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FJ810580.1 gg_id:375861 Subsurface ecosystem resilience: Long-term attenuation subsurface contaminants su FJ8105
AY328747.1 gg_id:90051 drinking water system simulator clone DSSD49 AY3287
EF492933.1 gg_id:257753 Iron-manganese Nodule and Its Surrounding Soil soil around iron-manganese nodule EF4929
AB294323.1 gg_id:210077 Microbial structure deep coal seem groundwater stream clone SWB12 AB2943
EF492932.1 gg_id:247931 Iron-manganese Nodule and Its Surrounding Soil soil around iron-manganese nodule EF4929
DQ337089.1 gg_id:150172 subsurface water clone EV818SWSAP66 DQ337
DQ404884.1 gg_id:155647 contaminated sediment clone 654956 DQ404
AM935609.1 gg_id:561445 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM935
AB294324.1 gg_id:203879 Microbial structure deep coal seem groundwater stream clone SWB13 AB2943
AY922035.1 gg_id:113557 farm soil clone AKYG578 AY922(
DQ837224.1 gg_id:242598 Archaeal and pristine National Park Spain Donana coastal aquifer clone 49S1_1B_8 DQ837
EF540408.1 gg_id:226082 oil-shale semi-coke solid waste clone 1_24MK EF5404
EU133831.1 gg_id:241569 tallgrass prarie soil clone FFCH14189 EU1338
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AY221066.1 gg_id:86386 Mammoth cave clone CCM6a AY221(
FJ810590.1 gg_id:419579 Subsurface ecosystem resilience: Long-term attenuation subsurface contaminants su FJ8105
EF999347.1 gg_id:240278 Vertical and Methanotrophs Estuarine Sediments Pearl River Estuary sediments 6cm EF9993
EU133877.1 gg_id:237992 tallgrass prarie soil clone FFCH1801 EU1338
EF574185.1 gg_id:230954 site S25 near Coco's Island marine clone S25_529 EF5741
AY907807.1 gg_id:136986 identification picoplankton contrasting waters Arabian Sea water clone A714022 AY9078
EU477832.1 gg_id:267229 and validation prototype -based taxonomic microarray members genus Burkholderia EU4778
AY234747.1 gg_id:112317 soil isolate Ellin6095 AY2347
EU133863.1 gg_id:249993 tallgrass prarie soil clone FFCH8270 EU1338
EF516320.1 gg_id:223302 grassland soil clone FCPS762 EF5163
EF516424.1 gg_id:227269 grassland soil clone FCPU607 EF5164
EU881164.1 gg_id:352281 Karst region primary forest soil clone KPF200711-070 EU8811
EF516735.1 gg_id:219174 grassland soil clone FCPU655 EF5167
EF516835.1 gg_id:225073 grassland soil clone FCPS400 EF5168
EF019212.1 gg_id:209746 aspen rhizosphere clone Amb_16S_1908 EF0192
EF654711.1 gg_id:245246 suspended sludge anammox reactor clone KIST-JJY042 EF6547
FJ479088.1 gg_id:555896 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4790
DQ413068.1 gg_id:152782 Microbial -dependent and Approaches Anaerobic/Aerobic SBR Reactor EBPR sludge DQ413
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DQ297977.1 gg_id:142009 Microbial hydrocarbon contaminated soil clone UA5 DQ297

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EF516867.1 gg_id:226979 grassland soil clone FCPO570 EF5168
EF516029.1 gg_id:225920 grassland soil clone FCPS638 EF5160
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EU669638.1 gg_id:307844 soil clone S8-40 EU6696
EF516006.1 gg_id:226748 grassland soil clone FCPT739 EF5160
AY921954.1 gg_id:113273 farm soil clone AKYG1130 AY9219
EF632895.1 gg_id:235519 Unique microbial contrasting aquatic altitude Andean Altiplano (northern Chile) fresh EF6328
EF516769.1 gg_id:224647 grassland soil clone FCPS759 EF5167
AB294328.1 gg_id:207655 Microbial structure deep coal seem groundwater stream clone SWB17 AB2943
EF516759.1 gg_id:222745 grassland soil clone FCPT632 EF5167
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AB426185.1 gg_id:273001 -situ identification study benzene-degrading s under methanogenic condition anaerc AB4261
EF516394.1 gg_id:223219 grassland soil clone FCPP685 EF5163
EU528239.1 gg_id:281246 Seasonal Dynamics Mudflat Mouth Major Kentucky Lake Reservoir Tributary sedime EU5282
EF516152.1 gg_id:217704 grassland soil clone FCPS619 EF5161
EU223955.1 gg_id:236215 -RFLP microbes Qinghai-Tin rail soil clone 124 EU2239
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EU133850.1 gg_id:236450 tallgrass prarie soil clone FFCH16997 EU1338
EF516351.1 gg_id:226263 grassland soil clone FCPT411 EF5163
EF019531.1 gg_id:205301 aspen rhizosphere clone Elev_16S_1034 EF0195
EU881346.1 gg_id:336201 (maize-sweet cropping field) Karst region maize-sweet potato cropland soil clone KM EU8813
AY921981.1 gg_id:113247 farm soil clone AKYG1746 AY9219
EF520945.1 gg_id:221665 Stable isotope probing 15N2 noncultivated diazotrophs 30 year fal soil Caldwell field EF5209
DQ676312.1 gg_id:220761 Archaeal sediment and plankton freshwater pond suboxic freshwater-pond clone M DQ676
AB294330.1 gg_id:207373 Microbial structure deep coal seem groundwater stream clone SWB19 AB2943
EF020158.1 gg_id:207982 aspen rhizosphere clone Elev_16S_1590 EF0201
GQ396975.1 gg_id:553957 Functional unvegetated perhumid recently-deglaciated soils do not correlate shifts s GQ396
FJ466126.1 gg_id:509733 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea FJ4661
FJ479428.1 gg_id:583255 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4794
EU528189.1 gg_id:285197 Seasonal Dynamics Mudflat Mouth Major Kentucky Lake Reservoir Tributary sedime EU5281
EF580984.1 gg_id:277681 Survey Microbial Freshwater Calcareous Mats freshwater calcareous mat clone CM5 EF5809
EF516904.1 gg_id:218538 grassland soil clone FCPS542 EF5169
FJ444750.1 gg_id:551308 Cotton Rhizosphere cotton rhizosphere clone 4y-67 FJ4447
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AY921702.1 gg_id:114209 farm soil clone AKYG1579 AY9217

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GU208364.1 gg_id:576056 Study on Sediment Dongping Lake sediment clone Td4-20 GU208
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EF018962.1 gg_id:215229 aspen rhizosphere clone Amb_16S_1476 EF0189
AB488102.1 gg_id:551424 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSSUR0 AB488
EU404008.1 gg_id:355651 Microbial septic tank effluent and soil biozone infiltrative surface clean water clone (EU404(
EF516891.1 gg_id:222729 grassland soil clone FCPP448 EF5168
AM935489.1 gg_id:548533 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM935
EF590004.2 gg_id:234053 changes structure sediments Songhua River contaminated nitrobenzene -DGGE cloni EF590C
EF516321.1 gg_id:220011 grassland soil clone FCPN390 EF5163
AB286353.1 gg_id:204179 Reducing production and domination comamonadaceae reducing oxygen supply was AB286
AB286450.1 gg_id:205044 Reducing production and domination comamonadaceae reducing oxygen supply was AB286
DQ310741.1 gg_id:200807 Recurring seasonal dynamics microbial stream habitats riverine sediment clone WC(DQ310
EF516268.1 gg_id:224900 grassland soil clone FCPP617 EF5162
GQ396994.1 gg_id:593511 Functional unvegetated perhumid recently-deglaciated soils do not correlate shifts s GQ396
EF580928.1 gg_id:278471 Survey Microbial Freshwater Calcareous Mats freshwater calcareous mat clone CM1 EF5809
EU340157.1 gg_id:238343 on Aquatic Macrophytes Geothermally Active Area Sedge Bay Yellowstone Lake WY EU340
EU340165.1 gg_id:237526 on Aquatic Macrophytes Geothermally Active Area Sedge Bay Yellowstone Lake WY EU340
EU104188.1 gg_id:341168 Evidence Comamonadaceae determinants settling performance activated sludge clo EU104
CU924494.1 gg_id:561226 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU924
AF371865.1 gg_id:25562 swine intestine clone p-2552-9F5 AF3718
EU459462.1 gg_id:296722 capybara feces clone CAP_aah97f02 EU459
EU459519.1 gg_id:294489 capybara feces clone CAP_aah99a09 EU459
FJ535157.1 gg_id:574522 Contamination risk vegetables Arcobacter during post-harvest processing water carr FJ5351
AF418961.1 gg_id:38016 USA: Colorado Fort collins Horsetooth Reservoir clone HTG2 AF4189
EU778115.1 gg_id:356250 feces clone RL388_aao93c10 EU778
EF620467.1 gg_id:257876 Ralstonia sp. str. ISSDS-784 EF6204
EU978820.1 gg_id:536916 and metabolic potential metagenome glacier ice clone glb332c EU978
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EU652615.1 gg_id:277698 Seasonal variation microbial Yel Sea sediment clone B8S-8 EU652
EU443952.1 gg_id:263927 sp. str. s3-3 EU443
AF084862.1 gg_id:19894 Bdellovibrio sp. str. JS7 AF084
FJ203067.1 gg_id:324529 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c FJ2030
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EU443963.1 gg_id:269969 sp. str. w5-3 EU443

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EF188429.1 gg_id:346586 Microbial Altamira Cave clone 236 EF1884
AY947967.1 gg_id:141636 Synchrony and seasonality two temperate rivers USA: Massachusetts Ipswich River c AY9479
AJ288899.1 gg_id:49685 stolpii str. DSM 12778 AJ2888
EU805174.1 gg_id:311266 It's all ranking aquatic 250 miles Panama City clone 6C233166 EU8051
EU662557.1 gg_id:580005 Productivity- Chemolithoautotrophically Based Sulfidic Karst Systems floating microb EU6625
EU237338.1 gg_id:239851 Genes transcripts Eastern and Western Equatorial North Atlantic Ocean microbial as EU2373
DQ266898.1 gg_id:141116 Cloning and microorganism genes alkaline soil clone pGXAR13 DQ266
EF687517.1 gg_id:281539 Biogeochemistry iron- and sulfur-precipitating microbial mats (Nile Mediterranean) s EF6875
AB369189.1 gg_id:239066 Microbiological Assessment Circulation Mud Fluids During First Operation Drilling De AB3691
AY294221.1 gg_id:101065 sp. str. PNEc1 AY2942
EU101250.1 gg_id:254683 Sulfide/oxygen supply ratio predicts outcome competition among sulfur-oxidizing wa EU1012
GU119471.1 gg_id:564132 Threatened Corals Provide Microbial Habitats reef water clone Reef_F14 GU119
AB176175.1 gg_id:182905 Microbial Hydrothermal System Suiyo Seamount on Izu-Ogasawara Arc vent area wa AB1761
AJ278146.1 gg_id:22594 Bdellovibrio sp. str. SD1 sewage AJ2781
EF574402.1 gg_id:229914 site S25 near Coco's Island marine clone S25_746 EF5744
GQ351210.1 gg_id:590861 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Eastern GQ351
DQ676387.1 gg_id:218005 Archaeal sediment and plankton freshwater pond suboxic freshwater-pond clone M DQ676
DQ133926.1 gg_id:168155 Dominant microbial biofilms frasassi cave system Italy limestone-corroding stream b DQ133
AJ290009.1 gg_id:40173 Germany: Lake Fuchskuhle north basin clone FukuN9 FukuN9 AJ2900
GU369899.1 gg_id:518456 and mats vents Arc white filamentous microbial mat photic shal hydrothermal vent GU369
AJ292518.1 gg_id:38566 Bdellovibrio sp. W str. ATCC 27047 AJ2925
AF148939.1 gg_id:30112 Bdellovibrio str. BRP4 AF1489
EU050708.1 gg_id:247981 Microbial waters production water Daqing oil field clone DQ328-109 EU0507
AJ292759.1 gg_id:40800 Bdellovibrio HD100 str. HD 100 DSM 50701 AJ2927
EU050700.1 gg_id:244273 Microbial waters production water Daqing oil field clone DQ328-1 EU0507
DQ847445.1 gg_id:172283 human forearm skin clone GR2-101 DQ847
GQ113033.1 gg_id:410201 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ113
DQ413094.1 gg_id:152494 Microbial -dependent and Approaches Anaerobic/Aerobic SBR Reactor EBPR sludge DQ413
AB286607.1 gg_id:213370 Reducing production and domination comamonadaceae reducing oxygen supply was AB2866
FJ542862.1 gg_id:525171 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone A FJ5428
AM233527.1 gg_id:320761 Multiple symbionts two species co-occurring gutless oligochaete worms Mediterrar AM233
CU466777.1 gg_id:338371 Evry wastewater treatment plant anoxic basin clone CU4667
EF687743.1 gg_id:243041 Bdellovibrio sp. str. JSS EF6877
GQ039893.1 gg_id:416757 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor GQ039
AY294215.1 gg_id:105561 Bdellovibrio sp. str. MPA AY2942
EU104139.1 gg_id:353499 Evidence Comamonadaceae determinants settling performance activated sludge clo EU1041
DQ640659.1 gg_id:232532 full-scale EBPR sludge clone Skagenf81 DQ640

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EU884926.1 gg_id:337320 Bdellovibrio sp. str. JSF2 EU8849
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AY662018.1 gg_id:137132 uranium-contaminated groundwater clone 300A-H04 AY6620
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EU134406.1 gg_id:257948 tallgrass prarie soil clone FFCH7045 EU1344
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EU134527.1 gg_id:254193 tallgrass prarie soil clone FFCH9759 EU1345
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FJ202533.1 gg_id:352758 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2025
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EF516682.1 gg_id:224255 grassland soil clone FCPS531 EF5166
DQ129144.2 gg_id:189151 forest soil clone CWT ST01_F02 DQ129
EF442982.1 gg_id:239332 Desulfobacterium catecholicum str. Kette EF4429
FJ516957.1 gg_id:511303 semiarid 'Tablas de Daimiel National Park' wetland (Central Spain) unravelled upper s FJ5169
U12253.1 gg_id:10829 Desulfobulbus rhabdoformis str. M16 U12253
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EU844167.1 gg_id:341591 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8441
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DQ394978.1 gg_id:151814 harbor sediment clone VHS-B4-9 DQ394
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NR_029305.1 gg_id:590669 Desulfobulbus elongatus str. FP; DSM 2908 NR_029
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AJ535238.1 gg_id:77808 marine sediment above hydrate ridge clone Hyd24-21 proteobacterium AJ5352
AY355297.2 gg_id:105894 epibiontic clone C11-G5 AY3552
Y13672.1 gg_id:10794 Desulfocapsa sulfexigens str. SB164P1 Y13672
EU662381.1 gg_id:571160 Productivity- Chemolithoautotrophically Based Sulfidic Karst Systems microbial mat (EU6623
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FJ901718.1 gg_id:567131 phreatic limestone sinkholes northeastern Mexico biomat sediment cenote La Palita (FJ9017
DQ925886.1 gg_id:235454 Microbes and Thermal Gradients Temperature Hydrothermal Chimneys hydrotherm DQ925
EU101288.1 gg_id:249303 Sulfide/oxygen supply ratio predicts outcome competition among sulfur-oxidizing wa EU101
X95181.1 gg_id:10792 Desulfocapsa thiozymogenes str. Bra2 X95181
EU662622.1 gg_id:583279 Productivity- Chemolithoautotrophically Based Sulfidic Karst Systems floating microb EU662
EU101286.1 gg_id:250699 Sulfide/oxygen supply ratio predicts outcome competition among sulfur-oxidizing wa EU101
DQ521816.1 gg_id:159745 Anaerobic Methane Oxidizing ANME-1b Archaea Hypersaline Sediments Gulf Mexico DQ521
DQ676351.1 gg_id:217639 Archaeal sediment and plankton freshwater pond suboxic freshwater-pond clone M DQ676
FJ712571.1 gg_id:531935 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) k FJ7125
EU265788.1 gg_id:264490 epibiotic assemblage recently described Yeti Kiwa hirsuta (Kiwidae) surface crab hyc EU265
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GQ850564.1 gg_id:591035 bottom water northern Bering Sea clone d75 GQ850
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NC_006138.1 gg_id:128538 Desulfotalea psychrophila str. LSv54 NC_00
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AY770713.1 gg_id:110727 sea urchin Paracentrotus lividus clone PlS93 AY770
NR_024949.1 gg_id:534504 Desulfotalea arctica str. LSv514; DSM 12342 NR_02
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AM774321.2 gg_id:245906 Cultivation and situ quantification consistently demonstrate that two distinct group AM774
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AY592401.1 gg_id:103065 deep-sea mud volcano clone Amsterdam-2B-43; BC20-2B-43 AY5924
FN396662.1 gg_id:550643 constant flux thermophilic cold seabed Arctic marine surface sediment clone s5_0_V FN3966
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AF354148.1 gg_id:71200 marine methane seep clone 1431 AF3541
EU981255.1 gg_id:355558 sulfate reducing living bench scale aquifer column water clone A56_SW EU981
AB294977.1 gg_id:226332 -dependent & analyses hydrothermal system off Taketomi Island Japan microbial ma AB2949

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EU287257.1 gg_id:257411 Pacific arctic surface sediment clone S11-74 EU287
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DQ831543.1 gg_id:168864 Activity and sulphate-reducing contrasting sediments River Colne estuary UK marine DQ831
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AY355305.2 gg_id:101832 epibiontic clone C6-B1 AY355
AM404380.1 gg_id:567796 Hydrocarbon-fueled sulfate reduction can sustain long-lived tubeworm aggregation AM404
AY586398.1 gg_id:108445 fatty acid-degrading consortium clone FA-PB11 AY586
AY216446.1 gg_id:82114 temperate estuarine mud clone KM15 AY216
AY193139.1 gg_id:80324 marine sediment clone Bol88 AY193
EU528183.1 gg_id:281431 Seasonal Dynamics Mudflat Mouth Major Kentucky Lake Reservoir Tributary sedime EU528
DQ677861.1 gg_id:243494 Blood Falls Subglacial Outf Taylor Glacier Antarctica subglacial outf clone BF99_C161 DQ677
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AY998140.1 gg_id:126281 Continental deep subsurface geochemically structured within alternating shale-sand AY998
EU328056.1 gg_id:278259 dynamics during bioremediation crude oil contaminated moderate saline soil clone B EU328
EU652618.1 gg_id:279049 Seasonal variation microbial Yel Sea sediment clone C8S-16 EU652
GU302481.1 gg_id:569243 Spatial structure and activity sedimentary microbial underlying Beggiatoa spp. mat I GU302
DQ521817.1 gg_id:161410 Anaerobic Methane Oxidizing ANME-1b Archaea Hypersaline Sediments Gulf Mexico DQ521
EU662614.1 gg_id:550521 Productivity- Chemolithoautotrophically Based Sulfidic Karst Systems floating microb EU662
EU290696.1 gg_id:241222 microbial structure biogeochemical contrasting shelf sediments Namibian upwelling EU290
NR_026354.1 gg_id:571713 Desulfofustis glycolicus str. PerGlyS NR_02
EF632754.1 gg_id:249075 Unique microbial contrasting aquatic altitude Andean Altiplano (northern Chile) fresh EF6327
EU542499.1 gg_id:260510 Effects chemical structure concentration on pathways microbial during dechlorinatio EU542
FJ264778.1 gg_id:341813 Manganese and Iron Dependent Anaerobic Oxidation Methane methane seep sedime FJ2647
AB100012.1 gg_id:99697 inactive deep-sea hydrothermal vent chimneys clone IndB4-24 AB100
AJ866934.1 gg_id:130219 Desulfobulbus mediterraneus str. NA62 AJ8669
AB252437.1 gg_id:156393 Microbial extremely CO2 rich deep-sea sediment Marine sediments Yonaguni Knoll I AB252
L42613.1 gg_id:10809 Desulforhopalus vacuolatus str. ltk10 L42613
FJ712433.1 gg_id:516762 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) K FJ7124
AY771961.1 gg_id:112020 marine surface sediment clone SP22 AY771
DQ831556.1 gg_id:164944 Activity and sulphate-reducing contrasting sediments River Colne estuary UK marine DQ831
EU617846.1 gg_id:329676 Seasonal variation microbial Yel Sea sediment clone D13S-79 EU617
AY050586.1 gg_id:19356 MCB-contaminated groundwater-treating reactor clone GOUTA17 AY050
AJ241011.1 gg_id:10837 Norway:(Svalbard)Hornsund clone Sva0631 AJ2410
AM404330.1 gg_id:221162 aerobic and anaerobic methane oxidizers Arctic mud volcano(Haakon Mosby Mud V AM404
FJ712434.1 gg_id:517763 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) K FJ7124

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AJ241013.1 gg_id:10827 Norway:(Svalbard)Hornsund clone Sva0999 AJ2410
AM950241.1 gg_id:567396 Sulphide oxidation elemental sulphur membrane bioreactor: Performance and selec AM950
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AB294967.1 gg_id:223812 -dependent & analyses hydrothermal system off Taketomi Island Japan microbial ma AB294
EF687172.1 gg_id:282050 Biogeochemistry iron- and sulfur-precipitating microbial mats (Nile Mediterranean) ir EF6871
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AF420335.1 gg_id:71031 hydrothermal sediment clone AF420335 AF4203
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GQ249525.1 gg_id:581436 Microbial anaerobic sediments Bay Cadiz (Spain) marine sediment: 6-8 cm layer clor GQ249
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AB100004.1 gg_id:79377 inactive deep-sea hydrothermal vent chimneys clone IndB2-42 AB100
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AJ007373.1 gg_id:10840 environmental clone directly AJ0073
DQ513028.1 gg_id:161392 Microbial life fluids ridge flank crustal fluid clone FS142-27B-02 DQ513
GQ337170.1 gg_id:582065 Hydrography shapes biogeography deep Arctic Ocean water depth 410m clone CB1 GQ337

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EU236362.1 gg_id:299227 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg91D6 EU236
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EU491186.1 gg_id:260159 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak EU491
FJ205260.1 gg_id:513991 Prokaryotic deep-sea region East Lau Spreading Centre active hydrothermal field sedi FJ2052
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GQ349282.1 gg_id:593656 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ349
DQ154855.1 gg_id:139228 Diel Migration Restructures Hypersaline Microbial Mat hypersaline microbial mat cl DQ154
FJ264670.1 gg_id:340510 Manganese and Iron Dependent Anaerobic Oxidation Methane methane seep sedim FJ2646
EU937982.1 gg_id:317469 Biogeochemistry Iron Oxidation Circumneutral Freshwater Habitat riparian iron oxidi EU937
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EU386020.1 gg_id:274277 Biogeographical and microbes sediments on subseafloor sediment South China Sea c EU386
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FJ484693.1 gg_id:512592 microbial autonomous rover world's deepest phreatic sinkhole wall biomat El Zacator FJ4846
FJ264596.1 gg_id:303539 Manganese and Iron Dependent Anaerobic Oxidation Methane methane seep sedim FJ2645
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FJ902380.1 gg_id:594172 phreatic limestone sinkholes northeastern Mexico green biomat 8m deep cenote Car FJ9023
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FJ716318.1 gg_id:551732 Chlorobi dominate shal chemocline Bahamas Sawmill Sink column 10.3 m water dept FJ7163
FJ517130.1 gg_id:512958 semiarid 'Tablas de Daimiel National Park' wetland (Central Spain) unravelled water c FJ5171
DQ676358.1 gg_id:224366 Archaeal sediment and plankton freshwater pond suboxic freshwater-pond clone M DQ676
AY771962.1 gg_id:111849 marine surface sediment clone SR24 AY771
AJ306774.1 gg_id:66925 DCP-dechlorinating consortium clone SHA-72 AJ3067
GQ487920.1 gg_id:554266 Microbial metal soil polluted heavy metals clone T1-75 GQ487
AB188771.1 gg_id:114153 cold seep sediment clone SB1-2 AB188
EU491434.1 gg_id:259879 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X4 clone EU491
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FJ205257.1 gg_id:512306 Prokaryotic deep-sea region East Lau Spreading Centre active hydrothermal field sedi FJ2052
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FJ497387.1 gg_id:574286 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun FJ4973
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FJ746091.1 gg_id:570989 Microbial oligotrophic marine sediments: South Pacific Gyre ocean sediment 5306 m FJ7460
EU937853.1 gg_id:352286 Biogeochemistry Iron Oxidation Circumneutral Freshwater Habitat riparian iron oxidi EU9378
FJ746300.1 gg_id:508914 Microbial oligotrophic marine sediments: South Pacific Gyre ocean sediment 5306 m FJ7463
EU048685.1 gg_id:250097 and archaeal surface marine sediment Slope South China Sea clone MD2896-B28 EU0486
AY592672.1 gg_id:105663 deep-sea mud volcano clone Napoli-2B-50; BC07-2B-50 AY5926
EU287051.1 gg_id:253719 Pacific arctic surface sediment clone B78-87 EU2870
EU181482.1 gg_id:246264 Prokaryotic enhanced organic matter remineralization continental margin marine se EU1814

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AY592130.1 gg_id:100278 marine ANAMMOX sediment clone AY592130 AY592
FJ755771.1 gg_id:586023 vertical archaeal water and Lake Taihu sediment clone LT-SB-B77 FJ7557
X99235.1 gg_id:10401 Desulfohalobium retbaense str. HR100 (DSM 5692T) X99235
U48244.1 gg_id:10400 Desulfohalobium retbaense str. DSM 5692 U48244
EU296539.1 gg_id:241507 Desulfonatronospira aceticus str. AHT 6 EU2965
X99234.1 gg_id:10404 Desulfonatronovibrio hydrogenovorans str. Z-7935 (DSM 9292T) X99234
GU196828.1 gg_id:557238 Desulfonatronovibrio sp. str. AHT21 GU196
EF644847.1 gg_id:299192 genes and citrate lyase deep-sea microbial MAR Rainbow hydrothermal vent system EF6448
AF524933.1 gg_id:74638 Desulfonauticus submarinus str. 6N AF5249
FJ194951.1 gg_id:329685 Desulfonauticus sp. str. DSM 4206 FJ1949
EU245681.1 gg_id:241136 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M4-F1(EU2456
DQ103666.1 gg_id:136882 hypersaline endoevaporitic microbial mat clone E6bG07 DQ103
EU245471.1 gg_id:253107 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M2-A0: EU2454
EU245401.1 gg_id:237109 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M1-C0: EU2454
AB264617.1 gg_id:167257 Desulfothermus okinawensis str. TFISO9 (= JCM 13304 = DSM 17375) AB2646
NR_025378.1 gg_id:537936 Desulfomicrobium orale str. DSM 12838 NR_025
AY464939.1 gg_id:100488 Desulfocaldus terraneus str. P6.2 AY4649
DQ069204.1 gg_id:130717 gold mine clone MAB25 DQ069
AJ277886.1 gg_id:33526 Desulfomicrobium escambiense str. DSM 10707T AJ2778
DQ069227.1 gg_id:128063 gold mine clone SRB5 DQ069
Y14594.1 gg_id:10408 Desulfonatronum lacustre str. z-7951 Y14594
AY725424.1 gg_id:103231 Desulfonatronum cooperatoris str. Z-9799 AY7254
GQ863488.1 gg_id:550045 Desulfonatronum sp. str. HSRB-L1 GQ863
DQ088749.1 gg_id:129416 subsurface clone BE325FW032701CTS_hole1-63 DQ088
GQ493712.1 gg_id:546485 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
FJ363013.1 gg_id:361170 feces adult twins and mothers; TS148 clone TS148_a01h07 FJ3630
AY978908.1 gg_id:121944 human transverse colon mucosal biopsy clone NG04 AY9789
EF602909.1 gg_id:230078 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6029
EU454891.1 gg_id:305445 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K77S EU4548
EU505347.1 gg_id:258794 cecal contents Mus musculus strain C57BL/6J; myd4 clone myd4_aaa02h11 EU5053
EU452762.1 gg_id:309442 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N EU4527
EF096212.1 gg_id:180715 mouse cecum clone obob1_aaa02f06 EF0962
AY993240.1 gg_id:129830 mouse cecum clone C21_k13 AY9932
EF097816.1 gg_id:184560 mouse cecum clone SWPT20_aaa04c06 EF0978
AY991087.1 gg_id:131193 mouse cecum clone C13_O03 AY9910
EU455583.1 gg_id:344389 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU4555
EF097361.1 gg_id:199580 mouse cecum clone SWPT19_aaa01e10 EF0973
DQ071477.1 gg_id:234242 microbial cecum captive and free-living capercaillies (Tetrao urogallus) clone TuCc14 DQ071
DQ308598.1 gg_id:148623 sheep rumen enrichment clone 196.G06 DQ308
EU659693.1 gg_id:283392 Desulfovibrio africanus str. SR-1 EU6596
DQ365927.1 gg_id:154031 Desulfovibrio alaskensis str. IMP-7760 DQ365

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EU251185.1 gg_id:248227 Desulfovibrio sp. str. ds2-2 EU2511
U53462.1 gg_id:10445 Desulfovibrio bastinii str. SEBR 4225 U53462
NR_025766.1 gg_id:533801 Desulfovibrio bastinii str. SRL4225; DSM 16055 NR_025
FJ024714.1 gg_id:330860 Copper affects reduction and genetic enriched sulfate reducing coastal sediments exp FJ0247
DQ109922.1 gg_id:142678 Sulfate-reducing mats: Changing paradigms new discoveries salt pond nonlithifying DQ109
AY281345.1 gg_id:87605 Desulfovibrio sp. str. ANP3 AY2813
U85475.1 gg_id:10430 Desulfovibrio sp. str. BG50 U85475
AF230530.1 gg_id:30839 Desulfovibrio dechloracetivorans AF2305
FJ823871.1 gg_id:516368 Controlling accumulation fermentation inhibitors biorefinery recycle water microbial FJ8238
GQ503772.1 gg_id:577487 uranium mine tailing pond inlet water clone Jdgsrb019 GQ503
GQ503807.1 gg_id:585949 effulent treatment plant inlet clone Jdgsrb054 GQ503
AF098671.1 gg_id:10516 Desulfovibrio desulfuricans AF0986
AJ295680.1 gg_id:74474 Desulfovibrio intestinalis str. JG-G12 AJ2956
DQ526427.1 gg_id:160710 Desulfovibrio desulfuricans str. EFX-DES DQ526
GQ503792.1 gg_id:591259 uranium mine tailing pond inlet water clone Jdgsrb039 GQ503
GQ503771.1 gg_id:577327 uranium mine tailing pond inlet water clone Jdgsrb018 GQ503
GQ898871.1 gg_id:572458 strain Desulfovibrio enrichment medium DSMZ 163 inoculated water Jaduguda Urar GQ898
GQ503812.1 gg_id:539624 effulent treatment plant inlet clone Jdgsrb059 GQ503
GQ503798.1 gg_id:564326 uranium mine tailing pond inlet water clone Jdgsrb045 GQ503
FJ823874.1 gg_id:530538 Controlling accumulation fermentation inhibitors biorefinery recycle water microbial FJ8238
FJ823870.1 gg_id:521886 Controlling accumulation fermentation inhibitors biorefinery recycle water microbial FJ8238
AJ544687.2 gg_id:80009 Desulfovibrio brasiliensis str. LVform1 AJ5446
NR_025977.1 gg_id:570680 Desulfovibrio gabonensis str. SEBR 2840; DSM 10636 NR_025
AP010904.1 gg_id:384156 Desulfovibrio magneticus str. RS-1 AP0109
AJ582758.1 gg_id:96567 Desulfovibrio ferrireducens str. CY2 AJ5827
GU139267.1 gg_id:542453 lactate formate propionate hydrogen donors reductive dehalogenation trichloroeth GU139
GQ402775.1 gg_id:567650 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
EF562565.1 gg_id:235762 stable microbial consortia capable degrading complex organic matter paper pulp colu EF5625
NR_029118.1 gg_id:592620 Desulfovibrio putealis str. B7-43; DSM 16056 NR_029
CP001649.1 gg_id:516164 Desulfovibrio salexigens str. DSM 2638 CP0016
AF050100.1 gg_id:10448 Desulfovibrio senezii str. CVL; DSM 8436 AF0501
AY340820.1 gg_id:91518 sulfate-reducing fluidized-bed reactor clone SR_FBR_E5 AY3408
X86689.1 gg_id:10505 Desulfovibrio sp str. DMB X86689
GQ898881.1 gg_id:585282 strain Desulfovibrio enrichment medium DSMZ 163 inoculated water East Calcutta v GQ898
AB062810.1 gg_id:23507 termite gut homogenate clone BCf11-19 AB0628
GQ502605.1 gg_id:582695 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf6- GQ502
X95230.2 gg_id:10429 Desulfovibrio aespoeensis str. Aspo2 X95230
Y18049.1 gg_id:10442 Desulfovibrio zosterae Y18049
EU885150.1 gg_id:327333 microbial hindgut chamber Pomacanthus sexstriatus GI tract clone AB2 EU8851
FM178807.1 gg_id:351705 Monitoring abundance and expression 'dehalococcoides' species chloroethene-redu FM178

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GU174149.1 gg_id:558603 Microbial Bactrian camel estimated rumen clone XJC38 GU174
EU885102.1 gg_id:304312 microbial hindgut chamber Pomacanthus sexstriatus GI tract clone A3C12 EU885
EU885154.1 gg_id:337642 microbial hindgut chamber Pomacanthus sexstriatus GI tract clone AF9 EU885
FJ225426.1 gg_id:364203 Desulfovibrio sp. str. H1 FJ2254
EF577029.1 gg_id:264685 Desulfovibrio defluvii str. RB22 EF5770
FJ440030.1 gg_id:510683 Megamonas hypermegale colonization correlates Campylobacter jejuni exclusion pou FJ4400
AM418397.1 gg_id:179230 Desulfohimalaya abdulkalamii str. pwc AM418
AY746987.1 gg_id:100353 Desulfovibrio oxyvorans str. DvO5 AY7469
FJ172813.1 gg_id:354049 Qinghai Yak Ruminal and Fungi China rumen clone RB-4C1 FJ1728
EU850487.1 gg_id:319780 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF252 EU850
EU245278.1 gg_id:257276 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-H5-B11 EU245
EU885153.1 gg_id:316313 microbial hindgut chamber Pomacanthus sexstriatus GI tract clone AB12 EU885
U90726.1 gg_id:10427 Desulfovibrio profundus str. DSM 11384 500-1 U9072
AF053752.1 gg_id:10462 Desulfovibrio burkinensis str. HDv; DSM 6830 AF053
EU775070.1 gg_id:308451 Francois Langur feces clone FL_2aaa02h01 EU775
AB234535.1 gg_id:147874 termite gut homogenate clone MgMjR-025 AB2345
AB192287.1 gg_id:141741 termite gut homogenate clone RPK-26 AB192
AF056091.1 gg_id:10518 Desulfovibrio sp. str. UNSW3caefatS AF056
NR_026303.1 gg_id:562366 Desulfovibrio vietnamensis str. G3 100 ID95-371 NR_02
AB470954.1 gg_id:536904 Desulfovibrio sp. str. r49 AB470
EU885140.1 gg_id:350456 microbial hindgut chamber Pomacanthus sexstriatus GI tract clone A2C5 EU885
EU885104.1 gg_id:348053 microbial hindgut chamber Pomacanthus sexstriatus GI tract clone A3G4 EU885
AY649785.1 gg_id:102334 Desulfovibrio alkalitolerans str. RT2 AY649
CP000112.1 gg_id:143024 Desulfovibrio desulfuricans str. G20 CP000
FJ655908.1 gg_id:558435 Desulfovibrio sp. str. I9 FJ6559
FJ202471.1 gg_id:305033 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2024
AF053751.1 gg_id:10470 Desulfovibrio alcoholovorans str. DSM 5433 AF053
AF192152.1 gg_id:51535 Desulfovibrio piger str. ATCC29098 AF192
U53464.1 gg_id:10452 Desulfovibrio gracilis str. SEBR 6116 U53464
EU616635.1 gg_id:321186 digestive-tract microbiota Hirudo orientalis european medicinal leech Desulfovibrio (EU616
DQ447183.2 gg_id:156761 Desulfovibrio gigas str. DSM 1382; ATCC 19364 DQ447
EU885143.1 gg_id:335081 microbial hindgut chamber Pomacanthus sexstriatus GI tract clone AB10 EU885
AY726757.3 gg_id:107875 Desulfovibrio sp. SB1 AY726
DQ422859.1 gg_id:161406 Desulfovibrio bizertensis str. MB3 DQ422
AF371871.1 gg_id:30569 swine intestine clone p-2918-6C5 AF371
EU885152.1 gg_id:341908 microbial hindgut chamber Pomacanthus sexstriatus GI tract clone AE3 EU885
EU885101.1 gg_id:322341 microbial hindgut chamber Pomacanthus sexstriatus GI tract clone A3F9 EU885
AJ132721.1 gg_id:111852 deep-sea hydrothermal chimney clone CHA3-114 AJ1327
NR_025038.1 gg_id:564993 Desulfovibrio inopinatus str. HHQ 20; DSM 10711 NR_02
AY274444.1 gg_id:104557 Desulfovibrio sp. str. HS2 AY2744

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DQ186200.2 gg_id:243561 Desulfovibrio carbinoliphilus str. D41 DQ186
Y11984.3 gg_id:28397 Desulfovibrio alaskensis str. NCIMB 13491 Y11984
DQ841177.2 gg_id:195717 Desulfovibrio sp. str. AS36 DQ841
EF453987.2 gg_id:225093 termite hindgut clone 290cost002-P3L-1410 EF4539
AM947130.1 gg_id:270241 Desulfovibrio marrakechensis str. DSM 19337 AM947
CP001197.1 gg_id:529124 Desulfovibrio vulgaris 'Miyazaki F' str. Miyazaki F CP001
EF123506.1 gg_id:257510 Microbial disease microbial mats on Siderastrea siderea three regions wider Caribbea EF1235
U85468.1 gg_id:10463 Desulfovibrio sp. str. BG6 U85468
AF228128.2 gg_id:43170 Desulfovibrio sp. str. Pr1.2 AF2281
GQ502595.1 gg_id:585650 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf6- GQ502
NR_025765.1 gg_id:576099 Desulfovibrio longus str. SEBR 2582; DSM 6739 NR_025
AY274449.1 gg_id:105315 Desulfovibrio ferrophilus str. IS5 AY2744
X95231.1 gg_id:10444 Bacterial sp. X95231
NC_008011.1 gg_id:159002 Lawsonia intracellularis str. PHE/MN1-00 NC_008
AY976442.1 gg_id:118641 human ascending colon mucosal biopsy clone LZ39 AY9764
GQ867364.1 gg_id:588730 and prevalence blaTEM genes Arctic seals colon content clone WSp127 GQ867
EU381557.1 gg_id:265414 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid p EU3815
FJ833256.1 gg_id:572886 Microbial Ecology Crop Folivorous Hoatzin crop contents clone A3Q302_22F03 FJ8332
EU468458.1 gg_id:287520 okapi feces clone OK1_a06 EU4684
EU461101.1 gg_id:303251 red kangaroo feces clone KO1_aai44b11 EU4611
AB234532.1 gg_id:146574 termite gut homogenate clone MgMjD-084 AB2345
AB089110.1 gg_id:78137 termite gut homogenate clone Rs-N35 proteobacterium AB0891
AB192288.1 gg_id:143786 termite gut homogenate clone RPK-66 AB1922
X99501.1 gg_id:10486 Desulfovibrio sp. str. STL1 X99501
FJ374255.1 gg_id:365000 Inter- and intraspecific humivorous scarab beetle larvae (Pachnoda spp.) larval hindgu FJ3742
AB234538.1 gg_id:149936 termite gut homogenate clone MgMjR-064 AB2345
AB089109.1 gg_id:78006 termite gut homogenate clone Rs-M89 proteobacterium AB0891
EF454896.2 gg_id:220622 termite hindgut clone 290cost002-P3L-618 EF4548
X99504.1 gg_id:10485 Desulfovibrio sp. str. STL6 X99504
FJ374258.1 gg_id:361169 Inter- and intraspecific humivorous scarab beetle larvae (Pachnoda spp.) larval hindgu FJ3742
AB089105.1 gg_id:78148 termite gut homogenate clone Rs-K75 AB0891
AY532164.1 gg_id:137367 Desulfovibrio sp. str. ZIRB-2 AY5321
AB234531.1 gg_id:148238 termite gut homogenate clone MgMjD-065 AB2345
Y16942.1 gg_id:10572 Desulfurella propionica str. U-8 (DSM 10410) Y16942
Y16941.1 gg_id:10573 Desulfurella kamchatkensis str. K-119 (DSM 10409) Y16941
NR_026109.1 gg_id:566496 Desulfurella acetivorans str. A63; DSM 5264 NR_026
Y18292.1 gg_id:51780 Hippea maritima str. MH2T Y18292
FJ264595.1 gg_id:343915 Manganese and Iron Dependent Anaerobic Oxidation Methane methane seep sedime FJ2645
AB294284.1 gg_id:207880 Microbial structure deep coal seem groundwater clone YWB15 AB2942
AY062880.1 gg_id:38853 environmental electrode surface clone d14 AY0628
EU052251.1 gg_id:240954 degradation kinetics and current efficiency cells supplied anode microbial fuel cell fe EU0522

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NR_026407.1 gg_id:575070 Desulfuromonas thiophila str. NZ27 DSMZ 8987 NR_02
EU246142.1 gg_id:235638 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-P4-B12 EU246
AY062875.1 gg_id:52449 environmental electrode surface clone d9 AY062
AJ519664.1 gg_id:76391 uranium mill tailings soil sample clone GuBH2-AG-114 proteobacterium AJ5196
AB294287.1 gg_id:210461 Microbial structure deep coal seem groundwater clone YWB18 AB294
X79415.1 gg_id:10692 Desulfuromusa succinoxidans str. Gylac (DSM 8270) X79415
GQ433952.1 gg_id:554572 Subseafloor ocean crust microbial observatories: (F-through Osmo Colonization Syst GQ433
EU542456.1 gg_id:263005 Effects chemical structure concentration on pathways microbial during dechlorinatio EU542
NR_026154.1 gg_id:552396 Pelobacter acidigallici str. MaGal12T; DSM 2377 NR_02
GU180167.1 gg_id:581956 Impact coplanar PCBs on microbial activity anaerobic estuarine sediments sediment GU180
NR_026479.1 gg_id:539100 Malonomonas rubra str. GraMal1; DSM 5091 NR_02
FJ638573.1 gg_id:538924 Temperature dependent succession sulfate reducing muddy southwestern Taiwan hc FJ6385
AY280424.1 gg_id:101417 exterior deep-sea hydrothermal vent sulfide chimney Juan de Fuca Ridge Pacific Oce AY280
EU386013.1 gg_id:262433 Biogeographical and microbes sediments on subseafloor sediment South China Sea c EU386
GQ246309.1 gg_id:511753 Temporal and spatial China North Yel Sea sediments clone Sd1-28 GQ246
EU052244.1 gg_id:237074 degradation kinetics and current efficiency cells supplied anode microbial fuel cell fe EU052
DQ677843.1 gg_id:245056 Blood Falls Subglacial Outf Taylor Glacier Antarctica subglacial outf clone BF99_C24 DQ677
DQ309326.1 gg_id:145062 Desulfuromonas alkaliphilus str. Z-0531 DQ309
AJ441215.1 gg_id:74843 hydrothermal vent polychaete mucous clone P. palm C/A 79 AJ4412
EU052243.1 gg_id:252121 degradation kinetics and current efficiency cells supplied anode microbial fuel cell fe EU052
AY187308.1 gg_id:102591 Pelobacter masseliensis AY1873
EU617856.1 gg_id:346218 Seasonal variation microbial Yel Sea sediment clone C13S-139 EU617
AB355057.1 gg_id:236199 Monitoring and archaeal two heavy polluted areas lake Egypt based on sediment Ma AB355
AY998187.1 gg_id:115871 Continental deep subsurface geochemically structured within alternating shale-sand AY998
AY515473.1 gg_id:103018 bulk water German Wadden Sea October 1999 clone GWS-K17 AY5154
EU531802.1 gg_id:264753 unculturable volcanos Xinjiang mud volcano (salty) clone 285 EU5318
AB189359.1 gg_id:113759 cold seep sediment clone JT75-105 AB189
AY187304.2 gg_id:108676 Geopsychrobacter electrodiphilus str. A2 AY1873
EU735643.1 gg_id:329004 archaeal structures and pristine soils China oil contaminated soil Jidong Oilfield clone EU735
FM179908.1 gg_id:353366 Biogeochemical processes microbial Gullfaks and Tommeliten methane seeps (Nortl FM179
AY155599.1 gg_id:81506 Geothermobacter ehrlichii str. SS015 AY1555
GQ249592.1 gg_id:554911 Microbial anaerobic sediments Bay Cadiz (Spain) marine sediment: 12-14 cm layer cl GQ249
EF687392.1 gg_id:286079 Biogeochemistry iron- and sulfur-precipitating microbial mats (Nile Mediterranean) s EF6873
AF458286.1 gg_id:77161 Mono Lake California clone AF4582
NR_026076.1 gg_id:561012 Geobacter bremensis str. Dfr1; ATCC BAA-607 NR_02
AAVG01000086.1 gg_id:179082 Geobacter lovleyi str. SZ AAVG0
NC_007517.1 gg_id:141183 Geobacter metallireducens str. GS-15 NC_00
AY653551.1 gg_id:129581 Geobacter psychrophilus str. P11 AY6535
AJ534676.1 gg_id:76599 ground water deep-well injection disposal site radioactive wastes Tomsk-7 clone S15A AJ5346
AB488058.1 gg_id:581180 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSSUR0 AB488
AB486606.1 gg_id:576801 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCOR0 AB486

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NC_009483.1 gg_id:233864 Geobacter uraniumreducens str. Rf4 NC_00
NC_008609.1 gg_id:179753 Pelobacter propionicus str. DSM 2379 NC_00
AB307657.1 gg_id:262500 clay wall used Japanese traditional buildings clone R33 AB307
FJ793176.1 gg_id:532352 Archaea and Hot Spring Thailand Tao Dam hot spring clone TDB56 FJ7931
AJ617860.1 gg_id:109573 oxic-anoxic interphase flooded paddy soil clone D28213 AJ6178
AB487900.1 gg_id:590693 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSSUR0 AB487
GQ487953.1 gg_id:563942 Microbial metal soil polluted heavy metals clone T7-90 GQ487
EF515449.1 gg_id:222702 Electricigen Enrichment MFC upf microbial fuel cell anode clone 24e09 EF5154
FM204965.1 gg_id:569815 Prokaryote shifts and reductive dehalogenase redundancy response electron donor FM204
FJ461924.1 gg_id:548027 Microbial ecology industrial digestor mesophilic anaerobic reactor fed effluent chemi FJ4619
FJ461960.1 gg_id:557399 Microbial ecology industrial digestor mesophilic anaerobic reactor fed effluent chemi FJ4619
AJ307942.1 gg_id:18952 derived microbial 'pearl'- community clone sipK44 AJ3079
AB488320.1 gg_id:576040 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSSUR0 AB488
AB486133.1 gg_id:543299 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC AB486
AY922116.1 gg_id:113721 farm soil clone AKYH1470 AY922
AB487641.1 gg_id:591167 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNSR0 AB487
FJ461907.1 gg_id:544277 Microbial ecology industrial digestor mesophilic anaerobic reactor fed effluent chemi FJ4619
AB486599.1 gg_id:589964 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCOR0 AB486
GQ355025.1 gg_id:555760 structure between two geochemically distinct springs Alum Rock Park spring clone M GQ355
DQ138957.1 gg_id:139194 chemical fertilizer paddy soil clone JG135 DQ138
FJ269083.1 gg_id:326474 dissimilatory ferric iron reducers arsenic contaminated Hunan south China paddy soil FJ2690
GQ263990.1 gg_id:582001 Structure Simulated Level Waste Site simulated level waste site clone WC2_80 GQ263
AB486446.1 gg_id:590701 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC AB486
EF527427.1 gg_id:222124 Geobacter uraniumreducens str. Rf4 EF5274
AY947909.1 gg_id:142841 Synchrony and seasonality two temperate rivers USA: Massachusetts Ipswich River c AY947
FJ461957.1 gg_id:585743 Microbial ecology industrial digestor mesophilic anaerobic reactor fed effluent chemi FJ4619
AM713386.1 gg_id:239296 Heterogeneity microorganisms sediments caused pH coal-mining lake sediment Fe(AM713
DQ086800.1 gg_id:143335 Geobacter sp. str. CLFeRB DQ086
AB240241.1 gg_id:144252 microbial structure rhizosphere Phragmites bulk soil reed bed reactor laboratory clo AB240
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NR_026077.1 gg_id:552049 Geobacter pelophilus str. Dfr2; ATCC BAA-603 NR_02
AB307656.1 gg_id:259279 clay wall used Japanese traditional buildings clone R40 AB307
AB234266.1 gg_id:149023 Biotransformation Polychlorinated Dioxins Microbial Dynamics Sediment Microcosm AB234
FJ393130.1 gg_id:358635 Fusing Biology Engineering Improve Power Output Microbial Fuel Cells microbial fuel FJ3931
Y19190.1 gg_id:10733 Geobacter sp. str. CdA-2 Y19190
EF014495.1 gg_id:236914 Geobacter sp. G02 EF0144
AB240367.1 gg_id:144809 microbial structure Phragmites rhizosphere biofilm reed bed reactor laboratory clon AB240
DQ354751.1 gg_id:150927 subsurface water clone MS140BH1062003ms331 DQ354
CP001124.1 gg_id:312961 Geobacter bemidjiensis str. Bem CP001
AY013644.2 gg_id:23462 sample taken downstream landfill clone BVB71 landfill AY013

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DQ676355.1 gg_id:226377 Archaeal sediment and plankton freshwater pond suboxic freshwater-pond clone M DQ676
AF335183.1 gg_id:29370 Geobacter grbiciae str. TACP-5 AF335
DQ145535.1 gg_id:142149 Geobacter pickeringii str. G13 DQ145
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EF515364.1 gg_id:225124 Electricigen Enrichment MFC upf microbial fuel cell anode clone 23d10 EF5153
EF527233.1 gg_id:220762 Geobacter sp. Ply1 str. PLY1 EF5272
AJ009496.1 gg_id:10720 anaerobic TCB-transforming consortium clone SJA-152 AJ0094
Y19191.1 gg_id:10708 Geobacter sp. str. CdA-3 Y19191
FJ479238.1 gg_id:593010 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4792
AM713384.1 gg_id:258079 Heterogeneity microorganisms sediments caused pH coal-mining lake sediment Fe(AM713
EF527234.1 gg_id:220531 Geobacter sp. Ply4 str. PLY4 EF5272
AY395392.1 gg_id:104157 pasture soil clone EB1073 AY3953
AB488092.1 gg_id:552927 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSSUR0 AB488
EF515400.1 gg_id:224061 Electricigen Enrichment MFC upf microbial fuel cell anode clone 23h09 EF5154
AY737507.1 gg_id:105662 Geobacter hephaestius str. VeEG4 AY7375
NR_025895.1 gg_id:543004 Geobacter metallireducens str. GS-15; ATCC 53774 NR_02
AY214185.1 gg_id:82426 benzene-contaminated groundwater clone ZZ12C11 AY214
EF515282.1 gg_id:218355 Electricigen Enrichment MFC upf microbial fuel cell anode clone 22d02 EF5152
FM204997.1 gg_id:547916 Prokaryote shifts and reductive dehalogenase redundancy response electron donor FM204
EF515564.1 gg_id:217229 Electricigen Enrichment MFC full-scale anaerobic bioreactor sludge treating brewery EF5155
EU335191.1 gg_id:251985 Changes microbial metabolic and along hydrogeochemically variable profile saturate EU335
AB239707.1 gg_id:143933 microbial structure rhizosphere Phragmites bulk soil reed bed reactor laboratory clo AB239
AY297795.1 gg_id:89444 waterlogged archaeological wood clone pACH72 AY297
EF520540.1 gg_id:231136 structure lakes: what controls ? acid-impacted lake clone ADK-MOh02-53 EF5205
AY770971.1 gg_id:108346 water injection well Dagang oilfield clone W31 AY7709
AF223382.1 gg_id:32027 Trichlorobacter thiogenes AF2233
EF520542.1 gg_id:229376 structure lakes: what controls ? acid-impacted lake clone ADK-MOh02-26 EF5205
FM210335.1 gg_id:572312 Prokaryote shifts and reductive dehalogenase redundancy response electron donor FM210
EU335154.1 gg_id:244045 Changes microbial metabolic and along hydrogeochemically variable profile saturate EU335
AB447710.1 gg_id:570781 Microbial Structure and Dynamics Granules Expanded Granular Sludge Bed (EGSB) R AB447
AB262721.1 gg_id:255281 microorganisms shal subsurface Sarobetsu mire peat soil clone HSM050P-B-10 AB262
EU244079.1 gg_id:356946 16SrRNA probes river Leine sediment clone sl1361 EU244
FJ478832.1 gg_id:511698 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4788
FJ461926.1 gg_id:541076 Microbial ecology industrial digestor mesophilic anaerobic reactor fed effluent chemi FJ4619
EU134368.1 gg_id:252584 tallgrass prarie soil clone FFCH5218 EU1343
EF515297.1 gg_id:223706 Electricigen Enrichment MFC upf microbial fuel cell anode clone 22e08 EF5152
EF192881.1 gg_id:202514 sediments temperate artificial lake Rapel reservoir sediment clone Rap1_22D EF1928
AY922036.1 gg_id:113772 farm soil clone AKYG597 AY922
AB186850.1 gg_id:107711 polychlorinated dioxin dechlorinating microcosm clone TSBW04 AB186
AB488109.1 gg_id:590962 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSSUR0 AB488

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AB486722.1 gg_id:534035 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCOR(AB486
AY947936.1 gg_id:141881 Synchrony and seasonality two temperate rivers USA: Massachusetts Ipswich River c AY947
AB488329.1 gg_id:535240 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSSUR0 AB488
CP000142.1 gg_id:140482 Pelobacter carbinolicus str. DSM 2380 CP000
EU528245.1 gg_id:287305 Seasonal Dynamics Mudflat Mouth Major Kentucky Lake Reservoir Tributary sedime EU528
AF357914.2 gg_id:51450 Desulfuromonas michiganensis str. BRS1 AF357
U41562.1 gg_id:10667 Pelobacter venetianus U4156
DQ647155.1 gg_id:251658 Microbial structure -temperature oil-field produced water Troll formations North Se DQ647
AB243821.1 gg_id:240641 Methods Investigate Microbial Niigata oil well clone Niigata-10 AB243
AY570613.1 gg_id:108489 biodegraded Canadian oil reservoir clone PL-27B4 AY570
AB294283.1 gg_id:215360 Microbial structure deep coal seem groundwater clone YWB14 AB294
EU328027.1 gg_id:279210 dynamics during bioremediation crude oil contaminated moderate saline soil clone B EU328
GU180166.1 gg_id:537907 Impact coplanar PCBs on microbial activity anaerobic estuarine sediments sediment GU180
AM745207.1 gg_id:293270 Impact oil er hydrocarbons on microbial and activity Gulf Mexico cold seep marine s AM745
U23140.1 gg_id:10684 "Desulfuromonas acetexigens" U2314
AB186848.1 gg_id:103899 polychlorinated dioxin dechlorinating microcosm clone TSAC13 AB186
AY185329.1 gg_id:107087 Desulfuromonas sp. clone AKS68 AY185
X70955.1 gg_id:10668 Pelobacter acetylenicus str. WoAcy1 DSM2348 X70955
GQ433929.1 gg_id:580755 Subseafloor ocean crust microbial observatories: (F-through Osmo Colonization Syst GQ433
EU491247.1 gg_id:276607 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak EU491
EU134335.1 gg_id:243283 tallgrass prarie soil clone FFCH4372 EU134
EU669605.1 gg_id:329697 soil clone S11-29 EU669
GQ495396.1 gg_id:561622 terrestrial volcanic rocks Iceland Hnausahraun lava f clone Bas-7-39 GQ495
EF494339.1 gg_id:223032 Nunnock River granitic landscape clone NR.1.030 EF4943
EU335175.1 gg_id:243968 Changes microbial metabolic and along hydrogeochemically variable profile saturate EU335
EU236382.1 gg_id:299505 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg91H5 EU236
AF130847.1 gg_id:24509 Candidatus Entotheonella palauensis AF130
AM697535.1 gg_id:223474 sequencing libraries indoor dust clone BF0002D046 AM697
FJ466208.1 gg_id:534885 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea FJ4662
FJ479408.1 gg_id:559177 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4794
FJ542849.1 gg_id:531899 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone A FJ5428
EF516200.1 gg_id:224375 grassland soil clone FCPT594 EF5162
DQ450812.1 gg_id:159853 Microbial Alpine Tundra Wet Meadow Soil: Chloroflexi Cold Water-Saturated satura DQ450
AY792293.1 gg_id:119981 Humic Lake clone CrystalBog021E5 AY792
EU134440.1 gg_id:241214 tallgrass prarie soil clone FFCH11684 EU134
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DQ768113.1 gg_id:169959 Cystobacter minus str. DSM 14751 DQ768

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AJ233910.1 gg_id:10626 Angiococcus disciformis str. d4 AJ2339
AB218222.1 gg_id:148095 Archangium gephyra str. NBRC 100087 AB218
AJ233900.1 gg_id:10630 Cystobacter ferrugineus str. Cb fe13 AJ2339
DQ768109.1 gg_id:168891 Cystobacter fuscus str. DSM 2262 DQ768
DQ768115.1 gg_id:169963 Cystobacter velatus str. DSM 14718 DQ768
AJ233897.1 gg_id:10617 Cystobacter fuscus str. Cb f6 AJ2338
EU263004.1 gg_id:274606 Cystobacter fuscus str. Cb9737 EU263
AJ233902.1 gg_id:10621 Cystobacter ferrugineus str. Cb fe27 AJ2339
AM930267.1 gg_id:251539 Melittangium lichenicola str. DSM 14877 AM930
EU262995.1 gg_id:264353 Cystobacter fuscus str. Bj41 EU2629
DQ768107.1 gg_id:169848 Cystobacter armeniaca str. DSM 14710 DQ768
DQ768111.1 gg_id:163670 Cystobacter miniatus str. DSM 14712 DQ768
AJ970180.1 gg_id:133876 Stigmatella erecta str. DSM 16858 AJ9701
EU193069.1 gg_id:365027 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo EU193
AJ233911.1 gg_id:10627 Angiococcus disciformis str. d6 AJ2339
AJ233905.1 gg_id:10633 Cystobacter violaceus str. Cb vi29 AJ2339
AJ233944.1 gg_id:10652 Polyangium vitellinum str. Pl vt1 AJ2339
EF108312.1 gg_id:180118 Haliangium ochraceum str. GS1 EF1083
AB062751.1 gg_id:38718 Haliangium tepidum AB062
EU134537.1 gg_id:236984 tallgrass prarie soil clone FFCH18685 EU1345
FJ712545.1 gg_id:530479 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) k FJ7125
AB286567.1 gg_id:204372 Reducing production and domination comamonadaceae reducing oxygen supply was AB2865
GQ264394.1 gg_id:574674 Structure Simulated Level Waste Site simulated level waste site clone WW2_84 GQ264
AM072418.1 gg_id:137564 uranium mining waste pile soil clone JG35-2-JT67 AM072
EF018702.1 gg_id:204556 aspen rhizosphere clone Amb_16S_999 EF0187
FJ479136.1 gg_id:578408 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4791
GQ396851.1 gg_id:566634 Functional unvegetated perhumid recently-deglaciated soils do not correlate shifts s GQ396
EU134437.1 gg_id:242508 tallgrass prarie soil clone FFCH11506 EU1344
EU134439.1 gg_id:236963 tallgrass prarie soil clone FFCH11594 EU1344
EU676441.1 gg_id:300085 rhizosphere pioneer plants (Bahia xylopoda and Viguiera linearis) growing on metals· EU6764
AY921676.1 gg_id:113324 farm soil clone AKYH1423 AY9216
AJ518792.1 gg_id:76933 uranium mining waste pile clone JG37-AG-33 proteobacterium AJ5187
AJ519631.1 gg_id:74929 uranium mill tailings soil clone Sh765B-TzT-42 AJ5196
EU617834.1 gg_id:333636 Seasonal variation microbial Yel Sea sediment clone C13S-30 EU6178
EF516060.1 gg_id:217328 grassland soil clone FCPP560 EF5160
EU925860.1 gg_id:353947 sediments sediment station DBS1 northern Bering Sea clone 061F22 EU9258
AM490754.1 gg_id:542734 Linking and functional nutrient spiraling mats (USA) microbial mat sulfidic cave sprir AM490
DQ395973.1 gg_id:152024 deep-sea octacoral clone ctg_CGOGA72 DQ395
EU617837.1 gg_id:313196 Seasonal variation microbial Yel Sea sediment clone D13S-10 EU6178

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DQ640732.1 gg_id:228460 full-scale EBPR sludge clone Skagen129 DQ640
AY922085.1 gg_id:114341 farm soil clone AKYG989 AY922(
EU134548.1 gg_id:246356 tallgrass prarie soil clone FFCH2604 EU1345
EU335231.1 gg_id:256412 Changes microbial metabolic and along hydrogeochemically variable profile unsatura EU3352
AY862012.1 gg_id:112562 Queens Laundry berry community clone QLBB011 AY862(
FJ748771.1 gg_id:578632 Vertical and sulfate-reducing prokaryotes estuarine Southern China Pearl River Estuai FJ7487
EF515967.1 gg_id:224129 grassland soil clone FCPO510 EF5159
EF516802.1 gg_id:221219 grassland soil clone FCPS608 EF5168
EF516477.1 gg_id:218069 grassland soil clone FCPO701 EF5164
EU617835.1 gg_id:345106 Seasonal variation microbial Yel Sea sediment clone D13S-24 EU6178
EF999387.1 gg_id:244765 Vertical and Methanotrophs Estuarine Sediments Pearl River Estuary sediments 22cn EF9993
DQ811794.1 gg_id:173727 mangrove soil clone MSB-3B11 DQ811
FJ466420.1 gg_id:566988 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea FJ4664
EU652608.1 gg_id:279253 Seasonal variation microbial Yel Sea sediment clone B8S-115 EU6526
GU119139.1 gg_id:570059 Threatened Corals Provide Microbial Habitats clone Past_J10 GU119
AB286332.1 gg_id:204177 Reducing production and domination comamonadaceae reducing oxygen supply was AB2863
AY622263.1 gg_id:99343 subsurface soil clone B-BK96 AY6222
FM253665.1 gg_id:305498 Rock gold mine unusually microbial biofilm clone F04-2 FM253
FJ478686.1 gg_id:570453 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4786
FJ478958.1 gg_id:543753 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4789
AJ241020.1 gg_id:10682 Norway:(Svalbard)Hornsund clone Sva0679 AJ2410
GU208498.1 gg_id:592792 Study on Sediment Dongping Lake sediment clone Shf1-5 GU208
FJ466408.1 gg_id:548168 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea FJ4664
AJ576419.1 gg_id:102303 midgut homogenate Pachnoda ephippiata larva clone PeM65 AJ5764
EF580975.1 gg_id:277714 Survey Microbial Freshwater Calcareous Mats freshwater calcareous mat clone CM1: EF5809
EF999354.1 gg_id:244128 Vertical and Methanotrophs Estuarine Sediments Pearl River Estuary sediments 6cm EF9993
AY921674.1 gg_id:113379 farm soil clone AKYH1085 AY9216
EU445232.1 gg_id:563875 Isolation Weight Forest Topsoil Metagenomic tropical forest topsoil clone R84 EU445
GU118929.1 gg_id:546642 Threatened Corals Provide Microbial Habitats clone Past_O02 GU118
DQ906778.1 gg_id:254611 Oman subsurface soil clone 2A-7 DQ906
GQ264118.1 gg_id:551080 Structure Simulated Level Waste Site simulated level waste site clone WC3_53 GQ264
EU617833.1 gg_id:332464 Seasonal variation microbial Yel Sea sediment clone D13S-2 EU6178
AM997778.1 gg_id:572137 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A AM997
EU134286.1 gg_id:256241 tallgrass prarie soil clone FFCH3218 EU1342
EU134430.1 gg_id:239367 tallgrass prarie soil clone FFCH10899 EU1344
AY921878.1 gg_id:113228 farm soil clone AKYH1170 AY9218
EF580944.1 gg_id:278622 Survey Microbial Freshwater Calcareous Mats freshwater calcareous mat clone CM6(EF5809
EF019351.1 gg_id:207878 aspen rhizosphere clone Elev_16S_566 EF0193
EU861852.1 gg_id:345643 effects chronic fertilization on alpine tundra microbial implications carbon and nitrog EU8618
NC_009675.1 gg_id:250283 Anaeromyxobacter sp. str. Fw109-5 NC_00

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GQ397088.1 gg_id:532843 Functional unvegetated perhumid recently-deglaciated soils do not correlate shifts s GQ397
EU134349.1 gg_id:236268 tallgrass prarie soil clone FFCH6412 EU1343
FJ190071.1 gg_id:335745 Strain-specific probing strain and heterogeneous U(VI)-reducing Anaeromyxobacter s FJ1900
FJ190063.1 gg_id:353729 Strain-specific probing strain and heterogeneous U(VI)-reducing Anaeromyxobacter s FJ1900
EU134508.1 gg_id:241430 tallgrass prarie soil clone FFCH17129 EU1345
AM162453.1 gg_id:151071 and situ identification acidic sphagnum peat bog clone B88 AM162
FJ190066.1 gg_id:324580 Strain-specific probing strain and heterogeneous U(VI)-reducing Anaeromyxobacter s FJ1900
EU331407.1 gg_id:247762 Anaeromyxobacter dehalogenans str. DCP15 EU3314
FJ190072.1 gg_id:317365 Strain-specific probing strain and heterogeneous U(VI)-reducing Anaeromyxobacter s FJ1900
GQ402739.1 gg_id:579915 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
GQ402712.1 gg_id:582110 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
EU307086.1 gg_id:249072 Changes microbial metabolic and along hydrogeochemically variable profile unsatura EU3070
AY921809.1 gg_id:113159 farm soil clone AKYG886 AY9218
EF520536.1 gg_id:234490 structure lakes: what controls ? acid-impacted lake clone ADK-BTh02-17 EF5205
AF382397.1 gg_id:24157 Anaeromyxobacter dehalogenans str. 2CP-5 AF3823
FJ190062.1 gg_id:312494 Anaeromyxobacter dehalogenans str. FRC-W FJ1900
AB486683.1 gg_id:571531 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCOR AB4866
AJ233915.1 gg_id:10592 Myxococcus coralloides str. Cc c806 AJ2339
GU139156.1 gg_id:587638 Corallococcus macrosporus str. HBUM91004 GU139
EU263003.1 gg_id:259044 Corallococcus coralloides str. 0185-2 EU2630
EU263002.1 gg_id:263917 Corallococcus coralloides str. 0198-2 EU2630
GQ246607.1 gg_id:550449 Corallococcus exiguus str. HBUM94202 GQ246
AJ233931.1 gg_id:10589 Corallococcus exiguus str. Cc e12b AJ2339
AM930268.1 gg_id:247897 Melittangium lichenicola str. ATCC 25944 AM930
AJ811614.1 gg_id:106360 Corallococcus coralloides str. DSM 51301 AJ8116
AJ811612.1 gg_id:106050 Corallococcus coralloides str. DSM 52500 AJ8116
AJ811595.1 gg_id:105288 Corallococcus coralloides str. DSM 51651 AJ8115
EU262999.1 gg_id:265680 Corallococcus coralloides str. 0007-3 EU2629
AJ811593.1 gg_id:104972 Corallococcus coralloides str. DSM 51548 AJ8115
AJ811601.1 gg_id:100844 Corallococcus coralloides str. DSM 51492 AJ8116
AJ811604.1 gg_id:101327 Corallococcus coralloides str. DSM 52502 AJ8116
AJ811615.1 gg_id:106528 Corallococcus coralloides str. DSM 51408 AJ8116
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AY724799.1 gg_id:105036 Myxococcus xanthus str. UCDaV16 AY7247
AY072737.1 gg_id:17656 Myxococcus macrosporus str. 125-10-3 AY0727
AY072740.1 gg_id:21317 Myxococcus macrosporus str. 125-10-1 AY0727
AY724798.1 gg_id:104894 Myxococcus xanthus str. UCDaV5 AY7247
EU271853.1 gg_id:251509 Myxococcus stipitatus str. KYC1101 EU2718
GQ246570.1 gg_id:590399 Myxococcus stipitatus str. HBUM92079 GQ246
EU262651.1 gg_id:243378 Myxococcus fulvus str. KYC1136 EU2626
EU262655.1 gg_id:237067 Myxococcus fulvus str. KYC1198 EU2626

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AB218209.1 gg_id:150276 Myxococcus fulvus str. NBRC 100070 AB218
GU139153.1 gg_id:579552 Myxococcus stipitatus str. HBUM93501 GU139
AJ233929.1 gg_id:10614 Myxococcus xanthus str. DSM 435 (Mx x1) AJ2339
GQ246531.1 gg_id:576354 Myxococcus virescens str. HBUM93351 GQ246
AJ233927.1 gg_id:10612 Myxococcus virescens str. Mx v1 AJ2339
AJ233909.1 gg_id:10600 Angiococcus disciformis str. d1 AJ2339
EU262997.1 gg_id:276309 Myxococcus macrosporus str. Myxo9736 EU262
DQ768123.1 gg_id:163033 Pyxicoccus fallax str. DSM 14698 DQ768
GQ246547.1 gg_id:579922 Corallococcus macrosporus str. HBUM93406 GQ246
GQ246552.1 gg_id:534207 Corallococcus macrosporus str. HBUM93407 GQ246
GU139157.1 gg_id:589401 Myxococcus virescens str. HBUM91069 GU139
AJ233930.1 gg_id:10615 Myxococcus xanthus str. Mx x132 AJ2339
AJ811621.1 gg_id:102087 Corallococcus coralloides str. DSM 52496 AJ8116
GQ246541.1 gg_id:539091 Myxococcus virescens str. HBUM93307 GQ246
EU262992.1 gg_id:277585 Myxococcus fulvus str. 0189-5 EU262
GQ246525.1 gg_id:540091 Myxococcus fulvus str. HBUM93175 GQ246
AJ233917.1 gg_id:10602 Myxococcus fulvus str. Mx f2 AJ2339
AJ811622.1 gg_id:102241 Corallococcus coralloides str. DSM 52498 AJ8116
AJ233920.1 gg_id:10605 Myxococcus macrosporus str. Cc m7 AJ2339
AY724797.1 gg_id:104738 Myxococcus xanthus str. UCDaV1 AY724
AJ233925.1 gg_id:10610 Myxococcus virescens str. Mx v2 AJ2339
EU158297.1 gg_id:247490 Myxococcus sp. str. HBUM 91040 EU158
GQ246558.1 gg_id:532677 Myxococcus fulvus str. HBUM93132 GQ246
AF280855.1 gg_id:73433 bioreactor clone mle1-22 AF280
EU283398.1 gg_id:253563 consecutively aerated submerged treating domestic wastewater activated sludge m EU283
ABCS01000137.1 gg_id:235635 Plesiocystis pacifica str. SIR-1 ABCS0
EU134550.1 gg_id:256957 tallgrass prarie soil clone FFCH2652 EU134
AY921891.1 gg_id:135973 farm soil clone AKYH963 AY921
FJ152686.1 gg_id:304479 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX1A_ FJ1526
EU050860.1 gg_id:245344 libraries sediment Kings Bay Svalbard Arctic clone ss1_B_05_87 EU050
CU466781.1 gg_id:327106 Evry wastewater treatment plant anoxic basin clone CU466
FJ203639.1 gg_id:313265 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h FJ2036
DQ298325.1 gg_id:154699 studies on and nifH Lasiurus sindicus Sewan grass Thar Desert Rajasthan India rhizos DQ298
AB252740.1 gg_id:152915 Antimicrobial Cyclic Depsipeptides SMH-27-4A coastal soil AB252
AM997796.1 gg_id:546538 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A AM997
EU236309.1 gg_id:298699 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg1a2H2 EU236
AJ233941.1 gg_id:10642 Chondromyces robustus str. Cm a22 AJ2339
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DQ491070.1 gg_id:170538 Chondromyces pediculatus str. BICC 8609 DQ491

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AJ233938.1 gg_id:10639 Chondromyces apiculatus str. Cm a14 AJ2339
AY079453.1 gg_id:29731 Polyangium cellulosum str. So0089-1 AY0794
AF387627.1 gg_id:26373 Polyangium cellulosum str. 9741 AF3876
EU240490.1 gg_id:277159 Sorangium cellulosum str. So0184-1 EU2404
FJ479176.1 gg_id:580635 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4791
AY921933.1 gg_id:113748 farm soil clone AKYG909 AY9219
EU193074.1 gg_id:369028 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo EU1930
EU881272.1 gg_id:355920 (long-term grazing and burned annual) Karst region serious disturbance field soil clor EU8812
EU134398.1 gg_id:257391 tallgrass prarie soil clone FFCH6364 EU1343
FJ479473.1 gg_id:579806 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4794
DQ295908.1 gg_id:145144 Cohn's Crenothrix filamentous oxidizer unusual methane monooxygenase physical e DQ295
FJ660562.1 gg_id:551380 Correlation functional stability and dynamics full-scale wastewater treatment plant a FJ6605
EF516308.1 gg_id:218711 grassland soil clone FCPO632 EF5163
AJ617907.1 gg_id:109755 oxic-anoxic interphase flooded paddy soil clone D142119 AJ6179
EU134486.1 gg_id:245900 tallgrass prarie soil clone FFCH15612 EU1344
FJ478737.1 gg_id:535402 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4787
AJ833647.1 gg_id:108677 Byssophaga cruenta str. c2 = DSM 14553 AJ8336
AY493915.1 gg_id:136914 Fingerprinting aggregates soil clone 604 AY4939
AJ233948.1 gg_id:10657 Myxococcales str. NOSO-1 AJ2339
AM490752.1 gg_id:588131 Linking and functional nutrient spiraling mats (USA) microbial mat sulfidic cave sprir AM490
EU104167.1 gg_id:347524 Evidence Comamonadaceae determinants settling performance activated sludge clo EU1041
EU979074.1 gg_id:326414 Effects intercropping Rhizobium inoculation on microbial biomass and rhizosphere b EU9790
AF280858.1 gg_id:71817 bioreactor clone mle1-29 AF2808
EF018417.1 gg_id:203878 aspen rhizosphere clone Amb_16S_1034 EF0184
AB238772.1 gg_id:146819 shal subsurface Sarobetsu Mire peat soil clone HSM-SS-009 AB2387
EF580966.1 gg_id:278697 Survey Microbial Freshwater Calcareous Mats freshwater calcareous mat clone CM1 EF5809
EF112185.1 gg_id:187653 Stigmatella koreensis str. KYC-1019 EF1121
EU134339.1 gg_id:240506 tallgrass prarie soil clone FFCH3210 EU1343
EU134451.1 gg_id:250244 tallgrass prarie soil clone FFCH12289 EU1344
EU134540.1 gg_id:237206 tallgrass prarie soil clone FFCH18737 EU1345
FJ671175.1 gg_id:511742 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6711
AY725263.1 gg_id:102557 decayed velvetleaf seed clone S1-4-CL5 AY7252
DQ768124.1 gg_id:170014 Hyalangium minutum str. DSM 14724 DQ768
DQ129589.1 gg_id:137984 microarray level air two cities Texas urban aerosol clone AKIW811 DQ129
AM697153.1 gg_id:221410 sequencing libraries indoor dust clone BF0002B103 AM697
GQ007850.1 gg_id:501815 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ007
FJ152674.1 gg_id:336745 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX1A_ FJ1526
GQ264111.1 gg_id:568834 Structure Simulated Level Waste Site simulated level waste site clone WC3_40 GQ264
DQ768110.1 gg_id:172129 Cystobacter gracilis str. DSM 14753 DQ768

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EU386034.1 gg_id:274528 Biogeographical and microbes sediments on subseafloor sediment South China Sea c EU3860
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DQ228369.1 gg_id:141905 microbial compositions two subglacial possible role microbes chemical weathering p DQ228
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AY869685.1 gg_id:112279 ridge flank crustal fluids clone FS266-77B-03 AY8696
EU919813.1 gg_id:351152 Kongsfjorden western Spitsbergen Svalbard ocean water clone b132 EU9198
DQ015820.1 gg_id:140293 Antarctic lake water clone ELB19-125 DQ015
DQ396146.1 gg_id:154831 deep-sea octacoral clone ctg_NISA283 DQ396
DQ289938.1 gg_id:162701 Microbial Carbon and Nitrogen Cycling Sediments South Atlantic Bight Permeable Sh DQ289
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FM179869.1 gg_id:354477 Biogeochemical processes microbial Gullfaks and Tommeliten methane seeps (Nortl FM179
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EU491229.1 gg_id:262635 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak EU4912
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FM253643.1 gg_id:334324 Rock gold mine unusually microbial biofilm clone C01-2 FM253
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DQ289896.1 gg_id:165188 Microbial Carbon and Nitrogen Cycling Sediments South Atlantic Bight Permeable Sh DQ289
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FJ203391.1 gg_id:349173 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h FJ2033
FJ416109.1 gg_id:359523 sediments sediment station NEC5 Northern Bering Sea clone 084L59 FJ4161
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GU118825.1 gg_id:542878 Threatened Corals Provide Microbial Habitats clone Mfra_O14 GU118
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AF354155.1 gg_id:71658 marine methane seep clone 1510 AF354
EU734963.1 gg_id:344456 assemblages sediment station DBSE Northern Bering Sea clone 057D15 EU734
EU236344.1 gg_id:296500 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg5a2H11 EU236
AF317771.1 gg_id:136770 Nullarbor cave clone wb1_N15 AF317
GU230398.1 gg_id:581179 Multilevel approach along Rio de la Plata-South Atlantic Ocean coastal sediment clo GU230
FJ358881.1 gg_id:588965 and redox-stratified sediments marine reef sandy sediment clone SO51 FJ3588
EU287101.1 gg_id:255323 Pacific arctic surface sediment clone P13-8 EU287
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AM936057.1 gg_id:542911 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM936
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DQ331004.1 gg_id:159301 Guerrero Negro hypersaline microbial mat clone 10D2Z33 DQ331
AM490745.1 gg_id:592584 Linking and functional nutrient spiraling mats (USA) microbial mat sulfidic cave sprir AM490
GU362952.1 gg_id:555750 and archaeal biogeochemical cycling genes within Qiongdongnan basin Sea: pilot stu GU362
AF154094.1 gg_id:10677 hydrocarbon seep clone BPC065 AF154
EU246004.1 gg_id:253746 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-P1-D07 EU246
EU360307.1 gg_id:277150 microbial fuel cell enriched sediment clone FWS 711 EU360
DQ109919.1 gg_id:143327 Sulfate-reducing mats: Changing paradigms new discoveries salt pond nonlithifying DQ109
DQ676442.1 gg_id:217352 Archaeal sediment and plankton freshwater pond suboxic freshwater-pond clone M DQ676
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AF418175.1 gg_id:74171 Desulfobacter curvatus str. DSM 3379 AF4181
NR_025348.1 gg_id:572343 Desulfobacterium anilini str. Ani1; DSM 4660 NR_02
CP001087.1 gg_id:523103 Desulfobacterium autotrophicum str. HRM2 CP001
AY542197.1 gg_id:113166 Gulf Mexico seafloor sediments clone GoM HDB-06 AY542
AF026998.1 gg_id:10771 hot spring clone OPB16 AF026
AY771951.1 gg_id:111847 marine surface sediment clone SI28 AY771
GU362956.1 gg_id:533418 and archaeal biogeochemical cycling genes within Qiongdongnan basin Sea: pilot stu GU362
EU385666.1 gg_id:262547 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S EU385
AF029045.1 gg_id:10904 Benzene mineralizing consortium complete clone SB-21 consortium AF029
FJ716478.1 gg_id:566769 Uncultivated archaea sulfate-reducing biofilm Frasassi cave system anoxic lake water FJ7164
FJ485020.1 gg_id:566534 microbial autonomous rover world's deepest phreatic sinkhole biomat El Zacaton 114 FJ4850
GQ356929.1 gg_id:544180 Metal Dependent Marine Methane Oxidation methane seep sediment clone Fe_B_1 GQ356
AF029048.1 gg_id:10906 Benzene mineralizing consortium complete clone SB-30 consortium AF029
DQ330997.1 gg_id:159166 Guerrero Negro hypersaline microbial mat clone 09D2Z19 DQ330
AY592183.1 gg_id:99181 marine ANAMMOX sediment clone AY592183 AY592
FJ628304.1 gg_id:564870 transition and zone within near-shore basin: brackish water anoxic fjord Nitinat Lake FJ6283
FN396628.1 gg_id:565202 constant flux thermophilic cold seabed Arctic marine surface sediment clone s5_0_II FN396
FJ437822.1 gg_id:535056 Benthic okenone production Fayetteville New York Green Lake chemocline 20.5 m wa FJ4378
DQ109878.1 gg_id:142790 Sulfate-reducing mats: Changing paradigms new discoveries salt pan lithifying micro DQ109
AB177158.1 gg_id:132816 seafloor methane hydrate clone ODP1230B17.18 AB177
GU180164.1 gg_id:540242 Impact coplanar PCBs on microbial activity anaerobic estuarine sediments sediment GU180
AM086120.1 gg_id:145576 Abundance and archaea mesotrophic Lake Kinneret lake profundal sediment clone AM086
AM745206.1 gg_id:294510 Impact oil er hydrocarbons on microbial and activity Gulf Mexico cold seep marine s AM745
EU385798.1 gg_id:274378 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S EU385
EU385717.1 gg_id:276920 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S EU385
EU925857.1 gg_id:328502 sediments sediment station DBS1 northern Bering Sea clone 052E88 EU9258
FM164951.2 gg_id:395222 two Bulgarian geothermal springs hot spring clone S1-53 FM164
DQ811822.1 gg_id:164969 mangrove soil clone MSB-5A4 DQ811
EU245381.1 gg_id:238545 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M1-A0 EU2453
AY542227.1 gg_id:113116 Gulf Mexico seafloor sediments clone GoM IDB-15 AY5422
AM229200.1 gg_id:575796 Microbial vicinity and within hydrates Hydrate Ridge (Cascadia Margin) marine gas h AM229
EU385917.1 gg_id:270552 Stratified microbes sediments Core MD05-2902 subseafloor sediment South China S EU385
GU302479.1 gg_id:557390 Spatial structure and activity sedimentary microbial underlying Beggiatoa spp. mat h GU302
EU592476.1 gg_id:592826 Seasonal changes Salton Sea hypersaline sediment clone SSS17A EU5924
DQ521799.1 gg_id:159904 Anaerobic Methane Oxidizing ANME-1b Archaea Hypersaline Sediments Gulf Mexico DQ521
FN429786.1 gg_id:548583 Biogeochemistry -activity cold seep Larsen B area western Weddell Sea Antarctica m FN4297
FJ264650.1 gg_id:339335 Manganese and Iron Dependent Anaerobic Oxidation Methane methane seep sedim FJ2646
DQ676438.1 gg_id:221104 Archaeal sediment and plankton freshwater pond suboxic freshwater-pond clone M DQ676
DQ925877.1 gg_id:252087 Microbes and Thermal Gradients Temperature Hydrothermal Chimneys hydrotherm DQ925
AB015244.1 gg_id:10939 deepest cold-seep area Japan Trench clone JTB133 proteobacterium AB015

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AY197382.1 gg_id:86333 Guaymas Basin hydrothermal vent sediments clone B01R011 AY1973
AY197376.1 gg_id:86388 Guaymas Basin hydrothermal vent sediments clone B01R004 AY1973
AJ441316.1 gg_id:67542 Desulfobacula toluolica str. DSM 7467 AJ4413
CP000859.1 gg_id:255870 Desulfococcus oleovorans str. Hxd3 CP000
DQ103668.1 gg_id:132520 hypersaline endoevaporitic microbial mat clone E4aE11 DQ103
GQ249552.1 gg_id:546119 Microbial anaerobic sediments Bay Cadiz (Spain) marine sediment: 12-14 cm layer cl GQ249
EU246073.1 gg_id:238062 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-P2-H01 EU246
DQ397423.1 gg_id:159502 Guerrero Negro hypersaline microbial mat clone 04D2Z68 DQ397
GQ249596.1 gg_id:544699 Microbial anaerobic sediments Bay Cadiz (Spain) marine sediment: 12-14 cm layer cl GQ249
FJ712553.1 gg_id:521361 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) k FJ7125
AM176871.1 gg_id:160902 Recovery mangrove sediment clone SZB46 AM176
EU245312.1 gg_id:257695 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-H5-H01 EU2453
EU245273.1 gg_id:256695 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-H5-B05 EU2452
AF513951.1 gg_id:111956 hypersaline lake clone LA30-B27 AF5139
AJ620510.1 gg_id:108098 Olavius crassitunicatus endosymbiont AJ6205
EU245134.1 gg_id:241850 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-H2-G09 EU2451
AF099063.1 gg_id:10900 Desulfofaba gelida str. PSv29 AF0990
AB015240.1 gg_id:10907 deepest cold-seep area Japan Trench clone JTB16 AB0152
NR_028732.1 gg_id:592871 Desulfofrigus fragile str. LSv21; DSM 12345 NR_02
AB189366.1 gg_id:113570 cold seep sediment clone JT75-121 AB1893
FM242377.1 gg_id:349097 sequences sediment clone 19 T9d+oil FM242
EF125385.1 gg_id:194587 soil naked tidal flat sediment near mangrove clone MSB-1ax8 EF1253
FM242229.1 gg_id:322751 sequences sediment clone 96 T0h-oil FM242
AB530178.1 gg_id:583955 Monitoring Suez and Tokyo bays based on analyses marine sediment clone Suez..Ba AB5301
DQ351771.1 gg_id:147847 Microbial Adherent Sediment Particles Heavy Metal Contaminated North Sea Surfac DQ351
EF442994.1 gg_id:248725 Desulfotignum sp. str. DSM 7120 EF4429
AF233370.1 gg_id:31826 Desulfotignum balticum str. Sax (DSM 7044) marine mud AF2333
EU047532.1 gg_id:251611 Anaerobic degradation benzene marine and cell hybridization dominant phylotype b EU0475
EU047529.1 gg_id:235729 Anaerobic degradation benzene marine and cell hybridization dominant phylotype b EU0475
AM882605.1 gg_id:330092 Structure along hydrocarbon contamination coastal sediment oil polluted water pet AM882
EU386050.1 gg_id:264473 Biogeographical and microbes sediments on subseafloor sediment South China Sea c EU3860
AB240476.1 gg_id:143077 microbial structure rhizosphere biofilm Sapporo root-tip (0 40 mm) Phragmites Sosei AB2404
EU048686.1 gg_id:245974 and archaeal surface marine sediment Slope South China Sea clone MD2896-B29 EU0486
EF454380.2 gg_id:222931 termite hindgut clone 290cost002-P3L-2033 EF4543
EU487868.1 gg_id:561085 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU4878
EU885093.1 gg_id:305714 microbial hindgut chamber Pomacanthus sexstriatus GI tract clone A2A5 EU8850
FJ712462.1 gg_id:526057 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) k FJ7124
EF454653.2 gg_id:226987 termite hindgut clone 290cost002-P3L-2488 EF4546
EU622291.1 gg_id:289758 syntrophic partnerships deep-sea vents direct cell capture and metagenomics Eel Ri EU6222
AM490751.1 gg_id:537744 Linking and functional nutrient spiraling mats (USA) microbial mat sulfidic cave sprir AM490

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EF454687.2 gg_id:223294 termite hindgut clone 290cost002-P3L-2541 EF4546
AY542569.1 gg_id:113399 Gulf Mexico seafloor sediment clone GoM GB425 12B-61 AY5425
FJ484450.1 gg_id:571089 microbial autonomous rover world's deepest phreatic sinkhole wall biomat El Zacator FJ4844
AB234533.1 gg_id:145609 termite gut homogenate clone MgMjD-089 AB2345
AB240382.1 gg_id:150612 microbial structure Phragmites rhizosphere biofilm reed bed reactor laboratory clon AB2403
EU246159.1 gg_id:248560 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-P4-E05 EU2461
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AM882604.1 gg_id:333017 Structure along hydrocarbon contamination coastal sediment oil polluted water pet AM882
EU385937.1 gg_id:262118 Stratified microbes sediments Core MD05-2902 subseafloor sediment South China S EU3859
AM882591.1 gg_id:327370 Structure along hydrocarbon contamination coastal sediment oil polluted water pet AM882
DQ831539.1 gg_id:171382 Activity and sulphate-reducing contrasting sediments River Colne estuary UK marine DQ831
EU246034.1 gg_id:249930 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-P1-H08 EU2460
AM086154.1 gg_id:147459 Abundance and archaea mesotrophic Lake Kinneret lake profundal sediment clone AM086
EF014726.1 gg_id:225865 Candidatus Magnetoglobus multicelularis gen. sp. nov. multicellular magnetotactic p EF0147
AM086124.1 gg_id:146208 Abundance and archaea mesotrophic Lake Kinneret lake profundal sediment clone AM086
EF442981.1 gg_id:237295 Desulfocella sp. str. DSM 2056 EF4429
EU399670.1 gg_id:273059 and localization microbial consortium full-scale granular activated carbon anaerobic EU3996
FJ264667.1 gg_id:311003 Manganese and Iron Dependent Anaerobic Oxidation Methane methane seep sedim FJ2646
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DQ811835.1 gg_id:173313 mangrove soil clone MSB-5E7 DQ811
U45989.1 gg_id:10869 Desulfonema magnum str. DSM 2077 anaerobic mud seawater lagoon (Etang de Prevost U45989
AB189380.1 gg_id:114027 cold seep sediment clone JT75-319 AB1893
AB188779.1 gg_id:113838 cold seep sediment clone SB3-7 AB1887
FJ789839.1 gg_id:534671 Desulfobotulus sapovorans str. ATCC 33892; 1pa3 FJ7898
FM242270.1 gg_id:314257 sequences sediment clone 4 T0h-oil FM242
EU160523.1 gg_id:352459 diagnosis central-venous infections cultivation-dependent and techniques biofilm sc EU1605
FJ202141.1 gg_id:314793 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2021
EU385675.1 gg_id:272166 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S EU3856
DQ395063.1 gg_id:156126 harbor sediment clone VHS-B5-66 DQ395
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DQ811836.1 gg_id:173385 mangrove soil clone MSB-5F12 DQ811
AJ937698.1 gg_id:143680 Microbiological investigation methane- and hydrocarbon-discharging volcanoes Carp AJ9376
AY222304.1 gg_id:114278 host hindgut caecum clone Del 1 AY2223
AM882599.1 gg_id:326082 Structure along hydrocarbon contamination coastal sediment oil polluted water pet AM882
AB355082.1 gg_id:237712 Monitoring and archaeal two heavy polluted areas lake Egypt based on sediment Ma AB3550
EU622295.1 gg_id:294941 syntrophic partnerships deep-sea vents direct cell capture and metagenomics Eel Riv EU6222
FJ716993.1 gg_id:544106 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United King FJ7169
DQ630689.1 gg_id:159784 Unexpected many-celled magnetotactic prokaryote salt marsh clone mmp5 DQ630
EU570889.1 gg_id:556574 transition and zone within near-shore anoxic basin: Nitinat Lake depth 50 m clone Ni EU5708
U85470.1 gg_id:10934 Desulfobotulus sp. str. BG14 U85470

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EU386062.1 gg_id:275331 Biogeographical and microbes sediments on subseafloor sediment South China Sea c EU386
FM165241.1 gg_id:557184 seep chitineous tube vestimentiferan tubeworm Lamellibrachia sp. cold seeps clone FM165
FJ973581.1 gg_id:378495 Periodic sulfide irruptions impact microbial structure and hypersaline lake water colu FJ9735
FJ712482.1 gg_id:528626 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) K FJ7124
FJ485367.1 gg_id:566855 microbial autonomous rover world's deepest phreatic sinkhole wall biomat El Zacator FJ4853
AY082457.1 gg_id:67851 neutral pH mine biofilm clone 44a-B1-10 AY082
DQ630675.1 gg_id:160459 Unexpected many-celled magnetotactic prokaryote salt marsh clone mmp23 DQ630
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AJ704678.1 gg_id:109279 marine sediment clone HMMVPog-2 AJ7046
DQ415842.1 gg_id:157733 Dominant microbial limestone-corroding biofilms frasassi system Italy Frasassi sulfid DQ415
FN396636.1 gg_id:541666 constant flux thermophilic cold seabed Arctic marine surface sediment clone s5_0_II FN396
GU230401.1 gg_id:554116 Multilevel approach along Rio de la Plata-South Atlantic Ocean coastal sediment clo GU230
AY216443.1 gg_id:81354 temperate estuarine mud clone KM88 AY216
DQ630707.1 gg_id:160788 Unexpected many-celled magnetotactic prokaryote salt marsh clone mmp2_2 DQ630
DQ521813.1 gg_id:160182 Anaerobic Methane Oxidizing ANME-1b Archaea Hypersaline Sediments Gulf Mexic DQ521
FM242231.1 gg_id:317203 sequences sediment clone 189 T0h-oil FM242
FJ716967.1 gg_id:545744 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United King FJ7169
AJ704696.1 gg_id:109295 marine sediment clone HMMVBeg-44 AJ7046
GQ356986.1 gg_id:581992 Metal Dependent Marine Methane Oxidation methane seep sediment clone FeSO4_ GQ356
GQ249585.1 gg_id:587834 Microbial anaerobic sediments Bay Cadiz (Spain) marine sediment: 12-14 cm layer c GQ249
AM882600.1 gg_id:306625 Structure along hydrocarbon contamination coastal sediment oil polluted water pet AM882
FJ814756.1 gg_id:556875 Microbial assemblages Thioploca sheaths cold seep settings Monterey Bay Carmel Ca FJ8147
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AJ237607.1 gg_id:10870 Desulfobacterium indolicum str. DSM 3383 marine mud AJ2376
AY771939.1 gg_id:111869 marine surface sediment clone SI29 AY771
EU385785.1 gg_id:272732 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S EU385
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FJ517109.1 gg_id:549171 semiarid 'Tablas de Daimiel National Park' wetland (Central Spain) unravelled water c FJ5171
EU385687.1 gg_id:274595 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S EU385
AM882587.1 gg_id:340294 Structure along hydrocarbon contamination coastal sediment oil polluted water pet AM882

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AY053490.1 gg_id:39986 gas hydrate clone AT425_EubD9 AY0534
AJ620501.1 gg_id:353759 Olavius 3 endosymbiont O. ilvae Individual 5 AJ6205
FJ746111.1 gg_id:513493 Microbial oligotrophic marine sediments: South Pacific Gyre ocean sediment 5306 m FJ7461
DQ811817.1 gg_id:172929 mangrove soil clone MSB-4G8 DQ811
FM242225.1 gg_id:337177 sequences sediment clone 342 T0h-oil FM242
AB237684.1 gg_id:139771 microorganisms deep subsurface groundwater sedimentary rock milieu clone HDBW AB237
AY082461.1 gg_id:67845 neutral pH mine biofilm clone 44a-B1-17 AY0824
GU302442.1 gg_id:552223 Spatial structure and activity sedimentary microbial underlying Beggiatoa spp. mat GU302
AM774314.1 gg_id:243934 Cultivation and situ quantification consistently demonstrate that two distinct group AM774
EF999398.1 gg_id:237632 Vertical and Methanotrophs Estuarine Sediments Pearl River Estuary sediments 50cn EF9993
DQ630706.1 gg_id:161002 Unexpected many-celled magnetotactic prokaryote salt marsh clone mmp2_28 DQ630
AJ241022.1 gg_id:10909 Norway:(Svalbard)Hornsund clone Sva0405 AJ2410
DQ831553.1 gg_id:163459 Activity and sulphate-reducing contrasting sediments River Colne estuary UK marine DQ831
AJ831748.1 gg_id:102310 chemocline clone 166 AJ8317
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DQ630702.1 gg_id:160395 Unexpected many-celled magnetotactic prokaryote salt marsh clone mmp2_20 DQ630
FJ716406.1 gg_id:571102 Uncultivated archaea sulfate-reducing biofilm Frasassi cave system anoxic lake water FJ7164
AY851291.1 gg_id:148326 Algidimarina propionica str. AK-P AY8512
EF688206.1 gg_id:347101 Detection microbial sludge anaerobic wastewater treatment system clone 5A4_cons EF6882
EU717681.1 gg_id:425208 Ultrastructure tactic behaviour and potential sulfate reduction multicellular magnet EU717
U81720.2 gg_id:10893 anaerobic digestor clone vadinHA60 U8172
GQ356954.1 gg_id:576546 Metal Dependent Marine Methane Oxidation methane seep sediment clone Fe_B_1 GQ356
DQ811793.1 gg_id:173340 mangrove soil clone MSB-3ax11 DQ811
AB177130.1 gg_id:130033 seafloor methane hydrate clone ODP1230B1.06 AB177
AM774320.1 gg_id:248513 Cultivation and situ quantification consistently demonstrate that two distinct group AM774
EU160501.1 gg_id:325508 diagnosis central-venous infections cultivation-dependent and techniques biofilm sc EU160
U45991.1 gg_id:10897 Desulfonema ishimotonii str. DSM 9679 anaerobic intertidal mud flats Jadebusen (North U4599
EU617853.1 gg_id:345458 Seasonal variation microbial Yel Sea sediment clone D13S-20 EU617
EU246163.1 gg_id:248972 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-P4-E10 EU246
AM404371.1 gg_id:558344 Hydrocarbon-fueled sulfate reduction can sustain long-lived tubeworm aggregation AM404
AJ620497.1 gg_id:354146 Olavius 4 endosymbiont O. algarvensis Individual 2 AJ6204
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DQ397413.1 gg_id:159387 Guerrero Negro hypersaline microbial mat clone 02D2Z34 DQ397
AJ831753.1 gg_id:106553 chemocline clone 293 AJ8317
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EF061952.1 gg_id:182353 Xiamen China mangrove sediment clone XME29 EF0619
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DQ394960.1 gg_id:155401 harbor sediment clone VHS-B3-73 DQ394
EU542523.1 gg_id:267799 Effects chemical structure concentration on pathways microbial during dechlorinatio EU542
EF125387.1 gg_id:193460 soil naked tidal flat sediment near mangrove clone MSB-1B10 EF1253
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AJ535249.1 gg_id:77873 marine sediment above hydrate ridge clone Hyd89-61 proteobacterium AJ5352
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DQ831554.1 gg_id:171484 Activity and sulphate-reducing contrasting sediments River Colne estuary UK marine DQ831
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AM745204.1 gg_id:287932 Impact oil er hydrocarbons on microbial and activity Gulf Mexico cold seep marine s AM745
AY851292.1 gg_id:150305 Algidimarina butyricum str. AK-B AY851
DQ811797.1 gg_id:167399 mangrove soil clone MSB-3C3 DQ811
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DQ397436.1 gg_id:159112 Guerrero Negro hypersaline microbial mat clone 062DZ56 DQ397
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AM176857.1 gg_id:160904 Recovery mangrove sediment clone SZB57 AM176
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EU617854.1 gg_id:316203 Seasonal variation microbial Yel Sea sediment clone C13S-20 EU617
EU048693.1 gg_id:250681 and archaeal surface marine sediment Slope South China Sea clone MD2896-B42 EU048
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DQ811819.1 gg_id:169367 mangrove soil clone MSB-4H12 DQ811
DQ811816.1 gg_id:166688 mangrove soil clone MSB-4G6 DQ811
DQ404782.1 gg_id:155938 contaminated sediment clone 661234 DQ404
AF002671.1 gg_id:10776 Desulfobacca acetoxidans AF002
FJ902442.1 gg_id:548667 phreatic limestone sinkholes northeastern Mexico water column surface cenote Cara FJ9024
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AF523963.1 gg_id:101995 forested wetland clone FW106 AF523
FJ902422.1 gg_id:586511 phreatic limestone sinkholes northeastern Mexico water column surface cenote Cara FJ9024
FJ484032.1 gg_id:537190 microbial autonomous rover world's deepest phreatic sinkhole wall biomat El Zacator FJ4840
FJ484530.1 gg_id:554210 microbial autonomous rover world's deepest phreatic sinkhole wall biomat El Zacator FJ4845
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AY340836.1 gg_id:91627 sulfate-reducing fluidized-bed reactor clone SR_FBR_L13 AY340
AB262720.1 gg_id:239069 microorganisms shal subsurface Sarobetsu mire peat soil clone HSM050P-B-9 AB262
FJ516878.1 gg_id:558853 semiarid 'Tablas de Daimiel National Park' wetland (Central Spain) unravelled upper s FJ5168
DQ676381.1 gg_id:221935 Archaeal sediment and plankton freshwater pond suboxic freshwater-pond clone M DQ676
AM490653.1 gg_id:580869 Linking and functional nutrient spiraling mats (USA) microbial mat sulfidic cave sprir AM490
FJ437843.1 gg_id:511708 Benthic okenone production Fayetteville New York Green Lake 25 m water depth clor FJ4378
AF282177.1 gg_id:30060 Desulfomonile limimaris str. DCB-F AF282
AF282178.1 gg_id:31004 marine sediment clone Btol AF282
AJ316021.1 gg_id:42269 Desulfomonile sp. clone 624 AJ316
AM086646.1 gg_id:140135 Desulfomonile tiedjei str. DSM 6799 AM086
DQ133909.1 gg_id:164530 Dominant microbial biofilms frasassi cave system Italy limestone-corroding stream b DQ133
CT574193.1 gg_id:151947 Evry municipal wastewater treatment plant clone 060B12_B_SD_P93 CT5741
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CT573960.1 gg_id:155759 Evry municipal wastewater treatment plant clone 009F03_B_SD_P15 CT5739
FJ462108.1 gg_id:581591 Microbial ecology industrial digestor mesophilic anaerobic reactor fed effluent chemi FJ4621
EU407209.1 gg_id:275861 household biogas digester clone GW-26 EU407
CT574120.1 gg_id:155635 Evry municipal wastewater treatment plant clone 061D05_B_SD_P93 CT5741
AJ133795.1 gg_id:10858 Syntrophus sp AJ1337
EU104840.1 gg_id:265855 sulfate-reducing and methanogen sulfate-fed reactors libraries anaerobic biofilm rea EU1048
CT574027.1 gg_id:151989 Evry municipal wastewater treatment plant clone 008C04_B_SD_P15 CT5740
CT574029.1 gg_id:156244 Evry municipal wastewater treatment plant clone 008C02_B_SD_P15 CT5740
AB252682.1 gg_id:168756 and activities propionate-oxidizing that affected propionate concentration anaerobic AB2526
CR933148.1 gg_id:110803 Evry municipal wastewater treatment plant clone 012B10_B_SD_P15 CR9331
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DQ676391.1 gg_id:227149 Archaeal and plankton freshwater pond suboxic freshwater-pond sediment clone M DQ676
CT574164.1 gg_id:152984 Evry municipal wastewater treatment plant clone 060F04_B_SD_P93 CT5741
DQ501304.1 gg_id:187961 Seasonal dynamics free-living and particle- four lakes northeastern Germany freshw DQ501
GU202945.1 gg_id:592840 Effect pH on anode microbes MFC microbial fuel cell inoculated activated sludge wa: GU202
CT573944.1 gg_id:154331 Evry municipal wastewater treatment plant clone 009H01_B_SD_P15 CT5739
EU407210.1 gg_id:276971 household biogas digester clone GW-27 EU407
EU522631.1 gg_id:262404 hydrocarbon-degrading methanogenic microbial consortia settling basin Northern Al EU5226
AY661413.1 gg_id:107448 anaerobic hybrid reactor clone TTA_H37 AY6614
AB234260.1 gg_id:145632 Biotransformation Polychlorinated Dioxins Microbial Dynamics Sediment Microcosm AB2342

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EU399668.1 gg_id:271079 and localization microbial consortium full-scale granular activated carbon anaerobic EU399
AB186854.1 gg_id:99369 polychlorinated dioxin dechlorinating microcosm clone TSBZ03 AB186
AF229793.1 gg_id:37165 terephthalate-degrading consortium clone TA20 AF229
AJ306771.1 gg_id:66928 DCP-dechlorinating consortium clone SHA-42 AJ3067
AB288891.1 gg_id:203169 termite gut homogenate clone BOf2-22 AB288
FJ462058.1 gg_id:593849 Microbial ecology industrial digestor mesophilic anaerobic reactor fed effluent chemi FJ4620
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DQ521796.1 gg_id:159708 Anaerobic Methane Oxidizing ANME-1b Archaea Hypersaline Sediments Gulf Mexic DQ521
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DQ521792.1 gg_id:160618 Anaerobic Methane Oxidizing ANME-1b Archaea Hypersaline Sediments Gulf Mexic DQ521
FJ902117.1 gg_id:579169 phreatic limestone sinkholes northeastern Mexico orange biomat 8m deep cenote Ca FJ9021
AJ535254.1 gg_id:77896 marine sediment above hydrate ridge clone Hyd89-52 proteobacterium AJ5352
FJ462062.1 gg_id:587689 Microbial ecology industrial digestor mesophilic anaerobic reactor fed effluent chemi FJ4620
AM746089.1 gg_id:299409 Impact oil er hydrocarbons on microbial and activity Gulf Mexico cold seep marine s AM746
DQ811814.1 gg_id:173034 mangrove soil clone MSB-4G3 DQ811
CU922340.1 gg_id:534010 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU922
FN429788.1 gg_id:546409 Biogeochemistry -activity cold seep Larsen B area western Weddell Sea Antarctica m FN429
AB252432.1 gg_id:153221 Microbial extremely CO2 rich deep-sea sediment Marine sediments Yonaguni Knoll I AB252
EU644230.1 gg_id:283767 and Samoylov Island Lena active layer -centred polygon near surface horizon; Rim_T EU644
DQ067032.1 gg_id:133542 Lake Washington sediment clone pLW-41 DQ067
DQ404844.1 gg_id:150930 contaminated sediment clone 655974 DQ404
FJ902148.1 gg_id:592355 phreatic limestone sinkholes northeastern Mexico orange biomat 8m deep cenote Ca FJ9021
DQ415841.1 gg_id:158424 Dominant microbial limestone-corroding biofilms frasassi system Italy Frasassi sulfid DQ415
AF420337.1 gg_id:67800 hydrothermal sediment clone AF420337 AF4203
GU180161.1 gg_id:538685 Impact coplanar PCBs on microbial activity anaerobic estuarine sediments sediment GU180
EU101287.1 gg_id:237813 Sulfide/oxygen supply ratio predicts outcome competition among sulfur-oxidizing wa EU101
EU542439.1 gg_id:274550 Effects chemical structure concentration on pathways microbial during dechlorinatio EU542
FN429791.1 gg_id:586738 Biogeochemistry -activity cold seep Larsen B area western Weddell Sea Antarctica m FN429
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AF354149.1 gg_id:71121 marine methane seep clone 1513 AF3541
AM712339.1 gg_id:252529 detection and ly microbial Brothers Seamount Kermadec Arc New Zealand biofilm h AM712
EU522632.1 gg_id:269237 hydrocarbon-degrading methanogenic microbial consortia settling basin Northern Al EU522
AB177179.1 gg_id:128221 seafloor methane hydrate clone ODP1230B23.08 AB177
CR933196.1 gg_id:110185 Evry municipal wastewater treatment plant clone 008B10_B_SD_P15 CR9331
AY542210.1 gg_id:114116 Gulf Mexico seafloor sediments clone GoM HDB-32 AY5422
AB426198.1 gg_id:259940 -situ identification study benzene-degrading s under methanogenic condition anaerc AB4261

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EU592411.1 gg_id:535455 Seasonal changes Salton Sea hypersaline sediment clone SSS15N EU592
EU644111.1 gg_id:280179 and Samoylov Island Lena active layer -centred polygon near permafrost table; Rim_ EU644
AY211657.1 gg_id:95801 Gulf Mexico seafloor sediment clone GoM GC185 503E AY211
AY211680.1 gg_id:96542 Gulf Mexico seafloor sediment clone GoM GC234 621E AY211
AF482437.1 gg_id:77432 granular sludge clone R2b29 AF482
FJ902092.1 gg_id:566804 phreatic limestone sinkholes northeastern Mexico orange biomat 8m deep cenote Ca FJ9020
DQ521786.1 gg_id:160206 Anaerobic Methane Oxidizing ANME-1b Archaea Hypersaline Sediments Gulf Mexic DQ521
FJ462010.1 gg_id:593726 Microbial ecology industrial digestor mesophilic anaerobic reactor fed effluent chemi FJ4620
AJ583188.1 gg_id:94853 radioactive site ground water clone S15B-MN12 AJ5831
EU644229.1 gg_id:282165 and Samoylov Island Lena active layer -centred polygon near surface horizon; Rim_T EU644
AB525446.1 gg_id:570354 Segregated ANME-1 and -2 cold-seep marine sediments deep-sea methane seep sed AB525
DQ787721.1 gg_id:162776 holocene lake sediment clone SLB628 DQ787
FJ902107.1 gg_id:580738 phreatic limestone sinkholes northeastern Mexico orange biomat 8m deep cenote Ca FJ9021
AM745217.1 gg_id:294031 Impact oil er hydrocarbons on microbial and activity Gulf Mexico cold seep marine s AM745
AF385080.1 gg_id:28552 Desulfacinum subterraneum str. 101 AF385
AF170418.1 gg_id:73225 Desulfacinum sp. str. M40/2 CIV-2.3 AF1704
DQ006288.1 gg_id:123413 Desulfatimicrobium mahresensis str. SA1 DQ006
FN356276.1 gg_id:558010 Prokaryotic structure sulfate reducer activity -temperature reservoirs and without ni FN356
FN356315.1 gg_id:570270 Prokaryotic structure sulfate reducer activity -temperature reservoirs and without ni FN356
NR_027598.1 gg_id:544627 Syntrophobacter fumaroxidans MPOB str. MPOB; DSM 10017 NR_02
AAJF01000012.1 gg_id:134597 Syntrophobacter fumaroxidans str. MPOB AAJF01
GQ261306.1 gg_id:543826 Study on Sediment sediment Dongping Lake clone 1S2-18 GQ261
AB232801.1 gg_id:138526 Microbial mesophilic chemostat cultivation propionate-degrading methanogenic con AB232
FJ535519.1 gg_id:538615 Microbial digestion swine wastewater anaerobic UASB reactor clone SWADLP2-18 FJ5355
GU208398.1 gg_id:581775 Study on Sediment Dongping Lake sediment clone Fh1-17 GU208
GQ402720.1 gg_id:583853 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
CU920959.1 gg_id:535086 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU920
CU924062.1 gg_id:573309 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU924
CU921674.1 gg_id:543856 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU921
FJ484661.1 gg_id:571785 microbial autonomous rover world's deepest phreatic sinkhole wall biomat El Zacator FJ4846
X70905.1 gg_id:10750 Syntrophobacter wolinii str. defined co Desulfovibrio sp. DSM 2805 X70905
EF515568.1 gg_id:222770 Electricigen Enrichment MFC full-scale anaerobic bioreactor sludge treating brewery EF5155
AB232820.1 gg_id:139158 Microbial mesophilic chemostat cultivation propionate-degrading methanogenic con AB232
DQ415751.1 gg_id:157212 Dominant microbial limestone-corroding biofilms frasassi system Italy Frasassi sulfid DQ415
CU921434.1 gg_id:549201 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU921
FN646446.1 gg_id:589878 candidate division OP3 cells limonene Limonene degrading methanogenic s clone LiN FN646
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GQ402673.1 gg_id:585966 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
EF688226.1 gg_id:329449 Detection microbial sludge anaerobic wastewater treatment system clone 5E3_cons EF6882
DQ404834.1 gg_id:155072 contaminated sediment clone 655963 DQ404
U25627.1 gg_id:10762 Thermodesulforhabdus norvegica str. A8444 U2562

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EU134394.1 gg_id:237260 tallgrass prarie soil clone FFCH612 EU1343
GQ389113.1 gg_id:535437 quality deterioration drinking system during serious red water outbreak clone S67 GQ389
FJ205268.1 gg_id:558961 Prokaryotic deep-sea region East Lau Spreading Centre active hydrothermal field sedi FJ2052
EU373905.1 gg_id:267944 southern Cretan margin (eastern Mediterranean Sea) canyon and slope sediment clc EU3739
GU208360.1 gg_id:560302 Study on Sediment Dongping Lake sediment clone Td4-7 GU208
EF019335.1 gg_id:206015 aspen rhizosphere clone Elev_16S_545 EF0193
FJ478988.1 gg_id:560191 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4789
EU335317.1 gg_id:248449 Changes microbial metabolic and along hydrogeochemically variable profile unsatura EU3353
AM936205.1 gg_id:559827 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM936
GQ472446.1 gg_id:568881 Microbial Dongping Lake lake sediment clone 5T1-3 GQ472
AF523967.1 gg_id:63257 forested wetland clone FW136 AF5239
AY963427.1 gg_id:152097 structures and correlated ecological factors soils two evergreen broad-leaved forests AY9634
FJ478874.1 gg_id:593126 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4788
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AB426233.1 gg_id:275505 -situ identification study benzene-degrading s under methanogenic condition anaerc AB4262
GU208380.1 gg_id:565064 Study on Sediment Dongping Lake sediment clone Td2-11 GU208
AB128874.1 gg_id:103274 deep marine sediments Nankai Trough Japan; ODP Leg 190 clone 1174-1091-4 AB1288
EU134559.1 gg_id:243792 tallgrass prarie soil clone FFCH3288 EU1345
AY921794.1 gg_id:113824 farm soil clone AKYG681 AY9217
FJ478660.1 gg_id:573531 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4786
GQ259289.1 gg_id:564500 Microbial activities coastal marine sediments and water column Svalbard deep sedir GQ259
AF523886.1 gg_id:55388 forested wetland clone RCP2-54 AF5238
FJ479115.1 gg_id:540681 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4791
FJ479389.1 gg_id:559874 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4793
AM072417.1 gg_id:138410 Untersuchung Verschiebung der bakteriellen Populationen mit U(VI) inokulierten Bc AM072
FJ479315.1 gg_id:575779 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4793
GQ302546.1 gg_id:581532 prokaryotic sediment Shawan methods cold spring clone sw-xj100 GQ302
GU056068.1 gg_id:552030 Biologic Techniques Applied Microbial Prospecting China: Ban 876 Gas Oil Field Bein GU056
FJ479231.1 gg_id:593037 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4792
AJ296569.1 gg_id:38614 uranium mining mill tailing clone GR-WP33-30 AJ2965
CU921195.1 gg_id:543214 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU921
GU118124.1 gg_id:547351 Threatened Corals Provide Microbial Habitats clone Apal_A09 GU118
EF600558.1 gg_id:302892 soil clone E5-2 EF6005
EU202780.1 gg_id:326405 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo EU2027
FJ479565.1 gg_id:510105 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4795
AJ581602.1 gg_id:93483 soil near uranium mill tailings clone KCM-B-53 AJ5816
EF032748.1 gg_id:191331 cyanobacterial mat in lava cave clone HAVOmat120 EF0327
AM997325.1 gg_id:555867 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A AM997
FJ478489.1 gg_id:572174 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4784
GQ500719.1 gg_id:581516 Surveys Biofilms and Sediments Mammoth Cave Karst Aquifers Charon's Cascade sa GQ500

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GQ262847.1 gg_id:549915 Structure Simulated Level Waste Site simulated level waste site clone F1_28X2 GQ262
EF018612.1 gg_id:215602 aspen rhizosphere clone Amb_16S_891 EF0186
EF032749.1 gg_id:192369 cyanobacterial mat in lava cave clone HAVOmat133 EF0327
EF590024.2 gg_id:228859 changes structure sediments Songhua River contaminated nitrobenzene -DGGE cloni EF5900
EU617849.1 gg_id:331603 Seasonal variation microbial Yel Sea sediment clone D13S-11 EU6178
GU061491.1 gg_id:560172 and function microbial mesoscale eddy perturbations South China Sea clone CE1-DC GU061
FJ478639.1 gg_id:593827 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4786
GU230392.1 gg_id:586588 Multilevel approach along Rio de la Plata-South Atlantic Ocean coastal sediment clo GU230
EF032751.1 gg_id:195011 cyanobacterial mat in lava cave clone HAVOmat82 EF0327
AB240314.1 gg_id:144627 microbial structure Phragmites rhizosphere biofilm reed bed reactor laboratory clon AB2403
AJ519632.1 gg_id:77057 uranium mill tailings soil sample clone Sh765B-AG-71 proteobacterium AJ5196
AY289452.1 gg_id:89599 soil clone ABS-13 AY2894
FJ152850.1 gg_id:315633 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX5A_ FJ1528
AM997396.1 gg_id:572529 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A AM997
AM936195.1 gg_id:548041 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM936
EU050854.1 gg_id:254522 libraries sediment Kings Bay Svalbard Arctic clone ss1_B_02_28 EU0508
AJ518789.1 gg_id:75247 uranium mining waste pile near Johanngeorgenstadt soil clone JG37-AG-2 AJ5187
EF018554.1 gg_id:205913 aspen rhizosphere clone Amb_16S_816 EF0185
EU386119.1 gg_id:276230 Biogeographical and microbes sediments on subseafloor sediment South China Sea c EU3861
EU134520.1 gg_id:240393 tallgrass prarie soil clone FFCH8074 EU1345
FJ755756.1 gg_id:578972 vertical archaeal water and Lake Taihu sediment clone LT-SB-B12 FJ7557
EU134328.1 gg_id:249749 tallgrass prarie soil clone FFCH11550 EU1343
EU202763.1 gg_id:324982 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo EU2027
AB234261.1 gg_id:147174 Biotransformation Polychlorinated Dioxins Microbial Dynamics Sediment Microcosm AB2342
AB252957.1 gg_id:168547 Identification Shibayama lagoon Ishikawa Japan iron-oxidation biofilm clone 023 AB2529
EU881148.1 gg_id:323943 Karst region primary forest soil clone KPF200711-152 EU8811
EF471464.1 gg_id:262091 Fast Screening and Estuarine Operon Libraries whole surface water Chesapeake Bay EF4714
EF019530.1 gg_id:214844 aspen rhizosphere clone Elev_16S_1033 EF0195
GQ246353.1 gg_id:509231 Temporal and spatial China North Yel Sea sediments clone Cm1-16 GQ246
FJ479302.1 gg_id:535350 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4793
AB252435.1 gg_id:152635 Microbial extremely CO2 rich deep-sea sediment Marine sediments Yonaguni Knoll I' AB2524
EF076107.1 gg_id:244235 Sponge- microorganisms: ecology and biotechnological potential Bahamas: Little San EF0761
FJ478944.1 gg_id:512156 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4789
AY963383.1 gg_id:152964 structures and correlated ecological factors soils two evergreen broad-leaved forests AY9633
AF234748.1 gg_id:48147 sludge clone H16 AF2347
EF516526.1 gg_id:226074 grassland soil clone FCPP428 EF5165
AM935117.1 gg_id:565668 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM935
AM889194.1 gg_id:593414 structure superficial sediments Bizerte (Tunisia) southern Mediterranean coastal an AM889
EF125461.1 gg_id:182959 mangrove soil clone MSB-2H1 EF1254

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AJ347034.1 gg_id:104678 sponge clone TK13 AJ3470
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EF442978.1 gg_id:257733 Desulforhabdus sp. str. DDT EF4429
EU542438.1 gg_id:262663 Effects chemical structure concentration on pathways microbial during dechlorinatio EU5424
DQ984662.1 gg_id:242560 Anaerobic degradation unsaturated or saturated long chain fatty acids (LCFA) prese DQ984
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GU180163.1 gg_id:578505 Impact coplanar PCBs on microbial activity anaerobic estuarine sediments sediment GU180
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AJ306776.1 gg_id:66924 DCP-dechlorinating consortium clone SHA-117 AJ3067
AM176858.1 gg_id:161119 Recovery mangrove sediment clone SZB9 AM176
GQ402743.1 gg_id:543482 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
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AB091329.1 gg_id:60011 UASB granular sludge clone UI AB0913
AF229787.1 gg_id:29387 terephthalate-degrading consortium clone TA14 AF2297
CT573826.1 gg_id:152222 Evry municipal wastewater treatment plant clone 013H09_B_SD_P15 CT5738
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EU399669.1 gg_id:262088 and localization microbial consortium full-scale granular activated carbon anaerobic EU3996
EU399678.1 gg_id:275018 and localization microbial consortium full-scale granular activated carbon anaerobic EU3996
AJ009465.1 gg_id:10718 TCB-transforming consortium clone SJA-51 AJ0094
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EU399661.1 gg_id:263368 and localization microbial consortium full-scale granular activated carbon anaerobic EU3996
EU399675.1 gg_id:265878 and localization microbial consortium full-scale granular activated carbon anaerobic EU3996
GQ844327.1 gg_id:569150 Microbial full-scale produced water treatment plant biofilm anoxic tank clone BB-B2 GQ844
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CT574144.1 gg_id:156077 Evry municipal wastewater treatment plant clone 060H12_B_SD_P93 CT5741
CT574201.1 gg_id:151230 Evry municipal wastewater treatment plant clone 060B01_B_SD_P93 CT5742
GU208245.1 gg_id:541892 Study on Sediment Dongping Lake sediment clone 6B1-7 GU208
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AY862530.1 gg_id:109749 rice slurry clone TPD-48 AY8625

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DQ396250.1 gg_id:151404 deep-sea octacoral clone ctg_NISA104 DQ396
GQ348270.1 gg_id:546068 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ348
GQ348264.1 gg_id:590521 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ348
GQ349049.1 gg_id:566231 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ349
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GQ347064.1 gg_id:589130 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ347
GQ348641.1 gg_id:571912 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ348
FJ545636.1 gg_id:559552 Diveristy Seawater and Sediment Northern North Yel Sea seawater clone W2-63 FJ5456
GQ337087.1 gg_id:572986 Hydrography shapes biogeography deep Arctic Ocean water depth 1191m clone NB: GQ337
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GU083677.1 gg_id:581115 Microorganism Xiarinur soda lake sediment clone x72 GU083
FJ152921.1 gg_id:317973 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX4CI FJ1529
AY048892.1 gg_id:23990 rhizosphere clone Q3-6C17 AY048
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EU050847.1 gg_id:237789 libraries sediment Kings Bay Svalbard Arctic clone ss1_B_03_45 EU050
EU487900.1 gg_id:574097 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU487
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EF573310.1 gg_id:233830 Coco's Island site 23 marine clone S23_1409 EF5733
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GQ348578.1 gg_id:576386 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ348
AF371949.1 gg_id:23625 swine intestine clone p-4193-6Wa5 AF371
FJ484808.1 gg_id:509157 microbial autonomous rover world's deepest phreatic sinkhole wall biomat El Zacator FJ4848
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CU466767.1 gg_id:336493 Evry wastewater treatment plant anoxic basin clone CU466
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U70713.1 gg_id:4709 Cape Hatteras picoplankton clone OM27 U7071
FJ203134.1 gg_id:355193 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c FJ2031
EF574353.1 gg_id:234197 site S25 near Coco's Island marine clone S25_697 EF5743
EU101270.1 gg_id:257793 Sulfide/oxygen supply ratio predicts outcome competition among sulfur-oxidizing wa EU101
DQ330714.1 gg_id:159120 Guerrero Negro hypersaline microbial mat clone 01D1q147 DQ330
EU491257.1 gg_id:269593 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak EU491
DQ395799.1 gg_id:155720 deep-sea octacoral clone ctg_CGOF235 DQ395
EU925894.1 gg_id:346201 sediments sediment station DBS1 northern Bering Sea clone 115G73 EU925
GQ263929.1 gg_id:513958 Structure Simulated Level Waste Site simulated level waste site clone WC2_181 GQ263

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FJ484648.1 gg_id:572347 microbial autonomous rover world's deepest phreatic sinkhole wall biomat El Zacator FJ4846
GQ472419.1 gg_id:547121 Microbial Dongping Lake lake sediment clone 4F2-23 GQ472
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EF590018.2 gg_id:231749 changes structure sediments Songhua River contaminated nitrobenzene -DGGE cloni EF590
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EU335163.1 gg_id:239473 Changes microbial metabolic and along hydrogeochemically variable profile saturate EU335
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EF575257.1 gg_id:228296 site S25 near Coco's Island marine clone S25_1601 EF5752
FJ155026.1 gg_id:330159 seasonal fluctuation coastal Bohai Bay sequencing and RFLP ocean water clone W FJ1550
EF573912.1 gg_id:228667 site S25 near Coco's Island marine clone S25_256 EF5739
EU592442.1 gg_id:537106 Seasonal changes Salton Sea hypersaline sediment clone SSS66N EU5924
EU592440.1 gg_id:589629 Seasonal changes Salton Sea hypersaline sediment clone SSS64N EU5924
EU488121.1 gg_id:560324 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU488
EU488297.1 gg_id:556385 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU488
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DQ394901.1 gg_id:156343 harbor sediment clone VHS-B1-26 DQ394
GQ261790.1 gg_id:544072 shifts taxa and response localized organic loading deep sea sediment whale falls clo GQ261

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DQ811792.1 gg_id:167519 mangrove soil clone MSB-3A9 DQ811
EF520534.1 gg_id:232980 structure lakes: what controls ? acid-impacted lake clone ADK-BTe02-06 EF5205
EU861868.1 gg_id:343349 effects chronic fertilization on alpine tundra microbial implications carbon and nitrog EU8618
EU803844.1 gg_id:337066 It's all ranking aquatic Lake Gatun clone 5C231481 EU8038
DQ451526.1 gg_id:156878 forest soil clone FAC87 DQ451
DQ811827.1 gg_id:170103 mangrove soil clone MSB-5C4 DQ811
EF208655.1 gg_id:202296 Vertical and horizontal structure microbial sandy carbonate sediment clone CI35cm.2 EF2086
EF125419.1 gg_id:199002 soil naked tidal flat sediment near mangrove clone MSB-1F8 EF1254
EU491252.1 gg_id:276800 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak EU4912
DQ925889.1 gg_id:255773 Microbes and Thermal Gradients Temperature Hydrothermal Chimneys hydrotherm DQ925
EU050850.1 gg_id:238559 libraries sediment Kings Bay Svalbard Arctic clone ss1_B_09_96 EU0508
FJ535320.1 gg_id:536335 within iron-containing flocculent mats submarine volcanoes along Kermadec Arc sedi FJ5353
AM712338.1 gg_id:255844 detection and ly microbial Brothers Seamount Kermadec Arc New Zealand biofilm h AM712
AF420341.2 gg_id:67796 hydrothermal sediment clone AF420341 AF4203
AJ441235.1 gg_id:57453 hydrothermal vent polychaete mucous clone P. palm A 205 AJ4412
AF420340.1 gg_id:67797 hydrothermal sediment clone AF420340 AF4203
FJ712464.1 gg_id:517432 and Archaea Gas Hydrate Sediments (East Sea) Kazan Mud Volcano Anaximander Mo FJ7124
DQ017948.1 gg_id:136786 upland stream clone S-Btb7_40 DQ017
EU134544.1 gg_id:253026 tallgrass prarie soil clone FFCH2390 EU1345
FJ592579.1 gg_id:509119 Fumarole-supported islands biodiversity within hyperarid -elevation landscape on Pu FJ5925
EF573992.1 gg_id:230171 site S25 near Coco's Island marine clone S25_336 EF5739
EF574948.1 gg_id:230813 site S25 near Coco's Island marine clone S25_1292 EF5749
GQ347789.1 gg_id:541766 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ347
EU048624.1 gg_id:236563 Microbial surface marine sediment Xisha Trough South China Sea clone MD2902-B18 EU0486
EU386045.1 gg_id:274122 Biogeographical and microbes sediments on subseafloor sediment South China Sea c EU3860
EU373913.1 gg_id:275503 southern Cretan margin (eastern Mediterranean Sea) canyon and slope sediment cl EU3739
FJ745210.1 gg_id:570846 Transporter genes expressed coastal response dissolved organic carbon surface wate FJ7452
GQ346753.1 gg_id:568507 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ346
EU134378.1 gg_id:256515 tallgrass prarie soil clone FFCH5621 EU1343
AB486345.1 gg_id:559850 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC AB4863
DQ267495.1 gg_id:149878 Metagenomic group plankton 500m depth mesopelagic Antarctic waters clone DQ267
EF574148.1 gg_id:230908 site S25 near Coco's Island marine clone S25_492 EF5741
DQ154849.1 gg_id:139171 Diel Migration Restructures Hypersaline Microbial Mat hypersaline microbial mat cl DQ154
FJ485412.1 gg_id:558030 microbial autonomous rover world's deepest phreatic sinkhole wall biomat El Zacator FJ4854
AJ241001.1 gg_id:10681 Norway:(Svalbard)Hornsund clone Sva0485 AJ2410
AM882628.1 gg_id:350620 Structure along hydrocarbon contamination coastal sediment oil polluted water pet AM882
EF632708.1 gg_id:256201 Unique microbial contrasting aquatic altitude Andean Altiplano (northern Chile) wate EF6327
DQ103652.1 gg_id:131834 hypersaline endoevaporitic microbial mat clone E6aH12 DQ103
AM040101.1 gg_id:149432 sandy sediments clone Sylt 5 AM040

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AF382143.1 gg_id:79548 bacterioplankton clone ZA3735c AF382
GQ337096.1 gg_id:548348 Hydrography shapes biogeography deep Arctic Ocean water depth 1000m clone BB GQ337
FM242399.1 gg_id:328281 sequences sediment clone 86 T12d-oil FM242
EU735646.1 gg_id:322881 archaeal structures and pristine soils China oil contaminated soil Jidong Oilfield clone EU735
EU734937.1 gg_id:327296 assemblages sediment station DBSE Northern Bering Sea clone 028C19 EU734
AY375082.1 gg_id:98535 deep sea sediment clone B109 AY375
AJ240985.1 gg_id:10661 Norway:(Svalbard)Hornsund clone Sva0853 AJ2409
AM882631.1 gg_id:306845 Structure along hydrocarbon contamination coastal sediment oil polluted water pet AM882
DQ464344.1 gg_id:157072 Arcobacter skirrowii str. 449/80 DQ464
AY314755.1 gg_id:105549 Arcobacter cryaerophilus CCUG 17802 AY314
EU106662.1 gg_id:260782 Arcobacter nitrofigilis str. F2176 EU106
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AB262383.1 gg_id:161324 Microbial Ishigaki-jima Island Japan sea water Ishigaki Port clone IG-1-21 AB262
AB262379.1 gg_id:160905 Microbial Ishigaki-jima Island Japan sea water Ishigaki Port clone IG-1-16 AB262
AY922188.1 gg_id:113246 whalefall clone 131599 AY922
GQ348908.1 gg_id:558608 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ348
FJ497477.1 gg_id:589078 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun FJ4974
AF513455.1 gg_id:60384 Arcobacter sp. str. LA31B AF5134
DQ071284.1 gg_id:139697 dominate filamentous sulfur mat 13 degree north field East Pacific Rise deep-sea hy DQ071
AF314538.1 gg_id:36386 Arcobacter butzleri oN_107_00 AF3145
AB013832.1 gg_id:11163 NB1-k clone NB1-k AB0138
EU052247.1 gg_id:248438 degradation kinetics and current efficiency cells supplied anode microbial fuel cell fe EU052
FJ202344.1 gg_id:314840 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2023
EF648116.1 gg_id:251292 dynamics during produced water treatment aerobic activated sludge clone XJ22 EF6481
AY225610.1 gg_id:96366 pumice fragments exposed to Mid-Atlantic Ridge vent clone AT-pp13 AY2256
GU061286.1 gg_id:546186 Evaluation culturing methods cultivate previously Yel Sea intertidal beach seawater GU061
AJ607391.1 gg_id:102614 Arcobacter cibarius str. LMG 21996 AJ6073
EF515495.1 gg_id:222170 Electricigen Enrichment MFC full-scale anaerobic bioreactor sludge treating brewery EF5154
AY922205.1 gg_id:113754 whalefall clone 131644 AY922
FJ202783.1 gg_id:349369 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2027
FJ403064.1 gg_id:357886 Disease- changes healthy and diseased colonies Caribbean coral Montastrea faveolat FJ4030
EF123613.1 gg_id:239833 Microbial disease microbial mats on Siderastrea siderea three regions wider Caribbe EF1236
AJ271654.1 gg_id:51975 Arcobacter sp. D1a1 AJ2716
AM084124.1 gg_id:140216 Arcobacter sp. str. R-28214 AM084
AY570641.1 gg_id:108516 biodegraded Canadian oil reservoir clone PL-8D4 AY5706
FN429802.1 gg_id:534177 Biogeochemistry -activity cold seep Larsen B area western Weddell Sea Antarctica m FN4298
FJ202326.1 gg_id:315205 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2023
DQ917897.1 gg_id:227146 Microbial profiles bleached and wild-type Muricea elongata Arcobacter clone ME15 DQ917
AY035822.1 gg_id:70950 enriched coastal seawater overlying anoxic marine sediment sulfidicus AY0358
EU050947.1 gg_id:255076 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_02_37 EU0509

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DQ357825.1 gg_id:150082 Marine Hatchery: Balance Between Pathogenic and Potentially Probiotic Strains adu DQ357
DQ676433.1 gg_id:224791 Archaeal sediment and plankton freshwater pond suboxic freshwater-pond clone M DQ676
AB030594.1 gg_id:50542 groundwater clone 1021 AB0305
EU265967.1 gg_id:567689 transition and zone within near-shore anoxic basin: Nitinat Lake depth 50 m clone Ni EU2659
FJ660508.1 gg_id:561979 Correlation functional stability and dynamics full-scale wastewater treatment plant a FJ6605
EF688595.1 gg_id:284348 Biogeochemistry iron- and sulfur-precipitating microbial mats (Nile Mediterranean) s EF6885
GU061298.1 gg_id:560130 Evaluation culturing methods cultivate previously Yel Sea intertidal beach seawater GU061
FJ717168.1 gg_id:571505 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United King FJ7171
AY621116.1 gg_id:106004 Arcobacter butzleri str. ATCC 49616 AY6211
EF031092.1 gg_id:186810 Prokaryotic Tirez La Macha Spain endorheic hypersaline atalasohaline lake clone SalB EF0310
AY697901.1 gg_id:105639 Antarctica clone F3C43 AY6979
AB234539.1 gg_id:149689 termite gut homogenate clone MgMjD-024 AB2345
FJ203095.1 gg_id:346863 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c FJ2030
AB262386.1 gg_id:159735 Microbial Ishigaki-jima Island Japan sea water Ishigaki Port clone IG-1-27 AB2623
EU236320.1 gg_id:292623 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg1bF7 EU2363
AB015259.1 gg_id:11183 deepest cold-seep area Japan Trench clone JTB360 proteobacterium AB0152
AJ810558.1 gg_id:105006 superficial sediments clone AJ8105
DQ464340.1 gg_id:158050 Arcobacter butzleri str. 520H-2004 DQ464
GQ340204.1 gg_id:583784 Prokaryotic Marathonas Reservoir Greece water column clone VE07-08-BAC GQ340
AB013833.1 gg_id:11181 NB1-l clone NB1-l AB0138
GQ349268.1 gg_id:581309 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ349
EU781617.1 gg_id:322902 Bacteroides ureolyticus 4 EU7816
GQ167663.1 gg_id:581365 Campylobacter concisus str. ATCC 51561 GQ167
EU869312.1 gg_id:334581 Campylobacter cuniculorum str. 119/07 EU8693
NC_009715.1 gg_id:242986 Campylobacter curvus str. 525.92 NC_009
AY621301.1 gg_id:103129 Campylobacter fetus str. 23D AY6213
AF219233.1 gg_id:69901 Campylobacter fetus MGH 97-2126 AF2192
DQ174168.1 gg_id:151146 Campylobacter gracilis str. ATCC 33236 DQ174
DQ174161.1 gg_id:155173 Campylobacter helveticus str. NCTC 12470 DQ174
DQ174163.1 gg_id:154260 Campylobacter helveticus str. NCTC 12472 DQ174
U03022.1 gg_id:11247 Campylobacter helveticus U03022
CP000776.1 gg_id:257761 Campylobacter hominis str. ATCC BAA-381 CP0007
AF043422.1 gg_id:11239 Campylobacter cf. lanienae str. UB 992 AF0434
AF550661.1 gg_id:57347 Campylobacter mucosalis str. ATCC 49353 AF5506
FJ983015.1 gg_id:430191 Aspects Oral Microbiome root canal clone FJ9830
NZ_ACFU01000050.1 gg_id:469893 Campylobacter rectus str. RM3267 NZ_AC
NZ_ACVQ01000030.1 gg_id:470642 Campylobacter showae str. RM3277 NZ_AC
EU781616.1 gg_id:326311 Campylobacter showae 3 EU7816
X67775.1 gg_id:11227 Campylobacter sputorum str. biovar sputorum;LMG 7795 X67775
AB181364.1 gg_id:100818 Campylobacter lari str. A3 AB1813
AB181358.1 gg_id:105325 Campylobacter lari str. NCTC12893 AB1813

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AB181357.1 gg_id:105165 Campylobacter lari str. NCTC12892 AB1813
AB181359.1 gg_id:105482 Campylobacter lari str. NCTC12894 AB1813
AF550640.1 gg_id:57368 Campylobacter upsaliensis str. LMG 8851 AF5506
AF550632.1 gg_id:102123 Campylobacter lari str. LMG 11251 AF5506
GQ167658.1 gg_id:586732 Campylobacter upsaliensis str. RM3195 GQ167
DQ174156.1 gg_id:154704 Campylobacter showae str. CCUG 11641 DQ174
EU289113.1 gg_id:238608 microbiome cloacal openings urogenital and anal tracts tammar wallaby Macropus e EU2891
FJ832837.1 gg_id:542539 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J3Q301_10B02 FJ8328
AF219235.1 gg_id:70687 Campylobacter hyointestinalis MGH 97-2652 AF2192
AB301962.1 gg_id:219863 Campylobacter subsp. hyointestinalis str. 2831-1 AB3019
AF550641.1 gg_id:57366 Campylobacter upsaliensis str. LMG 8853 AF5506
EU289065.1 gg_id:253584 microbiome cloacal openings urogenital and anal tracts tammar wallaby Macropus e EU2890
AY554142.1 gg_id:113002 Campylobacter sp. str. BTP1 AY5541
AY554144.1 gg_id:113756 Campylobacter sp. str. WB1 AY5541
GQ167676.1 gg_id:542181 Campylobacter coli str. ATCC 33559 GQ167
AF372091.1 gg_id:66989 Campylobacter jejuni str. NCTC 11351 AF3720
EU559332.1 gg_id:549039 Campylobacter sp. str. MIT 97-5311 EU5593
AJ276874.1 gg_id:69947 Campylobacter faecalis str. 1433 stool sample isolate AJ2768
AB301961.1 gg_id:219965 Campylobacter subsp. hyointestinalis str. 2728-1 AB3019
AF550628.1 gg_id:55836 Campylobacter jejuni str. H99/240 AF5506
AF550647.1 gg_id:57361 Campylobacter helveticus str. CCUG 30563 AF5506
DQ174159.1 gg_id:154512 Campylobacter upsaliensis str. NZ5564-94 DQ174
AM933372.1 gg_id:541426 Campylobacter subantarcticus str. LMG 24374 AM933
GQ451185.1 gg_id:533613 Fecal Yunnan snub-nosed monkey feces clone J16 GQ451
AF097688.1 gg_id:11237 Campylobacter hyointestinalis subsp. lawsonii str. CHY8 subsp. AF0976
AB066098.1 gg_id:54599 Campylobacter lari str. CF89-12 Japanese strain AB0660
AJ620504.1 gg_id:108770 Campylobacter insulaenigrae str. NCTC 12927 AJ6205
DQ174164.1 gg_id:152100 Campylobacter helveticus str. E504-90 DQ174
EU623474.1 gg_id:278725 Campylobacter sp. str. 24/06 EU6234
AF550620.1 gg_id:57384 Campylobacter coli str. LMG 9220 AF5506
DQ174146.1 gg_id:151930 Campylobacter lari str. NZ145-95 DQ174
FJ609419.1 gg_id:573432 Campylobacter jejuni str. PRCC-3 FJ6094
EF621895.1 gg_id:243035 Campylobacter canadensis str. L268 EF6218
AF550655.1 gg_id:57353 Campylobacter showae str. LMG 12636 AF5506
EU470464.1 gg_id:302158 Grevy's zebra feces clone GZ_aaa03d07 EU4704
AY288304.1 gg_id:86812 Campylobacter lanienae str. L52 AY2883
EF621896.1 gg_id:240175 Campylobacter canadensis str. L267 EF6218
NR_028692.1 gg_id:561090 Sulfurospirillum barnesii str. SES-3; ATCC 700032 NR_028
EF462744.1 gg_id:295702 meta-genome level extreme microbial symbiosis dorsal surface deep sea hydrotherm EF4627
AB355036.1 gg_id:244687 Monitoring and archaeal two heavy polluted areas lake Egypt based on surface wate AB3550

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FJ791877.1 gg_id:573109 Unexpectedly archaeal species shift between rare and dominant over thousand year FJ7918
FJ792027.1 gg_id:534646 Unexpectedly archaeal species shift between rare and dominant over thousand year FJ7920
U85964.1 gg_id:11189 Sulfurospirillum arsenophilum str. MIT-13 U8596
AB286550.1 gg_id:206504 Reducing production and domination comamonadaceae reducing oxygen supply was AB286
AY548994.2 gg_id:103740 marine bone clone boneC3F4 AY548
FJ792107.1 gg_id:534811 Unexpectedly archaeal species shift between rare and dominant over thousand year FJ7921
FJ792301.1 gg_id:562673 Unexpectedly archaeal species shift between rare and dominant over thousand year FJ7923
AY548973.1 gg_id:102465 marine bone clone boneC15D1 AY548
DQ295747.1 gg_id:160847 Epsilonproteobacteria terrestrial caves and springs microbial mat sulfidic Warm spri DQ295
DQ925871.1 gg_id:249367 Microbes and Thermal Gradients Temperature Hydrothermal Chimneys hydrotherm DQ925
DQ228579.1 gg_id:141569 and physiological significance attached microorganisms rock-hosted deep-sea carbo DQ228
AF357199.1 gg_id:22148 Sulfurospirillum sp. str. 18.1 AF357
FJ792478.1 gg_id:534881 Unexpectedly archaeal species shift between rare and dominant over thousand year FJ7924
AY672509.1 gg_id:99157 hydrothermal vent 9 degrees North East Rise Pacific Ocean clone CH1_28_BAC_16SrR AY672
AY327877.2 gg_id:88092 surface vent snail foot clone SF_C11-F3 AY327
FJ640810.1 gg_id:512603 GeoChip-based metabolic microbial hydrothermal vent chimney 4143-1 Mothra field FJ6408
AY280408.1 gg_id:100828 exterior deep-sea hydrothermal vent sulfide chimney Juan de Fuca Ridge Pacific Oce AY280
AB234540.1 gg_id:146284 termite gut homogenate clone MgMjR-060 AB234
AY280434.1 gg_id:106449 exterior deep-sea hydrothermal vent sulfide chimney Juan de Fuca Ridge Pacific Oce AY280
AB192073.1 gg_id:143275 termite gut homogenate clone M2PT2-04 AB192
FN356324.1 gg_id:580201 Prokaryotic structure sulfate reducer activity -temperature reservoirs and without ni FN356
FJ485111.1 gg_id:541385 microbial autonomous rover world's deepest phreatic sinkhole water column El Zacat FJ4851
AY266270.1 gg_id:103575 oil production water clone CT1 AY266
DQ925875.1 gg_id:244236 Microbes and Thermal Gradients Temperature Hydrothermal Chimneys hydrotherm DQ925
FJ156092.1 gg_id:461508 Arcobacter mytili str. T234 FJ1560
AJ969453.1 gg_id:159487 Microbial black smoker s Mid Atlantic Ridge ecological implications rock fragments ch AJ9694
AB231076.1 gg_id:147107 termite gut wall clone NkW01-035 AB231
AJ441214.1 gg_id:106099 hydrothermal vent polychaete mucous clone P. palm C/A 39 AJ4412
AJ576349.1 gg_id:102626 hindgut homogenate Pachnoda ephippiata larva clone PeH32 AJ5763
AY192528.1 gg_id:111196 Flexispira rappini str. 205-2 AY192
AY192526.1 gg_id:109700 Flexispira rappini str. 204-1 AY192
AY126479.1 gg_id:131724 Flexispira rappini str. 205-1 AY1264
AF396078.1 gg_id:20816 Helicobacter cinaedi 30327 AF396
AF396081.1 gg_id:49270 Helicobacter cinaedi 31111 AF396
AB275325.1 gg_id:196588 Helicobacter cinaedi str. PAGU0621 (= 56) AB275
AF302108.1 gg_id:69782 Helicobacter sp. str. HC15880 AF302
AF118017.1 gg_id:11022 Flexispira rappini str. H1353 AF118
AF497810.1 gg_id:56169 Helicobacter cinaedi str. 94105 AF497
AF497807.1 gg_id:60772 Flexispira rappini str. FR106 AF497
AF072471.1 gg_id:10989 Helicobacter mesocricetorum str. MU97-1514 AF0724

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AY323502.1 gg_id:105862 Helicobacter canadensis ISL 793/92
DQ438113.1 gg_id:154548 Helicobacter canadensis str. L172
AY631946.1 gg_id:106403 Helicobacter canis str. MIT 51402
L13464.1 gg_id:11062 Helicobacter canis
DQ307736.1 gg_id:154375 Helicobacter equorum str. EqF2
AF506785.1 gg_id:72292 Helicobacter heilmannii str. WD1
AY686607.1 gg_id:111336 Helicobacter felis str. Lee DS2
M57398.2 gg_id:10994 Helicobacter felis str. CS1; ATCC 49179
AF103882.1 gg_id:11030 Helicobacter felis str. 1136-7
AY561831.1 gg_id:106123 Helicobacter ganmani str. ES-5
AY631951.1 gg_id:101810 Helicobacter ganmani str. MIT 99-5102
U07573.2 gg_id:11042 Helicobacter hepaticus str. Hh-1
AY554124.1 gg_id:114186 Helicobacter kirbridei str. BTP1F
AF333339.1 gg_id:27055 Helicobacter sp. str. MIT 99-5504
AF010140.1 gg_id:11040 Helicobacter muridarum str. UNSW 1.7st
M35048.2 gg_id:11057 Helicobacter mustelae str. ATCC 43772
AY554133.1 gg_id:113226 Helicobacter peregrinus str. RTP4S
DQ062214.1 gg_id:132728 Helicobacter sp. AGN-1
X67854.1 gg_id:11080 Helicobacter pylori str. ATCC 49396T
Z25741.1 gg_id:11013 Helicobacter pylori str. NCTC 11637
DQ062215.1 gg_id:132837 Helicobacter sp. GA-3
AY593989.1 gg_id:101118 Helicobacter pylori str. LPB 424-01
AF057163.1 gg_id:10974 Helicobacter sp
AF535198.1 gg_id:57708 Helicobacter pylori str. Lit81
M88137.2 gg_id:10945 Helicobacter trogontum str. ATCC 43966
AY034820.1 gg_id:47556 Helicobacter rappini str. H 95 S
AF225548.1 gg_id:28994 Helicobacter trogontum str. ATCC 49310
U96296.1 gg_id:10983 Helicobacter rodentium str. MIT 95-1707
AF506791.1 gg_id:64310 Helicobacter heilmannii str. P5
AF506790.1 gg_id:71558 Helicobacter heilmannii str. P4
AF506787.1 gg_id:73122 Helicobacter heilmannii str. P1
AY554121.1 gg_id:114199 Helicobacter vulpecula str. BTP7C
FJ667779.1 gg_id:548699 Helicobacter sp. 'pancake tortoise' str. FL-2007
AF292378.1 gg_id:72792 Helicobacter cetorum str. MIT 99-5656
AY554137.1 gg_id:113171 Helicobacter sp. str. BTP3S
M88152.2 gg_id:11054 Helicobacter sp. '91-266-11 Fox' str. 91-266-11 Fox
X81028.1 gg_id:10960 Helicobacter sp. str. Mainz
L36141.1 gg_id:10982 Helicobacter pullorum str. NCTC 12824
AF058768.1 gg_id:11034 Helicobacter heilmannii 1
AF506794.1 gg_id:64304 Helicobacter heilmannii str. TD1

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AF333341.1 gg_id:36371 Helicobacter marmotae str. MIT 98-6070 AF3333
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U96300.1 gg_id:11047 Helicobacter trogontum str. ATCC 43968 U96300
AF237612.1 gg_id:26677 Helicobacter sp. str. Wee Tee AF2376
AY034817.1 gg_id:49918 Helicobacter rappini str. 1 SU AY0348
Y18028.1 gg_id:10969 Helicobacter heilmannii str. AF53 Y18028
AB006148.1 gg_id:11016 Helicobacter suncus str. Kaz-2 AB0061
AJ249858.1 gg_id:41542 Helicobacter sp. blood isolate 964 AJ2498
AF127027.1 gg_id:10980 Candidatus Helicobacter bovis AF1270
AF506778.1 gg_id:64319 Helicobacter heilmannii str. C4E AF5067
AF103880.1 gg_id:11028 Helicobacter felis str. 390-9 AF1038
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AF333340.1 gg_id:49735 Helicobacter sp. str. MIT 99-5507 AF3333
AF506780.1 gg_id:72724 Helicobacter heilmannii str. CM1 AF5067
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AY742308.1 gg_id:102634 Helicobacter sp. str. MIT 02-6899 AY7423
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FJ484970.1 gg_id:513207 microbial autonomous rover world's deepest phreatic sinkhole water column El Zacat FJ4849
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AY191481.1 gg_id:93946 microbial mat sulfidic cave spring clone LKC1.114_6 AY1914
AY191468.1 gg_id:93668 microbial mat sulfidic cave spring clone LKC1.21_5 AY1914
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DQ295702.1 gg_id:160766 Epsilonproteobacteria terrestrial caves and springs microbial mat sulfidic stream Mil DQ295
GQ406165.1 gg_id:512611 Benthic submerged sinkhole ecosystems sediment clone BK-20-18 GQ406
EU101041.1 gg_id:238274 Sulfide/oxygen supply ratio predicts outcome competition among sulfur-oxidizing wa EU101
AB030601.1 gg_id:21738 groundwater clone 1043 AB030
AB030605.1 gg_id:22082 groundwater clone 1028 AB030
EU884110.1 gg_id:329225 Recently Evolved Symbiosis Between Chemoautotrophic and Cave-Dwelling Amphip EU884
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GQ390203.1 gg_id:557628 oxic-anoxic interface meromictic crater lake Lac Pavin clone Eub62D4 GQ390
AY510172.1 gg_id:109530 microbial mat cave sulfidic spring clone LKC3_127.39 AY510
DQ787703.1 gg_id:171036 holocene lake sediment clone SLB59 DQ787
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AF367492.1 gg_id:70730 deep-sea hydrothermal vent clone VC1.2-cl32 AF3674
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U15101.1 gg_id:11096 hydrothermal vent clone PVB_OTU_2 U1510
NC_007575.1 gg_id:144857 Thiomicrospira denitrificans str. ATCC 33889 NC_00
FJ437888.1 gg_id:547212 Benthic okenone production Fayetteville New York Green Lake 25 m water depth clor FJ4378
AF121884.1 gg_id:11109 phenol-degrading consortium clone Phenol-1 AF1218
DQ295573.1 gg_id:160062 Epsilonproteobacteria terrestrial caves and springs microbial mat sulfidic cave spring DQ295
FJ615170.1 gg_id:593488 Microbial dynamics seasonally fjord: British Columbia Saanich Inlet depth 10m anoxic FJ6151
EU491812.1 gg_id:268142 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU4918
DQ234141.2 gg_id:142794 determined library mangrove clone DS057 DQ234
FJ497618.1 gg_id:563303 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun FJ4976
FJ717090.1 gg_id:551059 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United Kingc FJ7170
DQ676325.1 gg_id:224044 Archaeal and plankton freshwater pond suboxic freshwater-pond sediment clone M DQ676
AY211683.1 gg_id:96203 Gulf Mexico seafloor sediment clone GoM GC234 633E AY2116
AY225615.1 gg_id:97077 iron-rich substrate exposed to Mid-Atlantic Ridge vent clone AT-cs10 AY2256
FN397808.1 gg_id:424252 geomicrobiological investigation sediments Gulf Cadiz GeoB 9072-1 anoxic sub-surfa FN3978
AJ441199.1 gg_id:57482 hydrothermal vent polychaete mucous clone P. palm C/A 78 AJ4411
AF355050.1 gg_id:48010 marine clone Arctic96B-13 AF3550
GQ356982.1 gg_id:592000 Metal Dependent Marine Methane Oxidation methane seep sediment clone FeSO4_ GQ356
AY225612.1 gg_id:97721 organic-rich substrate exposed to Mid-Atlantic Ridge vent clone AT-co23 AY2256
DQ676368.1 gg_id:222158 Archaeal sediment and plankton freshwater pond suboxic freshwater-pond clone M DQ676
FJ497273.1 gg_id:590030 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun FJ4972
EF218993.1 gg_id:215778 and Eukaryotic Hydrothermal Site East Rise Ridge Flank Abyssal Hill hydrothermal site EF2189
DQ228650.1 gg_id:141130 Microbial colonizing mineral surfaces within sulfide-microbial incubator clone CH2b1 DQ228
EF219001.1 gg_id:209624 and Eukaryotic Hydrothermal Site East Rise Ridge Flank Abyssal Hill hydrothermal site EF2190
U15106.1 gg_id:11103 hydrothermal vent clone PVB_OTU_6 U1510
AY280406.1 gg_id:100516 exterior deep-sea hydrothermal vent sulfide chimney Juan de Fuca Ridge Pacific Oce AY2804
GQ848465.1 gg_id:578863 Microbial sediments vents along East Lau Spreading Centre deep sea hydrothermal GQ848
FJ535290.1 gg_id:546926 within iron-containing flocculent mats submarine volcanoes along Kermadec Arc iron FJ5352
FJ717130.1 gg_id:551352 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United Kingc FJ7171
FJ717171.1 gg_id:533593 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United Kingc FJ7171
EF379628.1 gg_id:205139 sea water Victoria Harbor (Hong Kong) area clone VH-PA7-38 EF3796
EU652649.1 gg_id:279233 Seasonal variation microbial Yel Sea sediment clone B8S-4 EU6526
DQ836759.1 gg_id:169835 attached biomass denitrifying bioreactor clone DB-83 DQ836
AY218555.1 gg_id:82461 penguin droppings sediments clone KD1-140 AY2185
EU652651.1 gg_id:278362 Seasonal variation microbial Yel Sea sediment clone A8S-94 EU6526
FM242221.1 gg_id:343001 sequences sediment clone 259 T0h-oil FM242
EU652650.1 gg_id:277911 Seasonal variation microbial Yel Sea sediment clone C8S-4 EU6526
FJ717108.1 gg_id:569301 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United Kingc FJ7171
FJ535347.1 gg_id:510699 within iron-containing flocculent mats submarine volcanoes along Kermadec Arc sedi FJ5353
AB530237.1 gg_id:584301 Monitoring Suez and Tokyo bays based on analyses marine sediment clone Tokyo..B AB5302
AB188787.1 gg_id:113750 cold seep sediment clone SB5-24 AB1887
AB193899.1 gg_id:108823 deep-sea vent clone Mb-NB05 AB1938

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GQ261804.1 gg_id:560545 shifts taxa and response localized organic loading deep sea sediment whale falls clo GQ261
AY922199.1 gg_id:112883 whalefall clone 131631 AY9221
DQ228651.1 gg_id:142365 Microbial colonizing mineral surfaces within sulfide-microbial incubator clone CH2b1 DQ228
FJ717087.1 gg_id:562754 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United King FJ7170
AY216438.1 gg_id:82215 temperate estuarine mud clone KM51 AY2164
EU491805.1 gg_id:273299 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU4918
AY225613.1 gg_id:98692 pumice fragments exposed to Mid-Atlantic Ridge vent clone AT-pp6 AY2256
AB189375.1 gg_id:113264 cold seep sediment clone JT75-307 AB1893
FJ497428.1 gg_id:572725 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun FJ4974
AY672505.1 gg_id:107511 hydrothermal vent 9 degrees North East Rise Pacific Ocean clone CH1_22_BAC_16Sr AY6725
AB015257.1 gg_id:11113 deepest cold-seep area Japan Trench clone JTB146 proteobacterium AB0152
AJ441200.1 gg_id:57484 hydrothermal vent polychaete mucous clone P. palm C 92 AJ4412
EF999352.1 gg_id:237892 Vertical and Methanotrophs Estuarine Sediments Pearl River Estuary sediments 6cm EF9993
AM982624.1 gg_id:278960 microbial and slurry pig saw dust spent bedding clone PISD-AJC10 AM982
FJ535284.1 gg_id:512607 within iron-containing flocculent mats submarine volcanoes along Kermadec Arc iron FJ5352
EF218991.1 gg_id:206907 and Eukaryotic Hydrothermal Site East Rise Ridge Flank Abyssal Hill hydrothermal site EF2189
AY532570.1 gg_id:105327 uranium-contaminated aquifer clone 1013-28-CG21 AY5325
FJ497261.1 gg_id:566005 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun FJ4972
AB235234.1 gg_id:141016 symbiont AB2352
FJ437839.1 gg_id:513719 Benthic okenone production Fayetteville New York Green Lake 25 m water depth clo FJ4378
AB176111.1 gg_id:175999 Microbial Hydrothermal System Suiyo Seamount on Izu-Ogasawara Arc vent area wa AB1761
FM203379.1 gg_id:370488 Biogeography filamentous and epsilonproteobacterial ectosymbionts vent shrimp e FM203
AJ515714.1 gg_id:94683 deep-sea shrimp gut clone 4 AJ5157
FM203398.1 gg_id:371282 Biogeography filamentous and epsilonproteobacterial ectosymbionts vent shrimp e FM203
AP009179.1 gg_id:249880 Sulfurovum sp. str. NBC37-1 AP0091
EF462799.1 gg_id:293907 meta-genome level extreme microbial symbiosis dorsal surface deep sea hydrothern EF4627
AJ515716.1 gg_id:94327 deep-sea shrimp gut clone 15 AJ5157
EU555122.1 gg_id:259007 Microbial Sulfide Hydrothermal Vent Field Juan de Fuca Ridge Dudley hydrothermal EU5551
AY672497.1 gg_id:102782 hydrothermal vent 9 degrees North East Rise Pacific Ocean clone CH1_1_BAC_16SrR AY6724
FJ792125.1 gg_id:510296 Unexpectedly archaeal species shift between rare and dominant over thousand year FJ7921
FJ535278.1 gg_id:554288 within iron-containing flocculent mats submarine volcanoes along Kermadec Arc iron FJ5352
AY531596.1 gg_id:100070 Indian Ocean hydrothermal vent clone SF_C23-C4_shell AY5315
DQ228647.1 gg_id:144474 Microbial colonizing mineral surfaces within sulfide-microbial incubator clone CH2b1 DQ228
AY542560.1 gg_id:113844 Gulf Mexico seafloor sediment clone GoM GB425 02B-28 AY5425
GQ249521.1 gg_id:580475 Microbial anaerobic sediments Bay Cadiz (Spain) marine sediment: 6-8 cm layer clo GQ249
GQ357025.1 gg_id:533206 Metal Dependent Marine Methane Oxidation methane seep sediment clone FeOrig_ GQ357
AF449231.1 gg_id:61878 Riftia pachyptila's tube clone R103-B15 AF4492
AB476184.1 gg_id:536849 Compositional and functional transition epibiotic microbial hydrothermal vent galat AB4761
AY531576.1 gg_id:107839 Indian Ocean hydrothermal vent clone SF_C23-G3 AY5315
FJ535277.1 gg_id:540587 within iron-containing flocculent mats submarine volcanoes along Kermadec Arc iron FJ5352

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EU487998.1 gg_id:570269 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU4879
FJ497296.1 gg_id:541606 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun FJ4972
GU369887.1 gg_id:519900 and mats vents Arc white filamentous microbial mat photic shal hydrothermal vent GU369
FJ535276.1 gg_id:511548 within iron-containing flocculent mats submarine volcanoes along Kermadec Arc iron FJ5352
AY549001.2 gg_id:101316 marine bone clone sacC13A3 AY5490
FJ535285.1 gg_id:554836 within iron-containing flocculent mats submarine volcanoes along Kermadec Arc iron FJ5352
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AY531587.1 gg_id:104132 Indian Ocean hydrothermal vent clone SF_C23-D11_shell AY5315
AY672538.1 gg_id:105257 hydrothermal vent 9 degrees North East Rise Pacific Ocean clone CH9_1_BAC_16SrR AY6725
AB440171.1 gg_id:569838 Farming and harvesting filamentous vent- galatheid crab (Decapoda; Anomura) vent AB4401
AY531601.1 gg_id:104446 Indian Ocean hydrothermal vent clone SF_C23-C7_shell AY5316
FJ535304.1 gg_id:554479 within iron-containing flocculent mats submarine volcanoes along Kermadec Arc iron FJ5353
EU652643.1 gg_id:278085 Seasonal variation microbial Yel Sea sediment clone B8S-12 EU6526
EU555129.1 gg_id:268986 Microbial Sulfide Hydrothermal Vent Field Juan de Fuca Ridge Dudley hydrothermal EU5551
DQ071277.1 gg_id:139667 dominate filamentous sulfur mat 13 degree north field East Pacific Rise deep-sea hy DQ071
EF462802.1 gg_id:289264 meta-genome level extreme microbial symbiosis dorsal surface deep sea hydrotherm EF4628
AJ441206.1 gg_id:57471 hydrothermal vent polychaete mucous clone P. palm C/A 113 AJ4412
EF462624.1 gg_id:296130 meta-genome level extreme microbial symbiosis dorsal surface deep sea hydrotherm EF4626
AB530172.1 gg_id:559058 Monitoring Suez and Tokyo bays based on analyses marine sediment clone Suez..Ba AB5301
FM165251.1 gg_id:558481 seep chitineous tube vestimentiferan tubeworm Lamellibrachia sp. cold seeps clone FM165
AF420359.1 gg_id:67782 hydrothermal sediment clone AF420359 AF4203
AB205405.1 gg_id:115002 Alviniconcha aff. hessleri gill endosymbiont AB2054
EF462766.1 gg_id:300444 meta-genome level extreme microbial symbiosis dorsal surface deep sea hydrotherm EF4627
AY531572.1 gg_id:107247 Indian Ocean hydrothermal vent clone SF_C23-G9 AY5315
FJ712419.1 gg_id:526671 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) K FJ7124
AF029044.1 gg_id:11139 Benzene mineralizing consortium complete clone SB-17 AF0290
EF462668.1 gg_id:299697 meta-genome level extreme microbial symbiosis dorsal surface deep sea hydrotherm EF4626
AY531593.1 gg_id:99597 Indian Ocean hydrothermal vent clone SF_C23-E5_shell AY5315
AY225618.1 gg_id:98223 organic-rich substrate exposed to Mid-Atlantic Ridge vent clone AT-co12 AY2256
AY672511.1 gg_id:103076 hydrothermal vent 9 degrees North East Rise Pacific Ocean clone CH1_3f_BAC_16SrF AY6725
DQ270643.1 gg_id:142040 hydrothermal carbonate chimney clone LC1133B-58 DQ270
EU107475.1 gg_id:349595 Identification Ectosymbiont on Hair Inhabiting Hydrothermal Vents hair Shinkaia cro EU1074
AY225625.1 gg_id:98807 iron-rich substrate exposed to Mid-Atlantic Ridge vent clone AT-cs7 AY2256
FM165253.1 gg_id:558667 seep chitineous tube vestimentiferan tubeworm Lamellibrachia sp. cold seeps clone FM165
AB099998.1 gg_id:79591 inactive deep-sea hydrothermal vent chimneys clone IndB1-30 AB0999
DQ394973.1 gg_id:153118 harbor sediment clone VHS-B3-94 DQ394
EF462777.1 gg_id:288783 meta-genome level extreme microbial symbiosis dorsal surface deep sea hydrotherm EF4627
AY531595.1 gg_id:99906 Indian Ocean hydrothermal vent clone SF_C23-E10_shell AY5315
EU265786.1 gg_id:258528 epibiotic assemblage recently described Yeti Kiwa hirsuta (Kiwidae) surface crab hyc EU2657

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AJ575963.1 gg_id:95437 deep sea hydrothermal vent clone T3-Hot3-706 AJ5759
AY531597.1 gg_id:100222 Indian Ocean hydrothermal vent clone SF_C23-B7_shell AY5315
AM176867.1 gg_id:161081 Recovery mangrove sediment clone SZB13 AM176
EU265795.1 gg_id:262084 epibiotic assemblage recently described Yeti Kiwa hirsuta (Kiwidae) surface crab hyc EU2657
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AY197378.1 gg_id:83351 Guaymas Basin hydrothermal vent sediments clone B01R006 AY1973
FJ535271.1 gg_id:544300 within iron-containing flocculent mats submarine volcanoes along Kermadec Arc iron FJ5352
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EU265785.1 gg_id:277410 epibiotic assemblage recently described Yeti Kiwa hirsuta (Kiwidae) surface crab hyc EU2657
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AY531585.1 gg_id:103824 Indian Ocean hydrothermal vent clone SF_C23-C11_shell AY5315
AY225614.1 gg_id:96015 iron-rich substrate exposed to Mid-Atlantic Ridge vent clone AT-cs3 AY2256
AB232530.1 gg_id:151369 Prokaryotic gills deep-sea hydrothermal vent shrimp gill Alvinocaris longirostris clone AB2325
DQ270645.1 gg_id:143843 hydrothermal carbonate chimney clone LC1133B-68 DQ270
AY531600.1 gg_id:104287 Indian Ocean hydrothermal vent clone SF_C23-C8_shell AY5316
AY531591.1 gg_id:99285 Indian Ocean hydrothermal vent clone SF_C23-B1_shell AY5315
AY327882.1 gg_id:90455 surface vent snail foot clone SF_C4-D5 AY3278
AY225624.1 gg_id:97289 pumice fragments exposed to Mid-Atlantic Ridge vent clone AT-pp27 AY2256
AF420351.1 gg_id:67787 hydrothermal sediment clone AF420351 AF4203
EU617859.1 gg_id:345356 Seasonal variation microbial Yel Sea sediment clone D13S-42 EU6178
FJ799124.1 gg_id:510696 Microbial Responsible Intermediates Degradation Anaerobic Digestion System Deterr FJ7991
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DQ270655.1 gg_id:141448 hydrothermal carbonate chimney clone LC1404B-6 DQ270
FJ535259.1 gg_id:542712 within iron-containing flocculent mats submarine volcanoes along Kermadec Arc iron FJ5352
GQ167319.1 gg_id:562624 Microbial Life -13C Brine Ice-Sealed Antarctic ice-entrained brine 16.5 m Lake Vida c GQ167
FJ535292.1 gg_id:551198 within iron-containing flocculent mats submarine volcanoes along Kermadec Arc iron FJ5352
AF449253.1 gg_id:61855 Riftia pachyptila's tube clone R76-B151 AF4492
AY672522.1 gg_id:99252 hydrothermal vent 9 degrees North East Rise Pacific Ocean clone CH3_9_BAC_16SrRN AY6725
DQ071276.1 gg_id:140018 dominate filamentous sulfur mat 13 degree north field East Pacific Rise deep-sea hy DQ071
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AB440161.1 gg_id:549495 Farming and harvesting filamentous vent- galatheid crab (Decapoda; Anomura) vent AB4401
EF462696.1 gg_id:289073 meta-genome level extreme microbial symbiosis dorsal surface deep sea hydrotherm EF4626
AY531570.1 gg_id:106942 Indian Ocean hydrothermal vent clone SF_C23-H11 AY5315
AB239758.1 gg_id:149235 filamentous epibiont Vulcanolepas osheai AB2397
FJ535270.1 gg_id:533833 within iron-containing flocculent mats submarine volcanoes along Kermadec Arc iron FJ5352

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EU265789.1 gg_id:258893 epibiotic assemblage recently described Yeti Kiwa hirsuta (Kiwidae) surface crab hyc EU265
AM268719.1 gg_id:232342 Fluid chemistry and microbial southern hydrothermal field (Lilliput) on Mid-Atlantic AM268
AF154091.1 gg_id:11137 hydrocarbon seep clone BPC056 AF154
DQ071288.1 gg_id:139782 dominate filamentous sulfur mat 13 degree north field East Pacific Rise deep-sea hy DQ071
AB440162.1 gg_id:557961 Farming and harvesting filamentous vent- galatheid crab (Decapoda; Anomura) vent AB440
GQ261779.1 gg_id:573816 shifts taxa and response localized organic loading deep sea sediment whale falls clo GQ261
EF462627.1 gg_id:297366 meta-genome level extreme microbial symbiosis dorsal surface deep sea hydrotherm EF4626
EU487914.1 gg_id:538726 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU487
EF462714.1 gg_id:293356 meta-genome level extreme microbial symbiosis dorsal surface deep sea hydrotherm EF4627
AB193955.1 gg_id:108919 deep-sea vent clone Sd-EB04 AB193
EF462827.1 gg_id:292616 meta-genome level extreme microbial symbiosis dorsal surface deep sea hydrotherm EF4628
AY531571.1 gg_id:107097 Indian Ocean hydrothermal vent clone SF_C23-H10 AY5315
FJ535282.1 gg_id:538493 within iron-containing flocculent mats submarine volcanoes along Kermadec Arc iron FJ5352
DQ394936.1 gg_id:153573 harbor sediment clone VHS-B3-29 DQ394
AB188786.1 gg_id:113953 cold seep sediment clone SB5-11 AB188
FJ497361.1 gg_id:542661 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun FJ4973
AB278150.1 gg_id:177809 hydrothermal vent prokaryotes trapped 0.2- and 0.1-micro-m-filtrates obtained Mar AB278
AF121887.1 gg_id:11128 2-bromophenol-dehalogenating consortium clone 2BP-7 AF1218
FM203396.1 gg_id:423805 Biogeography filamentous and epsilonproteobacterial ectosymbionts vent shrimp e FM203
EF061978.1 gg_id:190937 Xiamen China mangrove sediment clone XME34 EF0619
AY327881.1 gg_id:88572 surface vent snail foot clone SF_C4-C4 AY3278
FJ497343.1 gg_id:549911 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun FJ4973
FJ497347.1 gg_id:582544 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun FJ4973
GU180158.1 gg_id:537179 Impact coplanar PCBs on microbial activity anaerobic estuarine sediments sediment GU180
EU107476.1 gg_id:343167 Identification Ectosymbiont on Hair Inhabiting Hydrothermal Vents hair Shinkaia cro EU107
EU662505.1 gg_id:571991 Productivity- Chemolithoautotrophically Based Sulfidic Karst Systems microbial mat EU662
EF462800.1 gg_id:293062 meta-genome level extreme microbial symbiosis dorsal surface deep sea hydrotherm EF4628
FJ497375.1 gg_id:581955 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun FJ4973
GQ249549.1 gg_id:575344 Microbial anaerobic sediments Bay Cadiz (Spain) marine sediment: 12-14 cm layer c GQ249
FJ264679.1 gg_id:328542 Manganese and Iron Dependent Anaerobic Oxidation Methane methane seep sedim FJ2646
EF687491.1 gg_id:284524 Biogeochemistry iron- and sulfur-precipitating microbial mats (Nile Mediterranean) s EF6874
FJ905647.1 gg_id:545620 s Tonga-Kermadec iron oxide chimney-like structure on Volcano 19 Tonga Arc clone V FJ9056
AY531592.1 gg_id:99437 Indian Ocean hydrothermal vent clone SF_C23-B12_shell AY5315
FJ497326.1 gg_id:571424 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun FJ4973
FJ717162.1 gg_id:554142 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United King FJ7171
FJ497317.1 gg_id:574124 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun FJ4973
FJ535287.1 gg_id:544443 within iron-containing flocculent mats submarine volcanoes along Kermadec Arc iron FJ5352
FJ497276.1 gg_id:586842 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun FJ4972
EF061975.1 gg_id:175519 Xiamen China mangrove sediment clone XME6 EF0619
AY672498.1 gg_id:102927 hydrothermal vent 9 degrees North East Rise Pacific Ocean clone CH1_10_BAC_16Sr AY6724

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L35520.1 gg_id:11121 Alvinella pompejana L3552
GU369898.1 gg_id:520798 and mats vents Arc white filamentous microbial mat photic shal hydrothermal vent GU369
AY327880.1 gg_id:88951 surface vent snail foot clone SF_C5-F8 AY327
FJ712566.1 gg_id:508922 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) FJ7125
DQ925872.1 gg_id:241522 Microbes and Thermal Gradients Temperature Hydrothermal Chimneys hydrotherm DQ925
EF462629.1 gg_id:295292 meta-genome level extreme microbial symbiosis dorsal surface deep sea hydrotherm EF462
GQ261802.1 gg_id:543184 shifts taxa and response localized organic loading deep sea sediment whale falls clo GQ261
AF420344.1 gg_id:67793 hydrothermal sediment clone AF420344 AF420
DQ295602.2 gg_id:159750 Epsilonproteobacteria terrestrial caves and springs microbial mat sulfidic spring Drin DQ295
FJ497396.1 gg_id:542332 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun FJ4973
EF462824.1 gg_id:302928 meta-genome level extreme microbial symbiosis dorsal surface deep sea hydrotherm EF462
AB187014.1 gg_id:101863 Suiyo seamount hydrothermal vent water 0.2micro-m filterable fraction clone SSM-E AB187
AY542550.1 gg_id:114277 Gulf Mexico seafloor sediment clone GoM GB425 02B-9 AY542
FJ902253.1 gg_id:571547 phreatic limestone sinkholes northeastern Mexico water column 32m deep cenote C FJ9022
FJ264760.1 gg_id:339147 Manganese and Iron Dependent Anaerobic Oxidation Methane methane seep sedim FJ2647
AY355304.2 gg_id:101665 epibiontic clone C11-C9 AY355
AB091292.1 gg_id:84230 Sulfurovum lithotrophicum str. 42BKT AB091
AY672512.1 gg_id:103225 hydrothermal vent 9 degrees North East Rise Pacific Ocean clone CH3_1_BAC_16SrR AY672
AY531604.1 gg_id:104899 Indian Ocean hydrothermal vent clone SF_C23-F6 AY531
AJ132737.1 gg_id:20059 hydrothermal vent clone Top-147 AJ1327
AY672506.1 gg_id:107659 hydrothermal vent 9 degrees North East Rise Pacific Ocean clone CH1_23_BAC_16Sr AY672
EU245507.1 gg_id:252330 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M2-D1 EU245
FJ165504.1 gg_id:539775 Microbially-enhanced Dissolution Karst Carbonates microbial biofilm Sonterra #8 well FJ1655
DQ295697.1 gg_id:160880 Epsilonproteobacteria terrestrial caves and springs floating microbial mat sulfidic gr DQ295
AF449236.1 gg_id:61874 Riftia pachyptila's tube clone R103-B37 AF449
AY672537.1 gg_id:105096 hydrothermal vent 9 degrees North East Rise Pacific Ocean clone CH9_6_BAC_16SrR AY672
AJ969446.1 gg_id:158924 Microbial black smoker s Mid Atlantic Ridge ecological implications rock fragments c AJ9694
GU390848.1 gg_id:530358 Dark hot springs: structure biofilms caves Acquasanta Terme (Italy) sulfidic cave stre GU390
AM745162.1 gg_id:292405 Impact oil er hydrocarbons on microbial and activity Gulf Mexico cold seep marine s AM745
AF420360.1 gg_id:67780 hydrothermal sediment clone AF420360.1 AF420
AF420342.1 gg_id:67795 hydrothermal sediment clone AF420342 AF420
AB105048.1 gg_id:93761 Hydrogenimonas thermophila str. EP1-55-1% AB105
AY261811.1 gg_id:83596 UASB reactor granular sludge clone PD-UASB-2 proteobacterium AY261
DQ295692.1 gg_id:161262 Epsilonproteobacteria terrestrial caves and springs floating microbial mat sulfidic gr DQ295
AY531574.1 gg_id:107543 Indian Ocean hydrothermal vent clone SF_C23-G7 AY531
AB278149.1 gg_id:184732 hydrothermal vent prokaryotes trapped 0.2- and 0.1-micro-m-filtrates obtained Mar AB278
AB175498.1 gg_id:106632 Thioreductor micantisoli str. BKB25Ts-Y AB175
EF467531.1 gg_id:213162 situ microelectrode voltammetry sulfur-oxidizing biofilms Frasassi sulfidic cave strear EF467
FJ497432.1 gg_id:556468 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun FJ4974
EF467559.1 gg_id:211322 situ microelectrode voltammetry sulfur-oxidizing biofilms Frasassi sulfidic cave strear EF467

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AM268717.1 gg_id:233206 Fluid chemistry and microbial southern hydrothermal field (Lilliput) on Mid-Atlantic AM268
AY280433.1 gg_id:106294 exterior deep-sea hydrothermal vent sulfide chimney Juan de Fuca Ridge Pacific Oce AY2804
DQ295651.1 gg_id:161606 Epsilonproteobacteria terrestrial caves and springs microbial mat sulfidic cave strea DQ295
EF462765.1 gg_id:299712 meta-genome level extreme microbial symbiosis dorsal surface deep sea hydrotherm EF4627
GU196200.1 gg_id:579980 Bioaugmentation improved recovery digesters after toxicant exposure lab-scale ana GU196
AB278151.1 gg_id:180340 hydrothermal vent prokaryotes trapped 0.2- and 0.1-micro-m-filtrates obtained Mar AB278
AY531573.1 gg_id:107393 Indian Ocean hydrothermal vent clone SF_C23-G8 AY5315
FJ799123.1 gg_id:584284 Microbial Responsible Intermediates Degradation Anaerobic Digestion System Deterr FJ7991
AJ441202.1 gg_id:57475 hydrothermal vent polychaete mucous clone P. palm C 140 AJ4412
DQ295708.1 gg_id:160328 Epsilonproteobacteria terrestrial caves and springs microbial mat sulfidic stream Mil DQ295
EF467511.1 gg_id:215667 situ microelectrode voltammetry sulfur-oxidizing biofilms Frasassi sulfidic cave strear EF4675
FJ485355.1 gg_id:545841 microbial autonomous rover world's deepest phreatic sinkhole wall biomat El Zacator FJ4853
DQ228655.1 gg_id:141137 Microbial colonizing mineral surfaces within sulfide-microbial incubator clone CH2b1 DQ228
EF462722.1 gg_id:296261 meta-genome level extreme microbial symbiosis dorsal surface deep sea hydrotherm EF4627
EU234099.1 gg_id:246280 receiving river and un techniques anaerobic process WWTP treating penicillin G prod EU2340
AJ576002.1 gg_id:98839 deep sea hydrothermal vent clone T6-Ph07-983 AJ5760
GU390742.1 gg_id:517462 Dark hot springs: structure biofilms caves Acquasanta Terme (Italy) sulfidic cave stre GU390
AY082468.1 gg_id:67838 neutral pH mine biofilm clone 44a-B1-40 AY0824
AY280427.1 gg_id:101920 exterior deep-sea hydrothermal vent sulfide chimney Juan de Fuca Ridge Pacific Oce AY2804
EF467460.1 gg_id:205100 situ microelectrode voltammetry sulfur-oxidizing biofilms Frasassi sulfidic cave strear EF4674
AB198587.1 gg_id:135519 termite gut fluid and protists fraction clone RsC01-014 AB1985
DQ295656.1 gg_id:160561 Epsilonproteobacteria terrestrial caves and springs microbial mat sulfidic cave strea DQ295
AF286053.1 gg_id:29701 Helicobacter rappini W.Tee-Yu AF2860
AY571498.1 gg_id:114816 termite gut clone RsaHf427 AY5714
GU369897.1 gg_id:528299 and mats vents Arc white filamentous microbial mat photic shal hydrothermal vent GU369
AY355299.2 gg_id:106198 epibiontic clone C11-E8 AY3552
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AY578096.1 gg_id:105995 Helicobacter bilis str. KI900 AY5780
AY251062.1 gg_id:103492 deep-sea hydrothermal biofilm Edmond vent field on Central Indian Ridge clone FT17 AY2510
EF462645.1 gg_id:297781 meta-genome level extreme microbial symbiosis dorsal surface deep sea hydrotherm EF4626
AF449237.1 gg_id:61872 Riftia pachyptila's tube clone R103-B43 AF4492
EF467591.1 gg_id:214381 situ microelectrode voltammetry sulfur-oxidizing biofilms Frasassi sulfidic cave strear EF4675
AY672507.1 gg_id:107804 hydrothermal vent 9 degrees North East Rise Pacific Ocean clone CH1_25_BAC_16Sr AY6725
EF462782.1 gg_id:290493 meta-genome level extreme microbial symbiosis dorsal surface deep sea hydrotherm EF4627
EU662427.1 gg_id:579840 Productivity- Chemolithoautotrophically Based Sulfidic Karst Systems microbial mat EU6624
U51874.2 gg_id:10979 Helicobacter sp. Dog-4 str. Dog-4; Eaton 1302 U51874
DQ071280.1 gg_id:140620 dominate filamentous sulfur mat 13 degree north field East Pacific Rise deep-sea hy DQ071
AY531583.1 gg_id:103545 Indian Ocean hydrothermal vent clone SF_C23-F3 AY5315
GU390798.1 gg_id:516081 Dark hot springs: structure biofilms caves Acquasanta Terme (Italy) sulfidic cave stre GU390

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AF420347.1 gg_id:67790 hydrothermal sediment clone AF420347.1 AF4203
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GQ355026.1 gg_id:565854 structure between two geochemically distinct springs Alum Rock Park spring clone M GQ355
L35522.1 gg_id:11150 Alvinella pompejana epibiont L35522
AJ969465.1 gg_id:157898 Microbial black smoker s Mid Atlantic Ridge ecological implications rock fragments ch AJ9694
EU864466.1 gg_id:334109 structures under selection pressure levels antibiotics Xiao River receiving treated ox\ EU8644
EF644836.1 gg_id:300292 genes and citrate lyase deep-sea microbial MAR Rainbow hydrothermal vent system EF6448
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GU390782.1 gg_id:516622 Dark hot springs: structure biofilms caves Acquasanta Terme (Italy) sulfidic cave stre GU390
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GU390711.1 gg_id:515047 Dark hot springs: structure biofilms caves Acquasanta Terme (Italy) sulfidic cave stre GU390
AY280435.1 gg_id:106612 exterior deep-sea hydrothermal vent sulfide chimney Juan de Fuca Ridge Pacific Oce: AY2804
NC_005090.1 gg_id:93903 Wolinella succinogenes str. DSM 1740 NC_005
AF273252.1 gg_id:29152 Wolinella succinogenes str. SeR-1 AF2732
AF068812.2 gg_id:11156 hydrothermal vent clone VC2.1 Bac12 AF0688
AY691429.1 gg_id:106012 Caminibacter sp. str. TB-1 AY6914
NR_028943.1 gg_id:571654 Caminibacter hydrogeniphilus str. AM1116; DSM 14510 NR_028
AF299128.1 gg_id:40818 S17sBac34 complete clone AF2991
AF068804.2 gg_id:11155 hydrothermal vent clone VC2.1 Bac30 AF0688
ABCJ01000004.1 gg_id:243079 Caminibacter mediatlanticus str. TB-2 ABCJ01
NR_028999.1 gg_id:579615 Caminibacter profundus str. CR; DSM 15016 NR_028
CP001279.1 gg_id:528797 Nautilia profundicola str. AmH CP0012
NR_025497.1 gg_id:566284 Nautilia lithotrophica str. 525; DSM 13520 NR_025
AM937002.1 gg_id:260087 Nautilia abyssi str. PH1209 AM937
AP009178.1 gg_id:247747 Nitratiruptor sp. str. SB155-2 AP0091
AB175499.1 gg_id:106788 Nitratiruptor tergarcus str. MI55-1 AB1754
AB167820.1 gg_id:136358 Lebetimonas acidiphila str. Pd55 AB1678
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FJ154522.1 gg_id:556258 Acidithiobacillus caldus str. Da FJ1545
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DQ646485.1 gg_id:238863 Acidithiobacillus ferrooxidans str. DX-AF-4 DQ646
EU079375.1 gg_id:243219 Acidithiobacillus ferrooxidans str. NF-01 EU0793
AB039820.1 gg_id:19750 Acidithiobacillus ferrooxidans str. NASF-1 AB0398

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DQ321746.1 gg_id:148463 Acidithiobacillus ferrooxidans str. yunnan1 DQ321
DQ909079.1 gg_id:170265 Acidithiobacillus ferrooxidans str. c DQ909
GU167981.1 gg_id:583008 Acidithiobacillus ferrooxidans GU167
AF359940.1 gg_id:21015 Acidithiobacillus thiooxidans str. KCTC 8929P AF3599
AJ879995.1 gg_id:127417 Acidithiobacillus ferrooxidans str. B4 AJ8799
DQ529311.1 gg_id:301400 Acidithiobacillus ferrooxidans str. DBS-1 DQ529
EU250259.1 gg_id:241484 acid mine drainage clone GXDC-45 EU250
EF446188.1 gg_id:210453 Prokaryotic and Ecology Floating Macroscopic Filaments Extreme Acidic River Rio Tint EF4461
FJ946877.1 gg_id:567607 Acidithiobacillus ferrooxidans str. NK-16 FJ9468
AY552091.1 gg_id:147725 Acidithiobacillus sp. str. CASQ22 AY552
FJ890908.1 gg_id:574423 Microbial heap: implications model and control process -grade copper bioleaching he FJ8909
EF612419.1 gg_id:248238 historic semiarid lead-zinc site mine tailings clone K6-C19 EF6124
EF059761.1 gg_id:188237 Acidithiobacillus ferrooxidans str. CHMS EF0597
X75266.1 gg_id:7484 Acidithiobacillus ferrooxidans X75266
FJ154519.1 gg_id:539257 Acidithiobacillus ferrooxidans str. F6 FJ1545
AM502930.1 gg_id:241149 Acidithiobacillus ferrooxidans str. LMT1 AM502
EU084698.1 gg_id:254158 Acidithiobacillus ferrooxidans str. DGS EU084
DQ159176.1 gg_id:139484 Wetland System Treating Acid Coal Mine Drainage wetland clone AMD 636 DQ159
EU250217.1 gg_id:253906 acid mine drainage clone GXDC-3 EU250
AJ459801.1 gg_id:66601 Thermithiobacillus tepidarius str. DSM 3134 AJ4598
AJ458408.1 gg_id:67017 Aeromonas encheleia str. LMG 16328 AJ4584
AJ458416.1 gg_id:67011 Aeromonas encheleia str. E195 = S 191 AJ4584
FJ940842.1 gg_id:419066 Aeromonas enteropelogenes str. CRX104 FJ9408
FJ940843.1 gg_id:465898 Aeromonas enteropelogenes str. CRX105 FJ9408
FJ940844.1 gg_id:457890 Aeromonas enteropelogenes str. CRX203 FJ9408
FJ940845.1 gg_id:394895 Aeromonas enteropelogenes str. CRX207 FJ9408
FJ966347.1 gg_id:411204 Aeromonas veronii str. 5CB1 FJ9663
FJ940820.1 gg_id:455969 Aeromonas veronii str. LNC205 FJ9408
FJ940816.1 gg_id:401894 Aeromonas jandaei str. LC208 FJ9408
EU770282.1 gg_id:320191 Aeromonas veronii str. IH118 EU770
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AF157690.1 gg_id:9454 Aeromonas media str. 86352 AF157
AY900170.1 gg_id:143274 Aeromonas hydrophila str. PCA0081 AY900
FJ940831.1 gg_id:449999 Aeromonas media str. pW28 FJ9408
EU488683.1 gg_id:545213 Aeromonas media str. 974a EU488
FJ168773.1 gg_id:559246 Aeromonas media str. 480a FJ1687
AF418218.1 gg_id:59117 Aeromonas media 5 AF418
GQ470996.1 gg_id:546104 Aeromonas hydrophila str. HQ070610B-1 GQ470
AM262152.1 gg_id:158666 Aeromonas media str. CDC 0862-83 AM262

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FJ494900.1 gg_id:424847 Aeromonas hydrophila str. B27
AF468055.1 gg_id:28522 Aeromonas hydrophila str. 45/90
EU488681.1 gg_id:543209 Aeromonas media str. 83a
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AY532688.1 gg_id:99610 Aeromonas molluscorum str. 93M
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GQ860945.2 gg_id:559436 Aeromonas simiae str. MDC 54
AF150699.1 gg_id:47441 Elbe River snow isolate Iso19neu Iso19neu_1356 snow
FJ233860.1 gg_id:313618 Aeromonas jandaei str. AE25
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AF170914.4 gg_id:9385 Aeromonas culicicola str. MTCC 3249
EU918692.1 gg_id:347086 Pasteurella multocida str. SXXG0802
AB027005.1 gg_id:9445 Aeromonas salmonicida str. NI-441 T83-k-sw-2 IS-205
EU770278.1 gg_id:327136 Aeromonas veronii str. IH101
EU770304.1 gg_id:316400 Aeromonas veronii str. MW17
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AY987741.1 gg_id:198899 Aeromonas hydrophila str. -32
FM999979.1 gg_id:516755 Aeromonas popoffii str. LMG 17546
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EU770270.1 gg_id:308207 Aeromonas veronii str. HH104
EU770296.1 gg_id:316179 Aeromonas punctata str. ME15
AY928478.1 gg_id:138908 Aeromonas veronii bv. Sobria str. A155
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EU770309.1 gg_id:352788 Aeromonas veronii str. WS03
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EU770271.1 gg_id:317346 Aeromonas veronii str. HQ103
FJ940797.1 gg_id:414411 Aeromonas punctata str. 4LNC310

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EU770290.1 gg_id:326583 Aeromonas veronii str. IQ304
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EU770275.1 gg_id:350629 Aeromonas hydrophila str. IB336
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EU770285.1 gg_id:332437 Aeromonas veronii str. IH323
EU770288.1 gg_id:353344 Aeromonas veronii str. IQ117
EU730930.1 gg_id:311549 Aeromonas eucrenophila str. 189
EU770274.1 gg_id:327072 Aeromonas hydrophila str. IB101
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GU205196.1 gg_id:585209 Aeromonas popoffii str. JW08
GU205192.1 gg_id:534484 Aeromonas allosaccharophila str. JNC912

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DQ195676.1 gg_id:140125 Zobellella taiwanensis str. ZT1T DQ195
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FJ681292.1 gg_id:530658 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6812

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FJ673998.1 gg_id:532469 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6739
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FJ676261.1 gg_id:529152 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6762
FJ678600.1 gg_id:524710 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6786
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FJ679573.1 gg_id:530904 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6795
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FJ679565.1 gg_id:527828 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6795
FJ679188.1 gg_id:520121 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6791
FJ673005.1 gg_id:530535 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6730
Y17599.1 gg_id:9351 Succinimonas amylolytica str. DSM 2873 Y17599
EF445219.1 gg_id:207757 dairy cow rumen clone NED4C12 EF4452
FJ440064.1 gg_id:511871 Megamonas hypermegale colonization correlates Campylobacter jejuni exclusion pou FJ4400
AJ420985.1 gg_id:29865 Anaerobiospirillum thomasii str. DSM 11806T AJ4209
FJ832419.1 gg_id:577393 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P1Q401_75C10 FJ8324
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FJ832403.1 gg_id:548716 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P1Q401_45E06 FJ8324
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EU381934.1 gg_id:271179 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU381
FJ952818.1 gg_id:443894 Alteromonas sp. str. 2tb4 FJ9528
GQ391974.1 gg_id:519442 Aestuariibacter sp. str. PaD1.02 GQ391
AB076557.1 gg_id:60317 Agarivorans albus str. MKT 82 AB0765
GQ200591.1 gg_id:544653 Agarivorans sp. str. WH0801 GQ200
DQ416550.1 gg_id:153331 s1cb18 DQ416
AF290480.1 gg_id:27315 cf. Alishewanella fetalis clone Llangefni 75 mite AF2904
AF144407.1 gg_id:33192 Alishewanella fetalis str. CCUG 30811 AF1444
AY093457.1 gg_id:55811 deep marine sediment clone MB-A2-102 AY0934
DQ256339.1 gg_id:142481 subsurface water clone EV818BHEB5102702SAS10 DQ256
AY820719.1 gg_id:109054 drilling fluid clone CCSD_DF2030_B15 AY8207
FJ040187.1 gg_id:347660 Alteromonas genoviensis str. I96 FJ0401
EU189225.1 gg_id:239877 Alteromonas marina str. MB 3 EU189
AY881234.1 gg_id:145384 Alteromonas marina SCH0402 AY8812
AF288360.1 gg_id:71626 Alteromonas alvinellae str. HY757 AF2883
AF386742.1 gg_id:44702 Alteromonas sp. str. 4BT AF3867
AJ319537.1 gg_id:71568 Alteromonas macleodii subsp. abyssi str. HYD657 subsp. AJ3195
AM931040.1 gg_id:239418 Alteromonas sp. str. BUS 07-8 AM931
DQ836766.1 gg_id:163484 Alteromonas simiduii str. BCRC 17572 DQ836
AF114499.1 gg_id:8878 attached marine recovered surface clone 17 proteobacterium AF1144
EF061429.1 gg_id:190836 Alteromonas sp. NJSX37 EF0614
EU982324.1 gg_id:322486 Alteromonas sp. str. UST010723-013 EU9823
FJ210814.1 gg_id:309174 Alteromonas sp. str. QDHT-19 FJ2108
DQ486510.1 gg_id:227411 Alteromonas sp. str. DG1302 DQ486
AF114505.1 gg_id:8883 attached marine recovered deep chlorophyll maximum depth clone 2 proteobacterium AF1145

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AF114504.1 gg_id:8882 attached marine recovered depth 400m clone 25 proteobacterium AF1145
AF114508.1 gg_id:8886 attached marine recovered surface clone 8 AF1145
AY428573.1 gg_id:105550 Alteromonas litorea str. TF-22 AY4285
Y18232.1 gg_id:19130 Alteromonas macleodii str. CH-518 Y18232
AY344429.1 gg_id:91492 Lake Kauhako 30 m clone K2-30-18 AY3444
AM885869.1 gg_id:240896 Alteromonas macleodii R-28696 AM885
AF114501.1 gg_id:8880 attached marine recovered surface clone 18 proteobacterium AF1145
AF114496.1 gg_id:8875 attached marine recovered deep chlorophyll maximum depth clone proteobacterium AF1144
EF574195.1 gg_id:228587 site S25 near Coco's Island marine clone S25_539 EF5741
DQ071162.1 gg_id:136631 marine surface water clone Surf1.42 DQ071
AM882576.1 gg_id:311934 Structure along hydrocarbon contamination coastal sediment oil polluted water pet AM882
AY165578.1 gg_id:81399 Antarctic pack ice Lasarev Sea Southern Ocean clone ANTXI/4_14-11 AY1655
AF468279.1 gg_id:80086 Arctic pack ice; northern Fram Strait; 80 31.1 N; 01 deg 59.7 min E clone ARKIA-118 AF4682
CP000388.1 gg_id:160590 Pseudoalteromonas atlantica str. T6c CP0003
AY697880.1 gg_id:104267 Antarctica clone F2C28 AY6978
U85854.1 gg_id:8873 Glaciecola pallidula str. ACAM 615T IC079 U85854
AY167284.2 gg_id:81210 Glaciecola sp. str. ANT9142 AY1672
AB238790.1 gg_id:140832 Glaciecola sp. #105 AB2387
AM941178.1 gg_id:284078 Microbes enriched seawater after addition coral mucus and reef waters mixture1-8 AM941
AM913910.1 gg_id:439090 antibiotic-active brown alga Laminaria saccharina Baltic Sea Saccharina latissima AM913
AJ240915.1 gg_id:73940 5' clone CHAB-XII-8 AJ2409
AY771709.1 gg_id:108683 Glaciecola mesophila str. S2-38 AY7717
AJ488501.1 gg_id:65357 Glaciecola mesophila str. KMM 241 AJ4885
Y18230.1 gg_id:202397 macleodii- and cellular rDNAs Mediterranean seawater mesocosm experiment Alterom Y18230
AJ548479.1 gg_id:89023 Glaciecola mesophila str. LMG 21855 AJ5484
AF173965.1 gg_id:71399 Alteromonas macleodii str. KT1113 AF1739
AY349463.1 gg_id:91221 Glaciecola sp. WHOI JT-6b AY3494
U73724.1 gg_id:8898 gas vacuolate str. 214.6 U73724
AJ293820.1 gg_id:39858 Glaciecola polaris str. LMG 21857 AJ2938
DQ784575.1 gg_id:162089 Glaciecola agarolytica str. NO2 DQ784
AY553295.1 gg_id:106840 Salinimonas chungwhensis str. BH030046 AY5532
EU583725.1 gg_id:272031 Alteromonas sp. str. JSM 073008 EU5837
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AB040465.1 gg_id:38060 Alteromonas sp. str. K AB0404
FJ024319.1 gg_id:368249 Prokaryotic and their role biogeochemical cycling marine basalts basalt Juan de Fuca I FJ0243
AB473549.1 gg_id:419632 Aestuariibacter sp. NT-2008 str. Sd 2-38 (= KMM 3894) AB4735
AY207502.1 gg_id:84007 Aestuariibacter salexigens str. JC2042 AY2075
AY207503.1 gg_id:83231 Aestuariibacter halophilus str. JC2043 AY2075
AB040466.1 gg_id:45496 Alteromonas sp. str. D AB0404
FJ202664.1 gg_id:350427 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2026

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EU188146.1 gg_id:347006 Uncultivated oceanic unicellular N2-fixing cyanobacteria are picoplankton unusual 7(EU188
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AM882575.1 gg_id:316071 Structure along hydrocarbon contamination coastal sediment oil polluted water pet AM882
EU287412.1 gg_id:256595 Pacific arctic surface sediment clone S26-112 EU287
AM990642.1 gg_id:277954 Alteromonas sp. MOLA 365 AM990
AY926461.1 gg_id:113825 Alteromonas hispanica str. B-35 AY9264
AB040464.1 gg_id:137101 Alteromonas sp. str. S AB0404
AB526336.1 gg_id:573848 Alteromonas sp. str. JAM-GA13 AB5263
Y18233.1 gg_id:8895 Alteromonas macleodii str. CH-460 Y18233
EU188189.1 gg_id:317008 Uncultivated oceanic unicellular N2-fixing cyanobacteria are picoplankton unusual 7(EU188
GQ495024.1 gg_id:581173 Pseudoalteromonas sp. str. W-14-2 GQ495
AM183347.1 gg_id:155988 Alishewanella baltica str. BA131 AM183
EU841485.1 gg_id:310357 Alishewanella sp. str. 205 EU8414
AB295494.1 gg_id:216998 Alteromonas sp. str. A14 AB2954
NR_027234.1 gg_id:540876 Algicola sagamiensis str. B-10-31; DSM 14643 NR_02
GU108538.1 gg_id:591045 active chemolithoautotrophic prokaryotes sulfidic zone Black pelagic redoxcline dete GU108
EU714266.1 gg_id:332103 Alteromonas sp. str. BG20 EU714
DQ913886.1 gg_id:276341 Celerinatantimonas diazotrophica J-G1-2 DQ913
AJ002006.1 gg_id:8823 Rheinheimera baltica str. OS140 Baltic # 166 AJ0020
DQ985066.1 gg_id:177157 Rheinheimera sp. str. JL1145 DQ985
GQ009534.1 gg_id:500133 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw77 GQ009
GQ280117.1 gg_id:570209 Rheinheimera aquimaris str. JS-47 GQ280
FJ170027.1 gg_id:325282 Rheinheimera sp. str. CF12-10 FJ1700
FJ821606.1 gg_id:569335 Rheinheimera sp. str. TPS16 FJ8216
DQ298025.2 gg_id:143812 Rheinheimera chironomi str. K19414 DQ298
FJ902308.1 gg_id:509338 phreatic limestone sinkholes northeastern Mexico biomat rock outcrop cenote La Pal FJ9023
AM117933.1 gg_id:143326 marine boreal sponge Geodia baretti Norway:Korsfjord AM117
GQ240227.1 gg_id:576918 Rheinheimera sp. str. BZ19 GQ240
EU662623.1 gg_id:594183 Productivity- Chemolithoautotrophically Based Sulfidic Karst Systems floating microb EU6626
GQ130023.1 gg_id:440958 Genetic inventory 'JPL-SAF' during MSL mission spacecraft assembly clean room floc GQ130
AY887010.1 gg_id:114447 fresh water clone 1.34.5 AY8870
FJ902639.1 gg_id:593719 phreatic limestone sinkholes northeastern Mexico biofilm 1m deep hydrothermal ver FJ9026
AY701891.1 gg_id:140048 Rheinheimera texana str. A62-14B AY7018
GU108532.1 gg_id:548750 active chemolithoautotrophic prokaryotes sulfidic zone Black pelagic redoxcline dete GU108
FN397813.1 gg_id:405654 geomicrobiological investigation sediments Gulf Cadiz GeoB 9072-1 anoxic sub-surfa FN3978
AY167340.1 gg_id:81146 Psychrobacter sp. str. ARK10133 AY1673

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AB011364.1 gg_id:8843 Colwellia psychrerythraea str. ATCC27364 AB011
FN397812.1 gg_id:392867 geomicrobiological investigation sediments Gulf Cadiz GeoB 9072-1 anoxic sub-surfa FN397
GU061308.1 gg_id:560509 Evaluation culturing methods cultivate previously Yel Sea intertidal beach seawater GU061
U85841.1 gg_id:8840 Colwellia psychrerythraea str. ACAM 604 U8584
AF001375.1 gg_id:8836 Colwellia psychrerythraea str. ATCC27364; ACAM 550T AF001
AF530145.1 gg_id:61116 Colwellia psychrerythraea str. MGP-41 AF530
AY167332.1 gg_id:82309 Colwellia rossensis str. ANT9271 AY167
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FJ905674.1 gg_id:560989 s Tonga-Kermadec iron oxide chimney-like structure on Volcano 19 Tonga Arc clone V FJ9056
DQ027051.1 gg_id:130223 Colwellia sp. str. MT41 DQ027
EF551378.1 gg_id:225725 Colwellia sp. str. BSw20516 EF5513
EU050773.1 gg_id:257619 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_01_78 EU050
DQ837294.1 gg_id:235556 Archaeal and pristine National Park Spain Donana coastal aquifer clone 49S1_1B_55 DQ837
DQ490038.1 gg_id:158539 Microbial life ridge flank crustal fluids clone ODP-70B-02 DQ490
AY167330.1 gg_id:81643 Colwellia sp. str. ANT9407 AY167
DQ351740.1 gg_id:146764 Microbial Adherent Sediment Particles Heavy Metal Contaminated North Sea Surfac DQ351
GQ350647.1 gg_id:559927 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ350
GQ848466.1 gg_id:581903 Microbial sediments vents along East Lau Spreading Centre deep sea hydrothermal GQ848
L10950.1 gg_id:8854 marine snow clone agg53 L10950
AY829231.2 gg_id:179606 Colwellia sp. IE7-5 AY829
EU394582.1 gg_id:309555 Coccolithophore bloom dynamics shape (NE-Atl) northern Bay Biscay pelagic particle EU394
DQ027052.1 gg_id:131520 Colwellia sp. str. KT27 DQ027
GU391219.1 gg_id:531807 Thalassomonas sp. str. JYr2 GU391
AY165571.1 gg_id:81437 Antarctic pack ice Lasarev Sea Southern Ocean clone ANTXI/4_14-151 sea AY165
AB094412.1 gg_id:97603 Colwellia piezophila str. Y223G AB094
AF419350.1 gg_id:74479 Colwellia sp. str. Ant5-9 AF419
EU491932.1 gg_id:271119 Abundance and microbial life ocean crust deep seawater East Pacific Rise clone EPR4 EU491
EU599214.3 gg_id:319654 Colwellia sp. str. KMD002 EU599
EU491916.1 gg_id:258657 Abundance and microbial life ocean crust deep seawater East Pacific Rise clone EPR4 EU491
DQ492707.1 gg_id:158794 Colwellia sp. str. BSi20061 DQ492
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EU491896.1 gg_id:259552 Abundance and microbial life ocean crust deep seawater East Pacific Rise clone EPR4 EU491
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AF530146.1 gg_id:103969 Colwellia sp. str. MGP-59 AF530
GU108544.1 gg_id:589927 active chemolithoautotrophic prokaryotes sulfidic zone Black pelagic redoxcline dete GU108
AY167264.1 gg_id:81818 Colwellia sp. str. ANT8203 AY167
DQ923440.1 gg_id:179604 Alteromonas sp. W-6 DQ923
DQ228659.1 gg_id:141317 Microbial colonizing mineral surfaces within sulfide-microbial incubator clone CH2b7 DQ228
DQ212914.1 gg_id:140089 Thalassomonas agarivorans str. TMA1 DQ212

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GQ848478.1 gg_id:584370 Microbial sediments vents along East Lau Spreading Centre deep sea hydrothermal GQ848
FJ717227.1 gg_id:553622 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United King FJ7172
FJ202297.1 gg_id:322290 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2022
GU230351.1 gg_id:594414 Multilevel approach along Rio de la Plata-South Atlantic Ocean coastal sediment clo GU230
FJ203045.1 gg_id:322845 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c FJ2030
AY643537.2 gg_id:131602 White plague like disease Eilat coral reef AY6435
AY194066.1 gg_id:81968 Thalassomonas ganghwensis str. JC2041 AY1940
FJ203217.1 gg_id:306276 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c FJ2032
EU491328.1 gg_id:269454 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak EU4913
U15115.1 gg_id:8864 hydrothermal vent clone PVB_OTU_12 U15115
FJ791872.1 gg_id:513615 Unexpectedly archaeal species shift between rare and dominant over thousand year FJ7918
FJ203091.1 gg_id:324976 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c FJ2030
AJ294747.1 gg_id:26868 Thalassomonas viridans str. XOM5 CECT 5082 DSM 13753 AJ2947
AY770724.1 gg_id:110997 sea urchin Paracentrotus lividus clone PIS53 AY7707
FJ952826.1 gg_id:382239 Colwellia sp. str. 1tb5 FJ9528
AB193748.1 gg_id:111458 Ferrimonas marina str. A2A-30 AB1937
AB252733.1 gg_id:243052 Paraferrimonas sedimenticola str. Mok-142 AB2527
GU391222.1 gg_id:528038 Ferrimonas sp. str. JYr13 GU391
FJ203654.1 gg_id:341133 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h FJ2036
EU620413.1 gg_id:278677 Ferrimonas balearica str. S8-05 EU6204
AB193752.1 gg_id:112098 Ferrimonas balearica str. A2A-18 AB1937
AB193755.1 gg_id:111912 Ferrimonas sp. str. A3B-58 AB1937
NR_027560.1 gg_id:549106 Idiomarina baltica OS145 str. OS145; DSM 15154 NR_027
NC_006512.1 gg_id:128686 Idiomarina loihiensis str. L2TR NC_006
AE017340.1 gg_id:128915 Idiomarina loihiensis str. L2TR AE0173
AY092077.1 gg_id:67499 Idiomarina loihiensis str. 53 AY0920
AY635468.1 gg_id:107632 Idiomarina seosinensis str. CL-SP19 AY6354
EU603445.1 gg_id:275762 Idiomarina seosinensis str. PTG4-5 EU6034
AY553081.1 gg_id:107227 Idiomarina loihiensis str. GSP41 AY5530
NR_029115.1 gg_id:557590 Idiomarina fontislapidosi str. F23; LMG 22169 NR_029
EU440964.1 gg_id:311612 Idiomarina seosinensis str. PR58-8 EU4409
DQ235566.1 gg_id:142194 biofilm water pipeline biofilms steel pipelines Gulf Mexico clone 20 DQ235
AY526862.1 gg_id:102489 Idiomarina ramblicola str. R22 AY5268
AY505529.1 gg_id:101950 Idiomarina loihiensis str. GSP13 AY5055
FM877003.1 gg_id:574998 Idiomarina sp. IT-2008 str. CVS-6 FM877
DQ234155.2 gg_id:144284 determined library mangrove clone DS071 DQ234
EF486355.1 gg_id:222466 Idiomarina salinae str. ISL-52 EF4863
GQ180187.1 gg_id:591011 Pseudidiomarina sp. str. SW5 GQ180
GQ246209.1 gg_id:577128 Pseudidiomarina sp. str. YCSA4 GQ246
DQ416777.1 gg_id:268666 Idiomarina sp. G2DM-8 DQ416
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EF212001.1 gg_id:214514 Pseudidiomarina sp. str. c121 EF2120
EU600202.2 gg_id:260949 Pseudidiomarina sp. str. 8C EU600
EU722654.1 gg_id:327394 Microbial athalassohaline Tirez lagoon (Spain) sediment clone SB43 EU722
EF554907.1 gg_id:222862 Idiomarina sp. str. G-He8 EF5549
GU458902.1 gg_id:562858 microbiota human male female forehead forearm and influence make-up skin clone GU458
X92129.1 gg_id:44150 Crater Lake isolate 11C1 X92129
GU471247.1 gg_id:517013 Idiomarina sp. str. 10-D-4 GU471
EF554896.1 gg_id:226059 Idiomarina sp. str. JK38 EF5548
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EF554906.1 gg_id:223511 Idiomarina sp. str. G-He7 EF5549
X92128.1 gg_id:32525 Lake Nakuru isolate 20N1 X92128
D21224.1 gg_id:8975 Moritella japonica str. DSK1 D21224
AF530133.1 gg_id:70982 Moritella sp. str. MGP-6 AF5301
AJ132226.1 gg_id:8977 Moritella viscosa str. NVI 88/478T AJ1322
AB189343.1 gg_id:112983 cold seep sediment clone JT58-18 AB1893
AJ297540.1 gg_id:48310 Moritella marina str. NCIMB 2263 AJ2975
AY700605.1 gg_id:109434 Australia: Great Barrier Reef clone PDA-OTU7 AY7006
AB183504.1 gg_id:105913 Moritella sp. str. 47A1 AB1835
AB008797.1 gg_id:8989 Moritella yayanosii str. DB21MT-5 AB0087
AY382585.1 gg_id:96373 Moritella sp. str. 2-2-2-1 AY3825
AB038033.1 gg_id:33284 Moritella marina str. ATCC15381T AB0380
NR_025380.1 gg_id:573974 Moritella abyssi str. 2693; JCM 11436 NR_025
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AB183499.1 gg_id:101616 Moritella sp. str. 38C1 AB1834
AB183496.1 gg_id:101122 Moritella sp. str. 36C1 AB1834
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AB013842.1 gg_id:8994 Shewanella sp. 7-1.E AB0138
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CR954246.1 gg_id:140486 Pseudoalteromonas haloplanktis str. TAC125 CR9542
CR954246.1 gg_id:140406 Pseudoalteromonas haloplanktis str. TAC125 CR9542
AY040230.1 gg_id:21879 Pseudoalteromonas translucida str. KMM520 AY0402
AF316144.1 gg_id:52879 Pseudoalteromonas issachenkonii str. KMM 3549; F13 AF3161
EU880522.1 gg_id:351145 Pseudoalteromonas elyakovii str. P18 EU8805
AF316142.1 gg_id:37455 Pseudoalteromonas issachenkonii str. KMM 3558; F2 AF3161
FJ457238.1 gg_id:568943 Pseudoalteromonas luteoviolacea str. S4060 FJ4572
FJ952795.1 gg_id:446774 Pseudoalteromonas sp. str. 1tc11 FJ9527
FJ200646.1 gg_id:308744 Pseudoalteromonas haloplanktis str. I 6 FJ2006
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FJ362488.1 gg_id:360655 Pseudoalteromonas sp. str. 4-9-11-2
FJ200651.1 gg_id:309736 Pseudoalteromonas porphyrae str. I 85
AF475096.1 gg_id:42828 Pseudoalteromonas porphyrae str. Q-1-6
DQ531952.1 gg_id:161487 Pseudoalteromonas sp. str. MJ5322
X82147.1 gg_id:8972 Pseudoalteromonas rubra str. ATCC 29570T
FJ457188.1 gg_id:539701 Pseudoalteromonas rubra str. S2676
FJ457197.1 gg_id:559457 Pseudoalteromonas ruthenica str. S2756
NZ_AAOH01000015.1 gg_id:156459 Pseudoalteromonas tunicata str. D2
AF295593.1 gg_id:19424 Pseudoalteromonas sp. str. ACEM-4
Z25522.1 gg_id:8973 Pseudoalteromonas tunicata str. D2
FJ497712.1 gg_id:590855 Pseudoalteromonas sp. str. VS-105
EU330355.1 gg_id:238270 Pseudoalteromonas sp. str. BSi20440
EU330364.1 gg_id:249895 Pseudoalteromonas sp. str. BSi20654
AJ874344.1 gg_id:110410 Pseudoalteromonas atlantica str. 01/110
EF673282.1 gg_id:249648 Pseudoalteromonas sp. str. BSi20628
U85855.1 gg_id:8913 Pseudoalteromonas prydzensis str. MB8-11
FJ952812.1 gg_id:419834 Pseudoalteromonas sp. str. 2ta8
DQ218321.1 gg_id:139718 Pseudoalteromonas sp. str. EBD
DQ492780.1 gg_id:157463 Pseudoalteromonas sp. str. BSi20598
AF366042.1 gg_id:27905 marine str. BB2AT2
DQ520891.1 gg_id:161179 Pseudoalteromonas sp. str. BSi20526
DQ985065.1 gg_id:177202 Pseudoalteromonas sp. str. JL1130
AF529062.1 gg_id:60988 Pseudoalteromonas citrea str. CIP 105339
AM111083.1 gg_id:140836 Pseudoalteromonas sp. str. 8049
X82139.1 gg_id:8918 Pseudoalteromonas tetraodonis str. IAM 14160T
EF551372.1 gg_id:220500 Pseudoalteromonas sp. str. BSw20508
FJ457152.1 gg_id:546070 Pseudoalteromonas sp. str. S1610
FJ200640.1 gg_id:341432 Pseudoalteromonas agarivorans str. C 36
AB231330.1 gg_id:137602 Pseudoalteromonas viridis str. G-1387 (=MBIC03135)
EF584014.1 gg_id:233255 Pseudoalteromonas sp. str. AS1
AM180744.1 gg_id:150838 Pseudoalteromonas citrea UL34
DQ537514.1 gg_id:161414 Pseudoalteromonas haloplanktis str. BSi20545
AM111018.1 gg_id:140829 Pseudoalteromonas sp. str. 7016
AM111094.1 gg_id:140955 Pseudoalteromonas sp. str. 8060
AB457045.1 gg_id:309901 Pseudoalteromonas sp. str. SB-A1
AM111086.1 gg_id:140902 Pseudoalteromonas sp. str. 8052
AM691088.1 gg_id:221420 Pseudoalteromonas carrageenovora str. EG27
AF539773.1 gg_id:84384 Pseudoalteromonas sp. str. E36
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AF082564.1 gg_id:8947 Pseudoalteromonas distincta str. KMM638T
X98336.1 gg_id:8944 Pseudoalteromonas antarctica str. CECT 4664 NF3
FJ457157.1 gg_id:566474 Pseudoalteromonas sp. str. S1688
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EU807989.1 gg_id:310988 Pseudoalteromonas haloplanktis str. AFMB-008041
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FJ040186.1 gg_id:308609 Pseudoalteromonas haloplanktis str. I2
DQ537512.1 gg_id:160870 Pseudoalteromonas elyakovii str. BSi20539
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AJ704790.1 gg_id:103112 Pseudoalteromonas sp. str. ws17
EU240534.1 gg_id:349996 Pseudoalteromonas viridis str. P1
AJ417594.1 gg_id:46753 Pseudoalteromonas agarivorans str. KMM 255
X82134.1 gg_id:8912 Pseudoalteromonas atlantica str. IAM 12927T
DQ537518.1 gg_id:161195 Pseudoalteromonas haloplanktis str. BSi20594

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FJ457185.1 gg_id:542853 Pseudoalteromonas rubra str. S2472
AF038846.1 gg_id:8907 Pseudoalteromonas gracilis str. B9
X82136.1 gg_id:8908 Pseudoalteromonas carrageenovora str. ATCC 12662T
FJ200644.1 gg_id:336893 Pseudoalteromonas elyakovii str. C 102
AY771728.1 gg_id:141235 Pseudoalteromonas nigrifaciens S3-28
DQ492775.1 gg_id:158978 Pseudoalteromonas sp. str. BSi20576
EF584090.1 gg_id:234336 Pseudoalteromonas sp. str. VHOS1
AM110980.1 gg_id:140920 Pseudoalteromonas sp. str. 3025
AF354597.1 gg_id:19398 marine clone Arctic96B-17
DQ005900.1 gg_id:130450 Pseudoalteromonas rubra str. C312
AY864628.1 gg_id:111346 Pseudoalteromonas sp. str. U50
DQ665793.1 gg_id:173097 Pseudoalteromonas elyakovii str. BSi20460
NC_007481.1 gg_id:140750 Pseudoalteromonas haloplanktis str. TAC125
AM111017.1 gg_id:140854 Pseudoalteromonas sp. str. 7015
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EF551371.1 gg_id:221998 Pseudoalteromonas sp. str. BSw20507
AM111034.1 gg_id:140870 Pseudoalteromonas sp. str. 7038
FJ200648.1 gg_id:350574 Pseudoalteromonas marina str. I 17
DQ492816.1 gg_id:157558 Pseudoalteromonas sp. str. BR003
AB257325.2 gg_id:180592 Pseudoalteromonas tetraodonis str. Do-17
EU849123.1 gg_id:348634 Pseudoalteromonas sp. str. LP621
AY682201.1 gg_id:107552 Pseudoalteromonas chazhmella str. R10SW10
DQ517879.1 gg_id:161373 Pseudoalteromonas elyakovii str. BSi20670
AB518970.1 gg_id:543117 Pseudoalteromonas sp. str. MB55
DQ492738.1 gg_id:158140 Pseudoalteromonas sp. str. BSi20316
AF313497.1 gg_id:111481 Pseudoalteromonas sp. str. A3
DQ923439.1 gg_id:187538 Pseudoalteromonas sp. W-5
AB257336.2 gg_id:182468 Pseudoalteromonas mariniglutinosa str. Do-52
AM110978.1 gg_id:140823 Pseudoalteromonas sp. str. 3023
EU330366.1 gg_id:235804 Pseudoalteromonas sp. str. BSi20411
AM111090.1 gg_id:140875 Pseudoalteromonas sp. str. 8056
AM110975.1 gg_id:140860 Pseudoalteromonas sp. str. 3020
NR_026222.1 gg_id:543735 Pseudoalteromonas nigrifaciens str. NCIMB 8614
AF045560.1 gg_id:8946 Pseudoalteromonas antarctica str. N-1
AB457051.1 gg_id:346476 Pseudoalteromonas sp. str. SB-E1
FJ200643.1 gg_id:320146 Pseudoalteromonas marina str. C 90
AJ507251.1 gg_id:59526 Pseudoalteromonas mariniglutinosa str. KMM 3635
FJ172090.1 gg_id:348422 Pseudoalteromonas sp. str. SBC7

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DQ492784.1 gg_id:158866 Pseudoalteromonas sp. str. BSi20612 DQ492
AY563031.1 gg_id:100315 Pseudoalteromonas marina str. Mano4 AY5630
AB049728.1 gg_id:51317 Pseudoalteromonas atlantica str. AR06 AB0497
DQ011614.1 gg_id:125030 Pseudoalteromonas ganghwensis str. FR1302 DQ011
FN554588.1 gg_id:566577 Pseudoalteromonas sp. str. HL4 FN5545
AM111074.1 gg_id:140761 Pseudoalteromonas sp. str. 8039 AM111
FJ425222.1 gg_id:367067 Pseudoalteromonas sp. str. K1-14 FJ4252
AF173963.1 gg_id:18661 Pseudoalteromonas atlantica str. KT0910 AF1739
DQ787199.1 gg_id:165819 Pseudoalteromonas arctica str. 37-1-2 DQ787
DQ492758.1 gg_id:157718 Pseudoalteromonas sp. str. BSi20343 DQ492
AM111078.1 gg_id:140967 Pseudoalteromonas sp. str. 8043 AM111
AF043742.1 gg_id:22902 Pseudoalteromonas distincta str. KMM 638T; ATCC700518 AF0437
FJ202088.1 gg_id:326316 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2020
EU050781.1 gg_id:246147 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_02_66 EU0507
FJ403097.1 gg_id:359108 Disease- changes healthy and diseased colonies Caribbean coral Montastrea faveolat FJ4030
EU930871.1 gg_id:342076 Pseudoalteromonas sp. str. KDW4 EU9308
EF101548.1 gg_id:192719 Psychromonas arctica str. KOPRI24930 EF1015
AB365349.1 gg_id:275002 Psychromonas heitensis str. 04HE-4-40 (= MBIC 08331) AB3653
NZ_AAQS01000017.1 gg_id:160611 Psychromonas ingrahamii str. 37 NZ_AA
U14582.1 gg_id:9115 gas vacuolate str.90-P<gv>1 U14582
AJ969456.1 gg_id:157483 Microbial black smoker s Mid Atlantic Ridge ecological implications rock fragments ch AJ9694
AF374385.1 gg_id:38990 Psychromonas arctica str. Pull 5.3 AF3743
AY548987.2 gg_id:99098 marine bone clone sacC3D3 AY5489
U85849.1 gg_id:9117 Psychromonas sp. str. IC004 U85849
AB304804.1 gg_id:236309 Psychromonas sp. str. JAMM 0394 AB3048
DQ009471.1 gg_id:126016 bacterioplankton clone SPOTSMAY03_890m29 DQ009
AB374544.1 gg_id:264272 Psychromonas sp. str. J42-3A AB3745
U73722.1 gg_id:9120 gas vacuolate str. 174 U73722
DQ027056.1 gg_id:133700 Psychromonas sp. str. CNPT3 DQ027
AB304807.1 gg_id:252707 Psychromonas sp. str. JAMM 0700 AB3048
AY167326.1 gg_id:81340 Psychromonas sp. str. ANT9265 AY1673
AJ519627.1 gg_id:76528 uranium mill tailings soil clone Sh765B-TzT-48 AJ5196
AF235108.1 gg_id:71948 Alteromonas sp. str. KT1114 AF2351
DQ530480.1 gg_id:166114 Psychromonas sp. str. gape-82 DQ530
AJ416756.1 gg_id:25724 Psychromonas profunda str. 2825 AJ4167
FM994680.1 gg_id:561093 gill and deep-sea limpet Pectinodonta sp. digestive tract host on sunken wood deptl FM994
EF542799.1 gg_id:224364 Shewanella algae str. YJ06114 EF5427

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AB201780.1 gg_id:138170 Shewanella kaireiae str. c952
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AF145921.1 gg_id:9077 Shewanella japonica str. KMM 3299
CP000851.1 gg_id:249615 Shewanella pealeana str. ATCC 700345
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CP000821.1 gg_id:253801 Shewanella sediminis str. HAW-EB3
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AF136392.1 gg_id:137029 Shewanella sp. str. ANA-3
NZ_AAUO01000015.1 gg_id:183742 Shewanella woodyi str. ATCC 51908

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AF005255.1 gg_id:9108 Shewanella putrefaciens str. MR-30 AF005
AF170300.1 gg_id:70300 Shewanella putrefaciens str. IR-1 AF170
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AF039055.1 gg_id:9060 Shewanella oneidensis str. SP-22 AF039
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AM269901.1 gg_id:159850 Shewanella sp. str. ES-5 AM269
AM180742.1 gg_id:146524 Shewanella gaetbuli UL19 AM180
DQ537513.1 gg_id:161502 Shewanella frigidimarina str. BSi20544 DQ537
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AF022402.1 gg_id:9027 Shewanella sp. ANG.209 str. ANG.strain 209 ANG.209 AF0224
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EF584058.1 gg_id:234701 Shewanella sp. str. HE5 EF5840
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DQ307731.1 gg_id:147165 Shewanella putrefaciens str. Hac411 DQ307
AF387347.1 gg_id:33931 Shewanella oneidensis str. DML7 AF3873
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AB205567.1 gg_id:114271 Shewanella colwelliana str. Q-06 AB205
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DQ514298.1 gg_id:160423 Shewanella frigidimarina str. BSs20181 DQ514
AB204519.1 gg_id:137352 Shewanella pneumatophori str. SCRC-2738 AB204
AF132878.1 gg_id:38945 Shewanella frigidimarina str. ACAM 557 AF1328
EU290154.1 gg_id:256999 Shewanella marinus str. C4 EU290
DQ167234.1 gg_id:139040 Shewanella sp. str. HJ039 DQ167
DQ520894.1 gg_id:159825 Shewanella frigidimarina str. BSi20531 DQ520
EF105397.1 gg_id:179131 Shewanella sp. str. IE9-1 EF1053
AJ288152.1 gg_id:22553 Shewanella sp. Bok-1-30-2 AJ2881
DQ351772.1 gg_id:147472 Microbial Adherent Sediment Particles Heavy Metal Contaminated North Sea Surfac DQ351
EU427307.1 gg_id:265579 Shewanella sp. MSI04 EU4273
FJ169987.1 gg_id:323759 Shewanella sp. str. E505-14 FJ1699
CP001252.1 gg_id:527693 Shewanella baltica str. OS223 CP0012
EF584096.1 gg_id:231545 Shewanella sp. str. WA3 EF5840
FM887036.1 gg_id:459403 Shewanella sp. str. JC19 FM887
U85905.1 gg_id:137215 Shewanella frigidimarina str. ACAM 588 ICP4 U85905
AJ288153.1 gg_id:19933 Shewanella sp. SK-3-30-1 AJ2881
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EF584069.1 gg_id:231993 Shewanella sp. str. LS9 EF5840
AB201782.1 gg_id:137622 Shewanella sedimentalis str. d943 AB2017
NC_009997.1 gg_id:238071 Shewanella baltica str. OS195 NC_009
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U91552.1 gg_id:9070 Shewanella putrefaciens str. F137 U91552
AF011335.1 gg_id:9032 Shewanella pealeana str. ANG-SQ1 AF0113
CP000931.1 gg_id:270483 Shewanella halifaxensis str. HAW-EB4 CP0009
GU362097.1 gg_id:575055 Shewanella sp. str. KTSW-7 GU362
EU073095.1 gg_id:335676 Shewanella sp. str. TS29 EU0730
AF039054.1 gg_id:24664 Shewanella oneidensis str. SP-7 AF0390
EU434392.1 gg_id:260399 Shewanella putrefaciens str. a324 EU4343
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EU180603.1 gg_id:242880 Shewanella putrefaciens str. S002 EU1806
GU289647.1 gg_id:586719 Shewanella sp. str. MEBiC05444T GU289
AF295592.1 gg_id:52642 Shewanella olleyana str. ACEM-9 AF2955
AB306516.1 gg_id:247972 Shewanella sp. str. MIB015 AB3065
AM990834.1 gg_id:278789 Shewanella sp. MOLA 59 AM990
AY170366.1 gg_id:69757 Shewanella waksmanii str. KMM 3823 AY1703
EU000237.1 gg_id:309277 Shewanella donghaensis str. KOPRI_22224 EU000
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AF173966.1 gg_id:54246 Shewanella baltica str. KT0246 AF173
AB094597.1 gg_id:83672 Shewanella surugaensis str. c959 AB094
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AY351983.1 gg_id:92948 Shewanella affinis str. KMM 3587 AY351
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NC_009831.1 gg_id:246705 Shewanella sediminis str. HAW-EB3 NC_00
AB013839.1 gg_id:9017 Shewanella sp. 3-8.C AB013
NR_025934.1 gg_id:540854 Cardiobacterium hominis str. 6573; ATCC 15826 NR_02
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DQ645464.1 gg_id:160756 Cardiobacterium valvarum VA1941 DQ645
CP000513.1 gg_id:226003 Dichelobacter nodosus str. VCS1703A CP000
AJ717394.1 gg_id:149350 Suttonella ornithocola str. B6/99/2 AJ717
X92131.1 gg_id:46026 Lake Elmenteita isolate 2E1 X92131
AF384209.1 gg_id:25151 Chromatium sp. str. NZ AF384
AM712619.1 gg_id:237043 Allochromatium phaeobacterium str. JA144 AM712
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NR_025315.1 gg_id:559119 Chromatium okenii str. DSM 169 NR_02
FJ437816.1 gg_id:541203 Benthic okenone production Fayetteville New York Green Lake chemocline 20.5 m wa FJ4378
AB478662.1 gg_id:548000 SSU sequences Alps Cadagno di Fuori submerged biofilm mats montane wetland clo AB478
DQ330802.1 gg_id:159452 Guerrero Negro hypersaline microbial mat clone 02D2Z45 DQ330
AJ223235.1 gg_id:7564 Lamprocystis purpurea str. DSM 4197 AJ2232
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AM941379.1 gg_id:304631 Marichromatium indicum str. JA210 AM941
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AM941377.1 gg_id:325577 Marichromatium indicum str. JA214 AM941
AM941046.1 gg_id:369706 Marichromatium indicum JA347 AM941
AJ889020.1 gg_id:112951 Marichromatium chilcum str. CH8 AJ889
FJ376391.1 gg_id:360805 Marichromatium purpuratum str. DSM 1711 FJ3763
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AF508991.1 gg_id:71278 Nitrosococcus oceani str. SWC19 AF508

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AJ298748.1 gg_id:77717 Nitrosococcus halophilus AJ2987
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AF112999.1 gg_id:7533 Thiocapsa roseopersicina str. M11 AF1129
AM779060.1 gg_id:261543 Thiocapsa subramanianii str. JA146 AM779
AJ581994.1 gg_id:141744 Thiocapsa marina str. BM-3 AJ5819
AF112998.1 gg_id:7532 Thiocapsa roseopersicina str. 5811 AF1129
EF581005.1 gg_id:278653 Thiocapsa roseopersicina str. KS1 EF5810
AJ277022.1 gg_id:71426 Thiococcus sp. str. A31 AJ2770
Y12373.3 gg_id:71248 Thiococcus pfennigii str. 4250 Y12373
FN293055.1 gg_id:570678 Thiococcus pfennigii str. 4252 = DSM 228 FN2930
FN293058.1 gg_id:536936 Thiocystis gelatinosa str. 4310 = DSM 215 FN2930
D50655.1 gg_id:7517 Thiocystis gelatinosa D50655
AJ224438.1 gg_id:7518 Thiocystis violascens str. DSM 168T AJ2244
EF149014.1 gg_id:188673 Thiocystis sp. str. Mog3 EF1490
AM086640.1 gg_id:139588 Thiocystis sp. str. 448.10 AM086
AJ971090.1 gg_id:172979 Thiorhodococcus mannitophagus str. WS AJ9710
Y11316.1 gg_id:7526 Thiorhodococcus minor str. CE2203 Y11316
AM748925.1 gg_id:245986 Thiophaeococcus mangrovi str. JA304 AM748
AB016986.1 gg_id:7570 Thiorhodovibrio winogradskyi str. MBIC2776T AB0169
AB294924.1 gg_id:225518 -dependent & analyses hydrothermal system off Taketomi Island Japan microbial ma AB2949
DQ867045.1 gg_id:196530 Microbial and methanogenic potential temperature water Japan natural gas field clo DQ867
FJ535065.1 gg_id:545461 microbial colonizing walls Karstic Slovenia cave wall biofilm clone 2PJM13 FJ5350
AF420353.1 gg_id:55790 hydrothermal sediment clone AF420353 AF4203
DQ811841.1 gg_id:166871 mangrove soil clone MSB-4C11 DQ811
DQ395021.1 gg_id:152376 harbor sediment clone VHS-B5-48 DQ395
FJ712412.1 gg_id:516020 and Archaea Gas Hydrate Sediments (East Sea) Kazan Mud Volcano Anaximander Mo FJ7124
AY225634.1 gg_id:95183 Mid-Atlantic Ridge hydrothermal sediment clone AT-s26 AY2256
EU373841.1 gg_id:265007 southern Cretan margin (eastern Mediterranean Sea) canyon and slope sediment clo EU3738
AM882514.1 gg_id:309379 Structure along hydrocarbon contamination coastal sediment oil polluted water pet AM882
GU369919.1 gg_id:524281 and mats vents Arc white microbial film on pebble aphotic zone shal hydrothermal v GU369
FJ203535.1 gg_id:340951 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h FJ2035
EU617747.1 gg_id:337743 Seasonal variation microbial Yel Sea sediment clone C13S-68 EU617
FM877665.1 gg_id:362822 Microbial several mining wastes Bulgaria vicinity uranium mine Sliven clone Sliv-109 FM877
DQ499304.1 gg_id:159535 acidic cave snottite biofilm clone CV55 DQ499
EU050785.1 gg_id:254811 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_01_66 EU050
GU061986.1 gg_id:593500 and function microbial mesoscale eddy perturbations South China Sea clone S-DCM- GU061
AY225631.1 gg_id:96909 Mid-Atlantic Ridge hydrothermal sediment clone AT-s2-13 AY2256
EU652572.1 gg_id:278349 Seasonal variation microbial Yel Sea sediment clone B8S-132 EU6525
DQ269059.1 gg_id:182899 marine macro-alga surface clone UA09 DQ269

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AY592343.1 gg_id:99715 deep-sea mud volcano clone Amsterdam-1B-40; BC20-1B-40 AY5923
FJ712551.1 gg_id:519028 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) k FJ7125
AY796036.1 gg_id:108755 gold mine bore hole clone 47mm23 AY7960
EU700150.1 gg_id:298462 Study on Shantou Bay Marine Sediments Microorganisms sediment clone STU8 EU7001
FJ545527.1 gg_id:533202 Diveristy Seawater and Sediment Northern North Yel Sea seawater clone W1-36 FJ5455
DQ289941.1 gg_id:173031 Microbial Carbon and Nitrogen Cycling Sediments South Atlantic Bight Permeable Sh DQ289
AY225628.1 gg_id:96854 Mid-Atlantic Ridge hydrothermal sediment clone AT-s3-68 AY2256
EF644798.1 gg_id:299470 genes and citrate lyase deep-sea microbial MAR Logatchev hydrothermal vent syster EF6447
EU491553.1 gg_id:268415 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR4C EU4915
DQ303270.1 gg_id:141619 Microbial ecology macroscopic filaments extreme Tinto River acidic river clone fa7 DQ303
GU061300.1 gg_id:574531 Evaluation culturing methods cultivate previously Yel Sea intertidal beach seawater GU061
DQ394966.1 gg_id:153375 harbor sediment clone VHS-B3-85 DQ394
FN396767.1 gg_id:555049 constant flux thermophilic cold seabed Arctic marine surface sediment clone s5_8_I_ FN3967
FJ484458.1 gg_id:553048 microbial autonomous rover world's deepest phreatic sinkhole wall biomat El Zacator FJ4844
DQ351781.1 gg_id:147516 Microbial Adherent Sediment Particles Heavy Metal Contaminated North Sea Surfac DQ351
AM040135.1 gg_id:145316 sandy sediments clone Sylt 39 AM040
GQ351146.1 gg_id:586541 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Eastern GQ351
EF646139.1 gg_id:247661 Potential interactions particle- anammox and archaeal partners namibian Namibian u EF6461
FJ205341.1 gg_id:551312 Prokaryotic deep-sea hydrothermal region East Lau Spreading Centre deep marine se FJ2053
AM889168.1 gg_id:584938 structure superficial sediments Bizerte (Tunisia) southern Mediterranean coastal an AM889
FM877664.1 gg_id:367915 Microbial several mining wastes Bulgaria vicinity uranium mine Sliven clone Sliv-80 FM877
FJ529318.1 gg_id:512678 Evidence vertical transmission symbionts adult embryo Caribbean sponge Svenzea ze FJ5293
AB099937.1 gg_id:79212 inactive deep-sea hydrothermal vent chimneys clone IheB2-13 AB0999
DQ469234.1 gg_id:158638 Microbial and ecology water Zhong Tiaoshan mine Shanxi province China AMD clone DQ469
GU118309.1 gg_id:589714 Threatened Corals Provide Microbial Habitats clone Dstr_I04 GU118
EU801093.1 gg_id:336892 It's all ranking aquatic Delaware Bay NJ clone 2C229409 EU8010
FJ205285.1 gg_id:564511 Prokaryotic deep-sea region East Lau Spreading Centre active hydrothermal field sedi FJ2052
DQ833482.1 gg_id:164256 detected analyses depth sediment Guanting Reservoir clone 35-8 DQ833
AJ536881.1 gg_id:78477 uranium waste soil clone JG30-KF-AS32 AJ5368
DQ234241.2 gg_id:143226 determined library mangrove clone DS159 DQ234
EF613006.1 gg_id:234358 acid mine drainage clone YSK16S-43 EF6130
FJ535355.1 gg_id:556389 Granulosicoccus sp. str. Z271 FJ5353
EU394558.1 gg_id:342967 Coccolithophore bloom dynamics shape (NE-Atl) northern Bay Biscay pelagic free-livi EU3945
EU439003.1 gg_id:540861 symbiont EU4390
FJ228294.1 gg_id:324503 sulfate-reducing enriched during bioremediation experiment sediments (Brandenburg FJ2282
DQ070793.1 gg_id:147722 Prokaryotic Structures Seafloor Basalts Varying Age and Juan de Fuca Ridge basalt gl DQ070
DQ396312.1 gg_id:154441 deep-sea octacoral clone ctg_NISA188 DQ396
EU491600.1 gg_id:270104 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU4916
EU617752.1 gg_id:341837 Seasonal variation microbial Yel Sea sediment clone C13S-45 EU6177
EU491687.1 gg_id:276375 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU4916

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GU208368.1 gg_id:577626 Study on Sediment Dongping Lake sediment clone Td1-10 GU208
FM213426.1 gg_id:354483 Chemosynthetic Bivalvia species mud volcanoes Gulf Cadiz host gill tissue clone Mer FM213
EU491699.1 gg_id:268263 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU491
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DQ396273.1 gg_id:156456 deep-sea octacoral clone ctg_NISA021 DQ396
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DQ070809.1 gg_id:149398 Prokaryotic Structures Seafloor Basalts Varying Age and Juan de Fuca Ridge basalt gl DQ070
DQ289928.1 gg_id:168507 Microbial Carbon and Nitrogen Cycling Sediments South Atlantic Bight Permeable Sh DQ289
EU491667.1 gg_id:262608 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU491
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AY532575.1 gg_id:106089 uranium-contaminated aquifer clone 1013-28-CG34 AY532
EF612420.1 gg_id:244634 historic semiarid lead-zinc site mine tailings clone K6-C62 EF6124
EU246808.1 gg_id:241908 polyphasic description Pocillopora meandrina Palmyra Atoll Calcinus obscurus abdon EU246
EU735667.1 gg_id:307033 archaeal structures oil contaminated and soils China pristine soil Jidong Oilfield clone EU735
FJ535071.1 gg_id:571233 microbial colonizing walls Karstic Slovenia cave wall biofilm clone 3PJM14 FJ5350
DQ811846.1 gg_id:165797 mangrove soil clone MSB-4G2 DQ811
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FM877661.1 gg_id:357872 Microbial several mining wastes Bulgaria vicinity uranium mine Sliven clone Sliv-13 FM877
EU491253.1 gg_id:274139 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak EU491
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GU198380.1 gg_id:546867 Metagenomic denitrifying sulfur-oxidizing consortium enriched marine sediment clo GU198
FJ205202.1 gg_id:563890 Prokaryotic deep-sea region East Lau Spreading Centre inactive hydrothermal field se FJ2052
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DQ269101.1 gg_id:180233 marine macro-alga surface clone DPC112 DQ269
GQ495417.1 gg_id:575230 terrestrial volcanic rocks Iceland Hnausahraun lava f clone Bas-7-60 GQ495
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EU700176.1 gg_id:296708 Study on Shantou Bay Marine Sediments Microorganisms sediment clone STU34 EU700
EU800034.1 gg_id:307663 It's all ranking aquatic Newport Harbour RI clone 1C227721 EU800
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FJ712427.1 gg_id:519729 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) K FJ7124
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EU491103.1 gg_id:271777 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak EU491
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GQ348554.1 gg_id:554477 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ348
GQ866093.1 gg_id:553108 Seasonal changes Norway lobster (Nephrops norvegicus) gut clone F1-2 GQ866
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FJ497646.1 gg_id:587676 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun FJ4976
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EU491843.1 gg_id:260428 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU491
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AM086641.1 gg_id:139719 Thiocystis sp. str. H1.1 AM086
EF644807.1 gg_id:297894 genes and citrate lyase deep-sea microbial MAR Logatchev hydrothermal vent syster EF6448
DQ431906.1 gg_id:213821 microorganisms catalyzing nitrogen removal and organic matter metabolism perme DQ431
FN397816.1 gg_id:429948 geomicrobiological investigation sediments Gulf Cadiz GeoB 9072-1 anoxic sub-surfa FN3978
GQ246407.1 gg_id:551973 Temporal and spatial China North Yel Sea sediments clone Ld1-12 GQ246
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AM997582.1 gg_id:542870 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A AM997
AM882565.1 gg_id:312010 Structure along hydrocarbon contamination coastal sediment oil polluted water pet AM882
FJ437960.1 gg_id:512465 Benthic okenone production Fayetteville New York Green Lake surface sediments 16. FJ4379
GU454932.1 gg_id:530809 Understanding short-chain fatty acids accumulation enhanced alkaline digestion: kir GU454
DQ498828.1 gg_id:160903 Thiocapsa sp. str. SC5 DQ498
EF125462.1 gg_id:177523 mangrove soil clone MSB-2H6 EF1254
EU491333.1 gg_id:261470 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak EU491
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GQ495440.1 gg_id:543963 terrestrial volcanic rocks Iceland Hnausahraun lava f clone Bas-7-84 GQ495
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AF406546.1 gg_id:60630 bacterioplankton clone AEGEAN_245 AF4065
FJ497635.1 gg_id:558137 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun FJ4976
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GQ141761.1 gg_id:435569 Microbial thriving -pH Rincon de la Vieja Volcano National Park Costa Rica superficia GQ141
EF076070.1 gg_id:256660 Sponge- microorganisms: ecology and biotechnological potential Bahamas: Little San EF076
AB426192.1 gg_id:267544 -situ identification study benzene-degrading s under methanogenic condition anaerc AB426
DQ925905.1 gg_id:254195 Microbes and Thermal Gradients Temperature Hydrothermal Chimneys hydrotherm DQ925
GQ406158.1 gg_id:593544 Benthic submerged sinkhole ecosystems sediment clone TS-45-9 GQ406
EF654696.1 gg_id:242116 mixed granule anammox reactor clone KIST-JJY027 EF6546
U24110.1 gg_id:7550 Gamma-proteobacterial endosymbiont U2411
DQ408758.1 gg_id:241921 endosymbionts gutless marine nematode Astomonema sp. sediments coral reef sed DQ408
EU555131.1 gg_id:265444 Microbial Sulfide Hydrothermal Vent Field Juan de Fuca Ridge Dudley hydrothermal EU555
DQ925881.1 gg_id:242627 Microbes and Thermal Gradients Temperature Hydrothermal Chimneys hydrotherm DQ925
EF125401.1 gg_id:193004 soil naked tidal flat sediment near mangrove clone MSB-1D8 EF1254
AB100006.1 gg_id:79132 inactive deep-sea hydrothermal vent chimneys clone IndB3-17 AB100
AM882566.1 gg_id:314376 Structure along hydrocarbon contamination coastal sediment oil polluted water pet AM882
EU050809.1 gg_id:253074 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_01_83 EU0508
AJ006212.1 gg_id:7572 Lamprocystis purpurea str. ML1 AJ0062
AB252426.1 gg_id:153466 Microbial extremely CO2 rich deep-sea sediment Marine sediments Yonaguni Knoll I' AB2524
EU491139.1 gg_id:272596 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak EU491
AB294972.1 gg_id:225408 -dependent & analyses hydrothermal system off Taketomi Island Japan microbial ma AB2949
DQ458038.1 gg_id:157435 acid mine drainage clone DX41 DQ458
AM282561.1 gg_id:193170 Thiorhodococcus kakinadaii str. JA130 AM282
AACY01032263.1 gg_id:105207 Sargasso Sea AACY0
EU491349.1 gg_id:260349 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X3 clone EU491
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AM997970.1 gg_id:541611 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A AM997
EU491101.1 gg_id:271612 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak EU491
EF208706.1 gg_id:202468 Vertical and horizontal structure microbial sandy carbonate sediment clone CI75cm.2 EF2087
EU617749.1 gg_id:332804 Seasonal variation microbial Yel Sea sediment clone D13S-16 EU617
NR_029333.1 gg_id:589849 Thiocystis violacea str. N. Pfennig 2711; DSM 207 NR_02
DQ676383.1 gg_id:219789 Archaeal sediment and plankton freshwater pond suboxic freshwater-pond clone M DQ676
EU491810.1 gg_id:261375 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU4918
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AJ002796.2 gg_id:7556 Thiohalocapsa halophila str. SG3202 AJ0027
DQ330805.1 gg_id:159272 Guerrero Negro hypersaline microbial mat clone 02D2Z63 DQ330
EU236358.1 gg_id:295840 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg91C2 EU2363
FM242313.1 gg_id:328728 sequences sediment clone 25 T9d-oil FM242
FJ264656.1 gg_id:346479 Manganese and Iron Dependent Anaerobic Oxidation Methane methane seep sedime FJ2646
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AJ620507.1 gg_id:108086 Olavius crassitunicatus endosymbiont AJ6205
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AY953181.1 gg_id:114439 anaerobic swine lagoon clone B-1O AY953

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AJ404006.1 gg_id:67655 Thiobaca trueperi str. BCH AJ4040
AF468306.1 gg_id:80943 Arctic sea ice; northern Fram Strait clone ARKICE-74 AF4683
EU035919.2 gg_id:305967 Insight microbial structure Norwegian deep-water Desmacidon sponge deep-sea cor EU0359
FM242312.1 gg_id:323358 sequences sediment clone 62 T9d-oil FM242
AY225632.1 gg_id:98768 Mid-Atlantic Ridge hydrothermal sediment clone AT-s3-1 AY2256
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AM176876.1 gg_id:160373 Recovery mangrove sediment clone SZB80 AM176
EF157171.1 gg_id:246738 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon EF1571
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AB247483.1 gg_id:149328 lab-scale EBPR sludge clone Run-SP84 AB2474
DQ834966.1 gg_id:239144 Methylohalomonas lacustra DQ834
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EU734910.1 gg_id:313480 assemblages sediment station DBSE Northern Bering Sea clone 001A1 EU7349
AJ620498.1 gg_id:353788 Olavius 1 endosymbiont O. ilvae Individual 2 AJ6204
FJ971729.1 gg_id:415655 microbial autrotrophic denitrification granular sludge clone R1-B5 FJ9717
FM955329.1 gg_id:546246 nematodes marine sediment FM955
AM282559.1 gg_id:192789 Thiorhodococcus bheemlicum str. JA132 AM282
DQ408757.1 gg_id:211956 morphological between endosymbionts and marine nematode Astomonema sp. Bal DQ408
EU617748.1 gg_id:327160 Seasonal variation microbial Yel Sea sediment clone D13S-78 EU617
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EF999974.1 gg_id:245668 Thiodictyon bacillosum str. DSM 234T EF9999
FJ712507.1 gg_id:529626 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) K FJ7125
EF999973.1 gg_id:257959 Thiodictyon elegans str. DSM 232T EF9999
AB186842.1 gg_id:103037 polychlorinated dioxin dechlorinating microcosm clone TSBX13 AB1868
GQ249599.1 gg_id:509542 Microbial anaerobic sediments Bay Cadiz (Spain) marine sediment: 12-14 cm layer cl GQ249
GQ347493.1 gg_id:540052 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ347
AF223299.1 gg_id:31454 marine sediment clone B2M60 AF2232
EU652571.1 gg_id:279434 Seasonal variation microbial Yel Sea sediment clone A8S-46 EU6525
FJ358866.1 gg_id:580890 and redox-stratified sediments marine reef sandy sediment clone OX79 FJ3588
FJ264672.1 gg_id:348014 Manganese and Iron Dependent Anaerobic Oxidation Methane methane seep sedim FJ2646
DQ867047.1 gg_id:186089 Microbial and methanogenic potential temperature water Japan natural gas field cl DQ867
GQ246364.1 gg_id:593033 Temporal and spatial China North Yel Sea sediments clone Cm1-27 GQ246
GU056102.1 gg_id:571289 Biologic Techniques Applied Microbial Prospecting China: Ban 876 Gas Oil Field Bein GU056
AB530206.1 gg_id:586045 Monitoring Suez and Tokyo bays based on analyses marine sediment clone Tokyo..B AB5302
AB530192.1 gg_id:549648 Monitoring Suez and Tokyo bays based on analyses marine sediment clone Suez..Ba AB5301
DQ269062.1 gg_id:190822 marine macro-alga surface clone DPC061 DQ269
EU134786.1 gg_id:243086 tallgrass prarie soil clone FFCH2627 EU1347

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EU236373.1 gg_id:297512 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg91G3 EU2363
AY225627.1 gg_id:96329 Mid-Atlantic Ridge hydrothermal sediment clone AT-s68 AY2256
FJ497388.1 gg_id:579158 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun FJ4973
EF632940.1 gg_id:242102 Unique microbial contrasting aquatic altitude Andean Altiplano (northern Chile) fresh EF6329
EU491429.1 gg_id:261838 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X4 clone EU4914
DQ811847.1 gg_id:164335 mangrove soil clone MSB-5C2 DQ811
DQ811843.1 gg_id:172303 mangrove soil clone MSB-4E4 DQ811
EF203207.1 gg_id:207236 phylotypes sediments Lake Kastoria Greece sediment clone Kas176B EF2032
FM877666.1 gg_id:366930 Microbial several mining wastes Bulgaria vicinity uranium mine Sliven clone Sliv-112 FM877
AY225635.1 gg_id:98613 Mid-Atlantic Ridge hydrothermal sediment clone AT-s80 AY2256
DQ811842.1 gg_id:171222 mangrove soil clone MSB-4D7 DQ811
AY328773.1 gg_id:88634 drinking water system simulator clone DSSD75 AY3287
DQ351776.1 gg_id:146277 Microbial Adherent Sediment Particles Heavy Metal Contaminated North Sea Surfac DQ351
FJ937836.1 gg_id:397082 Marine Sponge Gelliodes carnosa coastal waters Lingshui Bay Hainan Island South Ch FJ9378
EU236293.1 gg_id:290042 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg9Co20 EU2362
GU208274.1 gg_id:568003 Study on Sediment Dongping Lake sediment clone 6F3-6 GU208
GU118056.1 gg_id:580801 Threatened Corals Provide Microbial Habitats clone Apal_E11 GU118
AB188772.1 gg_id:114044 cold seep sediment clone SB1-7 AB1887
FJ205206.1 gg_id:559269 Prokaryotic deep-sea region East Lau Spreading Centre inactive hydrothermal field se FJ2052
GQ356981.1 gg_id:557781 Metal Dependent Marine Methane Oxidation methane seep sediment clone FeSO4_ GQ356
GU369933.1 gg_id:527507 and mats vents Arc white microbial film on pebble aphotic zone shal hydrothermal v GU369
EF612432.1 gg_id:244758 historic semiarid lead-zinc site mine tailings clone Fe-K6-C35 EF6124
EU491147.1 gg_id:261461 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak EU4911
DQ823153.1 gg_id:167115 Techniques Microbial Studies Oregon Caves National Monument Quad 3 off trail clo DQ823
AB189342.1 gg_id:113899 cold seep sediment clone JT58-17 AB1893
CP000453.1 gg_id:171890 Alkalilimnicola ehrlichei str. MLHE-1 CP0004
AJ404972.1 gg_id:46869 Alkalilimnicola halodurans 34Alc AJ4049
DQ217918.1 gg_id:142576 Alkalispirillum sp. str. AGDZ DQ217
DQ217919.1 gg_id:142198 Alkalispirillum sp. str. ALPs 2 DQ217
EU308278.1 gg_id:358039 Arhodomonas sp. str. 50B226a_1 EU3082
EU653291.1 gg_id:280943 Thiobacillus prosperus str. DSM 5130 EU6532
EU653290.1 gg_id:282074 Thiobacillus prosperus str. V6 EU6532
AY298904.1 gg_id:89646 Ectothiorhodosinus mongolicum str. M9 AY2989
EU590916.1 gg_id:265489 Ectothiorhodospira sp. str. PHS-1 EU5909
AM943124.1 gg_id:556051 Ectothiorhodospira variabilis str. WN21R AM943
AM902494.1 gg_id:571311 Ectothiorhodospira imhoffii str. JA319 AM902
FN293051.1 gg_id:562547 Halorhodospira halophila str. 9622 FN2930
AJ318525.1 gg_id:62637 Halorhodospira neutrophila str. SG 3301 AJ3185
FJ153016.1 gg_id:323860 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX4CI FJ1530
NZ_ABYM01000001.1 gg_id:349593 Thioalkalivibrio sp. str. HL-EbGR7 NZ_AB

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DQ103664.1 gg_id:130099 hypersaline endoevaporitic microbial mat clone E2aA03 DQ103
GU083688.1 gg_id:568686 Microorganism Xiarinur soda lake sediment clone x309 GU083
AF126545.1 gg_id:73895 Thialkalivibrio denitrificans AF126
EU709878.1 gg_id:341189 Thioalkalivibrio sp. HL-EbGR7 str. HL-EbGr7 EU709
AY360060.1 gg_id:93813 Thialkalivibrio thiocyanodenitrificans str. ARhD AY360
EU368849.1 gg_id:260942 Thiohalospira halophila str. HL18 EU368
EU169227.1 gg_id:245592 Thiohalospira alkaliphila str. ALgr 6sp EU169
EU908045.1 gg_id:341286 Thiorhodospira sp. str. SLG EU908
AJ006530.2 gg_id:7548 Thiorhodospira sibirica A12 AJ0065
EF157110.1 gg_id:244243 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon EF1571
EF105756.1 gg_id:202113 microbial two endoevaporitic salt crusts evaporitic crust Lindsey Lake New Mexico cl EF1057
DQ001657.1 gg_id:158793 Microbial seeps asphalt seep clone B91-13 DQ001
AM935440.1 gg_id:539161 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM935
AF339744.1 gg_id:40387 thermal vent clone V3 AF339
FM209168.1 gg_id:543583 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd FM209
AJ581598.1 gg_id:93189 soil near uranium mill tailings clone KCM-B-23 AJ5815
EF157167.1 gg_id:245899 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon EF1571
EU735681.1 gg_id:349780 archaeal structures oil contaminated and soils China pristine soil Jidong Oilfield clone EU735
FM242405.1 gg_id:309866 sequences sediment clone 1 T12d-oil FM242
FM209058.1 gg_id:541794 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd FM209
EF157096.1 gg_id:256594 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon EF1570
AJ581597.1 gg_id:94093 soil near uranium mill tailings clone KCM-B-112 AJ5815
AM935143.1 gg_id:536607 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM935
EF105729.1 gg_id:202055 microbial two endoevaporitic salt crusts evaporitic crust Lindsey Lake New Mexico cl EF1057
FJ152988.1 gg_id:321932 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX4C FJ1529
EF157181.1 gg_id:251900 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon EF1571
FJ153022.1 gg_id:306675 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX4C FJ1530
CU467452.1 gg_id:315091 Prokaryotic Tunisian saltern Saltern solar multipond clone CU467
EF103128.1 gg_id:186404 Natronocella acetinitrilica str. ANL 6-2 EF1031
EF105732.1 gg_id:203311 microbial two endoevaporitic salt crusts evaporitic crust Lindsey Lake New Mexico cl EF1057
DQ001686.1 gg_id:157622 Microbial seeps asphalt seep clone B101-25 DQ001
CU467468.1 gg_id:328117 Prokaryotic Tunisian saltern Saltern solar multipond clone CU467
AF513947.1 gg_id:62495 Ectothiorhodospiraceae clone LA7-B9 AF513
EF157075.1 gg_id:255083 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon EF1570
AB240322.1 gg_id:142319 microbial structure Phragmites rhizosphere biofilm reed bed reactor laboratory clon AB240
AF507818.1 gg_id:62740 Mono Lake at depth 2 m station 6 July 2000 clone ML602J-47 proteobacterium AF507
AM936356.1 gg_id:562653 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM936
EF105746.1 gg_id:203128 microbial two endoevaporitic salt crusts evaporitic crust Lindsey Lake New Mexico cl EF1057
EF157092.1 gg_id:256908 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon EF1570

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AJ294337.1 gg_id:76987 Halothiobacillus hydrothermalis HY-66 AJ2943
AF170419.1 gg_id:19288 Halothiobacillus kellyi str. BII-1 AF1704
EU124668.1 gg_id:242036 Thioalkalibacter halophilus str. ALCO1 EU124
AF173169.1 gg_id:44985 Halothiobacillus neapolitanus str. DSM 581 AF1731
EU196318.1 gg_id:239328 Halothiobacillus sp. NP37 EU1963
EU245085.1 gg_id:256790 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-H1-G02 EU245
EU101029.1 gg_id:246599 Sulfide/oxygen supply ratio predicts outcome competition among sulfur-oxidizing wa EU101
EU101026.1 gg_id:246095 Sulfide/oxygen supply ratio predicts outcome competition among sulfur-oxidizing wa EU101
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AF154088.1 gg_id:7760 hydrocarbon seep clone BPC028 AF154
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EU101080.1 gg_id:251622 Sulfide/oxygen supply ratio predicts outcome competition among sulfur-oxidizing wa EU101
GU196195.1 gg_id:587626 Bioaugmentation improved recovery digesters after toxicant exposure lab-scale ana GU196
AM950234.1 gg_id:554439 Sulphide oxidation elemental sulphur membrane bioreactor: Performance and selec AM950
AB473891.1 gg_id:549132 sequences Cadagno di Fuori biofilm mat alpine wetland varying conductivities clone AB4738
EU037214.1 gg_id:252299 Hot Spring Microbial Mat Khir Ganga India hot spring microbial mat clone MO20 EU037
GU390833.1 gg_id:530086 Dark hot springs: structure biofilms caves Acquasanta Terme (Italy) sulfidic cave stre GU390
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GU196237.1 gg_id:577717 Bioaugmentation improved recovery digesters after toxicant exposure lab-scale ana GU196
EU101158.1 gg_id:236588 Sulfide/oxygen supply ratio predicts outcome competition among sulfur-oxidizing wa EU101
GU390879.1 gg_id:515900 Dark hot springs: structure biofilms caves Acquasanta Terme (Italy) sulfidic cave stre GU390
DQ354745.1 gg_id:154107 subsurface water clone MS149BH1062003_5 DQ354
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EF467492.1 gg_id:214022 situ microelectrode voltammetry sulfur-oxidizing biofilms Frasassi sulfidic cave strear EF4674
DQ459215.1 gg_id:160856 Microbial consortia involved anaerobic degradation unsaturated and saturated LCFA DQ459
EU101162.1 gg_id:245464 Sulfide/oxygen supply ratio predicts outcome competition among sulfur-oxidizing wa EU101
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EU134704.1 gg_id:248771 tallgrass prarie soil clone FFCH11229 EU1347
GQ264259.1 gg_id:513055 Structure Simulated Level Waste Site simulated level waste site clone WW1_b62 GQ264
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EF605262.1 gg_id:262257 Steroidobacter denitrificans str. FS EF6052
EU202849.1 gg_id:313985 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo EU2028

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GQ500734.1 gg_id:593006 Surveys Biofilms and Sediments Mammoth Cave Karst Aquifers Charon's Cascade sa GQ500
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EU542478.1 gg_id:259999 Effects chemical structure concentration on pathways microbial during dechlorinatio EU5424
EF688386.1 gg_id:254180 soil clone F6-105 EF6883
GQ402680.1 gg_id:581215 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
EU202846.1 gg_id:326004 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo EU2028
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DQ984544.1 gg_id:235634 Mt. Nan-Jen soil clone IFD_90 DQ984
AB252886.1 gg_id:172615 Identification Shibayama lagoon Ishikawa Japan iron-oxidation biofilm clone 31 AB2528
EU669610.1 gg_id:320093 soil clone S11-50 EU669
EU150278.1 gg_id:277979 acidobacteria and soil Niwot Ridge LTER clone Ni_D05_SFDN EU150
AY963328.1 gg_id:156500 structures and correlated ecological factors soils two evergreen broad-leaved forests AY9633
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EU786122.1 gg_id:546319 cotton rhizosphere soil clone 3H-18 EU786
GQ094382.1 gg_id:422593 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ094
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EU150277.1 gg_id:277971 acidobacteria and soil Niwot Ridge LTER clone Ni_B09_SFDN EU150
DQ984567.1 gg_id:238284 Mt. Nan-Jen soil clone IFD_18 DQ984
FM200868.1 gg_id:556730 and distinct induced biofilm fouling operated under conditions laboratory-scale men FM200
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GQ214101.1 gg_id:551472 China loess clone P830 GQ214
EU037949.1 gg_id:244526 Metabolic Profiles Microbial Chlorinated Pesticides Contaminated Sites Three Geogr EU037
EF520572.1 gg_id:232138 structure lakes: what controls ? acid-impacted lake clone ADK-MOe02-45 EF5205
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EU193051.1 gg_id:364617 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo EU193
EU104062.1 gg_id:332574 Evidence Comamonadaceae determinants settling performance activated sludge clo EU104
EU409118.1 gg_id:274454 Impacted Mine Drainage Dabaoshan Mining Area mine drainage sediment clone DB EU409
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DQ659217.1 gg_id:225165 acid mine drainage clone DBS-Clone42 DQ659
EU134723.1 gg_id:255115 tallgrass prarie soil clone FFCH7151 EU134
AY221082.1 gg_id:85458 Mammoth Cave clone CCU5 AY221
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FJ672005.1 gg_id:516961 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6720
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EU193057.1 gg_id:366851 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo EU1930
FJ478844.1 gg_id:560106 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4788
AM935088.1 gg_id:545602 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM935
DQ297982.1 gg_id:142342 Microbial hydrocarbon contaminated soil clone UE4 DQ297
AJ582039.1 gg_id:93780 soil near uranium mill tailings clone JG36-GS-61 AJ5820
AY963329.1 gg_id:153003 structures and correlated ecological factors soils two evergreen broad-leaved forests AY9633
EF019218.1 gg_id:209393 aspen rhizosphere clone Elev_16S_386 EF0192
EU403986.1 gg_id:346948 Microbial septic tank effluent and soil biozone infiltrative surface clean water clone (EU4039
AY963404.1 gg_id:156448 structures and correlated ecological factors soils two evergreen broad-leaved forests AY9634
FJ152814.1 gg_id:327382 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX5A_ FJ1528
EU528221.1 gg_id:282013 Seasonal Dynamics Mudflat Mouth Major Kentucky Lake Reservoir Tributary sedime EU5282
DQ984542.1 gg_id:252012 Mt. Nan-Jen soil clone IFD_16 DQ984
GU454892.1 gg_id:532025 Understanding short-chain fatty acids accumulation enhanced alkaline digestion: kir GU454
EU134725.1 gg_id:242587 tallgrass prarie soil clone FFCH10003 EU1347
EU150260.1 gg_id:278275 acidobacteria and soil Niwot Ridge LTER clone Ni_D7P1 EU1502
FJ535069.1 gg_id:542880 microbial colonizing walls Karstic Slovenia cave wall biofilm clone 3PJM137 FJ5350
AB179525.1 gg_id:105999 sedimentary rock clone MIZ34 AB1795
DQ279336.1 gg_id:142645 Dynamic during maturation Tuber magnatum Pico ascoma Xanthomonas clone TM1 DQ279
EF409868.1 gg_id:206356 acid mine drainage clone YSK40-06 EF4098
DQ451502.1 gg_id:156972 forest soil clone FAC63 DQ451
EF516354.1 gg_id:218090 grassland soil clone FCPS764 EF5163
FJ744832.1 gg_id:551627 Transporter genes expressed coastal response dissolved organic carbon surface wate FJ7448
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EU150279.1 gg_id:278427 acidobacteria and soil Niwot Ridge LTER clone Ni_D06_SFDN EU1502
EU193052.1 gg_id:369332 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo EU1930
AM176834.1 gg_id:159956 Recovery mangrove sediment clone SZB11 AM176
GU061304.1 gg_id:576363 Evaluation culturing methods cultivate previously Yel Sea intertidal beach seawater GU061
EU491633.1 gg_id:258366 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU4916
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AY907782.1 gg_id:137174 identification picoplankton contrasting waters Arabian Sea water clone A712005 AY9077
FJ545453.1 gg_id:513570 Diveristy Seawater and Sediment Northern North Yel Sea sediment clone S1-23 FJ5454
EU491448.1 gg_id:261579 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X4 clone EU4914

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GQ246317.1 gg_id:511715 Temporal and spatial China North Yel Sea sediments clone Sd1-36 GQ246
EU491127.1 gg_id:276781 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak EU491
DQ351813.1 gg_id:146081 Microbial Adherent Sediment Particles Heavy Metal Contaminated North Sea Surfac DQ351
FJ202756.1 gg_id:338034 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2027
AJ567537.1 gg_id:90195 deep-sea sediment clone MBMPE11 AJ5675
DQ270631.1 gg_id:142048 hydrothermal carbonate chimney clone LC1446B-88 DQ270
EF125454.1 gg_id:175214 mangrove soil clone MSB-2F9 EF1254
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EU491671.1 gg_id:269207 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU491
EU373852.1 gg_id:265200 southern Cretan margin (eastern Mediterranean Sea) canyon and slope sediment clc EU3738
EU617762.1 gg_id:339270 Seasonal variation microbial Yel Sea sediment clone D13S-135 EU617
AB015576.1 gg_id:7632 deep-sea sediment clone BD6-6 AB015
EU617760.1 gg_id:353103 Seasonal variation microbial Yel Sea sediment clone D13S-8 EU617
FM242213.1 gg_id:305299 sequences sediment clone 305 T0h-oil FM242
FJ203584.1 gg_id:324521 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h FJ2035
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FJ416135.1 gg_id:366945 sediments sediment station NEC5 Northern Bering Sea clone 140J34 FJ4161
EU491722.1 gg_id:259776 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU491
EF174279.1 gg_id:181525 direct activated sludge compost maturation stage clone H49-814 EF1742
EF125451.1 gg_id:188380 mangrove soil clone MSB-2F4 EF1254
DQ334616.1 gg_id:175390 Impact metals on sediments heavy metal polluted marine sediment clone HB1-41-8 DQ334
EU287293.1 gg_id:239219 Pacific arctic surface sediment clone S11-110 EU287
FJ902650.1 gg_id:558486 phreatic limestone sinkholes northeastern Mexico biofilm 1m deep hydrothermal ver FJ9026
GQ259229.1 gg_id:512555 Microbial activities coastal marine sediments and column Svalbard deep water clone GQ259
EF061959.1 gg_id:194499 Xiamen China mangrove sediment clone XME27 EF0619
AY592131.1 gg_id:100439 marine ANAMMOX sediment clone AY592131 AY592
EF612422.1 gg_id:241321 historic semiarid lead-zinc mine tailings site soil clone OS-C47 EF6124
DQ395002.1 gg_id:155659 harbor sediment clone VHS-B4-54 DQ395
EU491622.1 gg_id:276755 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU491
FJ628326.1 gg_id:587067 transition and zone within near-shore basin: brackish water anoxic fjord Nitinat Lake (FJ6283
GU369930.1 gg_id:522232 and mats vents Arc white microbial film on pebble aphotic zone shal hydrothermal v GU369
EU925888.1 gg_id:327055 sediments sediment station DBS1 northern Bering Sea clone 099G35 EU9258
FJ202726.1 gg_id:304768 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2027
FJ545563.1 gg_id:553394 Diveristy Seawater and Sediment Northern North Yel Sea sediment clone S2-30 FJ5455
FJ479452.1 gg_id:564382 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4794
EF208680.1 gg_id:201369 Vertical and horizontal structure microbial sandy carbonate sediment clone CI5cm.BC EF2086
EU290675.1 gg_id:243727 microbial structure biogeochemical contrasting shelf sediments Namibian upwelling EU2906
GQ261760.1 gg_id:550306 shifts taxa and response localized organic loading deep sea sediment whale falls clo GQ261
AJ567539.1 gg_id:88336 deep-sea sediment clone MBMPE13 AJ5675
EU491447.1 gg_id:277437 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X4 clone EU491

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AM176878.1 gg_id:160646 Recovery mangrove sediment clone SZB50 AM176
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EU134721.1 gg_id:239488 tallgrass prarie soil clone FFCH6145 EU134
AY922078.1 gg_id:113125 farm soil clone AKYG940 AY922(
GQ472813.1 gg_id:581306 Biodiversity planktonic Northern surface water northern Bering Sea clone b44 GQ472
AM997308.1 gg_id:575214 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A AM997
AY225636.1 gg_id:97007 Mid-Atlantic Ridge hydrothermal sediment clone AT-s2-59 AY2256
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AJ633957.1 gg_id:114452 host's accessory nidamental gland clone 30ANG2 AJ6339
GQ259320.1 gg_id:557119 Microbial activities coastal marine sediments and water column Svalbard surface se GQ259
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EU652513.1 gg_id:277629 Seasonal variation microbial Yel Sea sediment clone C8S-5 EU652
EU488031.1 gg_id:572374 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU488(
GQ337138.1 gg_id:561386 Hydrography shapes biogeography deep Arctic Ocean water depth 1000m clone CB: GQ337
DQ396093.1 gg_id:155768 deep-sea octacoral clone ctg_NISA258 DQ396
EU491461.1 gg_id:259137 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X4 clone EU491
EU287183.1 gg_id:239964 Pacific arctic surface sediment clone P13-90 EU287
GQ246393.1 gg_id:593413 Temporal and spatial China North Yel Sea sediments clone Cm1-56 GQ246
EF540428.1 gg_id:227143 oil-shale semi-coke solid waste clone MK6 EF5404
EF208690.1 gg_id:202816 Vertical and horizontal structure microbial sandy carbonate sediment clone CI5cm.FC EF2086
EF597713.1 gg_id:247624 Metagenomics deep mediterranean warm bathypelagic habitat 3010m depth Ionian EF5977
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EU491388.1 gg_id:261546 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X3 clone EU491
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AY265348.1 gg_id:82929 Dermacentor variabilis symbiont AY2653
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AY264674.1 gg_id:89402 Arsenophonus nasoniae str. ATCC 49151 AY2646
DQ158206.1 gg_id:140266 Averyella dalhousiensis str. 9501-97 1 DQ158
DQ158205.1 gg_id:139645 Averyella dalhousiensis str. 521-86 14 DQ158
DQ158204.1 gg_id:140650 Averyella dalhousiensis str. 2362-79 4 DQ158
FJ360760.1 gg_id:325971 Enterobacter aerogenes str. PSB28 FJ3607
DQ481464.1 gg_id:157163 Averyella dalhousiensis str. VTan-2 DQ481
DQ068917.1 gg_id:139129 microbiota antlions (Myrmeleon mobilis) whole animal laboratory starved antlion O DQ068
EU438866.1 gg_id:297157 Enterobacter amnigenus 2 EU438
EU741245.1 gg_id:335722 Enterobacter sp. str. KB3 EU741
AB291632.1 gg_id:241040 Insecticidal predatory antlion species (Neuroptera: Myrmeleontidae) larvae Myrmel AB291
EU879089.1 gg_id:305870 Pantoea agglomerans str. HDDMN03 EU879
AM184285.1 gg_id:161053 Enterobacter ludwigii str. WAB1946 AM184
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AY676878.1 gg_id:135960 Baumannia cicadellinicola B14 AY6768
AY676887.1 gg_id:136270 Baumannia cicadellinicola B34 AY6768
AF465797.1 gg_id:79588 Baumannia cicadellinicola AF4657
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AY676895.1 gg_id:137136 Baumannia cicadellinicola F02 AY6768
AF465795.1 gg_id:79106 Baumannia cicadellinicola AF4657
AY676877.1 gg_id:135411 Baumannia cicadellinicola B13 AY6768
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AJ233418.1 gg_id:51229 Brenneria rubrifaciens str. DSM 4483 AJ2334
U80207.1 gg_id:10197 Brenneria rubrifaciens str. ATCC 29291 U80207
AM237373.1 gg_id:156214 Sodalis glossinidius OS-75 AM237
Z96097.1 gg_id:10201 Brenneria salicis str. LMG 2698 Z96097
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AB033773.1 gg_id:20966 Buchnera sp AB0337
AJ296755.1 gg_id:50183 Buchnera aphidicola (Maculolachnus submacula) (Maculolachnus AJ2967
FJ655495.1 gg_id:579584 Buchnera aphidicola (Stomaphis aphananthae) FJ6554
M63251.1 gg_id:9645 Buchnera aphidicola M6325
M63252.1 gg_id:9648 Buchnera aphidicola M6325
FJ655509.1 gg_id:587576 Buchnera aphidicola (Lachnus tropicalis) FJ6555

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AJ296752.1 gg_id:41602 Buchnera aphidicola (Baizongia pistaciae) AJ2967
EU334777.1 gg_id:308536 Buchnera aphidicola (Cinara cedri) str. BCce2-1 EU334
AJ296753.1 gg_id:36645 Buchnera aphidicola (Stomaphis quercus) AJ2967
AJ296747.1 gg_id:23181 Buchnera aphidicola (Pterocomma populeum) AJ2967
M63254.1 gg_id:9650 Buchnera aphidicola M6325
AJ296758.1 gg_id:23853 Buchnera aphidicola (Panaphis juglandis) AJ2967
M63250.1 gg_id:9642 Buchnera aphidicola M6325
M63253.1 gg_id:9647 Buchnera aphidicola M6325
Z19056.1 gg_id:9651 Buchnera aphidicola Z19056
AJ296750.1 gg_id:53693 Buchnera aphidicola (Pemphigus populi) AJ2967
AB064508.1 gg_id:40406 Buchnera aphidicola (Yamatocallis tokyoensis) #317 (Yamatocallis AB064
DQ418492.1 gg_id:171684 Buchnera aphidicola (Eriosoma lanigerum) str. Zhaotong DQ418
EU334773.1 gg_id:308102 Buchnera aphidicola (Cinara tujafilina) str. BCtu-1 EU334
M63255.1 gg_id:9653 Buchnera aphidicola M6325
AJ296754.1 gg_id:24924 Buchnera aphidicola (Tuberolachnus salignus) (Tuberolachnus AJ2967
FJ655507.1 gg_id:577120 Buchnera aphidicola (Lachnus roboris) FJ6555
Y11972.1 gg_id:202061 Buchnera aphidicola Y11972
L81121.1 gg_id:111650 Buchnera aphidicola L81121
AE016826.1 gg_id:146724 Buchnera aphidicola str. Bp (Baizongia pistaciae) AE0168
FJ655512.1 gg_id:510297 Buchnera aphidicola (Nippolachnus piri) FJ6555
Y11973.1 gg_id:9652 Buchnera aphidicola Y11973
AY518294.1 gg_id:105511 Buchnera aphidicola (Aphis fabae fabae) AY5182
FJ655500.1 gg_id:560641 Buchnera aphidicola (Stomaphis takahashii) FJ6555
DQ223869.1 gg_id:165272 Buttiauxella agrestis str. RT1 DQ223
DQ223870.1 gg_id:172544 Buttiauxella noackiae str. RT7 DQ223
DQ440549.1 gg_id:153634 Buttiauxella agrestis str. HS-39 DQ440
AF227860.1 gg_id:73465 Pantoea sp. str. 57916 AF2278
DQ223871.1 gg_id:167300 Buttiauxella agrestis str. P1 DQ223
AJ293684.1 gg_id:69815 Buttiauxella agrestis str. S3/3-203 AJ2936
AJ233402.1 gg_id:10052 Buttiauxella ferragutiae str. DSM 9390 AJ2334
FJ716025.1 gg_id:513551 Diet- gut microbiota Lumbricus rubellus fingerprinting technique and cloning intestina FJ7160
AJ233406.1 gg_id:10056 Buttiauxella warmboldiae str. DSM 9404 AJ2334
NR_025328.1 gg_id:575201 Buttiauxella brennerae str. S1/6-571; DSM 9396 NR_02
AJ293687.1 gg_id:69978 Buttiauxella noackiae str. BR 626 AJ2936
AJ233403.1 gg_id:10053 Buttiauxella gaviniae str. DSM 9393 AJ2334
AJ233400.1 gg_id:10050 Buttiauxella agrestis str. DSM 4586 AJ2334
X92552.1 gg_id:9961 "Candidatus camponotii" X92552
AY334368.1 gg_id:106321 Camponotus sansabeanus symbiont AY3343
AJ245598.1 gg_id:20928 USA clone 14/7 AJ2455
AJ245592.1 gg_id:17213 Peru clone 5-5 AJ2455

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AJ245596.1 gg_id:48707 Saint Kitts and Nevis clone 12/1 AJ2455
NC_012751.1 gg_id:431766 Candidatus Hamiltonella defensa 5AT (Acyrthosiphon pisum) str. T5A NC_01
AB067723.1 gg_id:28528 Megacopta punctatissima symbiont AB067
U91515.1 gg_id:10203 Candidatus Phlomobacter fragariae str. france fragariae U9151
AY136143.1 gg_id:86615 Brachycaudus cardui symbiont AY136
AY136152.1 gg_id:105167 Macrosiphum rosae symbiont AY136
AF293619.1 gg_id:25922 Macrosiphoniella ludovicianae symbiont AF293
FJ357496.1 gg_id:359629 symbionts clones English grain Sitobion avenae F. (Insecta: Homoptera) and host plan FJ3574
AF293627.1 gg_id:50997 Uroleucon solidaginis symbiont AF293
DQ228285.1 gg_id:150888 Acyrthosiphon pisum symbiont DQ228
AF493976.1 gg_id:82917 Cedecea davisae str. DSM 4568 AF493
DQ481466.1 gg_id:203232 Citrobacter freundii str. VTan-4 DQ481
DQ481470.1 gg_id:201655 Citrobacter freundii str. VTan-9 DQ481
EU468094.1 gg_id:299301 cheetah feces clone CE2_g02_2 EU468
GQ154806.1 gg_id:534457 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
GQ155543.1 gg_id:588290 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
DQ816142.1 gg_id:168998 mouse cecum clone aaa88f07 DQ816
GQ155506.1 gg_id:511336 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EU467996.1 gg_id:301223 cheetah feces clone CE2_g10 EU467
EU468053.1 gg_id:297805 cheetah feces clone CE2_a06_2 EU468
GQ155565.1 gg_id:556376 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EU540206.1 gg_id:283179 profile human microbiota antecubital fossa (inner elbow) skin clone nbt247b06 EU540
FJ658620.1 gg_id:509207 Metalworking Fluids and Aerosols Metallurgy Plant metalworking aerosol clone Sumn FJ6586
AY163805.1 gg_id:101294 Citrobacter freundii str. A1 AY163
AM184249.1 gg_id:160975 Citrobacter freundii str. WAB1908 AM184
DQ294286.1 gg_id:143708 Citrobacter freundii str. 8 DQ294
AY259630.1 gg_id:83212 Citrobacter freundii str. WA1 AY259
GQ154984.1 gg_id:532730 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
DQ817309.1 gg_id:173691 mouse cecum clone aaa72h09 DQ817
DQ816132.1 gg_id:167280 mouse cecum clone aaa88d04 DQ816
GQ155666.1 gg_id:589249 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
AB548827.1 gg_id:530232 Citrobacter freundii str. JCM 24062 AB548
GQ154694.1 gg_id:510488 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
FJ581026.1 gg_id:570627 Citrobacter freundii str. IITRL1 FJ5810
DQ192060.1 gg_id:166668 Citrobacter sp. I91-10 DQ192
EU528229.1 gg_id:280706 Seasonal Dynamics Mudflat Mouth Major Kentucky Lake Reservoir Tributary sedime EU528
DQ816596.1 gg_id:167950 mouse cecum clone aab20b03 DQ816
DQ816998.1 gg_id:169360 mouse cecum clone aaa94d12 DQ816
DQ294285.1 gg_id:141265 Citrobacter freundii str. 7 DQ294
EU365679.1 gg_id:258785 Citrobacter freundii str. M-8 EU365
FJ975807.1 gg_id:547342 Human gut microbiome adopts alternative state bowel transplantation ileum effluent FJ9758

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EU545403.1 gg_id:534741 Citrobacter freundii str. XW722 EU545
EF593056.1 gg_id:251387 Identification cultivable and non-cultivable Nisargruna biogas plant predigester slurry EF593
DQ517285.1 gg_id:161301 Citrobacter freundii str. BRN1 DQ517
GU374110.1 gg_id:530539 soil East Calcutta wetland clone SRC_NBB9 GU374
GQ155532.1 gg_id:579108 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
DQ223880.1 gg_id:168759 Citrobacter sp. str. P11 DQ223
GQ155589.1 gg_id:552805 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ154756.1 gg_id:510480 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
EU468065.1 gg_id:295328 cheetah feces clone CE2_b11_3 EU468
EF371903.1 gg_id:213847 Citrobacter freundii str. TF13 EF371
DQ192058.1 gg_id:170521 Citrobacter sp. I91-5 DQ192
FJ658534.1 gg_id:511169 Metalworking Fluids and Aerosols Metallurgy Plant metalworking aerosol clone Sumn FJ6585
DQ816058.1 gg_id:169128 mouse cecum clone aaa86g12 DQ816
GQ155569.1 gg_id:510363 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ155471.1 gg_id:509639 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ154907.1 gg_id:567301 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
AB548831.1 gg_id:522347 Citrobacter freundii str. JCM 24066 AB548
GQ154858.1 gg_id:564251 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
DQ816447.1 gg_id:169742 mouse cecum clone aab18b07 DQ816
GQ155467.1 gg_id:544556 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
AF025373.1 gg_id:9852 Citrobacter werkmanii str. CDC 0876-58 AF025
EF059839.1 gg_id:226460 Cronobacter dublinensis str. E465 EF059
EF059874.1 gg_id:223014 Cronobacter dublinensis str. E791 EF059
EF059879.1 gg_id:224695 Cronobacter dublinensis str. E799; NCTC9846 EF059
EF059878.1 gg_id:224208 Cronobacter dublinensis str. E798 EF059
EF059887.1 gg_id:219603 Cronobacter muytjensii str. E888 EF059
FJ906909.1 gg_id:552376 Cronobacter muytjensii str. Jor112 FJ9069
EF059875.1 gg_id:224339 Cronobacter muytjensii str. E793 EF059
EF059849.1 gg_id:224182 Cronobacter muytjensii str. E616 EF059
GU227684.1 gg_id:587272 Cronobacter sakazakii str. KYU35 GU227
GU227677.1 gg_id:534869 Cronobacter sakazakii str. KYU8 GU227
GU122211.1 gg_id:579605 Cronobacter muytjensii str. 05CHPL61 GU122
EF059861.1 gg_id:222245 Cronobacter turicensis str. E680 EF059
GU122184.1 gg_id:573255 Cronobacter sakazakii str. CDC 20-83; 05CHPL02 GU122
EU458321.1 gg_id:297419 spotted hyena feces clone HY1_d03 EU458
GU227685.1 gg_id:593345 Cronobacter sakazakii str. KYU37 GU227
FJ906905.1 gg_id:584098 Cronobacter muytjensii str. Jor77 FJ9069
GU122215.1 gg_id:557422 Cronobacter sakazakii str. 05CHPL65 GU122
FN543093.2 gg_id:569973 Cronobacter turicensis z3032 FN543
EF059892.1 gg_id:217736 Cronobacter subsp. dublinensis str. DES187 EF059
FN539031.1 gg_id:559715 Cronobacter sp. str. 040407/32 FN539

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EU348325.1 gg_id:353216 symbiont
EU072500.1 gg_id:246330 pentatomid symbionts host gut clone Mh1
CP001836.1 gg_id:520563 Dickeya dadantii str. Ech586
EF530560.1 gg_id:226472 Erwinia chrysanthemi str. ICMP 4649
EU526397.1 gg_id:263449 Erwinia chrysanthemi
AF520709.2 gg_id:61200 Erwinia chrysanthemi str. CFBP 1270
AF520712.1 gg_id:61196 Dickeya dieffenbachiae str. CFBP 2051
EU821584.1 gg_id:366934 Erwinia chrysanthemi str. A5307
AF520711.2 gg_id:61197 Dickeya zeae str. CFBP 2052
AF373199.1 gg_id:66727 Erwinia chrysanthemi str. 571
AB453281.1 gg_id:328862 Edwardsiella ictaluri str. PH-0744
GU176612.1 gg_id:588536 Edwardsiella ictaluri str. HSA-1
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FJ405305.1 gg_id:358984 Edwardsiella tarda str. K16
EU121410.1 gg_id:242592 Edwardsiella tarda str. EH-202
FJ405306.1 gg_id:369144 Edwardsiella tarda str. K17
FJ405294.1 gg_id:364464 Edwardsiella tarda str. K5
FJ405307.1 gg_id:367467 Edwardsiella tarda str. K18
FJ493544.1 gg_id:538059 Edwardsiella tarda str. H1
FJ405304.1 gg_id:358672 Edwardsiella tarda str. K15
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EU259315.1 gg_id:249457 Edwardsiella tarda str. LTB-4
FJ405296.1 gg_id:361185 Edwardsiella tarda str. K7
FJ405299.1 gg_id:366911 Edwardsiella tarda str. K10
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EU259316.1 gg_id:252748 Edwardsiella tarda str. WY37
FJ405293.1 gg_id:366652 Edwardsiella tarda str. K4
EU259317.1 gg_id:244611 Edwardsiella tarda str. WY28
FJ405300.1 gg_id:370021 Edwardsiella tarda str. K11
GQ337957.1 gg_id:540452 Edwardsiella tarda str. TsLt
AF015259.1 gg_id:9737 Edwardsiella tarda str. CDC 4411-68
NR_024768.1 gg_id:537841 Edwardsiella hoshinae str. JCM1679
FJ405298.1 gg_id:360292 Edwardsiella tarda str. K9
EF371905.1 gg_id:215399 Edwardsiella tarda str. TF17
EU231639.1 gg_id:256624 Edwardsiella ictaluri str. TCCC11053
FJ405308.1 gg_id:364288 Edwardsiella tarda str. K19
FJ405302.1 gg_id:359327 Edwardsiella tarda str. K13
EF467289.1 gg_id:227142 Edwardsiella tarda str. CD
EU181369.1 gg_id:248470 Rahnella sp. str. LR113
DQ645479.1 gg_id:159919 Escherichia coli str. F4-2
GQ264499.1 gg_id:586406 Structure Simulated Level Waste Site simulated level waste site clone WW3_48

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EU855207.1 gg_id:355066 Enterobacter sp. str. CTSP29 EU855
DQ855282.1 gg_id:216257 Enterobacter sp. str. FMB-1 DQ855
GQ260085.1 gg_id:561327 Enterobacter cloacae str. ICIRC107 GQ260
EU047701.1 gg_id:251565 Enterobacter aerogenes str. HC050612-1 EU047
EU047702.1 gg_id:256852 Enterobacter cloacae str. HC050612-4 EU047
EU047556.1 gg_id:249130 Enterobacter hormaechei str. TMPSB-T10 EU047
GU071202.1 gg_id:587429 Enterobacter sp. str. DIT 14 GU071
GQ260087.1 gg_id:564431 Enterobacter cloacae str. ICIRC10 GQ260
AJ508302.1 gg_id:80575 Enterobacter hormaechei str. CIP 103441 AJ5083
AY335554.1 gg_id:129942 Enterobacter aerogenes str. CBNU-20-1 AY335
DQ202394.1 gg_id:140607 Enterobacter cloacae str. B5 DQ202
GQ260081.1 gg_id:587124 Enterobacter cloacae str. ICIRC91 GQ260
EF210100.1 gg_id:203409 Enterobacter hormaechei str. Z2-7 EF2101
FJ868805.1 gg_id:541119 Enterobacter sp. str. BSRA1 FJ8688
EF446901.1 gg_id:214586 Enterobacter cloacae str. GW4 EF4469
AF130914.1 gg_id:10081 Pantoea endophytica str. A42 AF1309
GQ179978.1 gg_id:575168 Enterobacter hormaechei str. FS11 GQ179
AY995561.1 gg_id:115488 Enterobacter hormaechei AY995
AJ854063.3 gg_id:108298 Enterobacter nickellidurans str. NiVas 114 AJ8540
GQ260075.1 gg_id:512914 Enterobacter hormaechei str. ICIRC82 GQ260
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EU073021.1 gg_id:254448 Enterobacter cloacae HQ040619-1 EU073
CU915026.1 gg_id:448667 and dynamics adapted microbiota during degradation Tunisian zarzatine enriched se CU915
DQ837566.1 gg_id:172044 Enterobacter sp. XIV DQ837
AB244457.1 gg_id:257506 Enterobacter cloacae str. An20-1 AB244
FJ976587.1 gg_id:545162 Enterobacter aerogenes str. LCR78 FJ9765
FJ999766.1 gg_id:385869 Enterobacter hormaechei str. SP FJ9997
EF179825.1 gg_id:258793 sequences adult Anopheles darlingi (Diptera: Culicidae) mosquitoes clone 4.2 EF1798
Y17665.1 gg_id:10077 Enterobacter cloacae Nr. 3 Y17665
EF059890.1 gg_id:218876 Enterobacter hormaechei str. E904 EF0598
DQ273684.1 gg_id:144399 Evaluation two chromogenic media glucosidase and commercial oligonucleotide pro DQ273
AY217654.1 gg_id:84190 Escherichia senegalensis str. F1p AY2176
EU302833.1 gg_id:240810 Salmonella sp. str. DAP8 EU3028
GQ478377.1 gg_id:551552 olive endosymbiont 'Candidatus Erwinia dacicola' switches intracellular extracellular GQ478
GQ131582.1 gg_id:460735 Erwinia rhapontici str. 1OP1 GQ131
Z96087.1 gg_id:9805 Erwinia rhapontici str. LMG 2688 Z96087
GQ131583.1 gg_id:451112 Erwinia rhapontici str. 1OP6 GQ131
GQ131584.1 gg_id:410468 Erwinia rhapontici str. 3OP1 GQ131
U80206.1 gg_id:9811 Erwinia rhapontici str. ATCC 29283 U8020

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AM292080.1 gg_id:179624 Erwinia tasmaniensis str. Et2/99 AM292
AM055715.2 gg_id:149797 Erwinia pyrifoliae str. Ejp557 AM055
FJ594367.1 gg_id:569261 Erwinia amylovora str. EA312 FJ5943
FJ594360.1 gg_id:566379 Erwinia pyrifoliae str. WT19 FJ5943
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AF130964.1 gg_id:9814 Erwinia toletana str. A82 AF1309
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EF059869.1 gg_id:223949 Escherichia hermannii str. E757 EF0598
EU931561.1 gg_id:337373 Pantoea agglomerans str. ZFJ-6 EU9315
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GU339282.1 gg_id:563485 Pantoea ananatis str. EH55 GU339
DQ273680.1 gg_id:141117 Evaluation two chromogenic media glucosidase and commercial oligonucleotide pro DQ273
U80201.1 gg_id:9861 Pectobacterium cypripedii str. ATCC 29267 U80201
EU289448.1 gg_id:253617 metagenomic approach biosynthesis ansamycin endophytes or symbionts enriched s EU2894
EU681952.1 gg_id:281980 Erwinia persicina str. WD1608 EU6819
FM163487.1 gg_id:289103 Achromobacter xylosoxidans str. RE1 FM163
AM055711.1 gg_id:149811 Erwinia billingiae str. Eb661 AM055
GQ024758.1 gg_id:484912 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ024
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GQ043420.1 gg_id:423241 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw96 GQ043
GQ024848.1 gg_id:484822 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ024
AF141893.1 gg_id:71250 Erwinia amylovora str. BC202(=Ea491) AF1418
GQ024907.1 gg_id:484762 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ024
EU072495.1 gg_id:239362 pentatomid symbionts host gut clone Ah1 EU0724
EU362176.1 gg_id:351023 Erwinia sp. str. C3(2008) EU3621
FJ595863.1 gg_id:543943 Erwinia pyrifoliae str. WT36 FJ5958
AY373829.2 gg_id:101634 Salmonella subterranea str. FRC1 AY3738
GU124495.1 gg_id:582297 endosymbiotic (Stal) (rice brown planthopper) Enterobacteriales endosymbiont Nila GU124
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GQ024769.1 gg_id:484901 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ024
AJ233417.1 gg_id:9810 Erwinia rhapontici str. DSM 4484 AJ2334
EF469631.1 gg_id:221786 Dioxyna bidentis ex Bidens tripartita symbiont EF4696
AB480771.1 gg_id:539151 Erwinia tasmaniensis str. Acj 205 AB4807
GQ024837.1 gg_id:484833 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ024
AM294946.1 gg_id:174382 Erwinia persicina str. LPPA 408 AM294
EU336938.2 gg_id:537651 Flavobacterium sp. str. AG13 EU3369
AF289542.1 gg_id:20321 Erwinia amylovora EA G-5 AF2895
AF024613.1 gg_id:9827 Pantoea agglomerans str. TAC.XII.93.2 AF0246

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AY702662.1 gg_id:169365 Margalefia venezuelensis str. MS12 AY702
DQ532292.1 gg_id:171458 Geographical Variation Microbial Burden and Spacecraft Assembly Kennedy Space C DQ532
AB480775.1 gg_id:575074 Erwinia tasmaniensis str. Acj 211 AB480
FJ595871.1 gg_id:573072 Erwinia amylovora str. LMG2068 FJ5958
GQ097550.1 gg_id:395052 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw GQ097
EU926632.1 gg_id:350789 Escherichia albertii str. 1297-05-19 EU926
NC_010498.1 gg_id:263846 Escherichia coli str. SECEC SMS-3-5 NC_01
AE014073.1 gg_id:146636 Shigella flexneri 2a str. 2457T AE014
DQ411026.1 gg_id:151002 Escherichia coli str. FR-2 DQ411
CP000038.1 gg_id:138890 Shigella sonnei str. Ss046 CP000
CU928163.2 gg_id:544923 Escherichia coli str. UMN026 CU928
AP010953.1 gg_id:568499 Escherichia coli O26:H11 str. 11368 AP010
CP000800.1 gg_id:257376 Escherichia coli str. E24377A CP000
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NC_010498.1 gg_id:263843 Escherichia coli str. SECEC SMS-3-5 NC_01
AAJV02000011.1 gg_id:314537 Escherichia coli str. E22 AAJV0
AAJV02000007.1 gg_id:340407 Escherichia coli str. E22 AAJV0
CP000819.1 gg_id:520568 Escherichia coli B str. REL606 CP000
CP000800.1 gg_id:257373 Escherichia coli str. E24377A CP000
FM180568.1 gg_id:369791 Escherichia coli 0127:H6 str. E2348/69 FM180
CP000948.1 gg_id:270792 Escherichia coli substr. DH10B str. K-12 CP000
CU928158.2 gg_id:554727 Escherichia fergusonii 35469 str. ATCC 35469T CU928
AAKB02000001.1 gg_id:281891 Escherichia coli str. 53638 AAKB0
CU928163.2 gg_id:544920 Escherichia coli str. UMN026 CU928
CU928161.2 gg_id:563144 Escherichia coli str. S88 CU928
EU009185.1 gg_id:238337 Shigella dysenteriae str. FBD014 EU009
AF233451.1 gg_id:17857 Escherichia coli AF2334
EF620924.1 gg_id:255332 Escherichia coli str. SYW003 EF6209
CU928161.2 gg_id:563145 Escherichia coli str. S88 CU928
CU928164.2 gg_id:536217 Escherichia coli str. IAI39 CU928
EU470924.1 gg_id:291766 red panda feces clone RP_2aaa03c06 EU470
EU470476.1 gg_id:301376 red panda feces clone RP_1aaa02h07 EU470
FJ950549.1 gg_id:428533 Escherichia coli str. c247 FJ9505
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EU471177.1 gg_id:302439 red panda feces clone RP_3aaa04d05 EU471
EU472680.1 gg_id:288712 red panda feces clone RPSD_1aaa01d01 EU472
EU472729.1 gg_id:290328 red panda feces clone RPSD_1aaa02g10 EU472

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EU464663.1 gg_id:287701 African elephant feces clone AFEL_aai32g02 EU464
EU472690.1 gg_id:290223 red panda feces clone RPSD_1aaa02d03 EU472
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EU472703.1 gg_id:298606 red panda feces clone RPSD_1aaa02d11 EU472
AY319393.1 gg_id:90202 Escherichia coli str. 5.2 AY319
EU472746.1 gg_id:301855 red panda feces clone RPSD_1aaa01e12 EU472
EU472863.1 gg_id:302968 red panda feces clone RPSD_1aaa01f04 EU472
GQ047684.1 gg_id:444206 Topographical and Temporal Human Skin Microbiome skin palm clone nbw137h05c GQ047
EU465326.1 gg_id:302392 lion feces clone LI3_aah75d02 EU465
EU470870.1 gg_id:289907 red panda feces clone RP_2aaa03c09 EU470
EU471112.1 gg_id:290411 red panda feces clone RP_3aaa03e02 EU471
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EU470944.1 gg_id:301988 red panda feces clone RP_2aaa04d11 EU470
EU470756.1 gg_id:294273 red panda feces clone RP_2aaa02e05 EU470
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EU778391.1 gg_id:314335 Red Panda feces clone RPSD_1aaa02b11 EU778
EU472908.1 gg_id:294073 red panda feces clone RPSD_1aaa03d09 EU472
EU472772.1 gg_id:300828 red panda feces clone RPSD_1aaa04a05 EU472
EU009180.1 gg_id:242457 Shigella boydii str. FBD009 EU009
EU471213.1 gg_id:295208 red panda feces clone RP_3aaa04f02 EU471
EU470490.1 gg_id:295383 red panda feces clone RP_1aaa02e01 EU470
EU470986.1 gg_id:301184 red panda feces clone RP_2aaa04d09 EU470
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GQ025582.1 gg_id:466050 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ025
FJ949576.1 gg_id:444646 Escherichia coli str. G4 FJ9495
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EU472728.1 gg_id:289118 red panda feces clone RPSD_1aaa03e05 EU472
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GQ493756.1 gg_id:537192 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
EU470610.1 gg_id:300547 red panda feces clone RP_1aaa04e06 EU470
FJ673277.1 gg_id:516144 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6732

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EU458135.1 gg_id:294276 North American black bear feces clone BB2_c08 EU458
EU470636.1 gg_id:300616 red panda feces clone RP_1aaa01d05 EU470
GQ031087.1 gg_id:414691 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ031
EU471061.1 gg_id:296334 red panda feces clone RP_3aaa01c11 EU471
EU472176.1 gg_id:297981 francois langur feces clone FL_2aaa04b02 EU472
GQ069091.1 gg_id:449962 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ069
EU472840.1 gg_id:298307 red panda feces clone RPSD_1aaa02b06 EU472
EU470804.1 gg_id:298326 red panda feces clone RP_2aaa03f10 EU470
EU472779.1 gg_id:294637 red panda feces clone RPSD_1aaa01b05 EU472
EU472793.1 gg_id:288476 red panda feces clone RPSD_1aaa03g10 EU472
EU470706.1 gg_id:293949 red panda feces clone RP_1aaa04g08 EU470
EU472879.1 gg_id:303261 red panda feces clone RPSD_1aaa01b03 EU472
EU470669.1 gg_id:289152 red panda feces clone RP_1aaa03e06 EU470
EU472824.1 gg_id:292653 red panda feces clone RPSD_1aaa02c07 EU472
EU472655.1 gg_id:290927 red panda feces clone RPSD_1aaa01f11 EU472
CP000036.1 gg_id:144321 Shigella boydii str. Sb227 CP000
EU471278.1 gg_id:292133 red panda feces clone RP_3aaa01c09 EU471
GQ047978.1 gg_id:419099 Topographical and Temporal Human Skin Microbiome skin palm clone nbw139g11c1 GQ047
EU776531.1 gg_id:329008 Lion feces clone LI3_aah76c06 EU776
EU468090.1 gg_id:288116 cheetah feces clone CE2_f03_3 EU468
EU472825.1 gg_id:291515 red panda feces clone RPSD_1aaa01c06 EU472
GQ021879.1 gg_id:487789 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ021
EU472913.1 gg_id:288396 red panda feces clone RPSD_1aaa04e12 EU472
EU472700.1 gg_id:288620 red panda feces clone RPSD_1aaa03d10 EU472
EU471279.1 gg_id:292445 red panda feces clone RP_3aaa02f07 EU471
EU471202.1 gg_id:298795 red panda feces clone RP_3aaa03c11 EU471
EU472777.1 gg_id:302310 red panda feces clone RPSD_1aaa01c05 EU472
FJ678202.1 gg_id:518667 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6782
EU470927.1 gg_id:288122 red panda feces clone RP_2aaa04b12 EU470
GQ047075.1 gg_id:391950 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw GQ047
EU470902.1 gg_id:291899 red panda feces clone RP_2aaa04g09 EU470
EU771755.1 gg_id:335863 African elephant feces clone AFEL_aai32a02 EU771
EU472815.1 gg_id:292496 red panda feces clone RPSD_1aaa04a06 EU472
EU470628.1 gg_id:295268 red panda feces clone RP_1aaa03c11 EU470
EU472092.1 gg_id:291590 francois langur feces clone FL_1aaa02e10 EU472
EU467743.1 gg_id:289022 North American black bear feces clone BB1_b07 EU467
GQ047710.1 gg_id:418353 Topographical and Temporal Human Skin Microbiome skin palm clone nbw138c06c1 GQ047
DQ819115.1 gg_id:167150 mouse cecal microbiota-colonized zebrafish digestive tract clone aab26a07 DQ819
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EU472786.1 gg_id:297825 red panda feces clone RPSD_1aaa02b09 EU472

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EU470556.1 gg_id:293201 red panda feces clone RP_1aaa03b07 EU470
EF560788.1 gg_id:233865 Escherichia coli str. BEE3 EF5607
EU471295.1 gg_id:298340 red panda feces clone RP_3aaa03g05 EU471
EU470739.1 gg_id:289190 red panda feces clone RP_2aaa02e12 EU470
EU468348.1 gg_id:293649 lion feces clone LI2_aae47f10 EU468
GQ031673.1 gg_id:403434 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ031
EU471240.1 gg_id:289442 red panda feces clone RP_3aaa03h04 EU471
EU470710.1 gg_id:290311 red panda feces clone RP_1aaa04a05 EU470
EU470675.1 gg_id:301701 red panda feces clone RP_1aaa02e06 EU470
NC_011740.1 gg_id:471437 Escherichia fergusonii str. ATCC 35469 NC_01
EU471997.1 gg_id:292359 francois langur feces clone FL_1aaa02b11 EU471
EU472874.1 gg_id:298984 red panda feces clone RPSD_1aaa03c12 EU472
EU472807.1 gg_id:293337 red panda feces clone RPSD_1aaa03c08 EU472
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EU472693.1 gg_id:293094 red panda feces clone RPSD_1aaa04d06 EU472
EF620921.1 gg_id:238636 Escherichia coli str. SYW001 EF6209
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EU471056.1 gg_id:302667 red panda feces clone RP_3aaa04h09 EU471
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AF527826.1 gg_id:71573 Escherichia coli str. RREC II AF5278
EU472637.1 gg_id:296080 red panda feces clone RPSD_1aaa03f03 EU472
EU470517.1 gg_id:297922 red panda feces clone RP_1aaa02g03 EU470
EU458385.1 gg_id:291249 spotted hyena feces clone HY1_a06_1 EU458
EU472805.1 gg_id:295661 red panda feces clone RPSD_1aaa01d08 EU472
EU472917.1 gg_id:288548 red panda feces clone RPSD_1aaa03c05 EU472
GQ047930.1 gg_id:391527 Topographical and Temporal Human Skin Microbiome skin palm clone nbw139b10c GQ047
EU472662.1 gg_id:294561 red panda feces clone RPSD_1aaa04b05 EU472
EU778485.1 gg_id:305760 Red Panda feces clone RP_1aaa01h12 EU778
EU470629.1 gg_id:290610 red panda feces clone RP_1aaa01b03 EU470
NC_009800.1 gg_id:245367 Escherichia coli str. HS NC_00
FJ950548.1 gg_id:401252 Escherichia coli str. c249 FJ9505
EU470620.1 gg_id:300756 red panda feces clone RP_1aaa02h01 EU470
EU472834.1 gg_id:288233 red panda feces clone RPSD_1aaa02g06 EU472
EU471158.1 gg_id:289812 red panda feces clone RP_3aaa02c10 EU471
GU065251.1 gg_id:535199 Escherichia coli str. BDS3 GU065
X80733.1 gg_id:9684 Escherichia X80733
EU472760.1 gg_id:298347 red panda feces clone RPSD_1aaa03e07 EU472
GQ008489.1 gg_id:501176 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ008
EU471035.1 gg_id:291503 red panda feces clone RP_3aaa04d07 EU471
EU471245.1 gg_id:288664 red panda feces clone RP_3aaa03f02 EU471

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EU471044.1 gg_id:297206 red panda feces clone RP_3aaa04h10 EU471
NZ_AAKA01000007.1 gg_id:138896 Shigella boydii str. BS512 NZ_AA
GQ047653.1 gg_id:418972 Topographical and Temporal Human Skin Microbiome skin palm clone nbw137d03c GQ047
AF527827.1 gg_id:62512 Escherichia coli str. RREC I AF527
EU472717.1 gg_id:301245 red panda feces clone RPSD_1aaa04f12 EU472
GQ156189.1 gg_id:535325 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
EU470543.1 gg_id:293816 red panda feces clone RP_1aaa01a09 EU470
EU470705.1 gg_id:298055 red panda feces clone RP_1aaa03b10 EU470
AM184231.1 gg_id:161699 Shigella boydii str. WAB1890 AM184
EU470774.1 gg_id:289364 red panda feces clone RP_2aaa04f07 EU470
EU471270.1 gg_id:289897 red panda feces clone RP_3aaa04b12 EU471
GQ047626.1 gg_id:430240 Topographical and Temporal Human Skin Microbiome skin palm clone nbw137a04c1 GQ047
EU470550.1 gg_id:288891 red panda feces clone RP_1aaa01b09 EU470
EU470714.1 gg_id:296886 red panda feces clone RP_1aaa02h04 EU470
EU472197.1 gg_id:290652 francois langur feces clone FL_2aaa02g07 EU472
DQ818739.1 gg_id:173654 mouse cecal microbiota-colonized zebrafish digestive tract clone aab37d01 DQ818
GQ031721.1 gg_id:428655 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ031
GQ047960.1 gg_id:432277 Topographical and Temporal Human Skin Microbiome skin palm clone nbw139f02c1 GQ047
NC_011415.1 gg_id:322518 Escherichia coli str. SE11 NC_01
NC_011740.1 gg_id:471438 Escherichia fergusonii str. ATCC 35469 NC_01
EU472904.1 gg_id:300530 red panda feces clone RPSD_1aaa02e02 EU472
GQ047656.1 gg_id:430442 Topographical and Temporal Human Skin Microbiome skin palm clone nbw137d07c GQ047
AE014073.1 gg_id:146716 Shigella flexneri 2a str. 2457T AE014
EU471257.1 gg_id:298991 red panda feces clone RP_3aaa02h04 EU471
AP009240.1 gg_id:332176 Escherichia coli str. SE11 AP009
NC_009801.1 gg_id:241154 Escherichia coli str. E24377A NC_00
AF357563.1 gg_id:73454 mpn-isolate group 15 AF357
GQ025520.1 gg_id:413814 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ025
EU472812.1 gg_id:301009 red panda feces clone RPSD_1aaa03f05 EU472
EU472915.1 gg_id:291673 red panda feces clone RPSD_1aaa02f08 EU472
GQ069064.1 gg_id:438768 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ069
EU470553.1 gg_id:302025 red panda feces clone RP_1aaa04b03 EU470
EU708318.1 gg_id:348648 Ewingella americana str. CH6 EU708
EU678359.1 gg_id:284672 Ewingella americana str. CH5 EU678
U29438.1 gg_id:10324 Ewingella americana str. NCPPB 3905 U2943
AY581130.1 gg_id:101409 Ewingella americana B791 AY581
EU196321.1 gg_id:246905 Aranicola sp. NP34 EU196
AF010251.1 gg_id:10139 Klebsiella granulomatis str. KH 22 d peripheral blood monocytes AF010
AY369139.1 gg_id:94946 Klebsiella pneumoniae AY369
GQ098970.1 gg_id:467551 Topographical and Temporal Human Skin Microbiome skin palm clone nbw504e12c1 GQ098

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AF390083.1 gg_id:20393 Klebsiella oxytoca str. W-6 AF3900
AJ871859.1 gg_id:113127 Klebsiella oxytoca str. SB2908 AJ8718
AB353046.1 gg_id:257803 Klebsiella oxytoca str. No.6 AB3530
FJ816026.1 gg_id:577013 Klebsiella oxytoca str. GS-4-08 FJ8160
EF633998.1 gg_id:255739 Klebsiella pneumoniae str. M-4 EF6339
GU361112.1 gg_id:515224 Klebsiella oxytoca str. SHD-1 GU361
GQ075941.1 gg_id:461429 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ075
GU119910.1 gg_id:539869 Klebsiella oxytoca str. Bx-LA-0908 GU119
GQ098941.1 gg_id:392581 Topographical and Temporal Human Skin Microbiome skin palm clone nbw504b09c1 GQ098
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AF543283.1 gg_id:58294 Klebsiella oxytoca str. ChDC OS31 AF5432
AJ871861.1 gg_id:113052 Klebsiella oxytoca str. SB73 AJ8718
AB004754.1 gg_id:10108 Klebsiella oxytoca str. JCM1665 AB0047
AF319525.3 gg_id:71572 Klebsiella oxytoca AF3195
EU554427.1 gg_id:272485 Klebsiella oxytoca str. Ag01 EU5544
AJ871862.1 gg_id:113718 Klebsiella oxytoca str. SB3037 AJ8718
AJ871860.1 gg_id:113819 Klebsiella oxytoca str. SB2942 AJ8718
CP000964.1 gg_id:355056 Klebsiella pneumoniae str. 342 CP0009
EU048272.1 gg_id:254999 Klebsiella pneumoniae str. MG09 EU0482
GQ166862.1 gg_id:585007 Klebsiella pneumoniae str. EB6-THQ GQ166
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EU240959.1 gg_id:273616 Klebsiella pneumoniae str. YC-A42 EU2409
FJ593858.1 gg_id:514856 Klebsiella sp. str. AL060225_04 FJ5938
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AF394537.1 gg_id:64272 Klebsiella pneumoniae str. 342 AF3945
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DQ185604.1 gg_id:140302 Klebsiella pneumoniae str. Ac01 DQ185
GQ156091.1 gg_id:550532 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
DQ379507.1 gg_id:153149 Klebsiella pneumoniae str. TSL-4 DQ379
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GU594298.1 gg_id:514480 Klebsiella pneumoniae str. B16 GU594

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EU086097.1 gg_id:241026 Klebsiella pneumoniae str. HR9 EU086
EU419756.1 gg_id:258442 Klebsiella pneumoniae str. L17 EU419
GQ154831.1 gg_id:582392 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
GQ154786.1 gg_id:554543 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
EU360116.1 gg_id:578618 Klebsiella pneumoniae str. PB24 EU360
AF228920.1 gg_id:72626 Klebsiella pneumoniae str. NLEP98-0472 AF228
GU594297.1 gg_id:525542 Klebsiella pneumoniae str. A38 GU594
GQ497246.1 gg_id:568000 Klebsiella sp. str. A4-1 GQ497
GQ154902.1 gg_id:587608 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
EU661374.1 gg_id:277703 Klebsiella pneumoniae str. K8 EU661
GQ155332.1 gg_id:557261 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
Y11488.1 gg_id:136340 Klebsiella pneumoniae str. AB2844 Y11488
EU771689.1 gg_id:307981 African elephant feces clone AFEL2_aao29h01 EU771
GQ154976.1 gg_id:565044 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
GQ156442.1 gg_id:591675 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
AY292865.1 gg_id:89119 Klebsiella pneumoniae 521 AY292
AM184253.1 gg_id:161438 Klebsiella pneumoniae str. WAB1912 AM184
EU881978.1 gg_id:350702 Klebsiella pneumoniae str. HDDMN06 EU881
GQ154733.1 gg_id:588616 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
NC_012731.1 gg_id:375667 Klebsiella pneumoniae str. NTUH-K2044 NC_01
EU776082.1 gg_id:319632 Spotted hyena feces clone HY1_f06_2 EU776
GQ154886.1 gg_id:584377 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
AY905691.1 gg_id:112401 Klebsiella pneumoniae str. CICC10072 AY905
GQ155971.1 gg_id:593698 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GU374001.1 gg_id:527950 dental caries clone SRC_DSA16 GU374
EU435386.1 gg_id:265566 Klebsiella variicola str. V2 EU435
GQ155807.1 gg_id:512044 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ155715.1 gg_id:567857 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EF031070.1 gg_id:215320 Klebsiella sp. CA17 EF031
Y11487.1 gg_id:136339 Klebsiella pneumoniae str. ATCC 13883 Y11487
GQ155784.1 gg_id:534117 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
DQ835530.1 gg_id:243623 Klebsiella oxytoca str. 20 DQ835
FJ975814.1 gg_id:593892 Human gut microbiome adopts alternative state bowel transplantation ileum effluent FJ9758
AF511429.1 gg_id:73274 Klebsiella pneumoniae CCCO2 AF511
GQ155370.1 gg_id:544564 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ154739.1 gg_id:568190 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
NC_012731.1 gg_id:375666 Klebsiella pneumoniae str. NTUH-K2044 NC_01
GQ155329.1 gg_id:570828 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ154908.1 gg_id:510655 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
DQ379506.1 gg_id:151643 Klebsiella pneumoniae str. TSL-2 DQ379
AY114159.1 gg_id:63980 Klebsiella pneumoniae str. 402-2 AY114

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EU036754.1 gg_id:327015 Klebsiella sp. str. SA07 EU036
GQ154799.1 gg_id:540518 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
NC_012731.1 gg_id:375670 Klebsiella pneumoniae str. NTUH-K2044 NC_01
GU227150.1 gg_id:584676 Klebsiella oxytoca str. A9-2 GU227
GU193983.1 gg_id:584760 Klebsiella pneumoniae str. IITRBL3 GU193
AB072699.1 gg_id:76366 Klebsiella pneumoniae F-5-2 AB072
GQ154948.1 gg_id:578178 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
GQ155672.1 gg_id:535765 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EU352755.1 gg_id:269092 Klebsiella pneumoniae str. NK 2.bp-1 EU352
NC_012731.1 gg_id:375669 Klebsiella pneumoniae str. NTUH-K2044 NC_01
AF390084.1 gg_id:37558 Klebsiella pneumoniae str. DM-5 AF390
FJ422735.1 gg_id:367184 Klebsiella pneumoniae str. 2N3 FJ4227
FJ222552.1 gg_id:354585 Klebsiella pneumoniae str. MR-M1 FJ2225
GQ154979.1 gg_id:513309 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
GQ154789.1 gg_id:590681 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
EU661373.1 gg_id:279251 Klebsiella pneumoniae str. K11 EU661
AF453251.1 gg_id:44635 Klebsiella pneumoniae str. ASR1 AF453
GQ156110.1 gg_id:539997 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
X93214.1 gg_id:10144 Klebsiella pneumoniae str. DSM 30102 X93214
GQ154895.1 gg_id:593574 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
EF154517.1 gg_id:189557 Klebsiella sp. str. CW-D EF1545
GQ156187.1 gg_id:560253 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
DQ226215.1 gg_id:142418 Klebsiella oxytoca DR.Y14 DQ226
GQ166865.1 gg_id:583479 Klebsiella pneumoniae str. EB55-THQ GQ166
AY598354.1 gg_id:109687 Klebsiella pneumoniae str. MCM B-325 AY598
GQ154945.1 gg_id:585107 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
GQ154754.1 gg_id:575147 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
AF130981.1 gg_id:32663 Klebsiella pneumoniae str. ATCC13883 AF130
DQ444287.1 gg_id:153811 Klebsiella pneumoniae str. 2 DQ444
GQ155333.1 gg_id:558921 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
AB004752.1 gg_id:10135 Serratia liquefaciens str. JCM1245 AB004
EU333881.1 gg_id:259427 Klebsiella granulomatis str. K22-14 EU333
GU339255.1 gg_id:532790 Klebsiella pneumoniae str. EH25 GU339
GQ155711.1 gg_id:589879 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
CP001891.1 gg_id:527920 Klebsiella variicola str. -22 CP001
FJ975784.1 gg_id:564752 Human gut microbiome adopts alternative state bowel transplantation ileum effluent FJ9757
Y17668.1 gg_id:10149 Klebsiella pneumoniae str. Klebs313 Y17668
EU661378.1 gg_id:278276 Klebsiella pneumoniae str. K42 EU661
GQ154950.1 gg_id:510291 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
GQ156083.1 gg_id:588769 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
EF551363.1 gg_id:222010 Raoultella planticola str. Rs-2 EF5513

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GQ156192.1 gg_id:575548 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
NC_012731.1 gg_id:375665 Klebsiella pneumoniae str. NTUH-K2044 NC_01
GQ154748.1 gg_id:556070 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
GQ155398.1 gg_id:579246 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
DQ837568.1 gg_id:168382 Klebsiella sp. III DQ837
EU734822.1 gg_id:349243 Pseudomonas aeruginosa str. NBRAJG90 EU7348
GQ155863.1 gg_id:539970 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ155396.1 gg_id:509168 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EF091148.1 gg_id:213635 Klebsiella pneumoniae str. 99 EF0911
EF566882.1 gg_id:273896 Klebsiella pneumoniae EF5668
FJ947063.1 gg_id:512541 Klebsiella pneumoniae str. fJ1 FJ9470
GQ155406.1 gg_id:572306 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
AY660026.2 gg_id:123487 Xenorhabdus poinarii AY660
NC_012731.1 gg_id:375668 Klebsiella pneumoniae str. NTUH-K2044 NC_01
CP001891.1 gg_id:527919 Klebsiella variicola str. -22 CP0018
GQ154942.1 gg_id:575251 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
GQ155346.1 gg_id:542868 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
FJ975804.1 gg_id:548574 Human gut microbiome adopts alternative state bowel transplantation ileum effluent FJ9758
EU078621.1 gg_id:251954 Klebsiella pneumoniae str. HR16 EU078
FJ593857.1 gg_id:532313 Klebsiella sp. str. AL060224_03 FJ5938
EU360793.1 gg_id:262483 Klebsiella pneumoniae str. ECU-21 EU360
GQ155955.1 gg_id:536479 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
FJ975797.1 gg_id:593596 Human gut microbiome adopts alternative state bowel transplantation ileum effluent FJ9757
GQ155996.1 gg_id:571066 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
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GQ155924.1 gg_id:590080 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
NC_012731.1 gg_id:375671 Klebsiella pneumoniae str. NTUH-K2044 NC_01
GQ154887.1 gg_id:511908 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
EF127829.1 gg_id:197404 Klebsiella oxytoca str. LF-1 EF1278
GQ155740.1 gg_id:512312 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
FJ436718.1 gg_id:358763 Klebsiella pneumoniae str. FIUMS1 FJ4367
GQ155340.1 gg_id:511148 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ155822.1 gg_id:513383 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
AJ233420.1 gg_id:27939 Klebsiella pneumoniae str. DSM 30104 AJ2334
DQ223868.1 gg_id:166493 Kluyvera intermedia str. P3 DQ223
NR_028802.1 gg_id:564215 Kluyvera intermedia str. 256; ATCC 33110 NR_02
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AJ277978.1 gg_id:22764 Leclercia adecarboxylata str. WG 162 AJ2779
AY451327.1 gg_id:99716 Leclercia adecarboxylata str. TERIPS4040 AY4513

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AF157695.1 gg_id:10087 Enterobacter cloacae str. drh3 AF1576
AY335552.1 gg_id:137221 Pantoea agglomerans str. CBNU-14-1 AY3355
AJ232240.1 gg_id:10085 isolate: SS-Unknown-1129 clone AJ2322
FJ592988.1 gg_id:432552 Pantoea agglomerans str. SB-2 FJ5929
EU302838.1 gg_id:247855 Pantoea sp. str. DAP13 EU3028
AJ276393.1 gg_id:71494 Leclercia adecarboxylata str. LBV 449 AJ2763
DQ011248.1 gg_id:136462 genes Da Qing Oil field microbial indicates presence variety sulfate-reducing fermen DQ011
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FJ587505.1 gg_id:586247 Pantoea sp. str. C-4-1 FJ5875
FJ593002.1 gg_id:447010 Pantoea agglomerans str. ST-1 FJ5930
GQ337696.1 gg_id:568247 Enterobacter aerogenes str. S18 GQ337
AF511434.1 gg_id:65397 Enterobacter cloacae CCCO10 AF5114
FN555402.1 gg_id:509744 Pantoea sp. I-Bh20-21 FN5554
FM210031.1 gg_id:334606 Enterobacter cancerogenus str. T2P18 FM210
EF428996.1 gg_id:208785 Pantoea agglomerans str. GIST-CPs1 EF4289
AY691545.1 gg_id:103577 Pantoea agglomerans str. ChDC YP3 AY6915
GQ280809.1 gg_id:567944 Enterobacter sp. str. PE-R GQ280
FJ950684.1 gg_id:408750 Enterobacter ludwigii str. d44 FJ9506
EU590682.1 gg_id:258931 Pantoea agglomerans str. BH-18 EU5906
AM184264.1 gg_id:161559 Pantoea agglomerans str. WAB1925 AM184
AB004691.1 gg_id:10075 Pantoea agglomerans str. JCM1236 AB0046
AY488028.1 gg_id:99221 Enterobacter sp. str. BL-2 AY4880
EU557027.1 gg_id:266569 Enterobacter ludwigii str. KU201-3 EU5570
GQ070505.1 gg_id:376025 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw. GQ070
EF011164.1 gg_id:192215 Enterobacter hormaechei str. PT4 EF0111
DQ011253.1 gg_id:132962 stratum sewage clone 6 DQ011
EU302840.1 gg_id:257817 Pantoea sp. str. DAP15 EU3028
FM210030.1 gg_id:306906 Enterobacter cancerogenus str. R27c FM210
EF429005.1 gg_id:211593 Pantoea agglomerans str. GIST-Out2 EF4290
GQ374474.1 gg_id:533493 Pantoea agglomerans str. GS2 GQ374
AY792266.1 gg_id:123510 Humic Lake clone CrystalBog5A11 AY7922
AM184254.1 gg_id:160936 Pantoea agglomerans str. WAB1913 AM184
AM184266.1 gg_id:161444 Pantoea agglomerans str. WAB1927 AM184
EU884395.1 gg_id:368993 Enterobacter cloacae str. XA-2 EU8843
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EU164545.1 gg_id:239199 Enterobacter hormaechei 4 EU1645
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GQ284566.1 gg_id:547400 Enterobacter ludwigii str. AR1.22 GQ284

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DQ011254.1 gg_id:136479 genes Da Qing Oil field microbial indicates presence variety sulfate-reducing fermen DQ011
GQ374471.1 gg_id:570229 Pantoea agglomerans str. XJ1 GQ374
GQ856082.1 gg_id:556086 Leclercia adecarboxylata str. LMG 2803 GQ856
EF446899.1 gg_id:205646 Pantoea agglomerans str. AT2 EF4468
DQ392984.1 gg_id:156431 Pantoea agglomerans str. e DQ392
GU166185.1 gg_id:558052 intestinal tract larvae (Musca domestica) direct cloning and sequencing genes whea GU166
DQ358125.1 gg_id:163102 Morganella morganii str. AP28 DQ358
AB089243.1 gg_id:83678 Morganella morganii str. JCM1672 AB089
AY043168.1 gg_id:40697 Morganella morganii AY0431
DQ358138.1 gg_id:162198 Morganella psychrotolerans str. U2/6 DQ358
AB099401.1 gg_id:85614 Proteus vulgaris str. AU34 AB0994
AY792272.1 gg_id:121180 Humic Lake clone CrystalBog1F6 AY7922
AY616166.1 gg_id:104851 Pantoea agglomerans str. TJA 98.VII.6 AY6161
GU338400.1 gg_id:544871 Pantoea ananatis str. E-1-4 GU338
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AY924374.1 gg_id:114198 Pantoea agglomerans str. Sc-1 AY9243
AY741162.1 gg_id:163464 Pantoea agglomerans str. S33 AY7411
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AY898642.1 gg_id:112237 Pantoea ananatis str. BD 435 AY8986
GQ332198.1 gg_id:534397 Pantoea ananatis str. M408 GQ332
AB033602.1 gg_id:9868 Pantoea agglomerans AB0336
GQ383918.1 gg_id:592050 Pantoea ananatis str. 4CBJ1 GQ383
FJ611846.1 gg_id:509337 Pantoea ananatis str. LMG 2676 FJ6118
GU324264.1 gg_id:591038 Pantoea ananatis str. M471 GU324
EF602556.1 gg_id:228308 Pantoea ananatis str. ESS29 EF6025
FJ611812.1 gg_id:585566 Pantoea ananatis str. ATCC 27995 FJ6118
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DQ129257.1 gg_id:152527 microarray level air two cities Texas urban aerosol clone AKIW987 DQ129
AF130949.1 gg_id:9937 Pantoea agglomerans str. A87 AF1309
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EU849107.1 gg_id:351329 Pantoea agglomerans str. PSB-UJ2-21 EU8491
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GQ367483.1 gg_id:557905 Pantoea sp. str. A18/07 GQ367

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AF130899.1 gg_id:9913 Pantoea agglomerans str. A21	AF1308
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GQ169378.1 gg_id:537971 Pantoea eucalypti str. IEXa	GQ169
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FM202484.1 gg_id:345858 Pantoea agglomerans str. EV2	FM202
AF130933.1 gg_id:9888 Pantoea agglomerans str. A63	AF1309
EU598802.1 gg_id:267618 Pantoea agglomerans	EU5988
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NR_026047.1 gg_id:559459 Pectobacterium wasabiae str. SR91; ATCC 43316
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EF530558.1 gg_id:218029 Pectobacterium wasabiae str. ICMP 9121
EF530556.1 gg_id:225898 Pectobacterium vasculorum str. ICMP 4226
Z96090.1 gg_id:9790 Pectobacterium carotovorum str. LMG 2386
EF178668.1 gg_id:182325 Pectobacterium atrosepticum str. NZEC20
AY278669.1 gg_id:87761 Photorhabdus sp. str. MOL
Z76750.1 gg_id:10266 Photorhabdus temperata str. Mge1
AY296252.1 gg_id:88447 Photorhabdus temperata
AY280573.1 gg_id:91820 Photorhabdus asymbiotica subsp. australis str. MB
Z76752.1 gg_id:10225 Photorhabdus asymbiotica str. ATCC 43949
Z76749.1 gg_id:10224 Photorhabdus luminescens str. Q614
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FJ006729.1 gg_id:356553 Photorhabdus luminescens str. SRK8
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GQ359965.1 gg_id:579651 Plesiomonas shigelloides str. PIM23
AJ301682.1 gg_id:19524 Proteus mirabilis str. CIP103181T (ATCC29906T)
AJ634474.1 gg_id:105166 Proteus penneri str. ENT229
DQ453959.1 gg_id:154694 Proteus vulgaris str. T-6
DQ826507.1 gg_id:164105 Proteus vulgaris
EF194105.1 gg_id:203330 Proteus mirabilis D3
DQ777867.1 gg_id:166692 Proteus mirabilis
EU411047.1 gg_id:277121 Proteus mirabilis str. GK IV
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AB079370.1 gg_id:19687 Proteus mirabilis str. U1-2
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AM040492.1 gg_id:128082 Providencia rettgeri str. DSM 4542
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AY803746.1 gg_id:108983 Providencia stuartii str. PGS13
EF192136.1 gg_id:206430 Providencia vermicola ANU201
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AB161460.1 gg_id:155411 Providencia sp. str. WW2
DQ824552.1 gg_id:187905 human fecal clone RL185_aaj69e11
DQ824750.1 gg_id:194664 human fecal clone RL185_aaj72f10
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FM209488.1 gg_id:309913 Rahnella aquatilis str. TS18
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FJ811859.1 gg_id:587642 Rahnella aquatilis str. 2B-CDF
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EF685273.1 gg_id:239195 Hepialus gonggaensis sequencing libraries larva guts clone Hg09
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AB099400.1 gg_id:84971 Raoultella planticola str. 4131
EF515418.1 gg_id:220845 Electricigen Enrichment MFC upf microbial fuel cell anode clone 24b10
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FJ823046.1 gg_id:563810 Raoultella ornithinolytica str. gx-110

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U78182.1 gg_id:49258 Raoultella ornithinolytica str. CIP 103 364 T U7818
Y17662.1 gg_id:10128 Raoultella ornithinolytica str. 590681 Y17662
EF515201.1 gg_id:222043 Electricigen Enrichment MFC upf microbial fuel cell anode clone 21c07 EF5152
EF515264.1 gg_id:225880 Electricigen Enrichment MFC upf microbial fuel cell anode clone 22b06 EF5152
EU294412.1 gg_id:257519 Raoultella ornithinolytica str. 38 sullage EU294
EF433545.1 gg_id:211783 Klebsiella sp. str. WW2 EF4335
AB099403.1 gg_id:86319 Raoultella planticola str. ATCC 43176 AB099
EF515440.1 gg_id:217863 Electricigen Enrichment MFC upf microbial fuel cell anode clone 24d09 EF5154
EF515404.1 gg_id:224329 Electricigen Enrichment MFC upf microbial fuel cell anode clone 24a05 EF5154
Y17666.1 gg_id:10130 Raoultella ornithinolytica str. FSK9555 Y17666
AY770415.1 gg_id:134449 insect gut clone AY770
FJ975874.1 gg_id:566870 Human gut microbiome adopts alternative state bowel transplantation ileum effluent FJ9758
DQ333356.1 gg_id:149677 Raoultella planticola str. 33-4ch DQ333
FJ975862.1 gg_id:511415 Human gut microbiome adopts alternative state bowel transplantation ileum effluent FJ9758
AY946284.1 gg_id:114650 Kluyvera cryocrescens 27 AY946
Y17663.1 gg_id:10129 Raoultella planticola str. 7444 Y17663
GQ154930.1 gg_id:511427 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
EU256396.1 gg_id:243243 Bacillus megaterium str. SZN4 EU256
FJ975841.1 gg_id:562152 Human gut microbiome adopts alternative state bowel transplantation ileum effluent FJ9758
AF129444.1 gg_id:42955 Raoultella planticola str. ATCC 33558T AF129
GQ154871.1 gg_id:583590 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
GQ154720.1 gg_id:509089 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
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AF511435.1 gg_id:65398 Serratia fonticola CCCO11b AF511
GQ156035.1 gg_id:545206 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
X93215.1 gg_id:10127 Raoultella planticola str. DSM 3069 T X93215
FJ975867.1 gg_id:569459 Human gut microbiome adopts alternative state bowel transplantation ileum effluent FJ9758
GU374107.1 gg_id:525406 soil East Calcutta wetland clone SRC_NBB7 GU374
Y17659.1 gg_id:10126 Raoultella planticola str. ATCC33531T Y17659
GQ155652.1 gg_id:566917 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
FJ405282.1 gg_id:356864 Citrobacter sp. str. F41 FJ4052
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EU704230.1 gg_id:296868 human biliary stents clone KLONE12 EU704
GQ156448.1 gg_id:593522 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
EU560831.1 gg_id:565501 Assessment genetic Apriona germari (Hope) larvae normalization techniques intestir EU5608
DQ223874.1 gg_id:170406 Obesumbacterium proteus str. RT6 DQ223
EU939439.1 gg_id:329096 Fecal wild pygmy loris feces clone WF16S_295 EU939

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GQ154719.1 gg_id:542496 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
DQ133596.1 gg_id:138380 Pantoea agglomerans str. B1 DQ133
FJ823007.1 gg_id:533363 Raoultella ornithinolytica str. gx-49 FJ8230
GQ154944.1 gg_id:578463 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
EF608520.1 gg_id:234549 predatory Poecilus chalcites their response lab rearing and antibiotic treatment diges EF6085
EU560759.1 gg_id:538000 Assessment genetic intestinal flora Apriona germari (Hope) larvae -RFLP techniques EU560
DQ113752.1 gg_id:132380 dog duodenum clone D1-50 DQ113
GQ154965.1 gg_id:550873 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
GQ156483.1 gg_id:540487 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
GQ156476.1 gg_id:579281 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
GQ154749.1 gg_id:536503 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
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X93216.1 gg_id:10131 Raoultella planticola str. DR3 X93216
GQ156507.1 gg_id:535104 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
AF129443.1 gg_id:25616 Raoultella planticola str. ATCC 33531T AF1294
AB364958.1 gg_id:235818 Raoultella ornithinolytica str. R1 AB3649
GQ154797.1 gg_id:540793 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
AJ508301.1 gg_id:80910 Enterobacter kobei str. CIP 105566 AJ5083
EU870376.1 gg_id:315511 Enterobacter sp. str. SZDA EU8703
AF029226.1 gg_id:9779 Salmonella bongori str. JEO 4162 AF0292
EU014682.1 gg_id:241394 Salmonella bongori str. DSM 13772 EU0146
EF604050.1 gg_id:231538 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040
EF604013.1 gg_id:233727 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040
EF604026.1 gg_id:233581 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040
EF604059.1 gg_id:233315 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040
EF604025.1 gg_id:232625 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040
DQ344533.1 gg_id:147628 Salmonella serovar Typhimurium subsp. enterica DQ344
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EF604061.1 gg_id:230866 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040
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EF604057.1 gg_id:229934 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040
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EF604076.1 gg_id:234402 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040
EF604396.1 gg_id:229998 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6043

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EF604038.1 gg_id:231547 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040
EF604070.1 gg_id:234703 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040
EF604265.1 gg_id:232599 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6042
EU073022.1 gg_id:253204 Salmonella sp. 'group B' HQ010915-1 EU073
EF604087.1 gg_id:235257 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040
EF604376.1 gg_id:227666 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6043
EF604048.1 gg_id:233068 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040
EU118102.1 gg_id:249888 Salmonella enteritidis str. E3 EU118
EF604237.1 gg_id:227737 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6042
DQ683179.1 gg_id:165358 Salmonella paratyphi str. 50973 DQ683
EF604419.1 gg_id:228264 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6044
DQ153191.1 gg_id:138268 Salmonella typhimurium str. S1.I DQ153
EF604015.1 gg_id:230265 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040
EF604056.1 gg_id:229595 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040
EF605231.1 gg_id:228781 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6052
EU118104.1 gg_id:247090 Salmonella enteritidis str. E4 EU118
EF604039.1 gg_id:228911 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040
AB273733.1 gg_id:256256 Salmonella enterica subsp. houtenae str. GTC 1734 AB273
AF130890.2 gg_id:9770 Pantoea agglomerans str. A11 AF1308
EF604075.1 gg_id:230988 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040
EF604427.1 gg_id:231487 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6044
FJ609417.1 gg_id:572114 Salmonella enterica str. PRSC-1 FJ6094
EF604238.1 gg_id:233123 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6042
AF227869.1 gg_id:40959 Salmonella subsp. enterica serovar Typhimurium str. 65946 subsp. AF2278
NC_003197.1 gg_id:128871 Salmonella typhimurium LT2 str. LT2; SGSC 1412; ATCC 700720 NC_00
FJ377885.1 gg_id:363910 Salmonella typhi str. MR9 FJ3778
EF604017.1 gg_id:235063 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040
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EF604062.1 gg_id:230359 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040
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EF604003.1 gg_id:233622 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040
EF604016.1 gg_id:227916 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040
EF604423.1 gg_id:234837 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6044

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EF604394.1 gg_id:229717 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6043
EF604064.1 gg_id:232978 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040
Z47544.1 gg_id:9756 Salmonella typhi str. Ty2 ATCC 19430 Z47544
EF604385.1 gg_id:233497 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6043
EF604103.1 gg_id:232094 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6041
EF604429.1 gg_id:229314 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6044
EF604416.1 gg_id:231885 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6044
AB273736.1 gg_id:248512 Salmonella enterica subsp. arizonae str. GTC 1732 AB2737
AE008820.1 gg_id:34689 Salmonella typhimurium LT2 str. LT2; SGSC 1412; ATCC 700720 LT2 AE0088
EF604012.1 gg_id:228028 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040
EF605229.1 gg_id:234498 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6052
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EF604124.1 gg_id:232989 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6041
EF604049.1 gg_id:229879 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040
EU118106.1 gg_id:241765 Salmonella enteritidis str. E6 EU1181
EF604278.1 gg_id:229337 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6042
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EF604007.1 gg_id:231467 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040
EF604266.1 gg_id:232902 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6042
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EF605236.1 gg_id:231367 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6052
EF604252.1 gg_id:228883 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6042
AF008580.1 gg_id:52635 Salmonella enterica arizonae subsp. IIIa str. ATCC 13314T AF0085
EU118080.1 gg_id:247476 Salmonella paratyphi str. A5 EU1180
EU118113.1 gg_id:249809 Salmonella typhi str. T6 EU1181
EU118101.1 gg_id:251997 Salmonella enteritidis str. E2 EU1181
EF604366.1 gg_id:233919 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6043
AB273735.1 gg_id:255286 Salmonella enterica subsp. diarizonae str. GTC 1733 AB2737
EF604389.1 gg_id:228797 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6043
EF604006.1 gg_id:230459 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040
EF604041.1 gg_id:234900 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040

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EF604350.1 gg_id:230452 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6043
EF604231.1 gg_id:228528 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6042
EF605222.1 gg_id:228682 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6052
X80676.1 gg_id:9753 Salmonella sp str. ATCC 9712 X80676
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EF603990.1 gg_id:229961 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6039
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AB334771.1 gg_id:247431 Serratia proteamaculans str. MPU8	AB3347
EU024331.1 gg_id:240135 intestinal microflora Hepialus gonggaensis larvae RFLP larval gut clone Hg03	EU0243
EU554429.1 gg_id:275241 Pseudomonas fluorescens str. Ag03	EU5544
FJ527460.1 gg_id:563283 Pectobacterium subsp. carotovorum str. Ecc4-4	FJ5274
AM696803.1 gg_id:220457 sequencing libraries indoor dust clone BF0001A090	AM696
AM696807.1 gg_id:218471 sequencing libraries indoor dust clone BF0001A094	AM696
AM696726.1 gg_id:220805 sequencing libraries indoor dust clone BF0001A013	AM696
FJ469981.1 gg_id:544455 Serratia grimesii str. N10-1	FJ4699
U93263.1 gg_id:10181 Aranicola proteolyticus	U93263
AJ279002.1 gg_id:33276 Serratia fonticola str. IB4	AJ2790
DQ321559.1 gg_id:146025 gut- microorganisms larvae and adults southern pine beetle Dendroctonus frontalis	DQ321
AY253924.1 gg_id:83887 Serratia liquefaciens k 100	AY2539
FJ811865.1 gg_id:546427 Serratia liquefaciens str. 1-BCH	FJ8118
EU266583.1 gg_id:256972 Serratia plymuthica str. RG 6	EU2665
FJ527469.1 gg_id:569600 Pectobacterium subsp. carotovorum str. Ecc7-1	FJ5274
EU557336.1 gg_id:261400 Serratia sp. str. J440	EU5573
DQ103512.1 gg_id:131626 Serratia sp. F2	DQ103
GU292825.1 gg_id:541724 Serratia sp. str. L5	GU292
AM696720.1 gg_id:217962 sequencing libraries indoor dust clone BF0001A007	AM696
AY040208.1 gg_id:64290 Serratia proteamaculans	AY0402
FN556576.1 gg_id:526416 Serratia sp. str. JW65.6a	FN5565
EU236755.1 gg_id:250856 Serratia plymuthica str. R1	EU2367
EU031768.1 gg_id:249473 Serratia sp. str. BS18	EU0317
AM696754.1 gg_id:218671 sequencing libraries indoor dust clone BF0001A041	AM696
AB004751.1 gg_id:10186 Serratia rubidaea str. JCM1240	AB0047
AJ233429.1 gg_id:10169 Serratia fonticola str. DSM 4576	AJ2334
AJ279044.1 gg_id:27304 Serratia quinivorans subsp. quinovora str. CP6	AJ2790
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AM696780.1 gg_id:226629 sequencing libraries indoor dust clone BF0001A067	AM696
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AM696788.1 gg_id:222984 sequencing libraries indoor dust clone BF0001A075	AM696
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EU075114.1 gg_id:239779 Serratia sp. str. Lac5	EU0751
AM696779.1 gg_id:224560 sequencing libraries indoor dust clone BF0001A066	AM696
FJ790328.1 gg_id:387955 Serratia sp. C1(2009) str. C1	FJ7903
AM157437.1 gg_id:142918 Serratia proteamaculans mother C4	AM157

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DQ123840.1 gg_id:148321 Serratia liquefaciens str. JF-1116 DQ123
AJ306725.1 gg_id:27899 Serratia liquefaciens str. CIP 103238T AJ3067
AY573038.1 gg_id:101976 Yersinia sp. str. ARCTIC-P11 AY573
AJ233436.1 gg_id:10189 Serratia rubidaea str. DSM 4480 AJ2334
EU196322.1 gg_id:247118 Hafnia sp. NP33 EU196
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EF428994.1 gg_id:216947 Serratia sp. str. GIST-WP4w1 EF4289
AY243097.1 gg_id:85224 Serratia liquefaciens str. Hf1 AY243
AM696787.1 gg_id:219390 sequencing libraries indoor dust clone BF0001A074 AM696
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FJ655517.1 gg_id:554574 symbiont FJ6555
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NC_004337.1 gg_id:140570 Shigella flexneri 2a str. 301 NC_00

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s__endosymbiont of Columbicola columbae	6521
s__Sodalis glossinidius	6210
s__unclassified	4396
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NC_008258.1 gg_id:168839 Shigella flexneri 5 str. 8401 NC_00
AE014073.1 gg_id:146756 Shigella flexneri 2a str. 2457T AE014
EF643608.1 gg_id:249718 Shigella flexneri str. FBD001shig EF6436
NC_008258.1 gg_id:168833 Shigella flexneri 5 str. 8401 NC_00
NC_004741.1 gg_id:129308 Shigella flexneri 2a str. 2457T NC_00
EU467921.1 gg_id:293331 cheetah feces clone CE2_b06 EU467
GQ048030.1 gg_id:421118 Topographical and Temporal Human Skin Microbiome skin palm clone nbw140e08c1 GQ048
GQ141872.1 gg_id:410166 Escherichia coli str. petra-05 GQ141
EU766807.1 gg_id:342976 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU766
EF528266.1 gg_id:222400 Escherichia coli str. CICCHLJ Q41 EF5282
GQ155203.1 gg_id:543477 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EU458164.1 gg_id:296929 North American black bear feces clone BB2_g06 EU458
GQ007663.1 gg_id:502000 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ007
GU594305.1 gg_id:521179 Escherichia coli str. B50 GU594
GQ155258.1 gg_id:588262 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EU470621.1 gg_id:293683 red panda feces clone RP_1aaa03d04 EU470
X96966.1 gg_id:9686 Shigella dysenteriae X96966
GQ155109.1 gg_id:543251 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ155303.1 gg_id:577035 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ155087.1 gg_id:586921 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ155248.1 gg_id:548241 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
AY098487.1 gg_id:66579 Escherichia coli AK108 AY098
DQ819201.1 gg_id:162903 mouse cecal microbiota-colonized zebrafish digestive tract clone aab27a07 DQ819
GQ155047.1 gg_id:513655 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ155132.1 gg_id:551754 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EU472747.1 gg_id:293399 red panda feces clone RPSD_1aaa03h08 EU472
EU778502.1 gg_id:304899 Red Panda feces clone RPSD_1aaa03a11 EU778
GQ155304.1 gg_id:563327 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ047990.1 gg_id:441018 Topographical and Temporal Human Skin Microbiome skin palm clone nbw140a03c1 GQ047
GQ155143.1 gg_id:593967 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
AM184304.1 gg_id:159905 Shigella flexneri str. WAB1966 AM184
GQ155305.1 gg_id:578663 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ155234.1 gg_id:590391 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
AB303383.1 gg_id:246629 slender pigeon louse Columbicola columbae symbiont AB303
AY861702.1 gg_id:112007 Sodalis glossinidius str. GA-SG AY861
AF005235.1 gg_id:9987 primary endosymbiont Sitophilus oryzae str. SFr of AF005
AF548137.1 gg_id:96697 symbiont AF548
AM774412.1 gg_id:237905 Biostraticola tofi str. BF36 AM774
AF548139.1 gg_id:95263 symbiont AF548
AF548142.1 gg_id:95903 symbiont AF548
DQ133565.1 gg_id:148901 Preliminary survey insects (Hemiptera: Coccoidea) scale insect clone DQ133

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s__Citrobacter farmeri	4447
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s__Citrobacter farmeri	5990
s__Citrobacter rodentium	4772
s__Enterobacter radicincitans	6229
s__Kluyvera ascorbata	4413
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EF688008.1 gg_id:341714 Pantoea citrea str. LMG 22049 EF688
FJ617235.1 gg_id:570566 Tatumella morbirosei str. LMG 23359 FJ6172
AJ233437.1 gg_id:10066 Tatumella ptyseos str. DSM 5000 AJ2334
EU877956.1 gg_id:565203 Tatumella ptyseos str. UAPS07005 EU877
EU215774.1 gg_id:257750 Tatumella saanichensis str. 06-3099 EU215
FJ611886.1 gg_id:552042 Pantoea punctata str. LMG 22097 FJ6118
EF688007.1 gg_id:330933 Pantoea terrea str. LMG 22051 EF688
AY837748.1 gg_id:142906 Thorsellia anophelis str. CCUG 49520 H2.1 AY8377
GU185859.1 gg_id:535185 Citrobacter amalonaticus str. SA01 GU185
AB088049.1 gg_id:77675 Citrobacter sp. str. VA53 AB088
AB504755.1 gg_id:386435 Citrobacter farmeri AB504
EU030438.1 gg_id:350440 Citrobacter farmeri EU030
FN433041.1 gg_id:573221 Citrobacter farmeri CCM30B FN433
DQ187379.1 gg_id:140670 Citrobacter amalonaticus DQ187
AY379978.1 gg_id:98643 Salmonella sp. str. AHL 6 AY379
FN433046.1 gg_id:561185 Citrobacter farmeri CCM35B FN433
NR_028686.1 gg_id:586695 Citrobacter sedlakii str. I-75; CDC 4696-86 NR_02
EU931550.1 gg_id:335500 Klebsiella oxytoca str. ZFJ-11 EU931
AF176567.1 gg_id:71543 Kluyvera ascorbata str. CDC 2064/78 AF176
AM933758.1 gg_id:332628 Kluyvera ascorbata 4105 AM933
AJ627203.1 gg_id:106098 Kluyvera ascorbata 276 AJ6272
AF025370.1 gg_id:9766 Citrobacter amalonaticus str. CDC 9020-77 AF0253
GQ205104.1 gg_id:558666 Enterobacter sp. str. RF-100 GQ205
DQ923474.1 gg_id:235571 Enterobacter sp. str. g1 DQ923
FJ593851.1 gg_id:527723 Enterobacter sp. str. MTP_050512_17 FJ5938
AY683044.1 gg_id:137822 Enterobacter sp. str. CBMB30 AY683
EU753977.1 gg_id:315576 Enterobacter sp. str. FR7 EU753
NR_024861.1 gg_id:559750 Citrobacter farmeri str. CDC 2991-81; CIP 104553 NR_02
EF025329.1 gg_id:178177 Enterobacter cloacae subsp. dissolvens str. SREPS 3 EF0253
AB475140.1 gg_id:518801 Cimex lectularius endosymbiont str. SYDL AB475
GQ492450.1 gg_id:590760 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
AAJU02000050.1 gg_id:311814 Escherichia coli str. F11 AAJU0
EU773756.1 gg_id:323418 Cheetah feces clone CE2_h04_1 EU773
AB244469.1 gg_id:253351 Enterobacter cloacae str. NC1111 AB244
AM980865.1 gg_id:369200 Escherichia coli str. ATCC 35218 AM980
EU460669.1 gg_id:289561 polar bear feces clone PB2_aai24b09 EU460
AB244459.1 gg_id:248864 Citrobacter freundii str. C3-1 AB244
FJ811872.1 gg_id:586506 Enterobacter aerogenes str. 11-WCH FJ8118
GQ047957.1 gg_id:440793 Topographical and Temporal Human Skin Microbiome skin palm clone nbw139e11c1 GQ047
AY253921.1 gg_id:85035 Rahnella aquatilis m 46 AY253
GQ155272.1 gg_id:575075 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155

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GQ155218.1 gg_id:561972 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EU723822.1 gg_id:345487 Shigella sonnei str. HDDMG06 EU723
AB479110.1 gg_id:561984 Escherichia hermannii str. YS-11 AB479
GQ155226.1 gg_id:513466 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ155033.1 gg_id:572044 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EU472730.1 gg_id:290622 red panda feces clone RPSD_1aaa01a11 EU472
EU470818.1 gg_id:288035 red panda feces clone RP_2aaa01b05 EU470
ABHR01000009.1 gg_id:292182 Escherichia coli O157:H7 str. EC4401 ABHR0
EU472797.1 gg_id:295950 red panda feces clone RPSD_1aaa03d01 EU472
DQ441386.1 gg_id:184632 human intestinal biopsy clone CD135 DQ441
EF179843.1 gg_id:271664 sequences adult Anopheles darlingi (Diptera: Culicidae) mosquitoes clone 1.1 EF1798
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GQ491694.1 gg_id:593660 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
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EF189919.1 gg_id:365055 Pantoea stewartii 40G RT2A EF1899
EU466029.1 gg_id:295053 African elephant feces clone AFEL3_aao16b08 EU466
FN433049.1 gg_id:547245 Citrobacter braakii CCM33B FN433
EU460308.1 gg_id:299829 polar bear feces clone PB1_aai26c12 EU460
GQ155101.1 gg_id:565925 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ047977.1 gg_id:445372 Topographical and Temporal Human Skin Microbiome skin palm clone nbw139g10c GQ047
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FJ364672.1 gg_id:370240 feces adult twins and mothers; TS19 clone TS19_a01f10 FJ3646
EU460405.1 gg_id:294051 polar bear feces clone PB1_aai28b07 EU460
DQ818978.1 gg_id:168683 mouse cecal microbiota-colonized zebrafish digestive tract clone aab40d10 DQ818
DQ133536.1 gg_id:138463 Citrobacter freundii str. GM1 DQ133
EU470874.1 gg_id:300686 red panda feces clone RP_2aaa01h11 EU470
AJ223409.1 gg_id:9789 Pectobacterium cacticida AJ2234
EF608524.1 gg_id:228556 predatory Poecilus chalcites their response lab rearing and antibiotic treatment diges EF6085
AY227805.1 gg_id:100736 Pantoea dispersa UQ68J AY2278
GQ155135.1 gg_id:578405 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EF551364.1 gg_id:223793 Enterobacter cloacae str. Rs-35 EF5513
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EF643377.1 gg_id:236811 Mangroveibacter plantisponsor str. MSSRF40 EF6433

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GQ155237.1 gg_id:576536 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
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GQ155055.1 gg_id:509758 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ492249.1 gg_id:536894 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
EU470678.1 gg_id:290999 red panda feces clone RP_1aaa02d02 EU470
EF515346.1 gg_id:226413 Electricigen Enrichment MFC upf microbial fuel cell anode clone 23b11 EF5153
EU472809.1 gg_id:299738 red panda feces clone RPSD_1aaa02d05 EU472
EU596536.1 gg_id:273327 Pantoea agglomerans str. SZ009 EU596
EU289465.1 gg_id:240399 metagenomic approach biosynthesis ansamycin endophytes or symbionts enriched s EU289
AB548574.1 gg_id:531505 Escherichia coli str. JCM 24001 AB548
EU466771.1 gg_id:289838 African elephant feces clone AFEL2_aao29c08 EU466
EU472860.1 gg_id:295962 red panda feces clone RPSD_1aaa02g08 EU472
GQ155181.1 gg_id:512375 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ114745.1 gg_id:385051 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ114
EU472794.1 gg_id:294989 red panda feces clone RPSD_1aaa03a08 EU472
FJ683754.1 gg_id:530543 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6837
DQ248277.1 gg_id:142545 carbon tetrachloride contaminated soil clone TA2 DQ248
EU772604.1 gg_id:322410 North American Black Bear feces clone BB1_h09 EU772
GU166291.1 gg_id:588020 Pantoea sp. str. Y1 GU166
E05133.1 gg_id:28107 Escherichia coli E05133

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AB548828.1 gg_id:514244 Citrobacter freundii str. JCM 24063 AB5488
GQ304782.1 gg_id:585624 Shigella flexneri str. A6 GQ304
NC_008253.1 gg_id:162759 Escherichia coli str. 536 NC_008
GQ101929.1 gg_id:465791 Topographical and Temporal Human Skin Microbiome skin palm clone nbw501a07c1 GQ101
AJ010486.1 gg_id:9947 Enterobacter pyrinus str. KCTC2520 AJ0104
DQ785510.1 gg_id:171754 Pectobacterium carotovorum str. ZJR1 DQ785
EU472892.1 gg_id:289762 red panda feces clone RPSD_1aaa01f07 EU4728
GQ031973.1 gg_id:484652 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw: GQ031
AM419020.1 gg_id:196793 Rahnella sp. str. NJ-8 AM419
EU470589.1 gg_id:290393 red panda feces clone RP_1aaa03e10 EU4705
EU530394.1 gg_id:261413 mucosa adherent and invasive microbes adenoma colorectal cancer profile non-ader EU5303
AB004744.1 gg_id:10064 Enterobacter asburiae str. JCM6051 AB0047
EU887834.1 gg_id:349857 and RFLP slurry Nisargruna biogas plant aerobic predigester clone 11A EU8878
GU594302.1 gg_id:519860 Escherichia coli str. A23 GU594
GQ155206.1 gg_id:569366 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EF515196.1 gg_id:226252 Electricigen Enrichment MFC upf microbial fuel cell anode clone 21b10 EF5151
EF560793.1 gg_id:238066 Escherichia coli str. BEG21 EF5607
DQ818882.1 gg_id:166890 mouse cecal microbiota-colonized zebrafish digestive tract clone aab39b10 DQ818
GQ155211.1 gg_id:546826 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EU470583.1 gg_id:302277 red panda feces clone RP_1aaa04a10 EU4705
FJ906906.1 gg_id:571278 Cronobacter muytjensii str. Jor93 FJ9069
DQ068925.1 gg_id:139022 microbiota antlions (Myrmeleon mobilis) whole animal laboratory starved antlion O DQ068
AM184307.1 gg_id:160426 Pantoea agglomerans str. WAB1969 AM184
GQ009455.1 gg_id:500210 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw77 GQ009
GQ102029.1 gg_id:442720 Topographical and Temporal Human Skin Microbiome skin palm clone nbw502f06c1 GQ102
GQ155009.1 gg_id:566225 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
AP010960.1 gg_id:546416 Escherichia coli O111:H- str. 11128 AP0109
X80729.1 gg_id:9692 Escherichia coli str. PK3 X80729
GQ155095.1 gg_id:510292 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GU223214.1 gg_id:581700 Enterobacter cloacae str. SK_C-2 GU223
U92195.1 gg_id:9714 Salmonella enterica subsp. houtenae serovar Houten str. Sh1 subsp. U92195
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GQ491972.1 gg_id:550764 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
GQ031668.1 gg_id:440795 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ031
FJ009375.1 gg_id:338379 Enterobacter cancerogenus str. H3 FJ0093
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DQ392983.1 gg_id:156485 Pantoea agglomerans str. d DQ392
GQ154854.1 gg_id:511626 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154

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CP001790.1 gg_id:523633 Pectobacterium wasabiae str. WPP163 CP0017
GQ025498.1 gg_id:405896 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ025
GQ155325.1 gg_id:582831 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
FJ611867.1 gg_id:538150 Enterobacter cancerogenus str. LMG 2693 FJ6118
EF418614.1 gg_id:216720 Escherichia coli str. WR EF4186
GQ156571.1 gg_id:566976 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
EU466945.1 gg_id:296544 African elephant feces clone AFEL2_aao31f11 EU4669
GQ155259.1 gg_id:553265 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
CP000247.1 gg_id:169669 Escherichia coli str. 536 CP0002
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GU171376.1 gg_id:580156 Rahnella aquatilis str. 5YN04-01 GU171
AM157447.1 gg_id:141508 Escherichia coli mother V4 AM157
FJ906795.1 gg_id:568033 Erwinia chrysanthemi str. Lichuan2 FJ9067
FJ997269.1 gg_id:430317 Escherichia coli str. DSPV 247T FJ9972
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GQ155014.1 gg_id:538134 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
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EU780667.1 gg_id:307587 Pantoea sp. str. CWB304 EU7806
GQ031664.1 gg_id:465153 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ031
GQ155195.1 gg_id:582588 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EF446900.1 gg_id:210269 Enterobacter cloacae str. AW3 EF4469
GQ101953.1 gg_id:441943 Topographical and Temporal Human Skin Microbiome skin palm clone nbw501f08c1 GQ101
EF560774.1 gg_id:233520 Escherichia coli str. 228 EF5607
AM184220.1 gg_id:159834 Enterobacter cloacae str. WAB1878 AM184
EU937744.1 gg_id:329159 Enterobacter sakazakii str. JG 09 Iti 7 EU9377
DQ444288.1 gg_id:154803 Klebsiella oxytoca str. 17 DQ444
GQ047998.1 gg_id:430834 Topographical and Temporal Human Skin Microbiome skin palm clone nbw140a11c1 GQ047
GQ156028.1 gg_id:566205 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
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EU470480.1 gg_id:291647 red panda feces clone RP_1aaa02b02 EU4704
DQ068852.1 gg_id:139468 microbiota antlions (Myrmeleon mobilis) GI tract freshly caught antlion OTU9 clone DQ068
EU470518.1 gg_id:288607 red panda feces clone RP_1aaa01b06 EU4705
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CP001637.1 gg_id:524975 Escherichia coli str. DH1 CP0016
EU472906.1 gg_id:298938 red panda feces clone RPSD_1aaa02d07 EU4729
GQ155318.1 gg_id:509391 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
AY690711.1 gg_id:101221 Erwinia sp. str. MK01 AY6907
GQ048037.1 gg_id:462729 Topographical and Temporal Human Skin Microbiome skin palm clone nbw140f06c1 GQ048

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FJ370038.1 gg_id:359179 feces adult twins and mothers; TS55 clone TS55_a03g03 FJ3700
FJ976607.1 gg_id:540908 Enterobacter sp. str. LCR98 FJ9766
CU928161.2 gg_id:563140 Escherichia coli str. S88 CU928
AY834756.1 gg_id:110694 Rhodopseudomonas palustris str. 2c AY8347
GQ099129.1 gg_id:380807 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ099
DQ223872.1 gg_id:164430 Buttiauxella sp. str. P5 DQ223
NZ_AAJU01000010.1 gg_id:139105 Escherichia coli str. F11 NZ_AA
EU471308.1 gg_id:294785 red panda feces clone RP_3aaa03b08 EU4713
GQ155251.1 gg_id:594208 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ155172.1 gg_id:544931 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EU472722.1 gg_id:295041 red panda feces clone RPSD_1aaa03b06 EU4727
GQ416532.1 gg_id:565456 Temporal succession biological degreasing systems clone F7jun.10 GQ416
EU216734.1 gg_id:329496 Pantoea sp. str. LMG 5345 EU2167
Z96077.1 gg_id:10042 Enterobacter nimipressuralis str. LMG 10245-T Z96077
GQ025526.1 gg_id:446114 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ025
GQ095671.1 gg_id:410941 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw4 GQ095
AF130892.2 gg_id:10079 Pantoea endophytica str. A13 AF1308
GQ155872.1 gg_id:581530 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
AY253920.1 gg_id:86492 Rahnella aquatilis k 62 AY2539
GQ025170.1 gg_id:405718 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1 GQ025
AJ583836.1 gg_id:95192 Pantoea agglomerans str. Pa4842 AJ5838
GQ102051.1 gg_id:394557 Topographical and Temporal Human Skin Microbiome skin palm clone nbw502h07c1 GQ102
GQ155846.1 gg_id:510610 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
FJ969376.1 gg_id:394960 Pectobacterium carotovorum str. KKH3 FJ9693
CP000948.1 gg_id:270797 Escherichia coli substr. DH10B str. K-12 CP0009
EU468003.1 gg_id:290774 cheetah feces clone CE2_a06_1 EU4680
AE005174.2 gg_id:128878 Escherichia coli O157:H7 str. EDL933 AE0051
GQ155038.1 gg_id:554226 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ492044.1 gg_id:572998 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
EU472657.1 gg_id:297746 red panda feces clone RPSD_1aaa04c10 EU4726
DQ278909.1 gg_id:144626 Enterobacter sp. str. Eg8 DQ278
EF560790.1 gg_id:228008 Escherichia coli str. BEE13 EF5607
EU430750.1 gg_id:260369 Enterobacter sp. str. ZJUPD6 EU4307
NZ_ACGN01000123.1 gg_id:470367 Escherichia coli str. 83972 NZ_AC
DQ068760.1 gg_id:172586 Salmonella sp. str. Co9936 DQ068
AF395913.1 gg_id:38659 Enterobacter aerogenes AF3959
GQ492576.1 gg_id:535166 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
GQ101935.1 gg_id:375951 Topographical and Temporal Human Skin Microbiome skin palm clone nbw501b03c1 GQ101
GQ047665.1 gg_id:449134 Topographical and Temporal Human Skin Microbiome skin palm clone nbw137e10c1 GQ047
EU471071.1 gg_id:297139 red panda feces clone RP_3aaa03f12 EU4710
AB286558.1 gg_id:217008 Reducing production and domination comamonadaceae reducing oxygen supply was AB2865

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GQ114706.1 gg_id:453826 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ114
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AM184226.1 gg_id:160051 Enterobacter sp. str. WAB1884 AM184
AF520708.1 gg_id:61203 Dickeya dianthicola str. CFBP 1200 AF5207
EF489443.1 gg_id:219392 Pantoea agglomerans str. GIST-NKst1 EF4894
EF153300.1 gg_id:186788 identification gut fourth-instar red imported fire ant (Solenopsis Buren) larvae GI trac EF1533
EF560782.1 gg_id:233200 Escherichia coli str. BE33 EF5607
U90758.1 gg_id:10315 Rahnella genosp. 3 str. DSM 30078 U90758
AJ233409.1 gg_id:10306 Brenneria alni str. DSM 11811 AJ2334
EU761873.1 gg_id:346129 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1 EU7618
GQ155273.1 gg_id:591917 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EU464932.1 gg_id:290119 African elephant feces clone AFYEL_aaj65d02 EU4649
GQ025120.1 gg_id:438223 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1 GQ025
GQ025542.1 gg_id:460697 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ025
EU430755.1 gg_id:259306 Enterobacter sp. str. ZJUPD1 EU4307
EU430752.1 gg_id:267416 Enterobacter sp. str. ZJUPD4 EU4307
EU430753.1 gg_id:270355 Enterobacter sp. str. ZJUPD3 EU4307
DQ223881.1 gg_id:168597 Citrobacter gillenii str. P9 DQ223
NC_004431.1 gg_id:128802 Escherichia coli str. CFT073 NC_004
EU471669.1 gg_id:297637 Asiatic elephant feces clone AE1_aaa03f11 EU4716
DQ112330.1 gg_id:136199 Pantoea agglomerans str. RS-18 DQ112
EU470656.1 gg_id:287789 red panda feces clone RP_1aaa03g09 EU4706
DQ068872.1 gg_id:139038 microbiota antlions (Myrmeleon mobilis) whole animal freshly caught antlion OTU1(DQ068
GQ048022.1 gg_id:442026 Topographical and Temporal Human Skin Microbiome skin palm clone nbw140d07c GQ048
AM062693.1 gg_id:249744 Enterobacter amnigenus p412 AM062
EU471187.1 gg_id:291079 red panda feces clone RP_3aaa04e11 EU4711
GU185862.1 gg_id:587224 Enterobacter ludwigii str. HSBN1 GU185
GQ155216.1 gg_id:583212 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
AM491468.1 gg_id:213014 Aranicola sp. str. Nj-67 AM491
GQ101988.1 gg_id:430225 Topographical and Temporal Human Skin Microbiome skin palm clone nbw502b08c GQ101
GQ155035.1 gg_id:587112 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EU471045.1 gg_id:293597 red panda feces clone RP_3aaa02e12 EU4710
EU458408.1 gg_id:295685 spotted hyena feces clone HY1_f04 EU4584
GU374094.1 gg_id:526760 soil East Calcutta wetland clone SRC_NBB2 GU374
GQ047705.1 gg_id:399615 Topographical and Temporal Human Skin Microbiome skin palm clone nbw138b11c GQ047
DQ298156.1 gg_id:142765 Escherichia sp. SWM_Isolation_4 DQ298
EU472916.1 gg_id:287896 red panda feces clone RPSD_1aaa04b06 EU4729
U88545.1 gg_id:9669 Salmonella typhi str. St111 U88545
EU472820.1 gg_id:294893 red panda feces clone RPSD_1aaa03c03 EU4728

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FJ267520.2 gg_id:343017 Escherichia blattae str. DSM 4481 FJ2675
FJ683659.1 gg_id:523290 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6836
X80680.1 gg_id:9721 Shigella dysenteriae X80680
GU272220.1 gg_id:592196 Escherichia coli str. wz_1977 GU272
DQ223879.1 gg_id:168024 Enterobacter amnigenus str. P4 DQ223
EU472796.1 gg_id:292881 red panda feces clone RPSD_1aaa04e04 EU472
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EU554444.1 gg_id:273128 Enterobacter asburiae str. Ag18 EU554
GQ099291.1 gg_id:395047 Topographical and Temporal Human Skin Microbiome skin interdigital web space cl GQ099
EF446895.1 gg_id:210966 Acinetobacter radioresistens str. Philippines-11 EF4468
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GQ155878.1 gg_id:549556 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
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FJ975887.1 gg_id:534463 Human gut microbiome adopts alternative state bowel transplantation ileum effluent FJ9758
FJ593037.1 gg_id:572846 Pectobacterium wasabiae str. JU-1 FJ5930
GQ155094.1 gg_id:593339 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
CU928162.2 gg_id:547290 Escherichia coli str. ED1a CU928
EF620926.1 gg_id:254200 Escherichia coli str. WD02 EF6209
EF620923.1 gg_id:254591 Escherichia coli str. SYW004 EF6209
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NR_024706.1 gg_id:562424 Pseudomonas flectens str. ATCC 12775 NR_02
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EU239468.1 gg_id:255707 Enterobacter asburiae str. XJUHX-5 EU2394
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EU472837.1 gg_id:295363 red panda feces clone RPSD_1aaa02h08 EU472
GQ155060.1 gg_id:509438 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ031670.1 gg_id:381600 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ031
AB273742.1 gg_id:245432 Cedecea lapagei str. GTC 346 AB273
FJ405361.1 gg_id:358229 Rahnella aquatilis str. SPb FJ4053
EU471082.1 gg_id:295799 red panda feces clone RP_3aaa04g04 EU471
FJ366024.1 gg_id:361492 feces adult twins and mothers; TS25 clone TS25_a01g12 FJ3660
EU472850.1 gg_id:301348 red panda feces clone RPSD_1aaa03d12 EU472
FJ975869.1 gg_id:513372 Human gut microbiome adopts alternative state bowel transplantation ileum effluent FJ9758
ABHO01000013.1 gg_id:286158 Escherichia coli O157:H7 str. EC4196 ABHO
DQ347522.1 gg_id:147724 Paracoccus sp. B-1012 DQ347
DQ124676.1 gg_id:136582 Enterobacter aerogenes str. S2-1 DQ124
U90314.1 gg_id:9706 Salmonella subsp. enterica serovar Blockley str. Sb1 subsp. U90314
X80725.1 gg_id:9741 Escherichia coli str. ATCC 11775T X80725
FM180568.1 gg_id:369788 Escherichia coli 0127:H6 str. E2348/69 FM180
DQ068864.1 gg_id:139117 microbiota antlions (Myrmeleon mobilis) whole animal freshly caught antlion OTU1 DQ068
GQ493963.1 gg_id:583626 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
EU834264.1 gg_id:332053 Raoultella ornithinolytica str. DS44 EU834
EF178670.1 gg_id:180411 Erwinia chrysanthemi str. NZEC135 EF1786
EU857633.1 gg_id:366089 Shigella flexneri EU857
AM933754.1 gg_id:340632 Kluyvera cryocrescens 169 AM933
EU472757.1 gg_id:301762 red panda feces clone RPSD_1aaa02d04 EU472
EF560786.1 gg_id:231669 Escherichia coli str. BE45 EF5607
GQ025603.1 gg_id:416339 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ025
FJ811871.1 gg_id:552136 Enterobacter aerogenes str. 7-WCH FJ8118
EU773798.1 gg_id:346813 Cheetah feces clone CE2_e03 EU773
GQ047918.1 gg_id:402513 Topographical and Temporal Human Skin Microbiome skin palm clone nbw139a08c1 GQ047
EU778388.1 gg_id:354647 Red Panda feces clone RP_1aaa02f05 EU778
EU471154.1 gg_id:297213 red panda feces clone RP_3aaa03f09 EU471
AF024608.1 gg_id:9727 Pantoea agglomerans str. TAC.III.94.1 AF0246
GQ155244.1 gg_id:571288 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ025550.1 gg_id:382453 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ025
GU186121.1 gg_id:584341 Pantoea agglomerans str. IHB B 1383 GU186
EU460458.1 gg_id:293981 polar bear feces clone PB2_aai21b06 EU460

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GQ024535.1 gg_id:485135 Topographical and Temporal Human Skin Microbiome skin palm clone nbw123e03c1 GQ024
Z96089.1 gg_id:9989 Pectobacterium carotovorum str. LMG 2404-T Z96089
GQ154883.1 gg_id:547125 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
GQ025585.1 gg_id:403646 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ025
EU684953.1 gg_id:295125 Erwinia chrysanthemi str. E353 EU684
AB244472.1 gg_id:248467 Enterobacter aerogenes str. NC4211 AB244
GU594308.1 gg_id:531073 Escherichia coli str. AC3 GU594
EU470599.1 gg_id:303181 red panda feces clone RP_1aaa01f04 EU470
GQ101940.1 gg_id:429707 Topographical and Temporal Human Skin Microbiome skin palm clone nbw501b10c1 GQ101
FJ906923.1 gg_id:548205 Cronobacter sakazakii str. Jor183 FJ9069
GQ416891.1 gg_id:572750 Temporal succession biological degreasing systems clone F1jun.25 GQ416
FJ192752.1 gg_id:308904 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior FJ1927
EF515391.1 gg_id:220037 Electricigen Enrichment MFC upf microbial fuel cell anode clone 23g08 EF5153
GQ492620.1 gg_id:561719 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
GQ155307.1 gg_id:553345 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ493735.1 gg_id:590258 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
AM184247.1 gg_id:161342 Enterobacter aerogenes str. WAB1906 AM184
FJ405332.1 gg_id:367948 Escherichia coli str. 4059 FJ4053
EF560785.1 gg_id:232471 Escherichia coli str. BE42 EF5607
GQ155160.1 gg_id:585374 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ114876.1 gg_id:466445 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ114
AB273737.1 gg_id:236285 Trabulsiella guamensis str. GTC 1379 AB2737
EU240950.1 gg_id:272583 Enterobacter hormaechei str. YO-B EU2409
GQ085256.1 gg_id:409792 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw273b02c GQ085
AB548824.1 gg_id:529730 Citrobacter freundii str. JCM 24059 AB5488
GQ031696.1 gg_id:454885 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ031
GQ155185.1 gg_id:582498 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
AJ233421.1 gg_id:9796 Leminorella grimontii str. DSM 5078 AJ2334
FJ364615.1 gg_id:362183 feces adult twins and mothers; TS19 clone TS19_a01a10 FJ3646
EU471104.1 gg_id:297764 red panda feces clone RP_3aaa03f01 EU4711
FJ611877.1 gg_id:582578 Enterobacter sp. str. ATCC 27981 FJ6118
FJ404760.1 gg_id:368274 Mangroveibacter sp. str. WG-1 FJ4047
NZ_ABHL02000001.1 gg_id:316857 Escherichia coli O157:H7 str. EC4045 NZ_AB
NC_002655.2 gg_id:150516 Escherichia coli O157:H7 str. EDL933 NC_00
GQ155256.1 gg_id:545159 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
FJ608656.1 gg_id:566084 Klebsiella pneumoniae str. EP4 FJ6086
EU468018.1 gg_id:301955 cheetah feces clone CE2_c10_2 EU468
FJ178002.1 gg_id:333293 Escherichia coli str. AC 521 FJ1780
EU430751.1 gg_id:272055 Enterobacter sp. str. ZJUPD5 EU430
GQ492150.1 gg_id:537226 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492

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EU275356.1 gg_id:256517 Enterobacter amnigenus str. CONC4 EU275
GQ493157.1 gg_id:592185 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
NC_007946.1 gg_id:156719 Escherichia coli str. UTI89 NC_00
GQ069665.1 gg_id:467129 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ069
EU460420.1 gg_id:292398 polar bear feces clone PB1_aai28d07 EU460
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EF059884.1 gg_id:226386 Enterobacter pyrinus str. E872 EF0598
U90318.1 gg_id:9667 Salmonella enteritidis str. SE22 U9031
EF604220.1 gg_id:231694 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6042
FJ975783.1 gg_id:580915 Human gut microbiome adopts alternative state bowel transplantation ileum effluent FJ9757
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FJ997270.1 gg_id:422465 Escherichia coli str. DSPV 284T FJ9972
GQ045414.1 gg_id:378815 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ045
GQ155041.1 gg_id:590526 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ048012.1 gg_id:433171 Topographical and Temporal Human Skin Microbiome skin palm clone nbw140c06c1 GQ048
GQ154774.1 gg_id:512283 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
GQ085555.1 gg_id:400155 Topographical and Temporal Human Skin Microbiome skin palm clone nbw277e02c1 GQ085
FJ745300.1 gg_id:529154 Enterobacter sp. str. DHM-1T FJ7453
GQ101981.1 gg_id:447089 Topographical and Temporal Human Skin Microbiome skin palm clone nbw502a11c1 GQ101
EU471150.1 gg_id:289419 red panda feces clone RP_3aaa01h02 EU471
EU472682.1 gg_id:302297 red panda feces clone RPSD_1aaa01b01 EU472
EF604226.1 gg_id:231697 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6042
FM180568.1 gg_id:369789 Escherichia coli 0127:H6 str. E2348/69 FM180
CP001790.1 gg_id:523634 Pectobacterium wasabiae str. WPP163 CP001
NC_002655.2 gg_id:150515 Escherichia coli O157:H7 str. EDL933 NC_00
FJ976591.1 gg_id:586643 Enterobacter cloacae str. LCR82 FJ9765
EU471123.1 gg_id:297308 red panda feces clone RP_3aaa04c06 EU471
EU470963.1 gg_id:291712 red panda feces clone RP_2aaa01f10 EU470
GQ047956.1 gg_id:386610 Topographical and Temporal Human Skin Microbiome skin palm clone nbw139e10c1 GQ047
GQ155268.1 gg_id:536948 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EU472798.1 gg_id:287407 red panda feces clone RPSD_1aaa04f01 EU472
GQ069125.1 gg_id:405545 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ069
NC_008563.1 gg_id:176526 Escherichia coli str. APEC O1 NC_00
FJ463821.1 gg_id:363666 Escherichia coli str. 4107 FJ4638
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GQ016868.1 gg_id:492799 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw826d1 GQ016
GQ048034.1 gg_id:414459 Topographical and Temporal Human Skin Microbiome skin palm clone nbw140f03c1 GQ048

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AY941834.1 gg_id:114469 Pantoea agglomerans str. XW112 AY941
AB269763.1 gg_id:167919 Escherichia coli str. AE1-2 AB269
GQ155076.1 gg_id:587663 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EU471300.1 gg_id:297539 red panda feces clone RP_3aaa02b11 EU471
GQ099117.1 gg_id:373130 Topographical and Temporal Human Skin Microbiome skin interdigital web space cl GQ099
DQ836638.1 gg_id:165472 gut- microorganisms pupa and adults pine engraver gut Ips pini larva clone ips8e3 DQ836
GQ095896.1 gg_id:412687 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ095
NZ_AAJU02000034.1 gg_id:351276 Escherichia coli str. F11 NZ_AA
AB428447.1 gg_id:331682 Ewingella americana str. GLD AB428
FJ605379.1 gg_id:449339 Enterobacter cloacae str. AceL-1 FJ6053
AJ884896.1 gg_id:191235 Rahnella sp. N1EH1 AJ8848
GQ155165.1 gg_id:589437 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
Z14096.1 gg_id:9994 Parasite BEV of E.variegatus Z14096
GQ493261.1 gg_id:592641 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
GQ155053.1 gg_id:511492 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EU470684.1 gg_id:292570 red panda feces clone RP_1aaa03a02 EU470
DQ356903.1 gg_id:153848 Pantoea agglomerans str. P29 DQ356
GQ025092.1 gg_id:386644 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1 GQ025
EU470757.1 gg_id:292134 red panda feces clone RP_2aaa02d12 EU470
DQ347838.1 gg_id:145311 Enterobacter cloacae Ecl_IIT-BT08 DQ347
EF059824.1 gg_id:222822 Enterobacter sakazakii str. E283 EF0598
GU594312.1 gg_id:531208 Escherichia coli str. E36 GU594
FJ368408.1 gg_id:361452 feces adult twins and mothers; TS3 clone TS3_a04a06 FJ3684
GQ155271.1 gg_id:586018 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EU816587.1 gg_id:305982 Enterobacter sp. str. MB-2-2-4 EU816
EF604008.1 gg_id:228026 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6040
GQ047651.1 gg_id:462723 Topographical and Temporal Human Skin Microbiome skin palm clone nbw137c11c1 GQ047
EU472845.1 gg_id:300896 red panda feces clone RPSD_1aaa03f06 EU472
EU472732.1 gg_id:293451 red panda feces clone RPSD_1aaa02f03 EU472
EU420928.1 gg_id:274149 Citrobacter freundii str. SA-A5-98 EU420
GQ155187.1 gg_id:592787 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
FM180568.1 gg_id:369793 Escherichia coli 0127:H6 str. E2348/69 FM180
FJ823386.1 gg_id:592076 Escherichia coli str. TCP-1 FJ8233
FJ975788.1 gg_id:589157 Human gut microbiome adopts alternative state bowel transplantation ileum effluent FJ9757
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EF515421.1 gg_id:217233 Electricigen Enrichment MFC upf microbial fuel cell anode clone 24c02 EF5154
NZ_ABHT01000152.1 gg_id:260777 Escherichia coli O157:H7 str. EC4501 NZ_AB

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GQ155197.1 gg_id:585037 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EU472785.1 gg_id:299402 red panda feces clone RPSD_1aaa01c08 EU472
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EU535123.1 gg_id:280193 profile human microbiota antecubital fossa (inner elbow) skin clone nbt171c02 EU5351
EU464506.1 gg_id:297762 African elephant feces clone AFEL_aai30c11 EU4645
GQ048005.1 gg_id:385167 Topographical and Temporal Human Skin Microbiome skin palm clone nbw140b08c1 GQ048
AB273744.1 gg_id:236091 Erwinia aphidicola str. GTC 1688 AB2737
GQ154843.1 gg_id:553840 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
EU470615.1 gg_id:291008 red panda feces clone RP_1aaa04d04 EU4706
GQ025492.1 gg_id:441988 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ025
GQ026798.1 gg_id:457125 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ026
EU778387.1 gg_id:356210 Red Panda feces clone RPSD_1aaa04a08 EU7783
EU470573.1 gg_id:301959 red panda feces clone RP_1aaa03e03 EU4705
GQ154857.1 gg_id:580141 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
GQ047689.1 gg_id:449074 Topographical and Temporal Human Skin Microbiome skin palm clone nbw137h10c1 GQ047
CU928161.2 gg_id:563141 Escherichia coli str. S88 CU928
EF059842.1 gg_id:224891 Enterobacter asburiae str. E531 EF0598
EU467838.1 gg_id:297319 North American black bear feces clone BB1_b07_2 EU4678
GQ492166.1 gg_id:590121 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
GQ492874.1 gg_id:535252 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
FJ405333.1 gg_id:369236 Escherichia coli str. 4060 FJ4053
AY373830.1 gg_id:105259 Trabulsiella guamensis AY3738
AB198445.1 gg_id:135844 termite gut wall fraction clone RsW01-004 AB1984
GQ025599.1 gg_id:389061 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ025
GQ114854.1 gg_id:415761 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ114
U90316.1 gg_id:9661 Salmonella typhimurium str. Stm1 U90316
DQ068855.1 gg_id:138975 microbiota antlions (Myrmeleon mobilis) GI tract freshly caught antlion OTU6 clone DQ068
EU470655.1 gg_id:297290 red panda feces clone RP_1aaa04h06 EU4706
GQ031692.1 gg_id:383643 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ031

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EF191171.1 gg_id:189337 Escherichia coli dcm EF1911
EF515376.1 gg_id:225183 Electricigen Enrichment MFC upf microbial fuel cell anode clone 23e11 EF5153
GQ155116.1 gg_id:511824 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ155122.1 gg_id:569621 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EF428236.2 gg_id:218527 Enterobacter hormaechei str. HDYM-06 EF4282
GQ155942.1 gg_id:574837 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
DQ818881.1 gg_id:164892 mouse cecal microbiota-colonized zebrafish digestive tract clone aab39b09 DQ818
EF515182.1 gg_id:226172 Electricigen Enrichment MFC upf microbial fuel cell anode clone 21a07 EF5151
GQ047658.1 gg_id:400299 Topographical and Temporal Human Skin Microbiome skin palm clone nbw137d10c1 GQ047
GQ155319.1 gg_id:511367 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ493947.1 gg_id:532961 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
AP010953.1 gg_id:568503 Escherichia coli O26:H11 str. 11368 AP010
GQ102038.1 gg_id:456984 Topographical and Temporal Human Skin Microbiome skin palm clone nbw502g05c1 GQ102
CU928161.2 gg_id:563143 Escherichia coli str. S88 CU928
GQ069819.1 gg_id:465176 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw1 GQ069
FJ975865.1 gg_id:554433 Human gut microbiome adopts alternative state bowel transplantation ileum effluent FJ9758
FJ368169.1 gg_id:362886 feces adult twins and mothers; TS3 clone TS3_a01a10 FJ3681
EU472720.1 gg_id:289568 red panda feces clone RPSD_1aaa03g08 EU472
GQ155176.1 gg_id:512507 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
AM933757.1 gg_id:353249 Kluyvera cryocrescens 4701 AM933
CU928162.2 gg_id:547289 Escherichia coli str. ED1a CU928
NZ_ABHK01000009.1 gg_id:260250 Escherichia coli O157:H7 str. EC4206 NZ_AB
EU472859.1 gg_id:302247 red panda feces clone RPSD_1aaa03f11 EU472
GQ155100.1 gg_id:539752 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ047953.1 gg_id:434609 Topographical and Temporal Human Skin Microbiome skin palm clone nbw139e07c1 GQ047
EU472801.1 gg_id:295032 red panda feces clone RPSD_1aaa04g01 EU472
AF373203.1 gg_id:66723 Erwinia chrysanthemi str. GSPB 1406 AF3732
EU723875.1 gg_id:349834 Shigella sp. str. 121405 EU7238
GQ033388.1 gg_id:388657 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw1 GQ033
AY360397.1 gg_id:93777 Erwinia chrysanthemi str. S3-1 AY3603
EU275357.1 gg_id:250107 Pantoea agglomerans str. CONC7 EU2753
EU560857.1 gg_id:562063 Assessment genetic Apriona germari (Hope) larvae normalization techniques intestir EU5608
EU471032.1 gg_id:295686 red panda feces clone RP_2aaa01c11 EU4710
AB288903.1 gg_id:201514 termite gut homogenate clone BOf5-16 AB2889
GU594301.1 gg_id:516250 Escherichia coli str. A5 GU594
EF515211.1 gg_id:217868 Electricigen Enrichment MFC upf microbial fuel cell anode clone 21d06 EF5152
GQ155921.1 gg_id:548341 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
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EF608546.1 gg_id:230213 predatory Poecilus chalcites their response lab rearing and antibiotic treatment diges EF6085

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CP001637.1 gg_id:524976 Escherichia coli str. DH1 CP001
AM184214.1 gg_id:161150 Pantoea agglomerans str. WAB1872 AM184
EU472148.1 gg_id:288731 francois langur feces clone FL_2aaa02a09 EU472
EF515321.1 gg_id:219651 Electricigen Enrichment MFC upf microbial fuel cell anode clone 22h03 EF5153
EF011116.1 gg_id:199506 Enterobacter cancerogenus str. EBD EF0111
EF471230.1 gg_id:226404 Enterobacter sp. str. BBTR105 EF4712
CP001790.1 gg_id:523631 Pectobacterium wasabiae str. WPP163 CP001
AM157436.1 gg_id:141413 Escherichia coli mother C4 AM157
CP000247.1 gg_id:169667 Escherichia coli str. 536 CP000
EU470717.1 gg_id:302020 red panda feces clone RP_1aaa02h08 EU470
FJ368186.1 gg_id:366961 feces adult twins and mothers; TS3 clone TS3_a01c05 FJ3681
EU778424.1 gg_id:326151 Red Panda feces clone RPSD_1aaa01b11 EU778
AY804014.1 gg_id:112448 Escherichia coli str. T10 AY804
EU471322.1 gg_id:303145 red panda feces clone RP_3aaa04b03 EU471
GQ029738.1 gg_id:413180 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw926f08 GQ029
EU554433.1 gg_id:273281 Shigella boydii str. Ag07 EU554
EU472761.1 gg_id:301142 red panda feces clone RPSD_1aaa02f12 EU472
L10328.1 gg_id:9702 Escherichia coli L10328
EF560776.1 gg_id:232981 Escherichia coli str. BE14 EF5607
EF676101.1 gg_id:257345 Klebsiella oxytoca str. XJU-1 EF6761
GQ102000.1 gg_id:409168 Topographical and Temporal Human Skin Microbiome skin palm clone nbw502c09c1 GQ102
AJ854062.1 gg_id:108296 Serratia ureolytica str. NiVa 51 AJ854
GQ099091.1 gg_id:389986 Topographical and Temporal Human Skin Microbiome skin interdigital web space cl GQ099
GQ031106.1 gg_id:395646 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ031
FJ368221.1 gg_id:369163 feces adult twins and mothers; TS3 clone TS3_a01f08 FJ3682
CP000247.1 gg_id:169665 Escherichia coli str. 536 CP000
EU470534.1 gg_id:296475 red panda feces clone RP_1aaa04e05 EU470
EU471185.1 gg_id:290380 red panda feces clone RP_3aaa03b07 EU471
GQ927306.1 gg_id:540402 Enterobacter sp. str. M6 GQ927
EU761952.1 gg_id:316329 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1 EU761
FJ364654.1 gg_id:368156 feces adult twins and mothers; TS19 clone TS19_a01e03 FJ3646
GU186117.1 gg_id:593155 Enterobacter cloacae str. IHB B 1374 GU186
GU594309.1 gg_id:521580 Escherichia coli str. AB6 GU594
U88435.1 gg_id:10311 Rahnella sp. 'CDC 21234' str. CDC 21234 U88435
EU470575.1 gg_id:302778 red panda feces clone RP_1aaa03a07 EU470
EU999992.2 gg_id:343920 Enterobacter ludwigii str. T4384 EU999
EU240200.1 gg_id:236031 interfering detection phytoplasma universal phytoplasmic primers Mexico EU240
EU460602.1 gg_id:298145 polar bear feces clone PB2_aai23c03 EU460
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GQ099081.1 gg_id:403628 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ099
GQ155052.1 gg_id:574054 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
AF511430.1 gg_id:65406 Escherichia coli CCCO4 AF5114
AY344368.2 gg_id:91670 Lake Kauhako 30 m clone K2-30-35 AY3443
GQ098908.1 gg_id:406048 Topographical and Temporal Human Skin Microbiome skin palm clone nbw503g03c1 GQ098
FJ976582.1 gg_id:592530 Enterobacter cancerogenus str. LCR73 FJ9765
CP000247.1 gg_id:169666 Escherichia coli str. 536 CP000
EF102825.1 gg_id:257388 Enterobacter sp. str. G-226-1 EF1028
GQ154770.1 gg_id:589091 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
GQ025541.1 gg_id:431917 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ025
EF219421.2 gg_id:441069 Enterobacter cloacae str. ATCC 43560 EF2194
U92197.1 gg_id:9711 Salmonella subsp. enterica serovar Agona str. Sa1 subsp. U9219
GQ154820.1 gg_id:535230 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
GQ031713.1 gg_id:452836 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ031
NZ_ABHM02000001.1 gg_id:317271 Escherichia coli O157:H7 str. EC4042 NZ_AB
GQ155096.1 gg_id:594320 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
FJ859683.1 gg_id:573410 Enterobacter ludwigii str. BIHB 336 FJ8596
GQ155198.1 gg_id:586724 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
CP000468.1 gg_id:175186 Escherichia coli str. APEC O1 CP000
NC_008563.1 gg_id:176527 Escherichia coli str. APEC O1 NC_00
GQ155253.1 gg_id:582117 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
FJ976590.1 gg_id:581741 Enterobacter sp. str. LCR81 FJ9765
FJ811874.1 gg_id:593519 Enterobacter aerogenes str. 5-WCH FJ8118
ABHS01000007.1 gg_id:302893 Escherichia coli O157:H7 str. EC4486 ABHS0
X80726.1 gg_id:9698 Shigella sonnei X80726
FJ364922.1 gg_id:363434 feces adult twins and mothers; TS19 clone TS19_a04g07 FJ3649
FM180568.1 gg_id:369792 Escherichia coli 0127:H6 str. E2348/69 FM180
AAMJ02000006.1 gg_id:342676 Shigella dysenteriae str. 1012 AAMJ0
EU778390.1 gg_id:333367 Red Panda feces clone RPSD_1aaa01b09 EU778
EU554431.1 gg_id:273912 Shigella flexneri str. Ag05 EU554
AF400480.1 gg_id:18267 Secondary endosymbiont Bemisia tabaci clone TANZ3-2 of AF4004
DQ837613.1 gg_id:164437 structures honeybee intestines and their response insecticidal proteins gut clone HB DQ837
DQ026512.1 gg_id:134671 Xenorhabdus sp. str. PDBC SCX7 DQ026
GU480985.1 gg_id:521599 Xenorhabdus hominickii GU480
AB030020.1 gg_id:32418 Antonina crawii (Insecta Homoptera Pseudooccidae) symbiont AB030
AF286129.1 gg_id:21132 eubacterium Aleurodicus dugesii AF286
AF476107.1 gg_id:63935 Planococcus citri symbiont AF476
AY676889.1 gg_id:136328 Baumannia cicadellinicola B37 AY676
AF400474.1 gg_id:50143 Secondary endosymbiont Bemisia tabaci clone IND34 AF4004

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DQ068832.1 gg_id:139463 microbiota antlions (Myrmeleon mobilis) GI tract freshly caught antlion OTU7 clone	DQ068
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GU374099.1 gg_id:531978 soil East Calcutta wetland clone SRC_NBB4	GU374
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FJ655533.1 gg_id:592467 symbiont	FJ6555
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AB013087.1 gg_id:9649 symbiont	AB013
FJ655532.1 gg_id:542044 symbiont	FJ6555
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AF077608.1 gg_id:9978 symbiont	AF0776
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AF476101.1 gg_id:63942 Antonina pretiosa symbiont	AF4761
AF286127.1 gg_id:20298 symbiont	AF2861
NC_004344.2 gg_id:141977 Wigglesworthia glossinidia endosymbiont Glossina brevipalpis	NC_004
EF153305.1 gg_id:192342 identification gut red imported fire ant (Solenopsis Buren) GI tract Solenopsis invicta	EF1533
AB083059.1 gg_id:55799 Parabdella sp. symbiont	AB083
DQ211709.1 gg_id:164016 Xenorhabdus sp. str. FRM16	DQ211
D78008.1 gg_id:10301 Xenorhabdus japonica str. SK-1T (=IAM14265T)	D78008
GU480979.1 gg_id:529286 Xenorhabdus griffiniae str. T87	GU480
GQ923884.1 gg_id:589696 Xenorhabdus sp. str. KB-3	GQ923
DQ205450.1 gg_id:173648 Xenorhabdus sp. str. USNJ01	DQ205
GU480982.1 gg_id:526425 Xenorhabdus sp. str. R00I-293	GU480
GQ373385.2 gg_id:526191 Xenorhabdus sp. str. SGas1	GQ373
AY286478.1 gg_id:87839 Xenorhabdus nematophila	AY2864
FN667741.1 gg_id:524496 Xenorhabdus bovienii str. SS-2004	FN6677
AB243427.1 gg_id:160641 Xenorhabdus sp. str. MY8 IkWj136	AB2434
GU480989.1 gg_id:517099 Xenorhabdus szentirmaii	GU480

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AY278675.1 gg_id:86906 Xenorhabdus beddingii str. DSM4764
D78006.1 gg_id:10299 Xenorhabdus beddingii str. DSM4764
AY317154.1 gg_id:89531 Xenorhabdus bovienii str. CB54
GU480981.1 gg_id:527534 Xenorhabdus bovienii str. Monsanto
GU480988.1 gg_id:515326 Xenorhabdus bovienii str. Li6
DQ208305.1 gg_id:167325 Xenorhabdus bovienii str. TB20
DQ205453.1 gg_id:163330 Xenorhabdus bovienii str. USNY95
D78007.1 gg_id:10244 Xenorhabdus bovienii str. ATCC35271T
FJ860885.1 gg_id:545382 Xenorhabdus bovienii str. USAR01
X82252.1 gg_id:10246 Xenorhabdus bovienii str. DSM 4766
DQ329379.1 gg_id:146743 Xenorhabdus budapestensis str. CB43
GU480990.1 gg_id:529536 Xenorhabdus cabanillasii
GU480992.1 gg_id:520060 Xenorhabdus innexi
EU190977.1 gg_id:266440 Xenorhabdus kozodoii str. FR48
FJ860884.1 gg_id:591393 Xenorhabdus nematophila str. K97
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EU513180.1 gg_id:264777 Xenorhabdus poinarii str. SRK 1
DQ211703.1 gg_id:169069 Xenorhabdus poinarii str. AZ26
EU250472.1 gg_id:246846 Xenorhabdus poinarii str. Iran2
GU480993.1 gg_id:527414 Xenorhabdus stockiae str. T9
DQ646382.1 gg_id:161501 Yersinia kristensenii str. 03
AAYR01000001.1 gg_id:261186 Yersinia pestis biovar Antiqua str. UG05-0454
AF365943.1 gg_id:30561 Yersinia pseudotuberculosis str. 204
EU434476.1 gg_id:274633 Yersinia kristensenii str. b281
AJ232236.1 gg_id:10381 Yersinia pestis SS-Yp-114
FJ641890.1 gg_id:559301 Yersinia intermedia str. 5375
EF179132.1 gg_id:264397 Yersinia ruckeri str. CCUG 14190
NC_006155.1 gg_id:128947 Yersinia pseudotuberculosis IP 32953 str. IP32953
AJ627595.1 gg_id:107083 Yersinia kristensenii str. Y156
FJ641877.1 gg_id:543977 Yersinia intermedia str. Nr13/84
CP000720.1 gg_id:257703 Yersinia pseudotuberculosis str. IP 31758
AJ232239.1 gg_id:10384 Yersinia pestis SS-Yp-117
X75274.1 gg_id:10388 Yersinia pestis
FJ641882.1 gg_id:573766 Yersinia intermedia str. H9-36/83
DQ646383.1 gg_id:161584 Yersinia aldovae str. 04
EF515428.1 gg_id:224468 Electricigen Enrichment MFC upf microbial fuel cell anode clone 24c09
EF179120.1 gg_id:258690 Yersinia massiliensis str. CCUG 53444
NZ_AAYR01000015.1 gg_id:263525 Yersinia pestis biovar Antiqua str. UG05-0454
X75276.1 gg_id:10393 Yersinia rohdei
X75273.1 gg_id:10365 Yersinia frederiksenii

FN667
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