. str. Y5 DQ279
AY967730.1 gg_id:115234 Influence starvation ozone and selected isolates on survival southern Jasus edwardsi AY9677
FN377729.1 gg_id:593776 Marinobacterium sp. RS-21 FN3777
AY549003.2 gg_id:101658 marine bone clone sacC13A1 AY5490
EF379568.1 gg_id:206232 sea water Victoria Harbor (Hong Kong) area clone VH-PA5-10 EF3795
EF422409.1 gg_id:213472 Marinospirillum sp. str. ANL-isoa EF4224
GU291323.1 gg_id:589506 Anaerobic sulfide-oxidizing couple acidification and nitrogen cycling heavy metal we GU291
EU544727.1 gg_id:262299 free-living particle- aggregate- archaeal and Laptev Sea 0.22-1.0 um size fraction (fre EU5447
NR_024654.1 gg_id:541001 Pseudospirillum japonicum str. ATCC 19191 NR_024
FJ628206.1 gg_id:555032 transition and zone within near-shore basin: brackish water anoxic fjord Nitinat Lake FJ6282
FJ403057.1 gg_id:364908 Disease- changes healthy and diseased colonies Caribbean coral Montastrea faveolat FJ4030
AM747817.1 gg_id:311032 Oceaniserpentilla haliotidis AM747
AY136131.2 gg_id:155199 Oceanobacter sp. str. RED65 AY1361
FJ202960.1 gg_id:353341 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2029
GQ131677.1 gg_id:376032 Neptuniibacter sp. str. antisso-13 GQ131
AY549004.2 gg_id:101822 marine bone clone Osedax_sym1 AY5490
AY549002.2 gg_id:101490 marine bone clone sacC13A2 AY5490
AF140000.1 gg_id:8195 Oceanospirillum sp. str. ML-158 AF1400
AF140002.1 gg_id:27457 Oceanospirillum sp. str. ML-165 AF1400

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EF067915.1 gg_id:245142 endolithic microbes marine basalts aerobic enrichment s innoculated basalt Brown B EF0679
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GQ349823.1 gg_id:569636 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ349
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DQ123914.1 gg_id:154336 Oceanrickettsia ariakensis DQ123
DQ015830.1 gg_id:139543 Antarctic lake water clone ELB19-203 DQ015
GU061314.1 gg_id:578191 Evaluation culturing methods cultivate previously Yel Sea intertidal beach seawater GU061
FM242233.1 gg_id:333373 sequences sediment clone 26 T0h-oil FM242
FJ717225.1 gg_id:554141 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United King FJ7172
NR_025432.1 gg_id:537713 Oleiphilus messinensis str. ME102; DSM 13489 NR_02
EF067910.1 gg_id:251507 endolithic microbes marine basalts aerobic enrichment s innoculated basalt Brown B EF0679
AY007676.1 gg_id:26630 marine isolate NOR5 AY007
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AM882556.1 gg_id:337698 Structure along hydrocarbon contamination coastal sediment oil polluted water pet AM882
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EU161717.1 gg_id:255918 Haliea rubra str. CM41_15a EU161
EF632658.1 gg_id:236929 Unique microbial contrasting aquatic altitude Andean Altiplano (northern Chile) sedi EF6326
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AAVV01000015.1 gg_id:190442 marine str. HTCC2080 AAVV0
NZ_AAVT01000006.1 gg_id:189314 marine str. HTCC2143 NZ_AA
GU230327.1 gg_id:589757 Multilevel approach along Rio de la Plata-South Atlantic Ocean coastal water clone GU230
EU544810.1 gg_id:275233 free-living particle- aggregate- archaeal and Laptev Sea 1.0-60 um size fraction (sus EU5448
DQ009134.1 gg_id:126508 bacterioplankton clone SPOTSAPR01_5m162 DQ009
EU700144.1 gg_id:295036 Study on Shantou Bay Marine Sediments Microorganisms sediment clone STU2 EU700
AB015519.1 gg_id:8181 deep-sea sediment clone BD1-7 AB015
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EU491047.1 gg_id:265525 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount South Rift X EU491
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FN398053.1 gg_id:592957 Haliea sp. str. 7SM29 = CECT 7447 FN398
DQ513020.1 gg_id:159939 Microbial life fluids ridge flank crustal fluid clone FS142-64B-02 DQ513
EU544827.1 gg_id:277594 free-living particle- aggregate- archaeal and Laptev Sea 1.0-60 um size fraction (susp EU544
GQ348262.1 gg_id:563632 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ348
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EU652555.1 gg_id:279539 Seasonal variation microbial Yel Sea sediment clone D8S-18 EU652
EU236417.1 gg_id:302021 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg92F9 EU236
EF123465.1 gg_id:241462 Microbial disease microbial mats on Siderastrea siderea three regions wider Caribbea EF1234
GQ347825.1 gg_id:563082 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ347
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AM990941.1 gg_id:540228 along Egyptian Mediterranean coast mediterranean coastal waters 500 offshore 0.5 AM990
EF123461.1 gg_id:245864 Microbial disease microbial mats on Siderastrea siderea three regions wider Caribbea EF1234
EU287241.1 gg_id:246295 Pacific arctic surface sediment clone S11-58 EU287
EU544811.1 gg_id:265700 free-living particle- aggregate- archaeal and Laptev Sea 1.0-60 um size fraction (susp EU544
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EU544826.1 gg_id:273002 free-living particle- aggregate- archaeal and Laptev Sea 1.0-60 um size fraction (susp EU544
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AF468388.1 gg_id:80239 Arctic sea ice ARK10038 AF468
FJ905759.1 gg_id:510210 s Tonga-Kermadec iron oxide sediments Volcano 1 Tonga Arc clone V1F161b FJ9057
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EU491750.1 gg_id:272039 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU491
EU050825.1 gg_id:251646 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_07_55 EU050
AY386336.1 gg_id:96552 marine str. HTCC2223 AY386
EU010139.1 gg_id:235473 Biogeography Singapore seawaters seawater clone B24 EU010
DQ070803.1 gg_id:149537 Prokaryotic Structures Seafloor Basalts Varying Age and Juan de Fuca Ridge basalt gl DQ070
AB294961.1 gg_id:219188 -dependent & analyses hydrothermal system off Taketomi Island Japan microbial ma AB294
EU707310.1 gg_id:320148 sulfur oxidizing Wadden Sea sediments Janssand sediment -490cm clone JS9_43 EU707
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GQ347899.1 gg_id:555942 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ347
AM259790.1 gg_id:216671 Spatial sponge- Mediterranean Tethya aurantium sponge endosome clone TAI-8-20 AM259
EU491031.1 gg_id:271029 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount South Rift X EU491
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FJ205329.1 gg_id:544776 Prokaryotic deep-sea hydrothermal region East Lau Spreading Centre deep marine se FJ2053

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FJ203235.1 gg_id:320209 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c FJ2032
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AM997517.1 gg_id:563606 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A AM997
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EU544821.1 gg_id:259019 free-living particle- aggregate- archaeal and Laptev Sea 1.0-60 um size fraction (susp EU544
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AF452607.1 gg_id:55809 hypersaline Mono Lake clone ML310M-42 AF452
AF507823.1 gg_id:62733 Mono Lake at depth 17.5 m station 6 July 2000 clone ML617.5J-3 proteobacterium AF507
DQ403810.1 gg_id:154488 Reinekia blandensis str. MED 297 DQ403
AJ561121.1 gg_id:87543 Reinekea marinisedimentorum str. DSM 15388 AJ5611
GQ456131.1 gg_id:578010 Reinekea sp. IMCC4489 str. IMCC 4489 GQ456
GQ348323.1 gg_id:570256 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ348
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GQ441197.1 gg_id:532996 and dynamic mat present vs. active nitrogen-fixing microorganisms marine microbia GQ441
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GQ250189.1 gg_id:545665 Saccharospirillum sp. IMCC4453 str. IMCC 4453 GQ250
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AB193953.1 gg_id:108916 deep-sea vent clone Sd-EB02 AB193
AB499797.1 gg_id:573269 microbial hydrothermal vent and seep sponges-- thioautotrophic Japan:Sumisu Cald AB499
GQ345482.1 gg_id:590055 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ345
AB278146.1 gg_id:185252 hydrothermal vent prokaryotes trapped 0.2- and 0.1-micro-m-filtrates obtained Mar AB278
GQ346343.1 gg_id:550034 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ346
AB479080.1 gg_id:454474 Calyptogena nautilei symbiont AB479
EU403436.1 gg_id:275217 Calyptogena ponderosa endosymbiont 6 EU403
AB112462.1 gg_id:90596 Suiyo Seamount hydrothermal plume clone SUP05-30 AB112
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AM911378.2 gg_id:369008 Phenotype-specific (Scleractinia) their implications coral's nutrition health and cold- AM911
AY951931.1 gg_id:114761 Bathymodiolus azoricus thioautotrophic gill symbiont AY951

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GU117979.1 gg_id:581250 Threatened Corals Provide Microbial Habitats clone Acer_F12 GU117
EU491869.1 gg_id:267568 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU491
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EU050830.1 gg_id:255358 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_08_75 EU0508
AJ581349.1 gg_id:92209 Mediterranean sponge clone E01-9C-12 AJ5813
GQ337223.1 gg_id:591094 Hydrography shapes biogeography deep Arctic Ocean water depth 900m clone CB1 GQ337
EU800017.1 gg_id:313341 It's all ranking aquatic Newport Harbour RI clone 1C227703 EU800
FJ403058.1 gg_id:361395 Disease- changes healthy and diseased colonies Caribbean coral Montastrea faveolat FJ4030
EU005712.1 gg_id:264274 Major activity inside and outside natural iron-fertilized phytoplankton bloom 3 micro EU005
GU061256.1 gg_id:540813 Evaluation culturing methods cultivate previously Yel Sea intertidal beach seawater GU061
GQ349050.1 gg_id:557301 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ349
DQ015809.1 gg_id:140174 Antarctic lake water clone ELB16-104 DQ015
FM242300.1 gg_id:337520 sequences sediment clone 3 T9d-oil FM242
EU050829.1 gg_id:255625 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_07_49 EU0508
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DQ666548.1 gg_id:170688 Actinobacillus capsulatus str. 266/5603 DQ666
DQ229009.1 gg_id:160043 Haemophilus parasuis str. ME4 DQ229
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AF268962.1 gg_id:31672 Actinobacillus indolicus str. H1269 AF2689
EF396307.1 gg_id:246454 Actinobacillus indolicus WB52/06-1 EF3963
DQ229002.1 gg_id:160636 Actinobacillus pleuropneumoniae 262/04 DQ229
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EF173404.1 gg_id:213833 Actinobacillus porcitonsillarum str. WT2A EF1734
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AF015299.1 gg_id:9589 Actinobacillus suis str. CCM5586 AF0152
AY362900.1 gg_id:106038 Actinobacillus ureae str. CCUG 2139 AY3629
AJ295746.3 gg_id:52835 Haemophilus parahaemolyticus str. NCTC 8479T AJ2957
AY029174.1 gg_id:69899 Actinobacillus arthritidis str. 13/225/95 AY0291
AF268949.1 gg_id:73428 Actinobacillus minor str. H1473 AF2689
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AY465359.1 gg_id:109412 Actinobacillus equuli str. B96/12; JF2421 AY4653
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EF396305.1 gg_id:244335 Haemophilus parasuis WB25/06-1 EF3963

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AF145255.1 gg_id:9586 Actinobacillus capsulatus str. 63595 AF1452
EU746660.2 gg_id:347029 Actinobacillus minor str. 202 EU7466
AF359941.1 gg_id:21084 Acidithiobacillus thiooxidans str. KCTC 8928P AF3599
ACQL01000137.1 gg_id:384731 Actinobacillus minor str. NM305 ACQL0
AF224295.1 gg_id:73432 Actinobacillus capsulatus str. P796 AF2242
DQ926691.1 gg_id:180536 Actinobacillus porcitonsillarum str. 71123 DQ926
EF173412.1 gg_id:212302 Actinobacillus porcitonsillarum str. WT7N EF1734
DQ229007.1 gg_id:160015 Actinobacillus minor 2134 DQ229
AF381187.1 gg_id:70103 Actinobacillus cf. equuli str. CCUG 19799 AF3811
DQ926692.1 gg_id:191170 Actinobacillus porcitonsillarum str. 73706 DQ926
AF268948.1 gg_id:74197 Actinobacillus minor str. H1470 AF2689
AF247720.1 gg_id:58548 Actinobacillus equuli str. I5445/4 AF2477
GQ074426.1 gg_id:385551 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw162g GQ074
FJ435959.1 gg_id:367622 Actinobacillus minor str. 33PN FJ4359
AF247723.1 gg_id:70395 Actinobacillus lignieresii str. F 264 AF2477
AF247717.1 gg_id:58549 Actinobacillus arthritidis str. F 141 AF2477
AF224285.1 gg_id:72378 Actinobacillus capsulatus str. CCUG 37035 AF2242
AF268945.1 gg_id:27164 Actinobacillus minor str. H1284 AF2689
AF247722.1 gg_id:73342 Actinobacillus lignieresii str. F 127 AF2477
AB512009.1 gg_id:562676 Aggregatibacter actinomycetemcomitans str. OMZ534 AB5120
AB548673.1 gg_id:531143 Aggregatibacter actinomycetemcomitans str. JCM 12985 AB5486
CP001607.1 gg_id:518655 Aggregatibacter aphrophilus str. NJ8700 CP0016
AF227858.1 gg_id:49556 str. 86355 AF2278
AF224299.1 gg_id:17538 Haemophilus segnis str. MCCM 00337 AF2242
EU826042.1 gg_id:551715 Avibacterium sp. str. HP95 EU8260
AY498868.1 gg_id:104700 Haemophilus paragallinarum str. NCTC 11296T AY4988
AY498871.1 gg_id:99711 Haemophilus paragallinarum str. SA7177 AY4988
AY498870.1 gg_id:99555 Haemophilus paragallinarum str. Modesto AY4988
NC_006300.1 gg_id:471413 Mannheimia succiniciproducens str. MBEL55E NC_00
AY029193.1 gg_id:22261 Mannheimia succiniciproducens str. MBEL55E AY0291
DQ841185.1 gg_id:186374 Pasteurella trehalosi str. 06-106810 DQ841
AY757729.1 gg_id:111227 Pasteurellaceae I6 AY7577
AF227862.1 gg_id:31902 Pasteurella sp. str. 37234 AF2278
AY172730.1 gg_id:91205 Bisgaard taxon 32 str. 5108/S2/90 AY1727
AY172729.1 gg_id:91016 Bisgaard taxon 32 str. HPA106 AY1727
EU331064.1 gg_id:578335 Chelonobacter oris str. 1662 EU3310
EU331067.1 gg_id:590073 Chelonobacter oris str. 17123 EU3310
AY362926.1 gg_id:99165 Pasteurella testudinis str. CCUG 19802 AY3629
GQ423354.1 gg_id:563660 Gallibacterium anatis str. Yu-ZMD-XP-3-QG GQ423
GQ423350.1 gg_id:551687 Gallibacterium anatis str. Yu-ZMD-XP-1-QG-3 GQ423

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AY038594.1 gg_id:73007 Gallibacterium anatis str. Hom.3 AY0385
AF224310.1 gg_id:74034 Actinobacillus cf. salpingitidis CCUG 28018 salpingitidis AF2243
AY038591.1 gg_id:64296 Gallibacterium genomosp. 1 str. Gerl.3191 AY0385
EU339201.1 gg_id:571594 Gallibacterium genomosp. 3 str. F448 EU3392
EU339196.1 gg_id:534387 Gallibacterium melopsittaci str. F450 EU3391
EU423995.1 gg_id:569567 Gallibacterium trehalosifermentans str. B7/99/1 EU4239
FJ841971.3 gg_id:542079 Gallibacterium anatis str. Yu-JZ-YQ-5-SLG FJ8419
NC_002940.2 gg_id:129218 Haemophilus ducreyi str. 35000HP NC_00
EU185475.1 gg_id:239174 Haemophilus haemolyticus str. D62.2 EU1854
EU185365.1 gg_id:248286 Haemophilus haemolyticus str. 24P12H3 EU1853
EU185437.1 gg_id:253598 Haemophilus haemolyticus str. 61224 EU1854
EU185346.1 gg_id:243151 Haemophilus haemolyticus str. 14P38 EU1853
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EU185436.1 gg_id:243777 Haemophilus haemolyticus str. 60P12H2 EU1854
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EU185473.1 gg_id:252539 Haemophilus influenzae str. D152.1 EU1854
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GQ106447.1 gg_id:375695 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw! GQ106
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EF511057.1 gg_id:224454 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aerug EF5110
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DQ228991.1 gg_id:160451 Haemophilus parasuis VS7-1 DQ228

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AB370297.1 gg_id:271851 Haemophilus parasuis str. 332 AB370
FJ667952.1 gg_id:540531 Haemophilus parasuis str. Nagasaki FJ6679
DQ229016.1 gg_id:161508 Haemophilus parasuis RW DQ229
FJ667979.1 gg_id:513849 Haemophilus parasuis str. NO145 FJ6679
EU909653.1 gg_id:354221 Haemophilus sp. str. CCUG 17210 EU909
FJ558112.1 gg_id:526872 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5581
FJ667959.1 gg_id:560868 Haemophilus parasuis str. HS1075 FJ6679
EU185432.1 gg_id:245942 Haemophilus haemolyticus str. 58122 EU185
GQ091882.1 gg_id:376235 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ091
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AB078972.1 gg_id:30824 Haemophilus parasuis 312 AB078
EU185439.1 gg_id:239937 Haemophilus haemolyticus str. 654210 EU185
FJ558093.1 gg_id:517548 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5580
FJ983093.1 gg_id:414943 Aspects Oral Microbiome subgingival plaque clone FJ9830
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GQ114305.1 gg_id:423130 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw59 GQ114
GQ074383.1 gg_id:392625 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw162c GQ074
GQ116263.1 gg_id:457345 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw690c02 GQ116
GQ091843.1 gg_id:409269 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ091
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EU185461.1 gg_id:235553 Haemophilus haemolyticus str. 93P10H4 EU185
X87978.1 gg_id:9509 Haemophilus influenzae str. 16N X87978
AY362910.1 gg_id:102232 Haemophilus parasuis str. Bakos B26 AY362
AY005033.1 gg_id:72532 subgingival dental plaque clone BJ095 AY005
GQ083015.1 gg_id:429541 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ083
DQ228998.1 gg_id:160846 Haemophilus parasuis P015/96 DQ228
EU909656.1 gg_id:340606 Haemophilus sp. str. CCUG 18082 EU909
AJ290754.2 gg_id:44396 Haemophilus parainfluenzae str. P1525 AJ2907
EU137565.1 gg_id:261499 Bartonella-positive fleas: and assembly patterns Oropsylla hirsuta (prairie dog flea) C EU137
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EU909680.1 gg_id:307019 Haemophilus sp. str. PN24 EU909
AB176910.1 gg_id:114966 Histophilus somni str. 129Pt AB176
AF053901.1 gg_id:9609 Mannheimia granulomatis str. Ph13; CCUG 26828 AF053
DQ301924.2 gg_id:146654 Mannheimia granulomatis str. W4672/1 DQ301
AF053896.1 gg_id:9605 Mannheimia ruminalis str. HPA98; CCUG38466 AF053
AY425286.1 gg_id:107110 Mannheimia ruminalis str. HPA109 AY425
AY425283.1 gg_id:106648 Mannheimia ruminalis str. HPA113 AY425

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DQ301927.2 gg_id:148422 Mannheimia varigena str. H39 DQ301
U57069.1 gg_id:9606 Mannheimia haemolytica str. PH192 U5706
AY362913.1 gg_id:102691 Mannheimia granulomatis str. ATCC 49244 AY3629
AF224287.1 gg_id:38515 Pasteurella haemolytica str. CCUG 28148 AF2242
AF053891.1 gg_id:9614 Mannheimia glucosida str. P737; CCUG 38459 AF0538
U57072.1 gg_id:9590 Mannheimia haemolytica str. PH704 U5707
DQ301923.1 gg_id:145499 Mannheimia glucosida str. P933 DQ301
AF224286.1 gg_id:72830 Mannheimia sp. MCCM 00145 AF2242
U57070.1 gg_id:9601 Mannheimia haemolytica str. PH40 U5707
AY425282.1 gg_id:106492 Mannheimia varigena str. V1835 AY4252
AY508828.1 gg_id:105688 Nicoletella semolina str. CCUG 43643 AY5088
U66492.1 gg_id:9498 Pasteurella aerogenes str. P U6649
EF579842.1 gg_id:278925 Pasteurella canis str. Group868/2 EF5798
DQ211736.1 gg_id:171809 Pasteurella mairii str. JF3176 DQ211
EU652767.1 gg_id:286210 Pasteurella subsp. multocida str. Pmww07824 EU6527
AY299318.1 gg_id:103885 Pasteurella multocida str. PM80 AY2993
AY507110.1 gg_id:104353 Pasteurella multocida str. X225 AY5071
AB279579.1 gg_id:187444 Pasteurella sp. str. V6 AB2795
AY299315.1 gg_id:103457 Pasteurella multocida str. PM64 AY2993
AY362925.1 gg_id:99002 Pasteurella stomatis str. CCUG 17979 AY3629
AY299319.1 gg_id:104032 Pasteurella multocida str. PM82 AY2993
AF224296.1 gg_id:69985 Pasteurella pneumotropica str. NCTC 10827 AF2242
AY362920.1 gg_id:107231 Pasteurella dagmatis str. CCUG 12397 AY3629
AY299316.1 gg_id:103590 Pasteurella multocida str. PM106 AY2993
FJ832327.1 gg_id:579924 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P1Q301_30F04 FJ8323
FJ976392.1 gg_id:552339 Interindividual healthy human oral microbiota mouth clone 24B192 FJ9763
AY362918.1 gg_id:103434 Pasteurella caballi str. ATCC 49197 AY3629
AJ251339.1 gg_id:32352 Bisgaardia hudsonenesis str. 98-D-690B AJ2513
AY362917.1 gg_id:103283 Pasteurella bettyae str. CCUG 2042 AY3629
EU681975.1 gg_id:289990 microflora imbalances intestine dogs inflammatory bowel disease duodenum dog IBI EU6819
EU681998.1 gg_id:293231 microflora imbalances intestine dogs inflammatory bowel disease duodenum health EU6819
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AY172732.1 gg_id:91315 Bisgaard taxon 40 str. B301529/00/1 AY1727
AY465363.1 gg_id:109416 Actinobacillus rossii str. B96/45; JF2425 AY4653
AY362894.1 gg_id:101590 Actinobacillus muris str. NCTC 12432 AY3628
GQ111657.1 gg_id:453130 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ111
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AF224311.1 gg_id:36769 Haemophilus sp. str. MCCM 01557 AF2243

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X89379.1 gg_id:9511 Phocoenobacter uteri str. M1063U = NCTC 12872 X89379
AY362907.1 gg_id:107128 Haemophilus haemoglobinophilus str. CCUG 3714 AY3629
FJ960217.1 gg_id:571320 bottlenose dolphin upper respiratory tract blowhole clone D9A4_107 FJ9602
AF487728.1 gg_id:82586 Pasteurella gallinarum str. NCTC 11051 AF4877
GQ111114.1 gg_id:453851 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ111
DQ113707.1 gg_id:134081 Assssmnt alng cnn intstnl trct dg ilm cln I2-02 DQ113
AF224293.1 gg_id:35735 Pasteurella sp. str. MCCM 02539 AF2242
GQ072607.1 gg_id:457136 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw19 GQ072
EU826048.1 gg_id:579141 Avibacterium sp. str. MCCM 01291 EU8260
AF487729.1 gg_id:82728 Pasteurella gallinarum str. R44sv AF4877
AF224304.1 gg_id:71067 Pasteurella sp. str. MCCM 02120 AF2243
AY362922.1 gg_id:107519 Pasteurella langaaensis str. CCUG 15566 AY3629
DQ851143.1 gg_id:164515 Haemophilus simiae str. ROG53 DQ851
AY216870.1 gg_id:85860 Volucribacter amazonae str. B96/5 AY2168
NR_025724.1 gg_id:535122 Volucribacter psittacicida str. Gerl. 236/81; CCUG 47536 NR_025
AF509820.1 gg_id:60271 Acinetobacter baylyi str. B2 AF5098
FJ009376.1 gg_id:331932 Acinetobacter baylyi str. H2 FJ0093
AM410708.1 gg_id:194118 Acinetobacter baylyi str. A7 LUH9557 = ACI846 AM410
FJ976560.1 gg_id:584494 Acinetobacter soli str. LCR52 FJ9765
AF509821.1 gg_id:60274 Acinetobacter baylyi str. C5 AF5098
AF509822.1 gg_id:60277 Acinetobacter baylyi str. A7 AF5098
AM412162.1 gg_id:242026 Acinetobacter sp. str. P-110 AM412
FJ009371.1 gg_id:333962 Acinetobacter johnsonii str. H10 FJ0093
AY536009.1 gg_id:129982 sp. str. BCaL1 AY5360
FM177774.1 gg_id:518457 Acinetobacter berezinae str. LUH 9667 FM177
Z93444.1 gg_id:43948 Acinetobacter sp. str. ATCC 11171 Group eleven Z93444
AF509832.1 gg_id:60258 Acinetobacter genomosp. 11 str. A23 AF5098
FM177776.1 gg_id:522874 Acinetobacter guillouiae str. A23 = DSM 14960 FM177
AF143841.1 gg_id:69970 hydrocarbon-degrading consortium clone AF2-1D AF1438
FM177775.1 gg_id:531947 Acinetobacter guillouiae str. LUH 7013 FM177
Z93443.1 gg_id:8344 Acinetobacter sp. str. ATCC 17924 Group ten Z93443
FN395270.1 gg_id:384502 Acinetobacter sp. str. FR-W3CA FN3952
EU705457.1 gg_id:323060 Microbial Burden and Analyses Phoenix Spacecraft Assembly Kennedy Space Centre EU7054
FJ192308.1 gg_id:326859 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior FJ1923
FJ263916.1 gg_id:314055 Acinetobacter johnsonii str. BA2 FJ2639
AF509830.1 gg_id:56661 Acinetobacter tandoii str. 4N13 AF5098
FJ607355.1 gg_id:534204 Acinetobacter junii str. SeaH-As6s FJ6073
GQ488001.1 gg_id:535015 Microbial metal soil polluted heavy metals clone V8-111 GQ488
AY586400.2 gg_id:109340 Acinetobacter haemolyticus str. AR-46 AY5864
GQ409505.1 gg_id:545881 Acinetobacter sp. str. Du6 GQ409

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FJ193164.1 gg_id:343114 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior FJ1931
AY689035.1 gg_id:100228 Acinetobacter sp. str. 3C_8 AY689
GQ070596.1 gg_id:418636 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ070
DQ257427.1 gg_id:142775 Acinetobacter johnsonii str. CAI-14 DQ257
FJ191887.1 gg_id:343089 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior FJ1918
EU536549.1 gg_id:286873 profile human microbiota antecubital fossa (inner elbow) skin clone nbt215g07 EU5365
EU275352.1 gg_id:253188 Acinetobacter johnsonii str. CONC8 EU2753
FJ192142.1 gg_id:347156 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior FJ1921
DQ675069.1 gg_id:168062 microbial production water -temperature petroleum reservoir clone QHO-B26 DQ675
CU466803.1 gg_id:336593 Evry wastewater treatment plant anoxic basin clone CU466
FJ192398.1 gg_id:334639 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior FJ1923
EU705366.1 gg_id:309203 Microbial Burden and Analyses Phoenix Spacecraft Assembly Kennedy Space Centre EU7053
GU124494.1 gg_id:535160 endosymbiotic (Stal) (rice brown planthopper) Acinetobacter endosymbiont Nilapar GU124
FJ191727.1 gg_id:334971 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior FJ1917
AB196244.1 gg_id:115340 Acinetobacter johnsonii str. IC001 AB196
FJ900940.1 gg_id:563501 Polymorphism microbial reservoirs water cut stage oil field clone L-36 FJ9009
FJ192385.1 gg_id:316225 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior FJ1923
AY167841.1 gg_id:77294 Acinetobacter johnsonii str. SAFR-006 AY1678
FJ192696.1 gg_id:338444 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior FJ1926
DQ675057.1 gg_id:165070 microbial production water -temperature petroleum reservoir clone QHO-B9 DQ675
FJ192370.1 gg_id:310406 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior FJ1923
FJ192156.1 gg_id:320031 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior FJ1921
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AB369040.1 gg_id:537750 and microbial oils produced Asia petroleum crude oil (Qatar Land Light) clone PT-QTI AB369
AB369043.1 gg_id:573441 and microbial oils produced Asia petroleum crude oil (Qatar Land Light) clone PT-QTI AB369
GQ102953.1 gg_id:436668 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv GQ102
DQ675078.1 gg_id:165523 microbial production water -temperature petroleum reservoir clone QHO-B28 DQ675
FJ948288.1 gg_id:578231 Isolation and identification endophytic three medicinal plants leaf clone HQ FJ9482
FJ192211.1 gg_id:352732 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior FJ1922
FJ192879.1 gg_id:328708 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior FJ1928
GQ111297.1 gg_id:467170 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ111
EU169147.1 gg_id:241109 Acinetobacter johnsonii str. B33 EU169
GQ102212.1 gg_id:371878 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv GQ102
EU240429.1 gg_id:235992 Acinetobacter johnsonii str. B178 EU240
EU504845.1 gg_id:268774 cecal contents Mus musculus strain C57BL/6J; myd2 clone myd2_aaa03b10 EU5048
GQ102805.1 gg_id:450958 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv GQ102
GQ106991.1 gg_id:445417 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw543d0 GQ106
FJ192003.1 gg_id:322306 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior FJ1920
EU705479.1 gg_id:345817 Microbial Burden and Analyses Phoenix Spacecraft Assembly Kennedy Space Centre EU7054
FJ192503.1 gg_id:308433 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior FJ1925

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AF188300.1 gg_id:8391 Acinetobacter johnsonii str. P152 AF1883
FJ192666.1 gg_id:347685 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior FJ1926
FJ192917.1 gg_id:322094 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior FJ1929
GQ104230.1 gg_id:460452 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv GQ104
EF429006.1 gg_id:216324 Acinetobacter sp. str. GIST-OutAn1 EF4290
DQ675059.1 gg_id:170409 microbial production water -temperature petroleum reservoir clone QHO-B11 DQ675
FJ191867.1 gg_id:341096 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior FJ1918
FJ192302.1 gg_id:329438 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior FJ1923
GQ080422.1 gg_id:372278 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw: GQ080
GQ072927.1 gg_id:452753 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw202h03(GQ072
DQ675049.1 gg_id:169400 microbial production water -temperature petroleum reservoir clone QHO-B8 DQ675
FJ191856.1 gg_id:329425 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior FJ1918
AB369019.1 gg_id:576274 and microbial oils produced Asia petroleum crude oil (Arabian Medium) clone PT-ARI AB369(
AY277551.1 gg_id:89870 Acinetobacter lwoffii str. 1E AY2775
FJ672802.1 gg_id:521318 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6728
DQ834359.1 gg_id:165112 Acinetobacter sp. str. FLL8 DQ834
FJ373029.1 gg_id:311265 Acinetobacter lwoffii str. S3-2 FJ3730
DQ223660.1 gg_id:160030 Acinetobacter sp. zf-IRht15 DQ223
X86572.1 gg_id:8361 Acinetobacter sp str. AC-40 X86572
DQ371237.1 gg_id:155206 Acinetobacter lwoffii str. FORb DQ371
AF188302.1 gg_id:8363 Acinetobacter lwoffii str. A382 AF1883
AY176770.1 gg_id:78649 Acinetobacter lwoffii str. HJ7 AY1767
EU240445.1 gg_id:237709 Acinetobacter lwoffii str. B190 EU2404
AM412164.1 gg_id:249976 Acinetobacter sp. str. P-126 AM412
DQ144736.1 gg_id:139182 Acinetobacter lwoffii str. LS2 DQ144
FJ191915.1 gg_id:310933 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior FJ1919
AM495259.1 gg_id:250455 Acinetobacter radioresistens str. INBS1 AM495
FJ816058.1 gg_id:569388 Acinetobacter calcoaceticus str. PUCM1011 FJ8160
AM157426.1 gg_id:141393 Acinetobacter calcoaceticus mother C3 AM157
EU921462.1 gg_id:328793 Acinetobacter calcoaceticus str. HIRFA26 EU9214
EU118781.1 gg_id:245216 Acinetobacter calcoaceticus str. AGL 17 EU1187
GQ469890.1 gg_id:587465 Acinetobacter calcoaceticus str. PUCM1031 GQ469
FJ816055.1 gg_id:510012 Acinetobacter calcoaceticus str. PUCM1008 FJ8160
FJ009370.1 gg_id:334071 Acinetobacter calcoaceticus str. H11 FJ0093
AM410707.1 gg_id:177547 Acinetobacter calcoaceticus str. ACI34 = RUH 0583 AM410
FJ816049.1 gg_id:567940 Acinetobacter calcoaceticus str. PUCM1002 FJ8160
FJ816073.1 gg_id:543130 Acinetobacter calcoaceticus str. PUCM1026 FJ8160
EF601824.1 gg_id:228947 Acinetobacter sp. str. NX2 EF6018
EU921468.1 gg_id:321731 Acinetobacter calcoaceticus str. HIRGA36 EU9214
DQ536511.1 gg_id:161691 Acinetobacter rhizosphaerae str. BIHB 723 DQ536

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AM921638.1 gg_id:257154 Acinetobacter rhizosphaerae PhyCEm-460 AM921
AY277552.1 gg_id:90549 Acinetobacter calcoaceticus str. AVP2-2 AY2775
AY364536.1 gg_id:94206 Acinetobacter rhizosphaerae str. IH9 AY3645
FJ976570.1 gg_id:578667 Acinetobacter calcoaceticus str. LCR61 FJ9765
DQ129724.2 gg_id:248172 Acinetobacter calcoaceticus str. HPC399 DQ129
FJ373024.1 gg_id:327004 Acinetobacter schindleri str. W1-2 FJ3730
GQ080249.1 gg_id:459017 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw: GQ080
GU339299.1 gg_id:542053 Acinetobacter schindleri str. EH74 GU339
GU004025.1 gg_id:581771 heterotrophic nitrifying biofilm clone 16SN42 GU004
GQ082321.1 gg_id:426536 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw11 GQ082
GU004026.1 gg_id:554705 heterotrophic nitrifying biofilm clone 16SN43 GU004
AF509826.1 gg_id:60264 Acinetobacter tjernbergiae str. 7B02 AF5098
NR_028849.1 gg_id:537702 Acinetobacter towneri str. AB1110; DSM 14962 NR_02
AF509824.1 gg_id:60268 Acinetobacter towneri str. 2N01 AF5098
AJ275039.1 gg_id:54545 Acinetobacter ursingii str. LUH 4763 AJ2750
EU258609.1 gg_id:277749 Acinetobacter venetianus str. ACI574 EU258
GQ007238.1 gg_id:502426 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ007
AB286521.1 gg_id:210171 Reducing production and domination comamonadaceae reducing oxygen supply was AB2865
AF357182.1 gg_id:48029 Alvinella pompejana symbiont APG130A AF357
FJ674507.1 gg_id:518521 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6745
GQ451319.1 gg_id:569668 Fecal Yunnan snub-nosed monkey feces clone J341 GQ451
EF468657.1 gg_id:218490 Acinetobacter sp. str. TD5 EF4686
AY047216.1 gg_id:39106 Acinetobacter haemolyticus AY0472
EU467937.1 gg_id:293369 cheetah feces clone CE2_e09 EU4679
EU779466.1 gg_id:321405 Hartmann's Mountain Zebra feces clone AFZEB_aaj72f01 EU7794
EU467673.1 gg_id:302118 naked mole-rat feces clone molerat_2g12_1 EU4676
FJ976593.1 gg_id:550870 Acinetobacter sp. str. LCR84 FJ9765
FJ672033.1 gg_id:520896 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6720
EU779403.1 gg_id:311420 Hartmann's Mountain Zebra feces clone AFZEB_aaj70a08 EU7794
AY633608.1 gg_id:101304 Acinetobacter seohaensis str. SW-100 AY6336
EU463254.1 gg_id:294712 naked mole-rat feces clone molerat_aai72d06 EU463
FJ672865.1 gg_id:517631 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6728
EU777000.1 gg_id:344560 Naked mole-rat feces clone molerat_2g01 EU7770
GQ077574.1 gg_id:415516 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1210e(GQ077
AM412161.1 gg_id:250903 Acinetobacter sp. str. P-134 AM412
FJ672928.1 gg_id:523993 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6729
AB207814.1 gg_id:167038 Acinetobacter psychrotolerans str. Ths AB2078
EU160535.1 gg_id:347520 diagnosis central-venous infections cultivation-dependent and techniques biofilm sc EU1605
EU604244.1 gg_id:274092 Acinetobacter baylyi str. 1477 EU6042
FJ193878.1 gg_id:338023 Genetic inventory 'KSC-Astrotek' spacecraft assembly clean room during DAWN missi FJ1938
EU463244.1 gg_id:290621 naked mole-rat feces clone molerat_aai72c02 EU463

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FJ851148.1 gg_id:569494 Acinetobacter sp. str. P4 FJ8511
U10875.1 gg_id:8400 Acinetobacter lwoffii str. ATCC 17925 U1087
FJ193928.1 gg_id:317023 Genetic inventory 'KSC-Astrotek' spacecraft assembly clean room during DAWN missi FJ1939
FJ193896.1 gg_id:356161 Genetic inventory 'KSC-Astrotek' spacecraft assembly clean room during DAWN missi FJ1938
EU124829.1 gg_id:245300 Gut microbes gut Helicoverpa armigera living on cotton plant clone 10 EU124
EU465090.1 gg_id:288912 African elephant feces clone AFYEL_aaj67h10 EU465
EF525671.1 gg_id:218350 Acinetobacter baumannii str. Serdang1 EF5256
DQ834354.1 gg_id:170113 Acinetobacter sp. str. FLL7 DQ834
FJ816048.1 gg_id:564236 Acinetobacter calcoaceticus str. PUCM1001 FJ8160
GQ088876.1 gg_id:380649 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ088
EU705448.1 gg_id:340228 Microbial Burden and Analyses Phoenix Spacecraft Assembly Kennedy Space Centre EU705
FJ193982.1 gg_id:333983 Genetic inventory 'KSC-Astrotek' spacecraft assembly clean room during DAWN missi FJ1939
GQ069608.1 gg_id:407828 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ069
FJ193755.1 gg_id:325011 Genetic inventory 'KSC-Astrotek' spacecraft assembly clean room during DAWN missi FJ1937
GQ080268.1 gg_id:431095 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ080
FJ477061.1 gg_id:533635 Acinetobacter xiamenensis str. KSL 4-102 FJ4770
Z93988.1 gg_id:8321 activated sludge clone T23 Z93988
DQ116000.1 gg_id:131304 bovine teat canal clone D-13 DQ116
DQ824717.1 gg_id:186196 human fecal clone RL185_aaj72b10 DQ824
DQ860032.1 gg_id:247964 anchovy intestinal microflora clone F1T DQ860
AF509827.1 gg_id:60263 Acinetobacter bouvetii str. 4B02 AF5098
FJ674492.1 gg_id:519299 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6744
GQ097172.1 gg_id:411031 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw GQ097
DQ187381.1 gg_id:139909 Acinetobacter calcoaceticus DQ187
EU560851.1 gg_id:563369 Assessment genetic Apriona germari (Hope) larvae normalization techniques intestir EU5608
AF526908.2 gg_id:62949 Acinetobacter radioresistens str. 50v1 AF5269
EF436374.1 gg_id:215173 library-based ruminal water buffalo (Bubalus bubalis) rumen fluid clone BRC88 EF4363
EU352764.1 gg_id:276866 Acinetobacter haemolyticus str. NK 2.BH-7 EU3527
Z93982.1 gg_id:8320 activated sludge clone T58 Z93982
FJ675544.1 gg_id:523482 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6755
AF509828.1 gg_id:60261 Acinetobacter grimontii str. 17A04 AF5098
AF336348.1 gg_id:40632 Acinetobacter sp. str. Wuba16 AF3363
FJ672724.1 gg_id:528677 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6727
EU921471.1 gg_id:351367 Acinetobacter baumannii str. HIRGP40 EU9214
FJ193816.1 gg_id:354830 Genetic inventory 'KSC-Astrotek' spacecraft assembly clean room during DAWN missi FJ1938
EU337120.1 gg_id:513402 Acinetobacter sp. str. 1B3 EU3371
AF189695.1 gg_id:48977 Acinetobacter sp. str. BC187 AF1896
AF159045.1 gg_id:8371 Acinetobacter calcoaceticus str. A2 AF1590
FJ671697.1 gg_id:522240 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6716
FJ816080.1 gg_id:536705 Acinetobacter calcoaceticus str. PUCM1503 FJ8160

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GQ045794.1 gg_id:391261 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ045
AJ303014.1 gg_id:73559 Acinetobacter sp. str. LBV326 (97 10 4186) AJ3030
EU360111.1 gg_id:582701 Acinetobacter calcoaceticus str. PB16 EU3601
EF432578.2 gg_id:206376 Acinetobacter calcoaceticus str. HB1-1 EF4325
Z93447.1 gg_id:8313 Acinetobacter sp. str. ATCC 17905 Group TU14 Z93447
DQ834356.1 gg_id:171431 Acinetobacter sp. str. SLH4 DQ834
EU513394.1 gg_id:277540 Acinetobacter calcoaceticus str. TMPSB-D12 EU5133
EF205268.1 gg_id:199813 Arctic gold mine fracture water clone Lupin-1130m-1-MDA-aci1 EF2052
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EU918130.1 gg_id:332182 Acinetobacter junii str. PM-8 EU9181
FJ527818.1 gg_id:540395 Acinetobacter sp. str. KSL5401-037 FJ5278
GQ284482.1 gg_id:590067 Acinetobacter sp. str. TDWCW1 GQ284
AY823621.1 gg_id:115347 Acinetobacter calcoaceticus str. SW1 AY8236
EU594561.1 gg_id:277462 Acinetobacter sp. str. 4-2 EU5945
FJ151628.1 gg_id:342972 Acinetobacter calcoaceticus str. HNR FJ1516
EU774032.1 gg_id:314572 Cheetah feces clone CE2_e07 EU7740
AB167206.1 gg_id:107919 Acinetobacter sp. str. c33 AB1672
FJ675182.1 gg_id:524252 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6751
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X80285.1 gg_id:8331 Acinetobacter calcoaceticus X80285
EU705523.1 gg_id:354028 Microbial Burden and Analyses Phoenix Spacecraft Assembly Kennedy Space Centre EU7055
FJ820996.1 gg_id:511035 Acinetobacter sp. str. PT22 FJ8209
DQ856498.1 gg_id:250517 intestinal microflora Chinese mitten crab (Eriocheir sinensis) clone C1A DQ856
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EU272861.1 gg_id:358174 Acinetobacter sp. str. MK28 EU2728
GQ174293.1 gg_id:414197 Acinetobacter sp. str. PP-2 GQ174
FJ263921.1 gg_id:318166 Acinetobacter septicus str. BA9 FJ2639
GQ092219.1 gg_id:403040 Topographical and Temporal Human Skin Microbiome skin palm clone nbw411b09c1 GQ092
AM412160.1 gg_id:247994 Acinetobacter sp. str. P-133 AM412
DQ464150.1 gg_id:158313 acid mine drainage clone D1-48 DQ464
EU073105.1 gg_id:350209 Acinetobacter sp. str. TS39 EU0731
FJ193900.1 gg_id:317914 Genetic inventory 'KSC-Astrotek' spacecraft assembly clean room during DAWN missi FJ1939
EF203410.1 gg_id:264736 Acinetobacter sp. str. URAM1 EF2034
FJ671719.1 gg_id:525292 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6717

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AY800383.1 gg_id:108973 Acinetobacter calcoaceticus AY8003
FJ193843.1 gg_id:324697 Genetic inventory 'KSC-Astrotek' spacecraft assembly clean room during DAWN missi FJ1938
FJ791167.1 gg_id:543942 Hydrocarbon degraders -grade long term automative hydrocarbon contamination oil- FJ7911
EU841481.1 gg_id:344669 Acinetobacter sp. str. 407 EU8414
EU467641.1 gg_id:291175 naked mole-rat feces clone molerat_2d03 EU4676
X89709.1 gg_id:8322 Acinetobacter sp str. DSM 587 X89709
GU370393.1 gg_id:518077 Acinetobacter sp. str. PD4 GU370
GQ383923.1 gg_id:582252 Acinetobacter sp. str. XJ127 GQ383
FM874549.1 gg_id:360440 occupant source house mattress dust clone MD03C05 FM874
AB176230.1 gg_id:191845 Microbial Hydrothermal System Suiyo Seamount on Izu-Ogasawara Arc vent area wa AB1762
FJ544395.1 gg_id:453868 Acinetobacter junii str. tu13 FJ5443
DQ341260.1 gg_id:147489 Acinetobacter lwoffii str. F78 DQ341
GQ045799.1 gg_id:415493 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ045
EU160530.1 gg_id:340699 diagnosis central-venous infections cultivation-dependent and techniques biofilm sci EU1605
FJ192953.1 gg_id:351059 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior FJ1929
EU661697.1 gg_id:286733 Acinetobacter baumannii str. NBRAJG76 EU6616
DQ441376.1 gg_id:190792 human intestinal biopsy clone CD125 DQ441
DQ824733.1 gg_id:194641 human fecal clone RL185_aaj72d05 DQ824
FJ672730.1 gg_id:516114 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6727
AY346313.2 gg_id:207698 Acinetobacter calcoaceticus str. HPC253 AY3463
FM213385.2 gg_id:347588 Acinetobacter sp. str. MN33 FM213
AY847284.1 gg_id:110290 Acinetobacter baumannii str. Ab8 AY8472
EF565936.1 gg_id:229145 Acinetobacter sp. str. NF4 EF5659
AJ293691.1 gg_id:71951 Acinetobacter parvus str. LUH4616 (Aci602) AJ2936
FN563424.1 gg_id:580752 Acinetobacter baumannii str. bpoe1353 FN5634
AJ278311.2 gg_id:35076 Acinetobacter schindleri str. LUH5832T AJ2783
EU467633.1 gg_id:287831 naked mole-rat feces clone molerat_2g07 EU4676
GQ045189.1 gg_id:445146 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ045
EF059532.1 gg_id:219882 Acinetobacter sp. JN18_V5_C EF0595
FJ672809.1 gg_id:528886 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6728
EU463223.1 gg_id:302877 naked mole-rat feces clone molerat_aai71h09 EU4632
FJ193977.1 gg_id:324684 Genetic inventory 'KSC-Astrotek' spacecraft assembly clean room during DAWN missi FJ1939
EU560788.1 gg_id:562084 Assessment genetic intestinal flora Apriona germari (Hope) larvae -RFLP techniques (EU5607
EU604241.1 gg_id:341709 Acinetobacter junii str. jfly-01 EU6042
Z93987.1 gg_id:8330 activated sludge clone T27 Z93987
FJ672176.1 gg_id:512623 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6721
EU221346.1 gg_id:235575 Acinetobacter calcoaceticus str. HM1C2 EU2213
EU730929.1 gg_id:353461 Acinetobacter johnsonii str. 178 EU7309
EU249988.1 gg_id:240369 Acinetobacter sp. str. PmeaMuc16 EU2499
EU160536.1 gg_id:328674 diagnosis central-venous infections cultivation-dependent and techniques biofilm sci EU1605

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EU921463.1 gg_id:345884 Acinetobacter calcoaceticus str. HIRFA27 EU921
FN433036.1 gg_id:565535 Acinetobacter beijerinckii CCM25B FN433
AJ633639.1 gg_id:99113 Acinetobacter sp. str. LMG M71 = ACI788 AJ6336
EU467631.1 gg_id:302583 naked mole-rat feces clone molerat_2f06 EU467
FJ674356.1 gg_id:525396 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6743
DQ824645.1 gg_id:184299 human fecal clone RL185_aaj71a07 DQ824
X81659.1 gg_id:8342 Acinetobacter species X81659
AF336353.1 gg_id:37719 Acinetobacter sp. str. Wuba39 AF3363
FJ263922.1 gg_id:304658 Acinetobacter septicus str. BA14 FJ2639
FJ816051.1 gg_id:564486 Acinetobacter calcoaceticus str. PUCM1004 FJ8160
X81668.1 gg_id:8375 Acinetobacter calcoaceticus X81668
EF188656.1 gg_id:351236 Microbial Altamira Cave clone 400 EF1886
EU090179.1 gg_id:250734 Acinetobacter calcoaceticus str. 11 EU0901
FJ976566.1 gg_id:591323 Acinetobacter calcoaceticus str. LCR58 FJ9765
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AY633607.1 gg_id:101152 Acinetobacter marinus str. SW-3 AY6336
FJ672939.1 gg_id:515715 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6729
EU467653.1 gg_id:289405 naked mole-rat feces clone molerat_2b02_1 EU467
FJ671896.1 gg_id:521562 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6718
EU463121.1 gg_id:290186 naked mole-rat feces clone molerat_aai70b10 EU463
EU160533.1 gg_id:353347 diagnosis central-venous infections cultivation-dependent and techniques biofilm sc EU1605
NR_028852.1 gg_id:591121 Acinetobacter gerneri str. 9A01; DSM 14967 NR_02
DQ856553.1 gg_id:244174 intestinal microflora Chinese mitten crab (Eriocheir sinensis) clone C3Q DQ856
FJ811875.1 gg_id:579258 Acinetobacter sp. str. MA3B-GFJ FJ8118
EF127901.2 gg_id:255893 Acinetobacter sp. str. Y3A EF1279
AJ295007.1 gg_id:36199 Acinetobacter venetianus str. ATCC 31012 AJ2950
EU382216.1 gg_id:263259 Acinetobacter sp. str. DZ0503SBS4 EU382
AB167222.1 gg_id:107933 Acinetobacter sp. str. c61 AB167
FJ976597.1 gg_id:509344 Acinetobacter calcoaceticus FJ9765
EU434432.1 gg_id:265496 Acinetobacter johnsonii str. a153 EU4344
FJ672184.1 gg_id:510837 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6721
GQ281071.1 gg_id:577164 Acinetobacter sp. str. NBCS09 GQ281
GQ258635.1 gg_id:542419 Acinetobacter soli str. SR2 GQ258
GQ039005.1 gg_id:441923 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu4 GQ039
FJ674942.1 gg_id:525865 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6749
FJ675650.1 gg_id:512333 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6756
FJ671967.1 gg_id:524433 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6719
EU934077.1 gg_id:333015 Acinetobacter sp. FR2_4 str. FR2_4con EU934
AF390087.1 gg_id:49347 Acinetobacter sp. str. Sea-9 AF390
AJ633641.1 gg_id:103039 Acinetobacter sp. str. LMG V90 = ACI792 AJ6336

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AF543466.1 gg_id:58303 Alkanindiges hongkongensis str. HKU9 AF5434
EU104153.1 gg_id:334424 Evidence Comamonadaceae determinants settling performance activated sludge clo EU1041
DQ640687.1 gg_id:228207 full-scale EBPR sludge clone Skagenf46 DQ640
GQ076362.1 gg_id:455948 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw36 GQ076
EU636038.1 gg_id:278473 Antarctic str. 3C8 EU636
DQ847440.1 gg_id:171048 human forearm skin clone GL2-47 DQ847
EU104133.1 gg_id:324983 Evidence Comamonadaceae determinants settling performance activated sludge clo EU1041
GQ464393.1 gg_id:548754 Detection during -ARDRA and sequencing frozen chicken storage container 90 days GQ464
DQ130041.1 gg_id:152336 microbial biota normal forearm human skin clone JEL30 DQ130
GQ076390.1 gg_id:392111 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw36 GQ076
GQ080410.1 gg_id:388165 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ080
DQ336992.1 gg_id:147715 subsurface water clone EV818CFSSAHH42 DQ336
DQ354732.1 gg_id:153465 subsurface water clone DR550SWSAEE45 DQ354
DQ354720.1 gg_id:155859 subsurface water clone DR550SWSAEE20 DQ354
EU104077.1 gg_id:307143 Evidence Comamonadaceae determinants settling performance activated sludge clo EU1040
AM905315.1 gg_id:238484 Microbial dynamics -arctic exposure hydrocarbons and bioremediation agent interti AM905
FJ380170.1 gg_id:370141 ornithogenic Ross Sea region Antarctica AB1 soil clone 13/4/4G FJ3801
DQ469231.1 gg_id:158223 Microbial and ecology water Zhong Tiaoshan mine Shanxi province China AMD clone DQ469
NR_029005.1 gg_id:591417 Enhydrobacter aerosaccus str. G; LMG 21877; ATCC 27094 NR_02
GQ054317.1 gg_id:379908 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw1108 GQ054
AY043376.1 gg_id:63603 Moraxella osloensis str. AU1220 AY0433
DQ153085.1 gg_id:219896 Moraxella bovoculi str. 371 DQ153
AF005167.1 gg_id:8243 Moraxella lacunata str. E3808 AF0051
AF005169.1 gg_id:8245 Moraxella lacunata str. NCTC 7911 AF0051
AF005161.1 gg_id:8237 Moraxella lacunata str. ATCC 17956 AF0051
AF005162.1 gg_id:8238 Moraxella lacunata str. E7992 AF0051
AF005178.1 gg_id:8274 Moraxella nonliquefaciens str. B6270/90 AF0051
AF005176.1 gg_id:8272 Moraxella nonliquefaciens str. P2581/88 AF0051
AF005186.1 gg_id:48597 Moraxella ovis str. ATCC 33078T AF0051
AF005185.1 gg_id:8278 Moraxella catarrhalis str. ATCC 25238T AF0051
FM873527.1 gg_id:360893 occupant source house mattress dust clone MA01E04 FM873
NR_028914.1 gg_id:585738 Moraxella canis str. N7; LMG 11194 NR_02
DQ647927.1 gg_id:222016 Moraxella bovis str. Tifton I DQ647
AM420053.1 gg_id:246528 Noma subgingival plaque clone 202G06(oral) AM420
AF005187.1 gg_id:8281 Moraxella caviae str. CCUG 355T AF0051
AF005188.1 gg_id:8261 Moraxella cuniculi str. CCUG 2154T AF0051
AF005189.1 gg_id:8249 Moraxella cuniculi str. CCUG 27179 AF0051
EF396294.1 gg_id:255045 Moraxella sp. CD12CA4 EF3962
GQ070485.1 gg_id:467388 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ070
AY212599.1 gg_id:100893 water 20 m downstream manure clone 148ds20 AY2125
DQ823176.1 gg_id:170920 Techniques Microbial Studies Oregon Caves National Monument Quad 3 on trail clo DQ823

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AY212663.1 gg_id:99626 water 20 m downstream manure clone 216ds20 AY2126
AY622230.1 gg_id:101684 subsurface soil clone C-CL42 AY6222
DQ660872.1 gg_id:237806 DongChuan copper pyrites PRC determined acid mine drainage (AMD) clone DC-II-2 DQ660
DQ458033.1 gg_id:158925 acid mine drainage clone DX63 DQ458
DQ354716.1 gg_id:153505 subsurface water clone DR550SWSAEE15b DQ354
DQ824588.1 gg_id:176013 human fecal clone RL185_aaj70b01 DQ824
AJ830006.1 gg_id:104541 Psychrobacter aquaticus str. CMS 58 AJ8300
AY842259.1 gg_id:110467 Psychrobacter celer str. SW-238 AY8422
AY771717.1 gg_id:108691 Psychrobacter fozii str. S2-83 AY7717
NC_007969.1 gg_id:157086 Psychrobacter cryohalolentis str. K5 NC_007
DQ270712.1 gg_id:141337 Psychrobacter sp. B-3151 DQ270
EU652044.1 gg_id:275703 Psychrobacter marincola str. aa-20 EU6520
AF441202.1 gg_id:44896 Psychrobacter jeotgali str. YKJ-105 AF4412
NR_025458.1 gg_id:562316 Psychrobacter marincola str. KMM 277 NR_025
AJ539104.1 gg_id:79510 Psychrobacter salsus str. DD48 AJ5391
AJ313425.1 gg_id:101537 Psychrobacter nivimaris str. 88/2-7 AJ3134
AB016054.1 gg_id:24089 Psychrobacter pacificensis str. NIBH P2J2 AB0160
AY057116.1 gg_id:27938 Psychrobacter meningitidis str. SGHMS AY0571
AB016056.1 gg_id:18681 Psychrobacter pacificensis str. NIBH P2J13 AB0160
AY167308.1 gg_id:82364 Psychrobacter glacincola str. ANT9253 AY1673
AY372913.1 gg_id:144095 marine sponge Rhabdastrella globostellata symbiont AY3729
EU434452.1 gg_id:269448 Psychrobacter pulmonis str. a40 EU4344
EU434447.1 gg_id:263373 Psychrobacter pulmonis str. a72 EU4344
EU434352.1 gg_id:276381 Psychrobacter pulmonis str. a161 EU4343
EU434446.1 gg_id:263158 Psychrobacter pulmonis str. a60 EU4344
AJ437696.1 gg_id:85442 Psychrobacter pulmonis str. CECT 5989T AJ4376
EU434362.1 gg_id:269048 Psychrobacter pulmonis str. a131 EU4343
NC_009524.1 gg_id:229173 Psychrobacter sp. str. PRwf-1 NC_009
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EU000245.1 gg_id:324143 Psychrobacter maritimus str. KOPRI_22337 EU0002
EU845548.1 gg_id:313200 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8455
EU880519.1 gg_id:311744 Psychrobacter nivimaris str. P24a EU8805
EF101551.1 gg_id:182841 Psychrobacter pulmonis str. KOPRI24933 EF1015
AY167281.1 gg_id:82289 Psychrobacter glacincola str. ANT9104 AY1672
EU433332.1 gg_id:271451 Psychrobacter sp. str. BSs20154 EU4333
AJ312213.1 gg_id:32985 Psychrobacter glacincola str. DSM 12194T AJ3122
DQ860047.1 gg_id:251317 anchovy intestinal microflora clone F2N DQ860
AM110989.1 gg_id:140965 Psychrobacter sp. str. 3035 AM110
EU434353.1 gg_id:264946 Psychrobacter pulmonis str. a163 EU4343
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AY497354.1 gg_id:106855 Psychrobacter sp. str. 20 AY4973

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AM111050.1 gg_id:140908 Psychrobacter sp. str. 7195 AM111
NR_027204.1 gg_id:566452 Psychrobacter arenosus str. R7; KMM 3659 NR_02
EU434405.1 gg_id:263288 Psychrobacter maritimus str. a336 EU434
GQ093417.1 gg_id:420929 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ093
EF101546.1 gg_id:181752 Psychrobacter aquimaris str. KOPRI24928 EF1015
AM111057.1 gg_id:140806 Psychrobacter sp. str. 7319 AM111
AY722804.1 gg_id:103680 Psychrobacter aquimaris str. SW-210 AY7228
AY864643.1 gg_id:110044 Psychrobacter sp. str. DVS7b AY8646
AY198113.1 gg_id:80503 Psychrobacter sp. HLA AY198
AY513645.1 gg_id:103196 Psychrobacter alimentarius str. JG-100 AY5136
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AY771724.1 gg_id:143446 Psychrobacter glacincola S3-14 AY771
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EU075123.1 gg_id:242630 Psychrobacter sp. str. En40 EU075
AM269904.1 gg_id:160677 Psychrobacter sp. str. ES-10 AM269
EU434395.1 gg_id:273089 Psychrobacter maritimus str. a325 EU4343
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EU370412.1 gg_id:266113 Psychrobacter faecalis str. 88Z1 EU370
AY864649.1 gg_id:110450 Psychrobacter sp. str. DVS6c AY8646
EU434433.1 gg_id:275103 Psychrobacter pulmonis str. a195 EU4344
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EU434386.1 gg_id:271742 Psychrobacter maritimus str. a281 EU4343
AJ609556.1 gg_id:100627 Psychrobacter frigidicola str. DSM 12411 AJ6095
EU834258.1 gg_id:312816 Psychrobacter frigidicola str. DS35 EU834
DQ337513.1 gg_id:147051 Psychrobacter psychrophilus BBDP29 DQ337
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U85876.1 gg_id:8300 Psychrobacter glacincola str. IC084 U85876
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EU845706.1 gg_id:335347 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU845
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EU915471.1 gg_id:326012 Psychrobacter phenylpyruvicus str. 123 EU915

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EF620447.1 gg_id:256056 Azotobacter vinelandii str. ISSDS-428 EF6204
EF620443.1 gg_id:238882 Azotobacter vinelandii str. ISSDS-423 EF6204
EF100152.1 gg_id:205128 Azotobacter beijerinckii str. ICMP 8673 EF1001

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AB429526.1 gg_id:333725 Azotobacter beijerinckii str. C4
GQ388971.1 gg_id:543932 quality deterioration drinking system during serious red water outbreak clone J20
FJ544363.1 gg_id:434412 Pseudomonas alcaligenes str. st5-2
GQ389014.1 gg_id:510529 quality deterioration drinking system during serious red water outbreak clone J62
FJ793191.1 gg_id:520731 Archaea and Hot Spring Thailand Tao Dam hot spring clone TDB96
AY835998.1 gg_id:110273 Pseudomonas alcaligenes M4-7
EF199996.1 gg_id:175542 Pseudomonas alcaligenes str. DIP1
AY651923.1 gg_id:105788 Pseudomonas alcaligenes str. S3
FJ455454.1 gg_id:570727 Pseudomonas alcaligenes str. PNP-Y3
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AB021376.1 gg_id:8523 Pseudomonas anguilliseptica str. NCMB 1949T
EU741649.1 gg_id:311673 Pseudomonas sp. str. BQNR
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GQ480478.1 gg_id:577261 Pseudomonas stutzeri str. MR-5
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AJ786814.1 gg_id:108090 Pseudomonas sp. R-23040
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AJ550465.1 gg_id:83510 Pseudomonas chlororaphis
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AF094722.1 gg_id:69974 Pseudomonas chlororaphis str. ATCC 13985
AY839234.1 gg_id:110012 Pseudomonas aurantiaca str. YC4963
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DQ813321.1 gg_id:165579 Pseudomonas sp. str. IBUN S1407
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EU158316.1 gg_id:239834 Pseudomonas sp. str. DK2
DQ682655.1 gg_id:164272 Pseudomonas aurantiaca str. NCIB 10068
AY216795.1 gg_id:81078 Pseudomonas chlororaphis 24_4
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FJ652607.1 gg_id:511076 Pseudomonas chlororaphis str. 30-84
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AY509898.1 gg_id:103725 Pseudomonas chlororaphis str. DSM 6698
EF620458.1 gg_id:255132 Pseudomonas chlororaphis str. ISSDS-592
AF530070.1 gg_id:72643 Pseudomonas citronellolis str. TERIDB9
EU170480.1 gg_id:250888 Pseudomonas aeruginosa str. L-4
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AY907566.1 gg_id:112473 Pseudomonas entomophila str. L48 AY9075
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AY263480.1 gg_id:82986 Pseudomonas sp. WR7#2 AY2634
FJ894412.1 gg_id:557030 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B2E; ear pu FJ8944
AJ288146.1 gg_id:73856 Pseudomonas sp. SK-1-3-1 AJ2881
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AM421976.1 gg_id:354955 Pseudomonas sp. str. NJ-24 AM421
AY581134.1 gg_id:102069 Pseudomonas lundensis b85 AY5811
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AY450556.1 gg_id:108450 Pseudomonas putida str. L AY4505
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EU730928.1 gg_id:354416 Pseudomonas fluorescens str. 166 EU7309
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FJ544330.1 gg_id:438282 Pseudomonas putida str. 813 FJ5443
FJ976084.1 gg_id:399673 Pseudomonas sp. str. 23jan04 FJ9760
EU434451.1 gg_id:274358 Pseudomonas libanensis str. a42 EU4344
DQ377751.1 gg_id:156328 Pseudomonas grimontii PD 10 DQ377
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GU213303.1 gg_id:535039 Pseudomonas sp. str. 4-13 GU213
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AB021401.1 gg_id:8733 Pseudomonas marginalis str. ATCC 10844T AB0214
EU184082.1 gg_id:255345 Pseudomonas lutea str. PSB2 EU1840
EU048319.1 gg_id:253104 Pseudomonas fluorescens str. CMG3047 EU0483

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EU111739.2 gg_id:547460 Pseudomonas migulae str. CT28 EU111
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AF386080.1 gg_id:58547 Pseudomonas mediterranea str. CFBP 5447 AF3860
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FJ472860.1 gg_id:545756 Pseudomonas pseudoalcaligenes str. JM8 FJ4728
FJ594992.1 gg_id:569922 Pseudomonas sp. str. CL-1 FJ5949
AF094734.1 gg_id:99890 Pseudomonas mendocina str. ATCC 25411 AF0947
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GQ110671.1 gg_id:451048 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ110
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EU937753.1 gg_id:311713 Pseudomonas sp. str. JG 10 Iti 8 EU9377
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EU927412.1 gg_id:319271 Pseudomonas mendocina str. 8-40B28 EU9274
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EF028693.1 gg_id:189438 Pseudomonas sp. str. BCL-53
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EU977740.1 gg_id:544679 Pseudomonas oryzihabitans str. 1P03PC
EU977588.1 gg_id:569674 Pseudomonas plecoglossicida str. 1P03MC
AB248284.1 gg_id:150864 Pseudomonas fulva str. 10 (= KMM 3881)
EU977738.1 gg_id:569323 Pseudomonas oryzihabitans str. 1P03PA
EU977587.1 gg_id:553834 Pseudomonas oryzihabitans str. 1P03MB
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AJ288148.1 gg_id:53166 Pseudomonas stutzeri Makran AJ2881
FJ671729.1 gg_id:526385 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6717
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EU771075.1 gg_id:338443 Pseudomonas stutzeri str. F22 EU7710
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AM933507.1 gg_id:334191 Pseudomonas veronii FB15 AM933
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AY512620.1 gg_id:102881 Pseudomonas veronii str. A1YC2-5 AY512
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AB506066.1 gg_id:576116 Pseudomonas sp. str. StFRB209 AB506
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AY277555.1 gg_id:89393 Pseudomonas sp. str. AGP3-7 AY2775
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AB088844.1 gg_id:79576 Pseudomonas sp. str. K23 AB0888
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EU539846.1 gg_id:280184 profile human microbiota antecubital fossa (inner elbow) skin clone nbt106c10 EU5398
EU538445.1 gg_id:282737 profile human microbiota antecubital fossa (inner elbow) skin clone nbt229g12 EU5384
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AB547166.1 gg_id:515561 Pseudomonas sp. str. DSP-S3 AB5471
FJ892984.1 gg_id:548837 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota HM2; ear p FJ8929
EU877075.1 gg_id:341197 Pseudomonas putida str. EC3_2001 EU8770
EU540274.1 gg_id:281449 profile human microbiota antecubital fossa (inner elbow) skin clone nbt113e10 EU5402
AJ846274.1 gg_id:106541 Pseudomonas sp. HHS8 AJ8462
EF471903.1 gg_id:217410 Pseudomonas sp. str. GW28-5 EF4719
AF320994.1 gg_id:33806 Pseudomonas tolaasii str. NZ027 AF3209
Z76669.1 gg_id:8639 Pseudomonas syringae str. LMG 1247t1T (; pathovar reference strain) Z76669
EU540055.1 gg_id:281519 profile human microbiota antecubital fossa (inner elbow) skin clone nbt112e11 EU5400
AY538263.1 gg_id:100141 Pseudomonas fluorescens str. PC17 AY5382
AB108691.1 gg_id:83881 Pseudomonas putida str. AN2 AB1086
EU538374.1 gg_id:280440 profile human microbiota antecubital fossa (inner elbow) skin clone nbt88b03 EU5383
FJ893864.1 gg_id:554161 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B1E; ear pu FJ8938
EF565945.1 gg_id:227761 Pseudomonas sp. str. 1043 EF5659
AF094726.1 gg_id:71021 Pseudomonas fluorescens str. ATCC 17386 AF0947
EU540294.1 gg_id:282548 profile human microbiota antecubital fossa (inner elbow) skin clone nbt114c12 EU5402
FJ893943.1 gg_id:549107 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B1E; ear pu FJ8939
AJ936933.1 gg_id:175024 Pseudomonas simiae AJ9369
FJ894257.1 gg_id:543206 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B2E; ear pu FJ8942
AY303316.1 gg_id:129966 Pseudomonas sp. str. ps6-35 AY3033
EU930815.1 gg_id:307397 Pseudomonas putida str. PC EU9308
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AF313466.1 gg_id:35880 Pseudomonas veronii AF3134
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FJ788425.1 gg_id:537584 Pseudomonas putida str. Rs-198 FJ7884

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AF411855.1 gg_id:27138 Pseudomonas sp. str. 5B AF411
FJ895023.1 gg_id:535208 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota BME; ear p FJ8950
AM111013.1 gg_id:140933 Pseudomonas sp. str. 7001 AM111
FJ894165.1 gg_id:567845 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B1E; ear pı FJ8941
FJ893919.1 gg_id:535538 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B1E; ear pı FJ8939
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FJ893323.1 gg_id:548944 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota WT1; ear p FJ8933
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DQ256083.1 gg_id:143611 Pseudomonas fluorescens str. sp-f DQ256
AB294558.1 gg_id:204838 Pseudomonas putida str. NCB0308-456 AB294
FJ892909.1 gg_id:538158 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota HM1; ear p FJ8929
DQ289076.1 gg_id:144195 Bacillus subtilis FM21 DQ289
FJ893397.1 gg_id:563933 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota WT1; ear p FJ8933
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AY303321.1 gg_id:131310 Pseudomonas sp. str. ps6-49 AY3033
EF016112.1 gg_id:195370 Pseudomonas sp. str. BSLY EF0161
AF374472.1 gg_id:67535 Pseudomonas costantinii str. CFBP 5705; HAMBI 2444 AF3744
EU538183.1 gg_id:283248 profile human microbiota antecubital fossa (inner elbow) skin clone nbt81g06 EU538
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FJ894960.1 gg_id:535843 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota BME; ear p FJ8949
EU169189.1 gg_id:237380 Pseudomonas tolaasii str. B34 EU169
DQ318867.1 gg_id:152043 Pseudomonas syringae str. 6 DQ318
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FJ893155.1 gg_id:557378 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota HM3; ear p FJ8931
EU434400.1 gg_id:270408 Pseudomonas fluorescens str. a342 EU434
EF153018.1 gg_id:184271 Pseudomonas corrugata str. P94 EF153
AJ249825.2 gg_id:74089 Pseudomonas putida str. GPo1 (TF4-1L) AJ2498
DQ402053.1 gg_id:155811 Pseudomonas fluorescens TC222 DQ402
FJ894348.1 gg_id:548110 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B2E; ear pu FJ8943
GU372931.1 gg_id:514461 Pseudomonas sp. str. CS3 GU372
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EU534747.1 gg_id:280344 profile human skin microbiota ear punch biopsy female C57BL/6J mouse clone nbt21 EU534
AF502594.1 gg_id:66559 Pseudomonas monteilii str. C11 AF502
AY900171.1 gg_id:142050 Pseudomonas fluorescens str. PCL1751 AY900
AF130950.1 gg_id:8581 Pseudomonas syringae str. A90 AF130
EU535916.1 gg_id:280150 profile human microbiota antecubital fossa (inner elbow) skin clone nbt06b10 EU535
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DQ257632.1 gg_id:147233 Pseudomonas putida str. MTCC 5110 DQ257
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AY690673.1 gg_id:99074 Sulfitobacter sp. str. GC07 AY690
AF100323.1 gg_id:8681 Pseudomonas thivervalensis str. SBK26; CFBP 11261T AF100
DQ536518.1 gg_id:161371 Pseudomonas poae str. BIHB 752 DQ536
EU434546.1 gg_id:258577 Pseudomonas fluorescens str. b59 EU434
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EU554430.1 gg_id:274557 Pseudomonas putida str. Ag04 EU554
GU186124.1 gg_id:548053 Pseudomonas fluorescens str. IHB B 1427 GU186
GQ174492.1 gg_id:446815 Pseudomonas sp. str. 32A GQ174
EU827496.1 gg_id:320652 Pseudomonas putida str. TFD49 EU827
FJ911604.1 gg_id:535159 Rhizobium sp. str. SPC RN2 FJ9116
GQ451221.1 gg_id:552947 Fecal Yunnan snub-nosed monkey feces clone J87 GQ451
FJ894687.1 gg_id:574364 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota BME; ear p FJ8946
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EF154274.1 gg_id:190873 Pseudomonas tolaasii str. 34 EF1542
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EF455752.1 gg_id:204831 Pseudomonas tolaasii ACCC 01267 EF4557
DQ288949.1 gg_id:144539 Pseudomonas putida TG11 DQ288
AJ889838.1 gg_id:113026 Pseudomonas avellanae str. BPIC 714 AJ8898
FJ894440.1 gg_id:542748 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B2E; ear pu FJ8944
NC_010322.1 gg_id:263559 Pseudomonas putida str. GB-1 NC_01
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FJ981653.1 gg_id:535517 Flea Vectors Plague clone XC7 FJ9816
AY574282.1 gg_id:140321 Pseudomonas putida str. S16 AY5742
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FM208263.1 gg_id:326340 Pseudomonas sp. str. DSM 8628 FM208
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FJ893183.1 gg_id:565882 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota HM3; ear p FJ8931
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EU434349.1 gg_id:260230 Pseudomonas fluorescens str. a258 EU4343
FJ894378.1 gg_id:556184 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B2E; ear pu FJ8943
EU601175.1 gg_id:279245 Pseudomonas putida str. PBRs5 EU601
FJ892805.1 gg_id:572626 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota HM1; ear p FJ8928
EF102852.1 gg_id:252507 Pseudomonas sp. str. G-229-23 EF1028
FJ605372.1 gg_id:451091 Pseudomonas plecoglossicida str. Fn-2 FJ6053
EU373377.1 gg_id:276371 Pseudomonas fluorescens str. HNR16 EU3733
EU652104.1 gg_id:274750 Pseudomonas sp. str. ybd-1 EU6521
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EU539844.1 gg_id:283892 profile human microbiota antecubital fossa (inner elbow) skin clone nbt106c05 EU5398
FJ422406.1 gg_id:360669 Pseudomonas fluorescens str. CB32 FJ4224
EU537106.1 gg_id:279854 profile human microbiota antecubital fossa (inner elbow) skin clone nbt220g07 EU5371
FJ894060.1 gg_id:561617 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B1E; ear pu FJ8940
GU186116.1 gg_id:589957 Pseudomonas putida str. IHB B 1369 GU186
FN675869.1 gg_id:518676 Pseudomonas trivialis RE*1-1-14 FN6758
EU538939.1 gg_id:285340 profile human microbiota antecubital fossa (inner elbow) skin clone nbt95f03 EU5389
EU360314.1 gg_id:261260 Pseudomonas fluorescens str. 2313 EU3603
FJ894338.1 gg_id:564449 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B2E; ear pu FJ8943
GQ499333.1 gg_id:539966 Pseudomonas putida str. M1 GQ499
DQ087528.1 gg_id:128047 Pseudomonas putida str. PBM11 DQ087
FJ894369.1 gg_id:536140 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B2E; ear pu FJ8943
AF320990.1 gg_id:37361 Pseudomonas tolaasii str. NCPPB 2325 AF3209
FJ893610.1 gg_id:549815 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota WT3; ear p FJ8936
NR_024909.1 gg_id:560291 Pseudomonas orientalis str. CFML 96-170; CIP 105540 NR_024
EU539533.1 gg_id:285381 profile human microbiota antecubital fossa (inner elbow) skin clone nbt241d02 EU5395
EU439425.1 gg_id:594417 Pseudomonas putida str. OK-St EU4394
FJ950631.1 gg_id:401370 Pseudomonas putida str. c255 FJ9506
EU434416.1 gg_id:264637 Pseudomonas fluorescens str. a1 EU4344
EU535748.1 gg_id:286344 profile human microbiota antecubital fossa (inner elbow) skin clone nbt10c12 EU5357
FM211694.1 gg_id:325970 Pseudomonas putida str. P9 FM211
FJ894346.1 gg_id:538400 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B2E; ear pu FJ8943
EF102849.1 gg_id:241842 Pseudomonas putida str. G-4-14-1 EF1028
AF482685.1 gg_id:66956 Pseudomonas sp. str. NMX AF4826
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AY738626.1 gg_id:102117 Pseudomonas putida AY7386
FJ893958.1 gg_id:571781 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B1E; ear pu FJ8939
EU540301.1 gg_id:283128 profile human microbiota antecubital fossa (inner elbow) skin clone nbt114f12 EU5403

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U81870.1 gg_id:8646 Pseudomonas sp. str. BI*7 U8187
AY303300.1 gg_id:129613 Pseudomonas sp. str. ps4-28 AY3033
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EF489479.1 gg_id:226767 Pseudomonas plecoglossicida EF4894
FJ894423.1 gg_id:538102 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B2E; ear pu FJ8944
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FJ893564.1 gg_id:549060 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota WT2; ear p FJ8935
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FJ418774.1 gg_id:366431 Pseudomonas syringae pv. tomato str. 2 FJ4187
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EU439421.1 gg_id:538528 Pseudomonas putida str. LH-S1 EU4394
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D84004.1 gg_id:8606 Pseudomonas oryzihabitans str. IAM1568 D84004
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DQ177468.1 gg_id:140357 Pseudomonas sp. str. Tibet-IIA21 DQ177
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EU855189.1 gg_id:307393 Pseudomonas fulva str. CTSP6 EU8551
EU540081.1 gg_id:283910 profile human microbiota antecubital fossa (inner elbow) skin clone nbt245b09 EU5400
AJ132993.1 gg_id:46263 Pseudomonas putida #HR9 AJ1329
EU538386.1 gg_id:279796 profile human microbiota antecubital fossa (inner elbow) skin clone nbt87h04 EU5383
EU538956.1 gg_id:285202 profile human microbiota antecubital fossa (inner elbow) skin clone nbt96a03 EU5389
FJ893421.1 gg_id:543846 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota WT1; ear p FJ8934
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EU162042.1 gg_id:243921 Pseudomonas sp. str. B2 EU1620
EU784140.1 gg_id:354316 Azotobacter sp. str. HY1141 EU7841
DQ314545.1 gg_id:149377 Pseudomonas sp. str. BWDY-41 DQ314
AY303255.1 gg_id:134368 Pseudomonas sp. str. ps10-14 AY3032
EU373390.1 gg_id:275232 Pseudomonas synxantha str. HNR22 EU3733
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EU434358.1 gg_id:271891 Pseudomonas libanensis str. a110 EU4343
FJ894768.1 gg_id:546879 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota BME; ear p FJ8947
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DQ482656.1 gg_id:158174 Pseudomonas putida str. Dsp-1 DQ482
FJ894373.1 gg_id:558838 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B2E; ear pı FJ8943
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EU538021.1 gg_id:283538 profile human microbiota antecubital fossa (inner elbow) skin clone nbt225a09 EU5380
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AY242068.1 gg_id:102312 Pseudomonas pv. syringae str. FG11 AY2420
EF526503.1 gg_id:218860 Pseudomonas putida str. NAPC3 EF5265
AY730552.1 gg_id:105687 Pseudomonas fluorescens str. VH060479 AY7305
AJ308311.1 gg_id:21401 Pseudomonas putida str. Biotype ICMP 13629; ATCC 17392 AJ3083
GU136489.1 gg_id:559336 Pseudomonas sp. str. DY1 GU136
EU538936.1 gg_id:280552 profile human microbiota antecubital fossa (inner elbow) skin clone nbt95e08 EU5389
AF170731.1 gg_id:8771 Pseudomonas sp. str. QSSC1-9 AF1707
FJ950635.1 gg_id:419521 Pseudomonas putida str. c315 FJ9506
FJ894174.1 gg_id:568497 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B1E; ear pı FJ8941
FJ894365.1 gg_id:561847 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B2E; ear pı FJ8943
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FJ894967.1 gg_id:544031 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota BME; ear p FJ8949
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EU534713.1 gg_id:285416 profile human skin microbiota ear punch biopsy female C57BL/6J mouse clone nbt18 EU5347
EU022591.1 gg_id:322456 Pseudomonas putida str. KBL2RM2 EU0225
FJ893927.1 gg_id:540978 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B1E; ear pı FJ8939
EU539515.1 gg_id:283300 profile human microbiota antecubital fossa (inner elbow) skin clone nbt104e09 EU5395
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FJ894815.1 gg_id:540259 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota BME; ear p FJ8948
EU540308.1 gg_id:284991 profile human microbiota antecubital fossa (inner elbow) skin clone nbt114h10 EU5403
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GU186122.1 gg_id:558279 Pseudomonas mandelii str. IHB B 1384 GU186
AY267197.1 gg_id:107228 Pseudomonas fluorescens str. SK1 AY2671
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EU037280.1 gg_id:252326 Pseudomonas sp. G3DM-33 EU0372
FM209481.1 gg_id:325760 Pseudomonas jessenii str. T2P28 FM209
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FJ982922.1 gg_id:468384 Pseudomonas putida str. ST13 FJ9829
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EU414476.1 gg_id:270637 Pseudomonas gingeri str. SDLi-1 EU4144
AF105390.1 gg_id:8640 Pseudomonas syringae 010297 AF1053
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AB021397.1 gg_id:8571 Pseudomonas asplenii str. ATCC 23835T AB0213
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Z76652.1 gg_id:8784 Pseudomonas agarici str. LMG 2112T () Z76652
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AB302395.1 gg_id:221239 Pseudomonas metavorans str. F-1 AB302
AY770691.1 gg_id:108393 Pseudomonas sp. str. FR1439 AY770
FJ894581.1 gg_id:543698 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B2E; ear pu FJ8945
DQ095882.1 gg_id:128167 Pseudomonas plecoglossicida str. R18 DQ095
FJ393302.1 gg_id:358881 Pseudomonas plecoglossicida str. TCCC11291 FJ3933
EU538458.1 gg_id:285690 profile human microbiota antecubital fossa (inner elbow) skin clone nbt230a11 EU538
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FM163468.1 gg_id:336095 Pseudomonas putida str. R20 FM163
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GU059580.1 gg_id:514857 Pseudomonas fluorescens str. 1206 GU059
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EU538170.1 gg_id:281603 profile human microbiota antecubital fossa (inner elbow) skin clone nbt81c12 EU538
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EU538166.1 gg_id:286284 profile human microbiota antecubital fossa (inner elbow) skin clone nbt81c07 EU538
EU535097.1 gg_id:282669 profile human skin microbiota ear punch biopsy female C57BL/6J mouse clone nbt18 EU535
FM202487.1 gg_id:344499 Pseudomonas tolaasii str. IEXb FM202
FJ893683.1 gg_id:549927 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota WT3; ear p FJ8936
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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
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FJ893603.1 gg_id:553179 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota WT3; ear p FJ8936
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EU111725.2 gg_id:558591 Pseudomonas migulae str. CT14 EU1117
AF348508.1 gg_id:74250 Pseudomonas corrugata str. ND9L AF3485
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EU538196.1 gg_id:283086 profile human microbiota antecubital fossa (inner elbow) skin clone nbt82e10 EU5381
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FJ893154.1 gg_id:549797 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota HM3; ear p FJ8931
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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
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EU537043.1 gg_id:281302 profile human microbiota antecubital fossa (inner elbow) skin clone nbt219e06 EU5370
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AY303254.1 gg_id:133637 Pseudomonas sp. str. ps10-13 AY3032
GQ260082.1 gg_id:545388 Pseudomonas fluorescens str. ICIRC97 GQ260
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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
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EU537190.1 gg_id:286488 profile human microbiota antecubital fossa (inner elbow) skin clone nbt68b06 EU5371
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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
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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
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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
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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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AM293678.1 gg_id:242660 Pseudomonas fluorescens str. PTA-268 AM293
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
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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
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EU821343.1 gg_id:342183 Pseudomonas mendocina str. LM7 EU8213
DQ530464.1 gg_id:164982 Pseudomonas sp. str. gap-f-39 DQ530
AJ316017.1 gg_id:29570 Paederus melanurus endosymbiont AJ3160
EF515488.1 gg_id:222712 Electricigen Enrichment MFC full-scale anaerobic bioreactor sludge treating brewery EF5154
FJ950669.1 gg_id:387747 Pseudomonas sp. str. d130 FJ9506
EU043330.1 gg_id:324324 Pseudomonas mendocina str. PASS3-slimb EU0433
DQ803319.1 gg_id:199647 human fecal clone RL311_aam23h11 DQ803
EU169149.1 gg_id:245779 Pseudomonas tolaasii str. B37 EU1691
DQ497784.1 gg_id:161169 Microbial within Ground Support Equipment and Flight Hardware Station's Internal DQ497
GU723305.1 gg_id:528277 Pseudomonas aeruginosa str. PSCMST2 GU723
EU373426.1 gg_id:265122 Pseudomonas aeruginosa str. YRR02 EU3734
AJ550466.1 gg_id:83866 Pseudomonas alcaliphila AJ5504
GQ388955.1 gg_id:511762 quality deterioration drinking system during serious red water outbreak clone J130 GQ388
Z76666.1 gg_id:8520 Pseudomonas pseudoalcaligenes str. LMG 1225T () Z76666
DQ095892.1 gg_id:134548 Pseudomonas plecoglossicida str. S3 DQ095
AB021373.1 gg_id:8434 Pseudomonas resinovorans str. ATCC 14235T AB0213
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
AY486387.1 gg_id:105677 Pseudomonas pseudoalcaligenes str. AU4510 AY4863
DQ279822.1 gg_id:144098 Pseudomonas sp. str. D14 DQ279
AY689052.1 gg_id:100960 Pseudomonas sp. str. 6C_12 AY6890
FJ901043.1 gg_id:549234 Polymorphism microbial reservoirs water cut stage oil field clone G-84 FJ9010
EF102842.1 gg_id:241788 Pseudomonas aeruginosa str. P-5-3 EF1028
FJ853495.1 gg_id:539000 Pseudomonas aeruginosa str. ZSL-2 FJ8534
EF608177.1 gg_id:573436 Pseudomonas aeruginosa str. HT25 EF6081
DQ459316.1 gg_id:157858 Pseudomonas aeruginosa str. NRRL B-14935 DQ459
FM955874.1 gg_id:549837 Pseudomonas sp. str. Asd M6-6 FM955
AY953147.1 gg_id:115164 Pseudomonas otitidis str. MCC10330 AY9531
EU272857.1 gg_id:363576 Pseudomonas aeruginosa str. MK50 EU2728
DQ270690.1 gg_id:143958 Pseudomonas sp. B-2051 DQ270
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EU857418.1 gg_id:314447 Pseudomonas putida str. BF-S5 EU8574
FJ462715.1 gg_id:550332 Pseudomonas citronellolis str. YS-8 FJ4627
EF101781.1 gg_id:181146 Effect carbon source addition method on enrichment salicylate-degrading organisms EF1017
EU579530.1 gg_id:263193 Pseudomonas pseudoalcaligenes str. R32 EU5795

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AY748891.1 gg_id:104313 Pseudomonas aeruginosa N17.35 AY748
EU109736.1 gg_id:256066 Pseudomonas aeruginosa str. CR-25 EU109
EF091149.1 gg_id:248422 Pseudomonas sp. str. 19rlim EF0911
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
AF139998.1 gg_id:53970 Pseudomonas sp. str. ML-124 AF1399
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
AB037546.1 gg_id:47079 Pseudomonas aeruginosa str. #47 AB0375
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L37366.1 gg_id:8488 Pseudomonas mendocina str. KR L37366
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GQ388928.1 gg_id:575928 quality deterioration drinking system during serious red water outbreak clone J105 GQ388
FJ657941.1 gg_id:573409 Metalworking Fluids and Aerosols Metallurgy Plant metalworking fluid clone Winter_ FJ6579
EU082809.1 gg_id:245977 Pseudomonas sp. str. MY0506 EU0828
DQ837570.1 gg_id:166237 Pseudomonas sp. K1 DQ837
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EF509324.1 gg_id:221914 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aerug EF5093

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FJ715961.1 gg_id:550759 Pseudomonas aeruginosa FJ7159
GQ388981.1 gg_id:511565 quality deterioration drinking system during serious red water outbreak clone J30 GQ388
EU286805.1 gg_id:257108 Pseudomonas sp. str. S3-3 EU2868
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FJ674967.1 gg_id:513753 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6749
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
Z76672.1 gg_id:70154 Pseudomonas aeruginosa str. DSM 50071T () Z76672
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AY443041.1 gg_id:105353 Pseudomonas sp. str. HS5322 AY4430
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AM697417.1 gg_id:225569 sequencing libraries indoor dust clone BF0001D032 AM697
EU539418.1 gg_id:285673 profile human microbiota antecubital fossa (inner elbow) skin clone nbt238e05 EU5394
EU939691.1 gg_id:309323 Pseudomonas sp. str. SC06 EU9396
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
EU308476.1 gg_id:357842 Pseudomonas sp str. TA022 EU3084
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
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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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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
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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
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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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EU537051.1 gg_id:280037 profile human microbiota antecubital fossa (inner elbow) skin clone nbt219f07 EU537
DQ282185.1 gg_id:144955 Pseudomonas fluorescens str. PGN-1 DQ282
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
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EF428995.1 gg_id:216433 Pseudomonas fluorescens EF4289
EU538158.1 gg_id:285771 profile human microbiota antecubital fossa (inner elbow) skin clone nbt81a05 EU538
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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_02
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_02
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 AF430

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AM111045.1 gg_id:140916 Pseudomonas sp. str. 7065 AM111
FN646596.1 gg_id:557247 Pseudomonas sp. SS-2009-PA4 str. PA4 FN6465
AJ249382.1 gg_id:22698 Pseudomonas frederiksbergensis str. JAJ28 AJ2493
EU539350.1 gg_id:283152 profile human microbiota antecubital fossa (inner elbow) skin clone nbt237c09 EU5393
EU538914.1 gg_id:285813 profile human microbiota antecubital fossa (inner elbow) skin clone nbt95a08 EU5389
GU272230.1 gg_id:548694 library dichlorvos treatment rape phyllosphere clone TF19 GU272
EU348741.1 gg_id:272086 Pseudomonas putida soil EU3487
EU537111.1 gg_id:279820 profile human microbiota antecubital fossa (inner elbow) skin clone nbt67a05 EU5371
EU538710.1 gg_id:286594 profile human microbiota antecubital fossa (inner elbow) skin clone nbt235e05 EU5387
AB440177.1 gg_id:535106 Pseudomonas costantinii AB4401
EU536997.1 gg_id:280285 profile human microbiota antecubital fossa (inner elbow) skin clone nbt218e01 EU5369
FJ893409.1 gg_id:569655 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota WT1; ear p FJ8934
EU535778.1 gg_id:283503 profile human microbiota antecubital fossa (inner elbow) skin clone nbt10f10 EU5357
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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
GQ497248.1 gg_id:544313 Pseudomonas sp. str. F2-2 GQ497
AM933508.1 gg_id:324712 Pseudomonas antarctica FB16 AM933
EU538247.1 gg_id:286083 profile human microbiota antecubital fossa (inner elbow) skin clone nbt83g04 EU5382
AY303293.1 gg_id:131271 Pseudomonas sp. str. ps4-16 AY3032
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AY622264.1 gg_id:99494 subsurface soil clone S-A1 AY6222
AB021381.1 gg_id:8570 Pseudomonas fuscovaginae str. MAFF 301177T AB0213
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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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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EU536974.1 gg_id:285745 profile human microbiota antecubital fossa (inner elbow) skin clone nbt217h10 EU5369
EF529516.1 gg_id:225502 Pseudomonas putida str. CM5001 EF5295
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FJ893112.1 gg_id:543418 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota HM3; ear p FJ8931
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FJ894864.1 gg_id:552364 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota BME; ear p FJ8948
AY263475.1 gg_id:82913 Pseudomonas sp. WE7#2b AY2634
EU536231.1 gg_id:279948 profile human microbiota antecubital fossa (inner elbow) skin clone nbt61c07 EU536
EU545156.1 gg_id:272623 Pseudomonas congelans str. SS157 EU5451
DQ086781.1 gg_id:128180 Pseudomonas fluorescens str. SKIN2 DQ086
GU198113.1 gg_id:589242 Pseudomonas fluorescens str. LMG 5849 GU198
EU834261.1 gg_id:345741 Pseudomonas plecoglossicida str. DS39 EU834
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
AY456712.1 gg_id:100571 Pseudomonas sp. str. SBW25 AY4567
GU391452.1 gg_id:563866 Pseudomonas sp. str. Gd1T GU391
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FJ950619.1 gg_id:389167 Pseudomonas putida str. c141 FJ9506
FJ976589.1 gg_id:572088 Pseudomonas putida str. LCR80 FJ9765
EU539815.1 gg_id:280992 profile human microbiota antecubital fossa (inner elbow) skin clone nbt105c12 EU5398
EU221400.1 gg_id:256776 Pseudomonas thivervalensis str. H2P1 EU2214
AF094738.1 gg_id:24808 Pseudomonas putida str. ATCC 17472 AF0947
AM111028.1 gg_id:140966 Pseudomonas sp. str. 7028 AM111
EU537168.1 gg_id:285451 profile human microbiota antecubital fossa (inner elbow) skin clone nbt67g02 EU5371
EF682071.1 gg_id:348246 Pseudomonas putida str. DN1.2 EF6820
AY259924.1 gg_id:91834 Pseudomonas filiscindens str. ATCC BAA-697 AY2599
DQ313381.1 gg_id:190384 Pseudomonas putida str. PCL1758 DQ313
EU439423.1 gg_id:536092 Pseudomonas putida str. QR2 EU4394
EU538074.1 gg_id:279760 profile human microbiota antecubital fossa (inner elbow) skin clone nbt81f06 EU5380
AB507253.1 gg_id:593521 Pseudomonas putida str. Pes207 AB5072
EU822884.1 gg_id:328707 Pseudomonas fluorescens str. MXX08012001 EU8228
AM110075.2 gg_id:257086 Pseudomonas sp. str. Ri71 AM110
AB046996.1 gg_id:106916 Pseudomonas fulva str. AJ 2129 AB0469
EU538204.1 gg_id:281728 profile human microbiota antecubital fossa (inner elbow) skin clone nbt82h11 EU5382
EF459522.1 gg_id:207295 Pseudomonas graminis KFC-45 EF4595
AY047218.1 gg_id:17462 Pseudomonas migulae AY0472
AB302401.1 gg_id:222217 Pseudomonas cinnamophila str. C-17 AB3024
EU169169.1 gg_id:251990 Pseudomonas aurantiaca str. B23 EU1691
EU647702.1 gg_id:272669 Pseudomonas mediterranea str. REG60 EU6477
EU538388.1 gg_id:279923 profile human microbiota antecubital fossa (inner elbow) skin clone nbt88a06 EU5383
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AB110608.1 gg_id:104753 Pseudomonas putida str. KF751 AB1106
DQ095884.1 gg_id:128118 Pseudomonas plecoglossicida str. R21 DQ095
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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
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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
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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
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U62131.1 gg_id:32280 Solemya terraeregina gill symbiont U62131
AM236336.1 gg_id:169677 thiotrophic endosymbiont Lucinoma aff. kazani AM236
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AB073120.1 gg_id:67480 Endosymbiont Lamellibrachia satsuma clone TUB163 AB0731

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EU290681.1 gg_id:241066 microbial structure biogeochemical contrasting shelf sediments Namibian upwelling EU2906
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EU580679.1 gg_id:269980 Autotrophic Thiomicrospira denitrificans-Like Catalyst Coupled Denitrification and Su EU5806
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EU287120.1 gg_id:235979 Pacific arctic surface sediment clone P13-27 EU2871
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EF455919.1 gg_id:217101 Thiohalomonas denitrificans str. HLD 15 EF4559
EU374712.1 gg_id:274344 Thiohalorhabdus denitrificans str. HLD 10 EU3747
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GQ346935.1 gg_id:561050 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ346
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AJ698862.1 gg_id:112014 Francisella philomiragia str. ATCC 25015 AJ6988
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DQ400508.1 gg_id:160152 Methylophaga marina str. KM5 DQ400
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AY375062.1 gg_id:97463 deep sea sediment clone B92 AY3750
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EU287255.1 gg_id:239634 Pacific arctic surface sediment clone S11-72 EU2872
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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
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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
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AF532775.1 gg_id:60451 marine sediment clone Limfjorden L9 AF5327
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AF532773.1 gg_id:60453 marine sediment clone Limfjorden L6 AF5327
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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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EU491688.1 gg_id:261914 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU491
AB263619.1 gg_id:178235 Thioploca sp. 'Lake Ogawara' AB263
AB042542.1 gg_id:18561 Thiothrix eikelboomii str. COM- AB042
AB042544.1 gg_id:37302 Thiothrix flexilis str. EJ1M-B AB042
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
AB042537.1 gg_id:18257 Thiothrix disciformis str. B2-8 AB042
DQ067608.1 gg_id:138619 Thiothrix sp. str. FBR0112 DQ067
FM165205.1 gg_id:544166 Succession structure biotrickling filter treating loads H2S terminal restriction fragme FM165
FM174321.1 gg_id:565016 biotrickling filter treating loads H2S biology tools clone H2SRC112 FM174
FM174322.1 gg_id:564802 biotrickling filter treating loads H2S biology tools clone H2SRC127 FM174
U32940.1 gg_id:7656 "Thiothrix ramosa" U3294
L79961.1 gg_id:135216 Thiothrix unzii str. A1; ATCC 49747 L79961
AB166732.1 gg_id:99902 Thiothrix sp. str. KRN-B2 AB166
AY510242.1 gg_id:110102 microbial mat cave sulfidic spring clone LKC3_156.41 AY510
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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AM882547.1 gg_id:333792 Structure along hydrocarbon contamination coastal sediment oil polluted water pet AM882
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EF632659.1 gg_id:251374 Unique microbial contrasting aquatic altitude Andean Altiplano (northern Chile) sedir EF6326
FJ712446.1 gg_id:532489 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) k FJ7124
EU050802.1 gg_id:255117 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_01_06 EU050
EU734980.1 gg_id:327786 assemblages sediment station DBSE Northern Bering Sea clone 074B2 EU734
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AM176874.1 gg_id:161459 Recovery mangrove sediment clone SZB41 AM176
DQ015812.1 gg_id:140611 Antarctic lake water clone ELB16-159 DQ015
AM997958.1 gg_id:539642 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A AM997
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FM179868.1 gg_id:333458 Biogeochemical processes microbial Gullfaks and Tommeliten methane seeps (Nortl FM179
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AB250579.1 gg_id:160900 and ecology Grotta Azzurra Palinuro Cape (Salerno Italy) microbial mat clone #6-4 AB2505
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FJ497283.1 gg_id:575773 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun FJ4972
EU287240.1 gg_id:236488 Pacific arctic surface sediment clone S11-57 EU287
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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 CB13 GQ337
GQ350551.1 gg_id:535210 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ350

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AF257292.2 gg_id:27722 marine clone DHB-2 AF2572
DQ300596.1 gg_id:147780 microbial ocean's interior amplicon single fosmid library pool 130m depth HOT static DQ300
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
GQ347341.1 gg_id:592135 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ347
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
AM935318.1 gg_id:556062 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM935
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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FJ444714.1 gg_id:585507 Cotton Rhizosphere cotton rhizosphere clone 4h-1 FJ4447
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
EU735652.1 gg_id:356150 archaeal structures oil contaminated and soils China pristine soil Jidong Oilfield clone EU735
AY292922.1 gg_id:101121 Vibrio fischeri EM17 AY2929
DQ026824.1 gg_id:227498 Vibrio fischeri str. PP3 DQ026
CP000020.1 gg_id:129275 Vibrio fischeri str. ES114 CP000
AY628647.1 gg_id:103863 Vibrio wodanis AY628
DQ146991.1 gg_id:146962 Vibrio sp. str. V776 DQ146
AB497068.1 gg_id:546558 Aliivibrio logei str. 11-2 AB497
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
DQ642809.1 gg_id:161003 Vibrio sp. 6(2006) DQ642
EU091324.1 gg_id:317079 Aliivibrio salmonicida PB1-8rrnB EU0913
EU091323.1 gg_id:304361 Aliivibrio salmonicida PB1-8rrnA EU0913
AY292929.1 gg_id:102250 Vibrio logei str. Srond101401 AY2929
FJ654064.1 gg_id:511531 Coral Reef Fish Feces and Gut Microbial Assemblages gut contents distal intestine clo FJ6540
Z19105.1 gg_id:9129 Melanocetus johnsoni symbiont Z19105
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
AY204488.1 gg_id:103923 Photobacterium leiognathi str. gachl1.1 AY2044
D25309.1 gg_id:9154 Photobacterium leiognathi str. ATCC25521 D25309
AY341442.1 gg_id:106555 Photobacterium mandapamensis str. ATCC 33981 AY3414
DQ978988.1 gg_id:183456 Photobacterium sp. S-7 DQ978
DQ219367.1 gg_id:142286 Photobacterium sp. str. 2220 DQ219
DQ534014.1 gg_id:160550 Photobacterium lutimaris str. DF-42 DQ534

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AY642168.1 gg_id:112325 Photobacterium phosphoreum str. calba.4.2 AY642
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AB166848.1 gg_id:102935 Photobacterium phosphoreum str. 127-1 AB1668
AB000278.1 gg_id:9163 Photobacterium iliopiscarium str. ATCC51760 AB000
EF067913.1 gg_id:245715 endolithic microbes marine basalts aerobic enrichment s innoculated basalt Brown B EF0679
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DQ317679.1 gg_id:160104 Photobacterium sp. str. OIM3 DQ317
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GQ386817.1 gg_id:582886 Photobacterium sp. str. CAIM 1206 GQ386
NC_006370.1 gg_id:129243 Photobacterium profundum str. SS9 NC_00
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AM279735.1 gg_id:160832 Salinivibrio aegyptiaca subsp. sharmensis str. BbAG AM279
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DQ513033.1 gg_id:160210 Microbial life fluids ridge flank crustal fluid clone FS142-3B-02 DQ513
AY551089.1 gg_id:102788 Ferrania halotolerans str. MACL01 AY551
DQ289936.1 gg_id:171395 Microbial Carbon and Nitrogen Cycling Sediments South Atlantic Bight Permeable Sh DQ289
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DQ923438.1 gg_id:176420 Vibrio sp. W-4 DQ923
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EU153251.1 gg_id:243117 Photobacterium sp. str. P16011A EU153
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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
AJ316169.1 gg_id:73534 Vibrio sp. str. LMG 19270 AJ3161
EU854927.1 gg_id:309342 Vibrio sp. 6H6 EU854
FJ952824.1 gg_id:402184 Vibrio sp. str. 2tc2 FJ9528
EU854890.1 gg_id:313041 Vibrio sp. 6A3 EU854
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AJ874359.1 gg_id:109806 Vibrio splendidus str. 01/100 AJ8743
EU660364.1 gg_id:297368 Vibrio parahaemolyticus str. CT12 EU660
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EU517637.1 gg_id:268839 Vibrio sp. str. 4E11 EU517
Z19081.1 gg_id:9246 Anomalops katoptron symbiont Z19081
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EU372926.1 gg_id:271355 Vibrio sp. str. S4 EU372
GQ906772.1 gg_id:575876 Pseudomonas fluorescens str. MR-6 GQ906
EU854833.1 gg_id:305431 Vibrio sp. 1E7 EU854
DQ922916.1 gg_id:226196 Vibrio comitatus str. GHG24 DQ922
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AJ414132.1 gg_id:74395 Vibrio sp. str. SYS6-01 AJ4141
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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
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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 AY562
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 EU833
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
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FJ457435.1 gg_id:511250 Vibrio sp. str. S2321 FJ4574
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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
AJ316194.1 gg_id:70306 Vibrio pacinii str. LMG 19999	AJ3161
FJ202493.1 gg_id:320634 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k	FJ2024
EU170469.1 gg_id:242658 Vibrio parahaemolyticus str. 070925	EU1704
EF488080.1 gg_id:224355 Vibrio porteresiae str. MSSRF31	EF4880
EU854924.1 gg_id:356007 Vibrio sp. 6E9	EU8549
EU854902.1 gg_id:348515 Vibrio sp. 6B5	EU8549
AM422800.1 gg_id:238361 Vibrio harveyi str. 04101	AM422
EF203212.1 gg_id:214385 Vibrio parahaemolyticus str. R22	EF2032
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
FJ203285.1 gg_id:339560 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c	FJ2032
NC_009783.1 gg_id:471502 Vibrio harveyi BAA-1116 str. ATCC BAA-1116; BB120	NC_009
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
GU064378.1 gg_id:544893 Vibrio parahaemolyticus str. 489	GU064
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
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FJ202872.1 gg_id:308237 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k	FJ2028
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EU517633.1 gg_id:262574 Vibrio sp. str. 4D5	EU5176

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AY940169.1 gg_id:114484 Vibrio midae str. SY9	AY9401
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
AY863432.1 gg_id:113088 Vibrio qinhuangdaora	AY8634
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
EU636231.1 gg_id:284716 Vibrio parahaemolyticus str. V7	EU6362
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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DQ304557.1 gg_id:144132 Vibrio harveyi str. FA-1
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AY911392.1 gg_id:112501 Vibrio shilonii str. MP-3
AY264926.1 gg_id:105905 Vibrio harveyi str. OVL 99-52331-
AY372930.1 gg_id:143887 marine sponge Rhabdastrella globostellata symbiont
Z19003.1 gg_id:9249 Kryptophanaron alfredi symbiont
GQ375456.1 gg_id:583549 Vibrio splendidus str. GHrC13
AY332401.1 gg_id:224717 Vibrio harveyi str. EHR1
GQ205448.1 gg_id:434247 Vibrio parahaemolyticus str. JGB080708-1
EF100710.1 gg_id:191629 Vibrio sp. str. V134
AB239476.1 gg_id:154281 Vibrio campbellii str. LC1-257
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AB470937.1 gg_id:566097 Vibrio harveyi str. r44
AB297941.1 gg_id:212446 Vibrio nigripulchritudo str. FPC1062
EU541605.1 gg_id:276875 Vibrio sp. str. CECT 7244
AY245190.1 gg_id:86266 Vibrio parahaemolyticus 21
X74714.1 gg_id:9230 Vibrio natriegens str. ATCC 14048T
AM778456.1 gg_id:252007 Vibrio sp. Y310
EU854864.1 gg_id:332457 Vibrio sp. 2F3
DQ995519.1 gg_id:175212 Vibrio alginolyticus str. A3G-2
EF584039.1 gg_id:233082 Vibrio sp. str. DS5
AY911391.1 gg_id:112498 Vibrio parahaemolyticus str. MP-2
X74690.1 gg_id:9234 Vibrio alginolyticus str. ATCC 17749T
Z19085.1 gg_id:9245 Photoblepharon palpebratus symbiont
GQ406675.1 gg_id:531375 Vibrio sp. str. PaD3.34b
EU854950.1 gg_id:319651 Vibrio sp. 7B2
EU660311.1 gg_id:295546 Vibrio parahaemolyticus str. V1
EU854896.1 gg_id:319020 Vibrio sp. 6B10
EU854928.1 gg_id:339400 Vibrio sp. 6H1
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EF584044.1 gg_id:237322 Vibrio sp. str. DS12
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AY876051.1 gg_id:128096 Vibrio sp. HB-8
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DQ497398.1 gg_id:159058 Vibrio parahaemolyticus str. 93A-5807
EU854826.1 gg_id:320027 Vibrio sp. 1E8

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AM162655.1 gg_id:142807 Listonella anguillarum str. 610
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AY494842.1 gg_id:100088 Vibrio cholerae str. SIO
AY426981.1 gg_id:101436 Vibrio ezurae str. HDS1-2
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AJ514915.1 gg_id:104527 Vibrio fortis str. LMG 21562
AY257971.1 gg_id:84052 Vibrio gallicus str. CIP 107864; HT 1-3
AB000390.2 gg_id:9208 Vibrio halioticoli str. IAM14596T
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EU031646.1 gg_id:235697 Vibrio harveyi str. AK1

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AB512477.1 gg_id:533825 Vibrio harveyi str. AM16
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AY332564.1 gg_id:91201 Vibrio harveyi str. EcGY020401
DQ995520.1 gg_id:178502 Vibrio harveyi str. B1X-1
GQ901063.1 gg_id:516123 Vibrio harveyi str. BBD-216-1b
GU262992.1 gg_id:587331 Vibrio harveyi str. 090212
AB506811.1 gg_id:429905 Vibrio harveyi str. KO-1
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GQ327950.1 gg_id:544280 Vibrio harveyi str. 090625
AB512473.1 gg_id:573785 Vibrio harveyi str. AM15
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X74693.1 gg_id:9214 Vibrio harveyi str. ATCC 35084T
AF134581.1 gg_id:9215 Vibrio harveyi
GQ406758.1 gg_id:524766 Vibrio sp. str. PaH2.13D1
AY254041.1 gg_id:82765 Vibrio hispanicus str. LMG 13211
U46579.1 gg_id:9286 Vibrio scophthalmi str. CECT 4638; A089
AB257339.2 gg_id:196408 Vibrio kanaloae str. Do-155
AB257330.2 gg_id:175599 Vibrio kanaloae str. Do-40
DQ068937.1 gg_id:128196 Vibrio metschnikovii str. ATCC 7708
AY837747.1 gg_id:141151 Vibrio metschnikovii str. CCUG 49718 E2.5
X97987.1 gg_id:9174 Vibrio sp str. VI737/19
X74719.1 gg_id:9170 Vibrio orientalis str. ATCC 33934T
DQ978991.1 gg_id:198609 Vibrio sp. S-10
DQ978993.1 gg_id:196541 Vibrio sp. S-12
GQ406597.1 gg_id:528119 Vibrio sp. str. PaD1.29
GQ406593.1 gg_id:517204 Vibrio sp. str. PaD1.21b
NR_029344.1 gg_id:559028 Vibrio pectenicida str. Ifremer A365; CIP 105190
AJ514914.1 gg_id:104376 Vibrio fortis str. LMG 21559
AF124055.3 gg_id:202555 Vibrio aerogenes str. FG1; CCRC 17041; ATCC 700797
FJ176463.1 gg_id:553847 Vibrio sp. str. J-S2-8
AF462458.1 gg_id:47306 Vibrio ruber str. VR1; JCM 11486; CCRC 17186
EU854910.1 gg_id:342299 Vibrio sp. 6C7
FJ952776.1 gg_id:421759 Vibrio sp. str. 2ta10
AJ345063.1 gg_id:94006 Vibrio hepatarius str. LMG 20362
GQ889354.1 gg_id:548764 Vibrio sp. str. Mj2
AB470936.1 gg_id:548949 Vibrio sp. str. r11
X99762.2 gg_id:9228 Vibrio diabolicus str. HE800
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DQ847123.1 gg_id:161711 Vibrio rhizosphaerae str. MSSRF3

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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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FM204858.1 gg_id:357595 Vibrio rotiferianus FM204
AY332407.1 gg_id:227760 Vibrio rumoiensis str. UDP1 AY3324
EU123937.1 gg_id:342373 Ulcerative enteritis Homarus americanus: case report and intestinal aerobic apparen EU123
DQ530292.1 gg_id:234292 Vibrio rumoiensis str. LAR3 DQ530
EF584027.1 gg_id:229162 Vibrio sp. str. BS11 EF5840
AY911395.1 gg_id:112524 Vibrio shilonii str. SW-2 AY9113
NZ_ABGR01000018.1 gg_id:238096 Vibrio campbellii str. AND4 NZ_AB
FJ176450.1 gg_id:570249 Vibrio natriegens str. T-C2-11 FJ1764
AY800101.1 gg_id:255891 Vibrio tapetis str. HH6087 AY8001
FN554604.2 gg_id:548927 Vibrio tapetis str. HJ4 FN5546
AY800099.1 gg_id:255639 Vibrio tapetis str. UK6 AY8000
AY129278.1 gg_id:78597 Vibrio tapetis str. LP2 AY1292
EF546255.1 gg_id:277789 Polymorphisms Vibrio vulnificus clone 03_C01 EF5462
EF546280.1 gg_id:279479 Polymorphisms Vibrio vulnificus clone 05_C08 EF5462
GQ392008.1 gg_id:527025 Vibrio sp. str. PaD2.27 GQ392
AJ515220.1 gg_id:69396 Vibrio splendidus str. LMG 10952 AJ5152
NR_025480.1 gg_id:547832 Vibrio chagasii str. R-3712; DSM 17138 NR_02
AJ515219.1 gg_id:74459 Vibrio splendidus str. TNNIII7 AJ5152
AJ515218.1 gg_id:56555 Vibrio splendidus str. TNEMF6 AJ5152
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
AY102326.1 gg_id:65459 heavy metal-contaminated soil clone a13128 AY1023
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
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g__Ignatzschineria
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g__Luteibacter

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s__Dyella ginsengisoli	17021
s__Dyella ginsengisoli	17397
s__Dyella japonica	17167
s__unclassified	16382
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s__unclassified	17332
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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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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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GQ263865.1 gg_id:554529 Structure Simulated Level Waste Site simulated level waste site clone WC2_11 GQ263
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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AY218606.1 gg_id:82101 penguin droppings sediments clone KD3-139 AY2186
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 AY6415
AY738260.1 gg_id:106659 Stenotrophomonas maltophilia str. TKW1 AY7382
AB194323.1 gg_id:138821 Stenotrophomonas maltophilia str. BL-12 AB1943
DQ192172.1 gg_id:139973 Stenotrophomonas maltophilia str. flds DQ192
AB299977.1 gg_id:224930 Stenotrophomonas maltophilia str. 26-3 (= KMM 3045) AB2999
EU857419.1 gg_id:344187 Stenotrophomonas maltophilia str. BF-S6 EU8574
EU239471.1 gg_id:239046 Pseudomonas geniculata str. XJUHX-9 EU2394
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 EU2394
EU239476.1 gg_id:257977 Pseudomonas geniculata str. XJUHX-18 EU2394
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 EU4344
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 AF5115
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 EU2394
EU779483.1 gg_id:349163 Hartmann's Mountain Zebra feces clone AFZEB_aaj71b07 EU7794

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EF221779.1 gg_id:200228 Stenotrophomonas sp. str. tap-11
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EU927145.1 gg_id:350559 Stenotrophomonas maltophilia str. G2
AF100733.1 gg_id:70857 Stenotrophomonas maltophilia VUN10003
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EF620466.1 gg_id:248993 Stenotrophomonas maltophilia str. ISSDS-782
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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
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FN395263.1 gg_id:392327 Stenotrophomonas maltophilia str. FR-W4Ba FN395
FJ184334.1 gg_id:316000 structure and physiology pyrene-degrading consortia growing biofilms model trickle c FJ1843
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EU056836.1 gg_id:255845 Stenotrophomonas maltophilia str. NK-ST EU056
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AJ293467.1 gg_id:43218 Stenotrophomonas maltophilia str. c5 AJ2934
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AB101446.1 gg_id:79280 Xanthomonas axonopodis str. S54 AB101
AJ786786.1 gg_id:108063 Xanthomonas sp. R-20819 AJ7867
AF508111.1 gg_id:66233 Thermomonas haemolytica TJ7 AF508
AF508105.1 gg_id:66237 Thermomonas haemolytica N22 AF508
EU665168.1 gg_id:562931 Soil are Changed Agricultural Practices agricultural soil clone Plot22-2B06 EU665
EU834276.1 gg_id:316695 Thermomonas brevis str. DS60 EU834
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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
AB355702.1 gg_id:245102 Thermomonas brevis str. S47 AB355
EU662613.1 gg_id:539739 Productivity- Chemolithoautotrophically Based Sulfidic Karst Systems floating microb EU662
EF633616.1 gg_id:250370 Thermomonas sp. str. lyso-lm521 EF6336

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AJ536871.1 gg_id:150596 s wastes primer pairs uranium mining waste pile soil clone JG30a-KF-75 AJ5368
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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
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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
AY218741.1 gg_id:82032 penguin droppings sediments clone KD5-86 AY218
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
AF159581.1 gg_id:7897 Xanthomonas pv. campestris str. L2 AF159
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
AB240508.1 gg_id:141461 microbial structure rhizosphere biofilm Sapporo root-base (80 160 mm) Phragmites S AB240
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 AY963
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 AY218
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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AY294012.1 gg_id:136003 activated sludge enriched nonylphenol ethoxylates clone S3A1 AY294(
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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
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FJ380132.1 gg_id:367350 ornithogenic Ross Sea region Antarctica AB1 soil clone 1/2/4D FJ3801
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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
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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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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 syr 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
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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
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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
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X99298.1 gg_id:7880 Xanthomonas campestris str. LMG 726 X99298
GU086451.1 gg_id:544600 Xanthomonas campestris str. N5 GU086
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NZ_ACHS01000481.1 gg_id:531786 Xanthomonas campestris pv. vasculorum str. NCPPB702 NZ_AC
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AY572961.1 gg_id:99262 Xanthomonas translucens pv. poae str. ATCC 33804 AY5729
EU723184.1 gg_id:344976 Xanthomonas sp. str. kmd_489 EU7231
GU373652.1 gg_id:527773 Xanthomonas pv. campestris str. XCC10 GU373
X95918.1 gg_id:7894 Xanthomonas albilineans str. LMG 494-T X95918
FJ606765.1 gg_id:539828 Xanthomonas arboricola pv. pruni str. LMG852 FJ6067
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
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EF101977.1 gg_id:174832 Xanthomonas axonopodis str. IP1-36 EF1019
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AY855862.1 gg_id:151559 Xanthomonas translucens pv. graminis Xtg18 AY8558
AB246809.1 gg_id:149852 Pseudomonas boreopolis str. Q-5 AB2468
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
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AF159572.1 gg_id:7844 Xylella fastidiosa str. PCE-FG; ATCC35881 AF1595
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DQ351751.1 gg_id:146140 Microbial Adherent Sediment Particles Heavy Metal Contaminated North Sea Surfac DQ351
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
AY344400.1 gg_id:91672 Lake Kauhako 30 m clone K2-30-7 AY344
AB193918.1 gg_id:108876 deep-sea vent clone Sc-NB04 AB193
GQ350808.1 gg_id:562101 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ350
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EF573230.1 gg_id:231910 Coco's Island site 23 marine clone S23_1329 EF5732
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EU344940.1 gg_id:262115 Hepialus gonggaensis guts equalized library larval gut clone Hg5-30 EU3449
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EF018382.1 gg_id:205209 aspen rhizosphere clone Amb_16S_760 EF0183
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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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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
Z21638.1 gg_id:4384 Leptospira wolbachii str. BIFLEXA CDC Z21638
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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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
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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
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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
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D45192.1 gg_id:4240 Borrelia miyamotoi str. HT31 D4519
D67023.1 gg_id:4170 Borrelia tanukii str. Hk501 D6702
EF570073.1 gg_id:279638 Borrelia burgdorferi str. SCW-42a EF570
L40596.1 gg_id:4283 Borrelia sp str. DN127 L40596
EU081286.1 gg_id:508944 Borrelia americana str. SCW-33 EU081
X85201.1 gg_id:4280 Borrelia burgdorferi str. DUNKIRK X8520
U28503.1 gg_id:4205 Borrelia duttonii U2850
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U42284.1 gg_id:4182 Borrelia anserina str. ES-1 U4228
EU135596.1 gg_id:318700 Borrelia valaisiana str. QSYSP4 EU135
DQ103657.1 gg_id:132946 hypersaline endoevaporitic microbial mat clone E2aA10 DQ103
DQ154846.1 gg_id:139275 Diel Migration Restructures Hypersaline Microbial Mat hypersaline microbial mat cl DQ154
DQ329736.1 gg_id:159199 Guerrero Negro hypersaline microbial mat clone 05D2Z74 DQ329
DQ103658.1 gg_id:134251 hypersaline endoevaporitic microbial mat clone E2aH12 DQ103
GU118739.1 gg_id:594444 Threatened Corals Provide Microbial Habitats clone Mfra_O15 GU118
AY605135.1 gg_id:99534 microbial mat clone IE043 AY605
EU246240.1 gg_id:255595 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-P5-F11 EU246
GU118767.1 gg_id:545372 Threatened Corals Provide Microbial Habitats clone Mfra_M16 GU118
AY605154.1 gg_id:100580 microbial mat clone IF058 AY605
EU246071.1 gg_id:240820 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-P2-G11 EU246
AY605174.1 gg_id:101818 microbial mat clone LH071 AY605
FM242277.1 gg_id:320359 sequences sediment clone 6bis T0h-oil FM242
DQ154805.1 gg_id:138982 Diel Migration Restructures Hypersaline Microbial Mat hypersaline microbial mat cl DQ154
AY605171.1 gg_id:101310 microbial mat clone LH042 AY605
FJ202296.1 gg_id:326880 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2022
AF104475.1 gg_id:3806 Olavius loisae endosymbiont 4 AF1044
AM493256.1 gg_id:348409 Multiple symbionts two species co-occurring gutless oligochaete worms Mediterrar AM493
AJ431239.1 gg_id:79373 Cytophaga sp. str. BHI80-86 AJ4312
AB186802.1 gg_id:100628 polychlorinated dioxin dechlorinating microcosm clone TSBW25 AB1868
EF515721.1 gg_id:219079 Electricigen Enrichment MFC full-scale anaerobic bioreactor sludge treating brewery EF5157
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
CU922644.1 gg_id:559340 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU922

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EU245523.1 gg_id:249436 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M2-F0 EU245
AY605126.1 gg_id:103618 microbial mat clone IE015 AY605
EU245802.1 gg_id:256467 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M6-E1 EU245
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AJ431240.1 gg_id:79117 Spirochaeta sp. str. BHI80-158 AJ4312
DQ154820.1 gg_id:139224 Diel Migration Restructures Hypersaline Microbial Mat hypersaline microbial mat cl DQ154
GU118646.1 gg_id:570244 Threatened Corals Provide Microbial Habitats clone Mfav_L02 GU118
AB121100.1 gg_id:99658 cold seep sediment clone JS624-4 AB121
EU245482.1 gg_id:255522 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M2-B0 EU245
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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
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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
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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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EU734981.1 gg_id:347105 assemblages sediment station DBSE Northern Bering Sea clone 075B7 EU7349
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
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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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AB088884.1 gg_id:78359 termite gut homogenate clone Rs-J14 sp. AB088
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
EF454002.2 gg_id:220062 termite hindgut clone 290cost002-P3L-1429 EF4540
AB084960.1 gg_id:69104 termite gut clone NkS21 AB084
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 AB062
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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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
GQ502643.1 gg_id:534577 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf7- GQ502
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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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
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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
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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
X93926.1 gg_id:3807 Spirochaeta asiatica str. Z-7591 X93926
AF166259.1 gg_id:37803 Spironema culicis str. BR91 AF1662
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
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GU139329.1 gg_id:593443 lactate formate propionate hydrogen donors reductive dehalogenation trichloroeth GU139
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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
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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
NR_028903.1 gg_id:591885 Anaerobaculum mobile str. NGA; DSM13181; ATCC BAA-54 NR_028
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
CU919006.1 gg_id:533770 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU9190
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
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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
AB062819.1 gg_id:19846 termite gut homogenate clone BCf4-02 AB0628
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
AB234551.1 gg_id:149454 termite gut homogenate clone MgMjR-058 AB2345
DQ307691.1 gg_id:144040 termite intestinal tract clone MTG-61 DQ307
AB299560.1 gg_id:254669 Motility Symbiont Termite Gut Flagellate Caduceia versatilis Member 'Synergistes' G AB2995
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
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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
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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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EU511554.1 gg_id:273187 cecal contents Mus musculus strain C57BL/6J; WD9 clone WD9_aak06e02 EU511
EU511346.1 gg_id:264641 cecal contents Mus musculus strain C57BL/6J; WD8 clone WD8_aak18g03 EU511
EU511034.1 gg_id:277428 cecal contents Mus musculus strain C57BL/6J; WD7 clone WD7_aal01f09 EU511
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EU511348.1 gg_id:260083 cecal contents Mus musculus strain C57BL/6J; WD8 clone WD8_aak18g05 EU511
EU508531.1 gg_id:275302 cecal contents Mus musculus strain C57BL/6J; MD2 clone MD2_aap35a03 EU508
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EU504622.1 gg_id:273734 cecal contents Mus musculus strain C57BL/6J; myd1 clone myd1_aaa03d01 EU504
EU507921.1 gg_id:274791 cecal contents Mus musculus strain C57BL/6J; MD24 clone MD24_aaa03e06 EU507
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EU509742.1 gg_id:258735 cecal contents Mus musculus strain C57BL/6J; WD10 clone WD10_aak48b11 EU509
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EU507618.1 gg_id:262103 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_aaa02a08 EU507
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EU505346.1 gg_id:275252 cecal contents Mus musculus strain C57BL/6J; myd4 clone myd4_aaa02h09
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EU508904.1 gg_id:262026 cecal contents Mus musculus strain C57BL/6J; MD6 clone MD6_aap38b10
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EU507144.1 gg_id:264111 cecal contents Mus musculus strain C57BL/6J; MD22 clone MD22_aaa02c04
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EU503726.1 gg_id:264512 cecal contents Mus musculus strain C57BL/6J; CRWD2 clone CRWD2_aaa03g04
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EU507105.1 gg_id:263436 cecal contents Mus musculus strain C57BL/6J; MD22 clone MD22_aaa01d11
EU511638.1 gg_id:272358 cecal contents Mus musculus strain C57BL/6J; WD9 clone WD9_aak08a10
EU507110.1 gg_id:268053 cecal contents Mus musculus strain C57BL/6J; MD22 clone MD22_aaa01f01
EU506770.1 gg_id:276156 cecal contents Mus musculus strain C57BL/6J; MD20 clone MD20_aap56a06
EU508273.1 gg_id:258736 cecal contents Mus musculus strain C57BL/6J; MD27 clone MD27_aaa01b03
EF099605.1 gg_id:181334 mouse cecum clone SWPT4_aaa01g04
EU508420.1 gg_id:260325 cecal contents Mus musculus strain C57BL/6J; MD2 clone MD2_aap33c07
EU507848.1 gg_id:259647 cecal contents Mus musculus strain C57BL/6J; MD24 clone MD24_aaa01h02
EU505410.1 gg_id:264645 cecal contents Mus musculus strain C57BL/6J; myd4 clone myd4_aaa04a06
EU510950.1 gg_id:276638 cecal contents Mus musculus strain C57BL/6J; WD6 clone WD6_aak52c02
EU506817.1 gg_id:261795 cecal contents Mus musculus strain C57BL/6J; MD20 clone MD20_aap56h02
EU508375.1 gg_id:277042 cecal contents Mus musculus strain C57BL/6J; MD27 clone MD27_aaa04c07
EU506604.1 gg_id:261326 cecal contents Mus musculus strain C57BL/6J; MD20 clone MD20_aap53b10
EU508929.1 gg_id:266817 cecal contents Mus musculus strain C57BL/6J; MD6 clone MD6_aap39b09
EU508441.1 gg_id:273802 cecal contents Mus musculus strain C57BL/6J; MD2 clone MD2_aap33e09
EU506669.1 gg_id:272190 cecal contents Mus musculus strain C57BL/6J; MD20 clone MD20_aap54b08
EU507690.1 gg_id:276757 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_aaa03c07
EU511255.1 gg_id:265361 cecal contents Mus musculus strain C57BL/6J; WD8 clone WD8_aak17b08
EU505497.1 gg_id:264699 cecal contents Mus musculus strain C57BL/6J; myd5 clone myd5_aaa01e06
EU507351.1 gg_id:260179 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_2aaa02a09
EU511453.1 gg_id:270231 cecal contents Mus musculus strain C57BL/6J; WD8 clone WD8_aak20e11
EU507804.1 gg_id:262219 cecal contents Mus musculus strain C57BL/6J; MD24 clone MD24_aaa01b02
EU511437.1 gg_id:270460 cecal contents Mus musculus strain C57BL/6J; WD8 clone WD8_aak20c06
EU507851.1 gg_id:265433 cecal contents Mus musculus strain C57BL/6J; MD24 clone MD24_aaa01h07
EU505321.1 gg_id:274384 cecal contents Mus musculus strain C57BL/6J; myd4 clone myd4_aaa02e01

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EU508639.1 gg_id:271756 cecal contents Mus musculus strain C57BL/6J; MD2 clone MD2_aap36f09
EU506764.1 gg_id:264481 cecal contents Mus musculus strain C57BL/6J; MD20 clone MD20_aap55h08
EU510765.1 gg_id:266227 cecal contents Mus musculus strain C57BL/6J; WD5 clone WD5_aak40h10
EU511037.1 gg_id:259314 cecal contents Mus musculus strain C57BL/6J; WD7 clone WD7_aal01g02
EU505265.1 gg_id:260007 cecal contents Mus musculus strain C57BL/6J; myd4 clone myd4_aaa01e08
EU507268.1 gg_id:273137 cecal contents Mus musculus strain C57BL/6J; MD22 clone MD22_aaa04g02
EU507889.1 gg_id:259741 cecal contents Mus musculus strain C57BL/6J; MD24 clone MD24_aaa02g07
EU511607.1 gg_id:264282 cecal contents Mus musculus strain C57BL/6J; WD9 clone WD9_aak07d09
EU505264.1 gg_id:268970 cecal contents Mus musculus strain C57BL/6J; myd4 clone myd4_aaa01e06
EU506704.1 gg_id:258419 cecal contents Mus musculus strain C57BL/6J; MD20 clone MD20_aap54g11
EU508537.1 gg_id:260583 cecal contents Mus musculus strain C57BL/6J; MD2 clone MD2_aap35b02
EU505385.1 gg_id:276790 cecal contents Mus musculus strain C57BL/6J; myd4 clone myd4_aaa03f06
EU508763.1 gg_id:260625 cecal contents Mus musculus strain C57BL/6J; MD4 clone MD4_aap50f09
EU504373.1 gg_id:276645 cecal contents Mus musculus strain C57BL/6J; CRWD6 clone CRWD6_aaa03c02
EU507092.1 gg_id:268381 cecal contents Mus musculus strain C57BL/6J; MD22 clone MD22_aaa01b08
EU505326.1 gg_id:261861 cecal contents Mus musculus strain C57BL/6J; myd4 clone myd4_aaa02e07
EU510815.1 gg_id:275230 cecal contents Mus musculus strain C57BL/6J; WD6 clone WD6_aak49f10
EU510996.1 gg_id:277246 cecal contents Mus musculus strain C57BL/6J; WD7 clone WD7_aal01b02
EU507968.1 gg_id:267744 cecal contents Mus musculus strain C57BL/6J; MD24 clone MD24_aaa04h08
EU508609.1 gg_id:259298 cecal contents Mus musculus strain C57BL/6J; MD2 clone MD2_aap36c03
EU510924.1 gg_id:270518 cecal contents Mus musculus strain C57BL/6J; WD6 clone WD6_aak51f12
EU504465.1 gg_id:264394 cecal contents Mus musculus strain C57BL/6J; CRWD6 clone CRWD6_aaa04h06
EU508654.1 gg_id:274263 cecal contents Mus musculus strain C57BL/6J; MD2 clone MD2_aap36h05
EU509080.1 gg_id:264601 cecal contents Mus musculus strain C57BL/6J; MD7 clone MD7_aap43c06
EU508631.1 gg_id:271916 cecal contents Mus musculus strain C57BL/6J; MD2 clone MD2_aap36e08
EU509668.1 gg_id:276430 cecal contents Mus musculus strain C57BL/6J; WD10 clone WD10_aak46h06
EU510822.1 gg_id:274196 cecal contents Mus musculus strain C57BL/6J; WD6 clone WD6_aak49g07
EU507406.1 gg_id:262058 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_2aaa02g09
EU509057.1 gg_id:260836 cecal contents Mus musculus strain C57BL/6J; MD7 clone MD7_aap42g10
EU505389.1 gg_id:266572 cecal contents Mus musculus strain C57BL/6J; myd4 clone myd4_aaa03f10
EU505423.1 gg_id:273017 cecal contents Mus musculus strain C57BL/6J; myd4 clone myd4_aaa04c06
EU504523.1 gg_id:273270 cecal contents Mus musculus strain C57BL/6J; myd1 clone myd1_aaa01g09
EF099211.1 gg_id:197429 mouse cecum clone SWPT2_aaa04a05
EU507094.1 gg_id:275623 cecal contents Mus musculus strain C57BL/6J; MD22 clone MD22_aaa01c02
EU507091.1 gg_id:275882 cecal contents Mus musculus strain C57BL/6J; MD22 clone MD22_aaa01b03
EU507233.1 gg_id:258892 cecal contents Mus musculus strain C57BL/6J; MD22 clone MD22_aaa03h12
EU506791.1 gg_id:263684 cecal contents Mus musculus strain C57BL/6J; MD20 clone MD20_aap56d05
EU511078.1 gg_id:273953 cecal contents Mus musculus strain C57BL/6J; WD7 clone WD7_aal02d04
EU507701.1 gg_id:267813 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_aaa03d08

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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
DQ796924.1 gg_id:180379 human fecal clone RL179_aao56e02 DQ796
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
AY977931.1 gg_id:124370 human cecum mucosal biopsy clone LG47 AY977
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
DQ796744.1 gg_id:198851 human fecal clone RL179_aao53h07 DQ796
EU467482.1 gg_id:292065 Sumatran orangutan feces clone orang1_h04_1 EU467
DQ800165.1 gg_id:184625 human fecal clone RL303_aal69a10 DQ800
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
NZ_ADFR01000011.1 gg_id:532556 Bulleidia extructa str. W1219 NZ_AD
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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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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DQ326852.1 gg_id:149140 Metagenomic gut microbiome healthy human stool clone E331 DQ326
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DQ794080.1 gg_id:183083 human fecal clone RL176_aan57g03 DQ794
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DQ057480.1 gg_id:136526 str. ic1391 DQ057
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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
DQ798576.1 gg_id:178236 human fecal clone RL181_aan98e03 DQ798
AY975735.1 gg_id:116787 human ascending colon mucosal biopsy clone Y182 AY975
DQ797930.1 gg_id:180338 human fecal clone RL302_aal93e08 DQ797
FJ372126.1 gg_id:360238 feces adult twins and mothers; TS9 clone TS9_a02a08 FJ3721
FJ371039.1 gg_id:370335 feces adult twins and mothers; TS5 clone TS5_a04c01 FJ3710
AJ576387.1 gg_id:104610 midgut homogenate Pachnoda ephippiata larva clone PeM18 AJ5763
GQ046231.1 gg_id:427628 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw GQ046
FJ370907.1 gg_id:362830 feces adult twins and mothers; TS5 clone TS5_a02f06 FJ3709
DQ327268.1 gg_id:145872 Metagenomic gut microbiome healthy human stool clone E812 DQ327
FJ370787.1 gg_id:363246 feces adult twins and mothers; TS5 clone TS5_a01c07 FJ3707
FJ370764.1 gg_id:362087 feces adult twins and mothers; TS5 clone TS5_a01a04 FJ3707
FJ369674.1 gg_id:360605 feces adult twins and mothers; TS51 clone TS51_a03e03 FJ3696
DQ797079.1 gg_id:194170 human fecal clone RL386_aao86g03 DQ797
FJ368379.1 gg_id:359304 feces adult twins and mothers; TS3 clone TS3_a03f08 FJ3683
FJ368229.1 gg_id:358899 feces adult twins and mothers; TS3 clone TS3_a01g05 FJ3682
FJ678559.1 gg_id:516982 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6785
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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
AB030220.1 gg_id:21822 Coprobacillus cateniformis str. JCM 10605 AB030
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
NZ_ABAW02000024.1 gg_id:470381 Eubacterium dolichum str. DSM 3991 NZ_AB
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
M23728.1 gg_id:15730 Erysipelothrix rhusiopathiae M2372
DQ462571.1 gg_id:157405 Erysipelothrix muris DQ462
AB055910.1 gg_id:78143 Erysipelothrix rhusiopathiae str. KG-BB2 AB055
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
EU771726.1 gg_id:309403 African elephant feces clone AFYEL_aaj65d04 EU771
DQ353900.1 gg_id:149744 Fecal Wild Gorilla (Gorilla beringei) wild gorilla feces clone Z2 DQ353
EU470295.1 gg_id:293994 Grevy's zebra feces clone GZ_aaa03h02 EU470
DQ353909.1 gg_id:149927 Fecal Wild Gorilla (Gorilla beringei) wild gorilla feces clone Z22 DQ353
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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AY128088.1 gg_id:60757 phototrophic sludge clone PSB-M-3 AY128
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
EU458790.1 gg_id:290793 Goeldi's marmoset feces clone CAL_f07_1 EU458
EU458745.1 gg_id:295903 Goeldi's marmoset feces clone CAL_c04_2 EU458
EU458772.1 gg_id:295432 Goeldi's marmoset feces clone CAL_b05_2 EU458
EU458780.1 gg_id:299091 Goeldi's marmoset feces clone CAL_c08_2 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
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DQ353903.1 gg_id:148303 Fecal Wild Gorilla (Gorilla beringei) wild gorilla feces clone Z5 DQ353
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EU510761.1 gg_id:276677 cecal contents Mus musculus strain C57BL/6J; WD5 clone WD5_aak40h01 EU510
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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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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
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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
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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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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
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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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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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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
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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
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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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Y16395.1 gg_id:15608 Rubus stunt phytoplasma Y16395
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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