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GQ263305.1 gg_id:591613 Structure Simulated Level Waste Site simulated level waste site clone FW1_a53 GQ263
DQ234507.2 gg_id:580066 Mucilaginibacter sp. RA1BR4 DQ234
AB240499.1 gg_id:143639 microbial structure rhizosphere biofilm Sapporo root-base (80 160 mm) Phragmites S AB2404
DQ311009.1 gg_id:147488 Flavobacterium sp. str. Xb-5 DQ311
EU787448.1 gg_id:332533 Flexibacter sp. str. R2A36-4 EU7874
EF125948.1 gg_id:512727 Biofilm-reactor Based Enrichment Utilizing Oligotrophic Concentrations Acyl-homose EF1259
AJ575720.1 gg_id:97995 lake water clone SW30 AJ5757
EF446146.1 gg_id:212927 Pedobacter lentus str. DS-40 EF4461
EU636060.1 gg_id:278598 Antarctic str. GA082 EU6360
EU734803.2 gg_id:305278 Pedobacter sp. str. 12157 EU7348
FJ674761.1 gg_id:523152 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6747
EF516106.1 gg_id:221402 grassland soil clone FCPO447 EF5161
AJ318181.1 gg_id:19131 Waste-gas biofilter clone BIsii5 AJ3181
EF157093.1 gg_id:240268 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon EF1570
FJ377315.1 gg_id:370124 Pedobacter sp. str. L2b-1 FJ3773
EU769182.1 gg_id:321863 velvetleaf seed clone S3-10-CL5 EU7691
DQ297969.1 gg_id:141304 Microbial hydrocarbon contaminated soil clone UA8 DQ297
EF516092.1 gg_id:225889 grassland soil clone FCPU417 EF5160
DQ984593.1 gg_id:238033 Mt. Nan-Jen litterfall clone IYF111 DQ984
NC_010830.1 gg_id:342865 Candidatus Amoebophilus asiaticus str. 5a2 NC_010
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FJ203649.1 gg_id:334714 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h FJ2036
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GU118732.1 gg_id:547706 Threatened Corals Provide Microbial Habitats clone Mfra_I15 GU118
EU236302.1 gg_id:302378 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg1a1A4 EU2363
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FJ203340.1 gg_id:347250 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c FJ2033
FJ203020.1 gg_id:355518 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c FJ2030
FJ203043.1 gg_id:311355 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c FJ2030
FJ203017.1 gg_id:330094 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c FJ2030
FJ203331.1 gg_id:315090 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c FJ2033
GU119035.1 gg_id:568584 Threatened Corals Provide Microbial Habitats clone Past_F02 GU119
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AF215634.1 gg_id:33872 Acanthamoeba spp. symbiont AF2156
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DQ314214.1 gg_id:146310 Heterodera glycines symbiont DQ314
EF092220.1 gg_id:275952 Persistent Axinella corrugata hingobacteriales clone B255_A11 EF0922
EU340220.1 gg_id:241269 on Aquatic Macrophytes Geothermally Active Area Sedge Bay Yellowstone Lake WY EU3402
AY862784.2 gg_id:161615 prokaryotic genetic Salar de Atacama Northern Chile athalassohaline lake water clon AY8627
AB015585.1 gg_id:2576 deep-sea sediment clone BD7-10 AB0155
EU236422.1 gg_id:290158 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg92G12 EU2364
EU156156.1 gg_id:250980 thermal spring microbial and functional genes Coffee Pots Hot Spring clone pCOF_65 EU1561
AY862060.1 gg_id:202103 Hydrogen and bioenergetics Yellowstone geothermal ecosystem Washburn Spring 3 AY8620
EU245415.1 gg_id:238437 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M1-D0 EU2454
EF648019.1 gg_id:253575 dynamics during produced water treatment aerobic activated sludge clone HB5 EF6480
GQ356162.1 gg_id:582163 biomarkers ammonia oxidation activity anaerobic ammonium-oxidation (Anammox) GQ356
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AB240228.1 gg_id:143475 microbial structure rhizosphere Phragmites bulk soil reed bed reactor laboratory clo AB2402
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EU181485.1 gg_id:255060 Prokaryotic enhanced organic matter remineralization continental margin marine se EU1814
EU385882.1 gg_id:261758 Stratified microbes sediments Core MD05-2902 subseafloor sediment South China S EU3858
EF157182.1 gg_id:247643 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon EF1571
AF445671.1 gg_id:74751 travertine hot spring clone SM1D02 AF4456
AJ390445.1 gg_id:30354 soil clone PBS-II-34 AJ3904
GU172181.1 gg_id:591575 Microbial Eucalyptus plantation soil clone DSM-R9 GU172
EU156145.1 gg_id:254219 thermal spring microbial and functional genes Coffee Pots Hot Spring clone pCOF_65 EU1561
AB252429.1 gg_id:155382 Microbial extremely CO2 rich deep-sea sediment Marine sediments Yonaguni Knoll I AB2524
AF419685.1 gg_id:71654 Guaymas Basin hydrothermal sediment clone CS_B038 AF4196
EF515667.1 gg_id:217919 Electricigen Enrichment MFC full-scale anaerobic bioreactor sludge treating brewery EF5156
EU981282.1 gg_id:344869 sulfate reducing living bench scale aquifer column water clone A32_SW EU9812
EU522662.1 gg_id:262018 hydrocarbon-degrading methanogenic microbial consortia settling basin Northern Al EU5226
EU638713.1 gg_id:349253 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU6387
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EF515591.1 gg_id:227180 Electricigen Enrichment MFC full-scale anaerobic bioreactor sludge treating brewery EF5155
AY713479.1 gg_id:151718 first genome fragment marine sponge- candidate phylum Poribacteria transposase s AY7134

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FJ652532.1 gg_id:536466 aerobic and anaerobic ammonia-oxidizing marine sponges Atlantic Ocean water colu FJ6525
FJ479322.1 gg_id:569418 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4793
AB177139.1 gg_id:134010 seafloor methane hydrate clone ODP1230B10.20 AB177
AY093477.1 gg_id:63105 deep marine sediment clone MB-C2-106 AY0934
FJ873292.1 gg_id:564399 Vertical and archaea methane-rich cold seep located base sediments Okhotsk Sea clo FJ8732
EU491224.1 gg_id:263735 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak EU491
EU385929.1 gg_id:260188 Stratified microbes sediments Core MD05-2902 subseafloor sediment South China S EU385
AB177164.1 gg_id:134487 seafloor methane hydrate clone ODP1230B2.02 AB177
U68437.2 gg_id:3042 Chlamydia muridarum str. SFPD U6843
AY661797.1 gg_id:103676 Chlamydia suis str. 32XII AY661
U76710.2 gg_id:3022 Chlamydophila abortus str. EBA U7671
AB001785.1 gg_id:2944 Chlamydophila felis str. Fe-145 AB001
AB001775.1 gg_id:3035 Chlamydophila pecorum str. Bo-Maeda AB001
AE017160.1 gg_id:90574 Chlamydophila pneumoniae str. TW-183 AE017
AB001779.1 gg_id:2966 Chlamydophila psittaci str. Bud-1 AB001
AB001791.1 gg_id:2976 Chlamydophila psittaci str. Ohmiya AB001
AB001807.1 gg_id:2992 Chlamydophila psittaci str. PCM55 AB001
U68419.2 gg_id:3019 Chlamydophila psittaci str. turkey strain NJ1; Tk-NJ U6841
E17339.1 gg_id:44021 Chlamydia psittaci Prt/GCP1 E17339
E17340.1 gg_id:36508 Chlamydia psittaci Prk/Daruma E17340
E17343.1 gg_id:36991 Chlamydia pecorum Bo/Maeda E17343
DQ011662.1 gg_id:158932 Chlamydia sp. CH301104 DQ011
NC_005861.1 gg_id:471187 Candidatus Protochlamydia amoebophila str. UWE25 NC_00
FJ532294.1 gg_id:579758 Protochlamydia naegleriophila str. CRIB41 S156 FJ5322
FJ976105.1 gg_id:561599 Parachlamydia acanthamoebae str. cvE20 FJ9761
AF478463.2 gg_id:580742 New parachlamydial phylotypes detected s human clinical nasal washing clone cvC7 AF4784
AF177275.1 gg_id:24341 Neochlamydia hartmannellae str. A1Hsp AF1772
AY223862.1 gg_id:83246 Candidatus Rhabdochlamydia porcellionis clone RKPsHep porcellionis AY2238
EU090707.1 gg_id:249365 Chlamydia-Like Respiratory Pneumonia Patients clinical respiratory s German patient EU090
EU133918.1 gg_id:253897 tallgrass prarie soil clone FFCH17845 EU1339
AY140911.1 gg_id:89923 Fritschea eriococci AY1409
EF177461.1 gg_id:217851 Xenoturbella westbladi UUZM 57848 symbiont EF1774
U68460.2 gg_id:2935 Simkania negevensis str. Z U68460
DQ124300.1 gg_id:152262 Criblamydia sequanensis str. CRIB-18 DQ124
EU074225.1 gg_id:320922 Estrella lausannensis str. CRIB 30 EU0742
AF448722.3 gg_id:583814 New chlamydial lineages s freshwater clone cvE6 AF4487
DQ444442.1 gg_id:171324 Anaerobic ammonium oxidation tropical freshwater system (Lake Tanganyika) fresh DQ444
AF448723.3 gg_id:584073 New chlamydial lineages s freshwater clone cvE9 AF4487
AY184804.1 gg_id:100535 Waddlia sp. str. G817 AY1848
AF042496.1 gg_id:2936 Waddlia chondrophila str. WSU 86/1044 AF0424

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FJ810559.1 gg_id:408758 Subsurface ecosystem resilience: Long-term attenuation subsurface contaminants su FJ8105
GU208405.1 gg_id:560369 Study on Sediment Dongping Lake sediment clone Fh2-11 GU208
AM490699.1 gg_id:565618 Linking and functional nutrient spiraling mats (USA) microbial mat sulfidic cave sprir AM490
DQ640726.1 gg_id:230544 full-scale EBPR sludge clone Skagen107 DQ640
FJ810562.1 gg_id:467449 Subsurface ecosystem resilience: Long-term attenuation subsurface contaminants su FJ8105
FM207902.1 gg_id:310286 Anaerobic p-xylene mineralization activated sludge and fresh water sediment denitr FM207
GU208220.1 gg_id:581318 Study on Sediment Dongping Lake sediment clone 3C3-5 GU208
AM490708.1 gg_id:565419 Linking and functional nutrient spiraling mats (USA) microbial mat sulfidic cave sprir AM490
AM162482.1 gg_id:152302 and situ identification acidic sphagnum peat bog clone B44 AM162
DQ501337.1 gg_id:196940 Seasonal dynamics free-living and particle- four lakes northeastern Germany freshw DQ501
AB486984.1 gg_id:578382 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCORC AB486
AB252950.1 gg_id:172221 Identification Shibayama lagoon Ishikawa Japan iron-oxidation biofilm clone 392 AB2529
AY221073.1 gg_id:83562 Mammoth cave clone CCM9b AY221
AB252951.1 gg_id:170662 Identification Shibayama lagoon Ishikawa Japan iron-oxidation biofilm clone 397 AB2529
FJ810563.1 gg_id:373685 Subsurface ecosystem resilience: Long-term attenuation subsurface contaminants su FJ8105
GU208359.1 gg_id:561793 Study on Sediment Dongping Lake sediment clone Td4-4 GU208
FJ485389.1 gg_id:509237 microbial autonomous rover world's deepest phreatic sinkhole wall biomat El Zacator FJ4853
AF445702.1 gg_id:46550 green sulfur clone SM1H02 AF445
AY555793.1 gg_id:106021 Bor Khlueng hot spring clone PK74 AY555
DQ088767.1 gg_id:134457 subsurface clone BE325FW032701CTS_hole1-17 DQ088
AY741701.1 gg_id:99903 borehole water gold mine clone TTMF57 AY741
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NC_002932.3 gg_id:143083 Chlorobium tepidum str. TLS NC_00
AM050125.1 gg_id:188667 Chlorobium limicola str. C1 AM050
EF560696.1 gg_id:226020 Chlorobaculum macestae str. M EF5606
AM050131.1 gg_id:192472 Pelodictyon luteolum str. E1P1 AM050
AY693833.1 gg_id:103776 anaerobic sludge clone EUB42 AY6938
NR_029321.1 gg_id:540816 Chlorobaculum thiosulfatiphilum str. 6230; DSM 249 NR_02
EF560700.1 gg_id:222254 Chlorobaculum parvum str. X EF5607
NC_007514.1 gg_id:141021 Chlorobium chlorochromatii str. CaD3 NC_00
NZ_AASE01000013.1 gg_id:171289 Chlorobium ferrooxidans str. DSM 13031 NZ_AA
NZ_AAJD01000008.1 gg_id:131048 Prosthecochloris vibrioformis str. DSM 265 NZ_AA
NC_011026.1 gg_id:347501 Chloroherpeton thalassium str. ATCC 35110 NC_01
AF170103.1 gg_id:202092 Chloroherpeton thalassium AF170
CP000096.1 gg_id:143111 Pelodictyon luteolum str. DSM 273 CP000
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AJ291827.1 gg_id:19433 Prosthecochloris vibrioformis str. CHP 3402 AJ2918
FJ716270.1 gg_id:513209 Chlorobi dominate shal chemocline Bahamas Sawmill Sink column 10.3 m water dept FJ7162
AJ888468.1 gg_id:113834 Prosthecochloris sp. str. 4Vi AJ8884

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AY293405.1 gg_id:88021 travertine terrace Yellowstone Hot Springs clone SM2B09 AY2934
NC_010803.1 gg_id:292136 Chlorobium limicola str. DSM 245 NC_01
EF153291.1 gg_id:189071 Chlorobium sp. str. ShCl03 EF1532
EF654662.1 gg_id:256699 Chlorobium phaeobacteroides str. G-gCphb03 EF6546
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DQ676424.1 gg_id:217425 Archaeal and plankton freshwater pond suboxic freshwater-pond sediment clone M DQ676
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GQ339136.1 gg_id:515456 Comprehensive Investigation on Iron Cycling Freshwater Seep ing Microscopy Cultiv GQ339
GU183591.1 gg_id:582049 Structures Reduced and Oxidized Aquifer lower Aqueous Arsenic Titas Bangladesh a GU183
GQ339118.1 gg_id:529782 Comprehensive Investigation on Iron Cycling Freshwater Seep ing Microscopy Cultiv GQ339
AB240289.1 gg_id:144037 microbial structure Phragmites rhizosphere biofilm reed bed reactor laboratory clon AB240
AF234699.1 gg_id:25315 sludge clone A12b AF2346
DQ520166.1 gg_id:160290 shal China sequences hypertrophic freshwater lake clone ML-5-66.2 DQ520
EF648096.1 gg_id:255310 dynamics during produced water treatment aerobic activated sludge clone HB107 EF6480
AB288917.1 gg_id:202747 termite gut homogenate clone BOf8-10 AB2889
AF445657.1 gg_id:30516 travertine hot spring clone SM1B09 AF4456
EF126253.1 gg_id:277457 Phototrophic microbial build laminated Fe-formations on Sulawesi Indonesia mesoph EF1262
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AY921840.1 gg_id:114305 farm soil clone AKYH1119 AY9218
EF126257.1 gg_id:263133 Phototrophic microbial build laminated Fe-formations on Sulawesi Indonesia mesoph EF1262
EU133924.1 gg_id:253338 tallgrass prarie soil clone FFCH3953 EU1339
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EU133919.1 gg_id:239595 tallgrass prarie soil clone FFCH12071 EU1339
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EF632929.1 gg_id:241447 Unique microbial contrasting aquatic altitude Andean Altiplano (northern Chile) fresh EF6329
AY118151.1 gg_id:60815 benzene-degrading nitrate-reducing consortium clone Cart-N2 bacterium AY1181
AB240328.1 gg_id:141738 microbial structure Phragmites rhizosphere biofilm reed bed reactor laboratory clon AB2403
AB192128.1 gg_id:142983 termite gut homogenate clone M2PB4-57 AB1921
DQ413108.1 gg_id:153791 Microbial -dependent and Approaches Anaerobic/Aerobic SBR Reactor EBPR sludge DQ413
FJ356024.1 gg_id:360408 Targeted FACS enrichment groups lab scale systems anaerobic:aerobic lab-scale EBPR FJ3560
AY118152.1 gg_id:60814 benzene-degrading nitrate-reducing consortium clone Cart-N3 bacterium AY1181
DQ676315.1 gg_id:222624 Archaeal and plankton freshwater pond suboxic freshwater-pond sediment clone M DQ676
AB192127.1 gg_id:141121 termite gut homogenate clone M2PT2-67 AB1921
GQ356164.1 gg_id:588073 biomarkers ammonia oxidation activity anaerobic ammonium-oxidation (Anammox) GQ356
EF515342.1 gg_id:224048 Electricigen Enrichment MFC upf microbial fuel cell anode clone 23b07 EF5153
AB192126.1 gg_id:142772 termite gut homogenate clone M1NP2-57 AB1921
DQ018819.1 gg_id:135521 Unique Microbial Anaerobic Swine Lagoons anaerobic swine lagoon clone C-156 DQ018
AF027006.1 gg_id:2640 hot spring clone OPB88 AF0270

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DQ324902.1 gg_id:148867 Geochemical and bioenergetic variability across systems Yellowstone National Park DQ324
DQ645243.1 gg_id:164804 Microbial and oxidation activity biofilms within Alvord Desert Basin Southeastern Or DQ645
AY861796.1 gg_id:112647 Obsidian Pool prime community clone OPPB063 AY8617
EU283596.1 gg_id:278344 Model Early Earth Harbors Deeply Divergent Divisions Anderson Lake clone A309 EU2835
FN429794.1 gg_id:588053 Biogeochemistry -activity cold seep Larsen B area western Weddell Sea Antarctica m FN4297
EU937844.1 gg_id:337082 Biogeochemistry Iron Oxidation Circumneutral Freshwater Habitat riparian iron oxidi EU9378
AM490707.1 gg_id:564034 Linking and functional nutrient spiraling mats (USA) microbial mat sulfidic cave sprir AM490
AB195898.1 gg_id:109186 Anaerobic sludge clone N25 AB1958
EU234260.1 gg_id:255151 river and un techniques downstream Wang Yang River receiving penicillin G producti EU2342
AM997556.1 gg_id:572568 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A AM997
EF562071.1 gg_id:256995 Subsurface microbial deep-granitic-fracture water colorado Henderson Molybdenum EF5620
FJ710780.1 gg_id:540639 Abundance and microbial long-term operated anammox biofilm reactors initiated ino FJ7107
AB234252.1 gg_id:149719 Biotransformation Polychlorinated Dioxins Microbial Dynamics Sediment Microcosm AB2342
AB486936.1 gg_id:577176 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCOR(AB4869
EF467561.1 gg_id:216233 situ microelectrode voltammetry sulfur-oxidizing biofilms Frasassi sulfidic cave strear EF4675
FJ710734.1 gg_id:591641 Abundance and microbial long-term operated anammox biofilm reactors initiated ino FJ7107
FJ416082.1 gg_id:363429 sediments sediment station NEC5 Northern Bering Sea clone 014K15 FJ4160
EF203206.1 gg_id:213866 phylotypes sediments Lake Kastoria Greece sediment clone Kas175B EF2032
DQ404811.1 gg_id:154683 contaminated sediment clone 655939 DQ404
EU644107.1 gg_id:282378 and Samoylov Island Lena active layer -centred polygon near permafrost table; Rim_ EU6441
GQ487886.1 gg_id:578784 Microbial metal soil polluted heavy metals clone T1-6 GQ487
AB186805.1 gg_id:101101 polychlorinated dioxin dechlorinating microcosm clone TSAC14 AB1868
AY340841.1 gg_id:91023 sulfate-reducing fluidized-bed reactor clone SR_FBR_L83 AY3408
AY741700.1 gg_id:99743 borehole water gold mine clone TTMF87 AY7417
EU101178.1 gg_id:255842 Sulfide/oxygen supply ratio predicts outcome competition among sulfur-oxidizing wa EU1011
DQ925883.1 gg_id:252875 Microbes and Thermal Gradients Temperature Hydrothermal Chimneys hydrotherm DQ925
GU369881.1 gg_id:517364 and mats vents Arc white filamentous microbial mat photic shal hydrothermal vent GU369
AB355060.1 gg_id:247813 Monitoring and archaeal two heavy polluted areas lake Egypt based on sediment Ma AB3550
AY327874.1 gg_id:88595 surface vent snail foot clone SF_C4-C6 AY3278
FJ545477.1 gg_id:547407 Diveristy Seawater and Sediment Northern North Yel Sea sediment clone S1-48 FJ5454
DQ337042.1 gg_id:147607 subsurface water clone EV818EB5CPSAJJ39 DQ337
AB179693.1 gg_id:102361 groundwater 0.2 m-captured fraction clone KNA6-EB22 AB1796
FJ484546.1 gg_id:533163 microbial autonomous rover world's deepest phreatic sinkhole wall biomat El Zacator FJ4845
AB117714.1 gg_id:103839 autotrophic nitrifying biofilm clone NB-10 AB1177
DQ521481.1 gg_id:185950 Antarctic lake ice cover clone ANTLV1_C12 DQ521
AF234733.1 gg_id:53925 sludge clone S14 AF2347
FJ481330.1 gg_id:565487 Microbes marine sponges sponge tissue clone XB3E04F FJ4813
EU134161.1 gg_id:248283 tallgrass prarie soil clone FFCH18628 EU1341
AF445738.1 gg_id:47497 travertine hot spring clone SM2G06 AF4457
AM490723.1 gg_id:540671 Linking and functional nutrient spiraling mats (USA) microbial mat sulfidic cave sprir AM490

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CU466712.1 gg_id:324279 Evry wastewater treatment plant anoxic basin clone CU466
X84576.2 gg_id:71617 mixed genomic activated sludge clone SBR2037 X84576
DQ404819.1 gg_id:154220 contaminated sediment clone 655947 DQ404
EU134165.1 gg_id:243950 tallgrass prarie soil clone FFCH1946 EU134
FJ478663.1 gg_id:583735 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4786
AJ347035.1 gg_id:60174 sponge clone TK16 AJ3470
EF516563.1 gg_id:223701 grassland soil clone FCPT422 EF5165
EF516958.1 gg_id:219899 grassland soil clone FCPS653 EF5169
AF173817.1 gg_id:2727 Antarctic lake ice clone LB3-100 AF1738
GQ397094.1 gg_id:535410 Functional unvegetated perhumid recently-deglaciated soils do not correlate shifts s GQ397
EU133974.1 gg_id:251353 tallgrass prarie soil clone FFCH9554 EU1339
DQ017911.1 gg_id:131339 upland stream clone S-Rwb_62 DQ017
EU134013.1 gg_id:248412 tallgrass prarie soil clone FFCH5168 EU1340
EU051342.1 gg_id:249472 soil clone BJ-204 EU0513
AY921746.1 gg_id:113259 farm soil clone AKYH905 AY9217
AY922012.1 gg_id:113017 farm soil clone AKYG434 AY9220
EU134153.1 gg_id:249503 tallgrass prarie soil clone FFCH17716 EU1341
FM253644.1 gg_id:308698 Rock gold mine unusually microbial biofilm clone C04-2 FM253
FJ479099.1 gg_id:576689 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4790
FJ481242.1 gg_id:546971 Microbes marine sponges sponge tissue clone XA2F07F FJ4812
AM490722.1 gg_id:584712 Linking and functional nutrient spiraling mats (USA) microbial mat sulfidic cave sprir AM490
EF019589.1 gg_id:215379 aspen rhizosphere clone Elev_16S_1110 EF0195
AY921926.1 gg_id:114246 farm soil clone AKYH973 AY9219
EF126266.1 gg_id:270948 Phototrophic microbial build laminated Fe-formations on Sulawesi Indonesia mesoph EF1262
FM253645.1 gg_id:316115 Rock gold mine unusually microbial biofilm clone C05-2 FM253
FJ152730.1 gg_id:306793 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX5A_ FJ1527
AF445676.1 gg_id:30131 travertine hot spring clone SM1D10 AF4456
AM259916.1 gg_id:240136 Chondrilla nucula-specific sponge mesohyl clone CN69 AM259
AY921673.1 gg_id:112841 farm soil clone AKYG659 AY9216
EF515553.1 gg_id:227415 Electricigen Enrichment MFC full-scale anaerobic bioreactor sludge treating brewery EF5155
AM935617.1 gg_id:534001 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM935
AY426440.1 gg_id:105100 full-scale anaerobic UASB bioreactor treating paper mill wastewater clone B15 AY4264
AJ306749.1 gg_id:66944 DCP-dechlorinating consortium clone SHA-147 AJ3067
AB046413.1 gg_id:44630 Anaerolinea thermophila AB0464
CU922908.1 gg_id:564996 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU9229
AB274513.1 gg_id:214594 packed-bed reactor clone CFB-24 AB2745
AB234255.1 gg_id:149727 Biotransformation Polychlorinated Dioxins Microbial Dynamics Sediment Microcosm AB2342
AY921672.1 gg_id:113861 farm soil clone AKYH789 AY9216
AY921883.1 gg_id:112889 farm soil clone AKYG493 AY9218
AB240304.1 gg_id:143935 microbial structure Phragmites rhizosphere biofilm reed bed reactor laboratory clone AB2403

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EF198026.1 gg_id:195376 Microbial structures and thermophilic methanogenic consortia anaerobic mesophilic EF198
EU542512.1 gg_id:264526 Effects chemical structure concentration on pathways microbial during dechlorinatio EU542
DQ478736.1 gg_id:158754 UASB reactor treating brewery wastewater clone CLONG3 DQ478
AB447642.1 gg_id:579753 Microbial Structure and Dynamics Granules Expanded Granular Sludge Bed (EGSB) R AB447
AB274515.1 gg_id:214216 packed-bed reactor clone CFB-26 AB274
EF688367.1 gg_id:242454 soil clone F6-01 EF6883
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EF125459.1 gg_id:191839 mangrove soil clone MSB-2G5 EF1254
EU283567.1 gg_id:278710 Model Early Earth Harbors Deeply Divergent Divisions Anderson Lake clone A379 EU283
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GQ093932.1 gg_id:430848 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ093
GU390735.1 gg_id:529542 Dark hot springs: structure biofilms caves Acquasanta Terme (Italy) sulfidic cave stre GU390
GQ347430.1 gg_id:588075 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ347
AM162480.1 gg_id:153300 and situ identification acidic sphagnum peat bog clone B71 AM162
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FJ793156.1 gg_id:518088 Archaea and Hot Spring Thailand Tao Dam hot spring clone TDB09 FJ7931
AY531577.1 gg_id:99031 Indian Ocean hydrothermal vent clone SF_C23-G2 AY531
GQ396855.1 gg_id:559525 Functional unvegetated perhumid recently-deglaciated soils do not correlate shifts GQ396
CU466710.1 gg_id:341107 Evry wastewater treatment plant anoxic basin clone CU466
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EU245299.1 gg_id:244008 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-H5-F01 EU245
AM943597.1 gg_id:269159 Microbial dolomite formation Lagoa Vermelha Brazil carbonaceous sediments hype AM943
GQ246419.1 gg_id:510365 Temporal and spatial China North Yel Sea sediments clone Ld1-24 GQ246
EF125407.1 gg_id:182748 soil naked tidal flat sediment near mangrove clone MSB-1E5 EF1254
EU050928.1 gg_id:253945 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_03_41 EU050
GU180177.1 gg_id:534587 Impact coplanar PCBs on microbial activity anaerobic estuarine sediments sediment GU180
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AF154100.1 gg_id:1295 hydrocarbon seep clone GCA112 AF154

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EU181507.1 gg_id:255643 Prokaryotic enhanced organic matter remineralization continental margin marine se EU181
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EU245353.1 gg_id:237424 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-H6-E05 EU245
EU488497.1 gg_id:549616 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU488
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EU245567.1 gg_id:252001 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M3-B0 EU245
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EU245923.1 gg_id:240978 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M8-C0 EU245
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GQ850583.1 gg_id:571883 bottom water northern Bering Sea clone d147 GQ850
EU245598.1 gg_id:252162 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M3-E0 EU245
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DQ330158.1 gg_id:159124 Guerrero Negro hypersaline microbial mat clone 072DZ38 DQ330
DQ330169.1 gg_id:159407 Guerrero Negro hypersaline microbial mat clone 08D2Z40 DQ330
DQ394929.1 gg_id:151554 harbor sediment clone VHS-B3-9 DQ394
DQ330199.1 gg_id:159389 Guerrero Negro hypersaline microbial mat clone 10D2Z16 DQ330
FJ638585.1 gg_id:512964 Temperature dependent succession sulfate reducing muddy southwestern Taiwan hc FJ6385
DQ330198.1 gg_id:159395 Guerrero Negro hypersaline microbial mat clone 10D2Z17 DQ330
EU246094.1 gg_id:243415 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-P3-C04 EU246

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EU245948.1 gg_id:239373 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M8-E1 EU245
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EU245058.1 gg_id:238582 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-H1-C02 EU245
GQ143765.1 gg_id:443913 Level Continental Shelf Sediment and Phylum-level lineages Phylum Planctomycetes GQ143
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FM242278.1 gg_id:322996 sequences sediment clone 17bis T0h-oil FM242
FJ478819.1 gg_id:574527 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4788
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EU669650.1 gg_id:304270 soil clone S8-80 EU669
FJ710715.1 gg_id:589667 Abundance and microbial long-term operated anammox biofilm reactors initiated ino FJ7107
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EF594052.1 gg_id:233441 mixed granule anammox reactor clone KIST-JJY020 EF594
EU374068.1 gg_id:272558 southern Cretan margin (eastern Mediterranean Sea) canyon and slope sediment cl EU374
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EU488398.1 gg_id:550672 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU488
EF061968.1 gg_id:184557 Xiamen China mangrove sediment clone XME13 EF0619
EF205579.1 gg_id:211551 among geographically regions central Tibet geothermal spring mat clone TP7 EF2055
DQ463699.2 gg_id:173719 distinct Lake Tanganyika anoxic hypolimnion clone TK-SH16a DQ463
EU488293.1 gg_id:533639 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU488
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AM490737.1 gg_id:570248 Linking and functional nutrient spiraling mats (USA) microbial mat sulfidic cave sprir AM490
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FJ746327.1 gg_id:509084 Microbial oligotrophic marine sediments: South Pacific Gyre ocean sediment 5306 m FJ7463
FJ746247.1 gg_id:509572 Microbial oligotrophic marine sediments: South Pacific Gyre ocean sediment 5306 m FJ7462
EU385894.1 gg_id:268805 Stratified microbes sediments Core MD05-2902 subseafloor sediment South China S EU3858
FJ746244.1 gg_id:553966 Microbial oligotrophic marine sediments: South Pacific Gyre ocean sediment 5306 m FJ7462
FJ455877.1 gg_id:513961 Variations archaeal and sulfate-methane transition zone continental margin sediment FJ4558
DQ811877.1 gg_id:171074 mangrove soil clone MSB-5B1 DQ811
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EF208698.1 gg_id:202905 Vertical and horizontal structure microbial sandy carbonate sediment clone CI75cm.2 EF2086
EF061971.1 gg_id:192578 Xiamen China mangrove sediment clone XME55 EF0619
EF061967.1 gg_id:199390 Xiamen China mangrove sediment clone XME3 EF0619

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EU522648.1 gg_id:264388 hydrocarbon-degrading methanogenic microbial consortia settling basin Northern Al EU522
EU644236.1 gg_id:281467 and Samoylov Island Lena active layer -centred polygon near surface horizon; Rim_T EU644
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CU923939.1 gg_id:562686 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU923
CU926201.1 gg_id:534784 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU926
CU917838.1 gg_id:556268 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU917
CU920969.1 gg_id:547682 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU920
CU925406.1 gg_id:565436 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU925
EF515504.1 gg_id:224766 Electricigen Enrichment MFC full-scale anaerobic bioreactor sludge treating brewery EF5155
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CU918551.1 gg_id:552199 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU918
CU919033.1 gg_id:534657 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU919
CU920569.1 gg_id:569566 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU920
EF515594.1 gg_id:218815 Electricigen Enrichment MFC full-scale anaerobic bioreactor sludge treating brewery EF5155

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CU918328.1 gg_id:543552 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU918
CU920613.1 gg_id:542582 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU920
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AB539936.1 gg_id:547418 Evidence syntrophic acetate oxidation coupled hydrogenotrophic methanogenesis -t AB539
EU487924.1 gg_id:549880 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU487
EU488227.1 gg_id:565887 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU488
FJ977397.1 gg_id:567707 effluent treated soil clone CS9 FJ9773
AF445659.1 gg_id:74684 travertine hot spring clone SM1B12 AF445
AB240467.1 gg_id:143650 microbial structure rhizosphere biofilm Sapporo root-tip (0 40 mm) Phragmites Sosei AB240
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DQ329898.1 gg_id:159186 Guerrero Negro hypersaline mat clone 02D2Z14 DQ329
AY921832.1 gg_id:113374 farm soil clone AKYG1561 AY921
AJ431247.1 gg_id:103391 Dehalococcoides sp. str. BHI80-52 AJ4312
CU921045.1 gg_id:553193 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU921
AJ009480.1 gg_id:2710 chlorobenzene-degrading consortium clone SJA-101 AJ0094
EF125425.1 gg_id:185193 mangrove soil clone MSB-2B11 EF1254
GU180178.1 gg_id:555085 Impact coplanar PCBs on microbial activity anaerobic estuarine sediments sediment GU180
AJ306793.1 gg_id:66911 DCP-dechlorinating consortium clone SHD-14 AJ3067
FM955656.1 gg_id:563339 Study Prokaryotic Some Selected Niches Western Ghats India water clone BCWCSP1 FM955
DQ811868.1 gg_id:169619 mangrove soil clone MSB-3E6 DQ811
FJ973585.1 gg_id:419583 Periodic sulfide irruptions impact microbial structure and hypersaline lake water colu FJ9735
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DQ394948.1 gg_id:153171 harbor sediment clone VHS-B3-54 DQ394
EF515576.1 gg_id:226739 Electricigen Enrichment MFC full-scale anaerobic bioreactor sludge treating brewery EF5155
EF203180.1 gg_id:208032 phylotypes sediments Lake Kastoria Greece sediment clone Kas19B EF2031
AY214200.1 gg_id:81161 benzene-contaminated groundwater clone ZZ14AC19 AY214
CU918692.1 gg_id:560513 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU918
AY548939.1 gg_id:100980 ANAMMOX sludge clone 1-20 AY548
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AY426455.1 gg_id:102061 full-scale anaerobic UASB bioreactor treating paper mill wastewater clone E10 AY4264
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AB487122.1 gg_id:594201 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNIR0 AB4871
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EF516324.1 gg_id:225605 grassland soil clone FCPU564 EF5163
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DQ128817.2 gg_id:186887 no tillage soil clone HSB NT53_E04 DQ128
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EF515997.1 gg_id:217684 grassland soil clone FCPP418 EF5159
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GQ015160.1 gg_id:494503 Topographical and Temporal Human Skin Microbiome skin palm clone nbw765b09c GQ015
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EU134015.1 gg_id:244349 tallgrass prarie soil clone FFCH5128 EU134
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EU134006.1 gg_id:245129 tallgrass prarie soil clone FFCH5499 EU134
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DQ289898.1 gg_id:169145 Microbial Carbon and Nitrogen Cycling Sediments South Atlantic Bight Permeable Sh DQ289
FJ623297.1 gg_id:582257 Efficient polyhydroxyalkanoates production waste-activated submitted process seque FJ6232
AM935699.1 gg_id:552001 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM935
FJ542929.1 gg_id:509986 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone B FJ5429
EU104334.1 gg_id:349891 Evidence Comamonadaceae determinants settling performance activated sludge clo EU104
DQ269088.1 gg_id:177331 marine macro-alga surface clone DPC004 DQ269
EU421855.1 gg_id:262783 Un-culturable Indian Himalayas soil under glacier Lahaul-Spiti Valley clone KC-9 EU4218
AM086103.1 gg_id:146618 Abundance and archaea mesotrophic Lake Kinneret lake profundal sediment clone (AM086
FN563245.1 gg_id:582127 Impact changing HRT OLR on prokaryotes involved biomethanizitaion and fuzzy logic FN563
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AJ278167.1 gg_id:65481 anaerobic bioreactor clone SHD-71 AJ2781
FJ529287.1 gg_id:551159 Evidence vertical transmission symbionts adult embryo Caribbean sponge Svenzea ze FJ5292
AB257633.1 gg_id:265961 Microbial few millimeters be surface dolomite rock 'Val Piora' Alps 1965 meters abov AB2576
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AM176891.1 gg_id:160746 Recovery mangrove sediment clone SZB48 AM176
FJ481351.1 gg_id:580216 Microbes marine sponges sponge tissue clone XC1G09 FJ4813
EU529736.1 gg_id:272484 FACS SBR EBPR system clone H94 EU529
FN396715.1 gg_id:556929 constant flux thermophilic cold seabed Arctic marine surface sediment clone s5_8_II FN3967
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FJ481363.1 gg_id:578919 Microbes marine sponges sponge tissue clone XE1A01 FJ4813
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U20797.1 gg_id:13753 marine clone SAR202 U2079

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GU118655.1 gg_id:556998 Threatened Corals Provide Microbial Habitats clone Mfav_L15 GU118
EU491393.1 gg_id:273086 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X3 clone EU491
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AM997386.1 gg_id:569629 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A AM997
GQ350036.1 gg_id:577420 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ350
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GQ347250.1 gg_id:536270 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ347
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GU118688.1 gg_id:561516 Threatened Corals Provide Microbial Habitats clone Mfav_F17 GU118
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AY534097.1 gg_id:101670 Sargasso Sea clone SAR250 AY534
GQ337162.1 gg_id:569652 Hydrography shapes biogeography deep Arctic Ocean water depth 410m clone CB1 GQ337
EF076113.1 gg_id:238932 Sponge- microorganisms: ecology and biotechnological potential Bahamas: Little San EF0761
GQ337281.1 gg_id:561898 Hydrography shapes biogeography deep Arctic Ocean water depth 996m clone NB0 GQ337
AY704387.1 gg_id:111406 oceanic crust clone CTD005-74B-02 AY704
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FJ481362.1 gg_id:583588 Microbes marine sponges sponge tissue clone XD2H09 FJ4813
GQ346854.1 gg_id:580967 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ346
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AY592108.1 gg_id:104227 marine ANAMMOX sediment clone AY592108 AY592
GU118595.1 gg_id:584893 Threatened Corals Provide Microbial Habitats clone Mfav_A11 GU118
GU118631.1 gg_id:576491 Threatened Corals Provide Microbial Habitats clone Mfav_I09 GU118
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GU118524.1 gg_id:564046 Threatened Corals Provide Microbial Habitats clone Mfav_C19 GU118
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AF005747.2 gg_id:13754 deep subsurface paleosol clone H1.2.f AF005
AJ567556.1 gg_id:90508 deep-sea sediment clone MBMPE42 AJ5675
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GU118534.1 gg_id:578581 Threatened Corals Provide Microbial Habitats clone Mfav_C17 GU118
FJ481355.1 gg_id:510043 Microbes marine sponges sponge tissue clone XD2B11 FJ4813
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AAUI01000026.1 gg_id:191282 Chloroflexus aggregans str. DSM 9485 AAUI0

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EU245131.1 gg_id:251486 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-H2-F12 EU245
AJ308501.1 gg_id:71275 Chloroflexus aurantiacus str. DSM 637 AJ3085
AB041226.1 gg_id:17199 Roseiflexus castenholzii str. HLO8 AB041
AB166782.1 gg_id:107332 EBPR sludge clone UTFS-OF06-31 AB166
EU589291.1 gg_id:273949 China Ningxia rice paddy field soil clone 2_C1 EU589
NC_009523.1 gg_id:235028 Roseiflexus sp. str. RS-1 NC_00
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AB079639.1 gg_id:41211 Kouleothrix aurantiaca str. MYSI AB079
FN594697.1 gg_id:579686 and arsenic mobilization rock biofilms ancient biofilom gold mine Zloty Stok clone b7 FN594
AY921852.1 gg_id:113942 farm soil clone AKYG724 AY921
X84565.2 gg_id:1281 sludge clone SBR2022 X84565
EF520511.1 gg_id:230687 structure lakes: what controls ? acid-impacted lake clone ADK-MOe02-82 EF5205
EU335386.1 gg_id:253621 Changes microbial metabolic and along hydrogeochemically variable profile unsatura EU335
AF507694.1 gg_id:65689 forest soil clone S095 AF507
EU134099.1 gg_id:241781 tallgrass prarie soil clone FFCH12331 EU134
EU881212.1 gg_id:329622 Karst region natural restoration land soil clone KNR200711-149 EU881
EU134100.1 gg_id:240467 tallgrass prarie soil clone FFCH12357 EU134
EU134120.1 gg_id:248223 tallgrass prarie soil clone FFCH14454 EU134
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GU118012.1 gg_id:590439 Threatened Corals Provide Microbial Habitats clone Apal_D13 GU118
DQ329906.1 gg_id:159054 Guerrero Negro hypersaline microbial mat clone 02D2Z24 DQ329
EU246315.1 gg_id:253655 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-P6-G07 EU246
AF146832.2 gg_id:73897 Oscillochloris sp. str. R AF146
NC_009972.1 gg_id:245517 Herpetosiphon aurantiacus str. ATCC 23779 NC_00
AF039293.1 gg_id:1266 Herpetosiphon geysericola str. ATCC23076 AF0392
AF004928.2 gg_id:74423 Dehalococcoides ethenogenes str. strain 195 AF0049
NC_002936.3 gg_id:109890 Dehalococcoides ethenogenes str. 195 NC_00
EU385770.1 gg_id:272948 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S EU385
AB177317.1 gg_id:132805 seafloor methane hydrate clone ODP1251B13.5 AB177
EU385739.1 gg_id:269946 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S EU385
AB177189.1 gg_id:135968 seafloor methane hydrate clone ODP1230B3.02 AB177
EU487871.1 gg_id:534610 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU487
AY704392.1 gg_id:111801 oceanic crust clone FS117-42B-02 AY704
GQ143778.1 gg_id:406679 Level Continental Shelf Sediment and Phylum-level lineages Phylum Planctomycetes GQ143
FJ746273.1 gg_id:533019 Microbial oligotrophic marine sediments: South Pacific Gyre ocean sediment 5306 m FJ7462
FJ746218.1 gg_id:513194 Microbial oligotrophic marine sediments: South Pacific Gyre ocean sediment 5306 m FJ7462
AM943570.1 gg_id:260482 Microbial dolomite formation Lagoa Vermelha Brazil carbonaceous sediments hype AM943
AY592728.1 gg_id:105090 deep-sea mud volcano clone Napoli-3B-61; BC07-3B-61 AY592

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FJ746184.1 gg_id:510245 Microbial oligotrophic marine sediments: South Pacific Gyre ocean sediment 5306 m FJ7461
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EU385867.1 gg_id:273645 Stratified microbes sediments Core MD05-2902 subseafloor sediment South China S EU3858
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EU181494.1 gg_id:257219 Prokaryotic enhanced organic matter remineralization continental margin marine se EU1814
AF005745.1 gg_id:13747 deep subsurface paleosol clone t0.6.f AF0057
U81649.2 gg_id:13743 anaerobic digestor clone vadinBA26 U81649
FJ810554.1 gg_id:461677 Subsurface ecosystem resilience: Long-term attenuation subsurface contaminants su FJ8105
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EU679418.1 gg_id:573684 Dehalogenimonas lykanthroporepellens str. BL-DC-8 EU6794
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AB300091.1 gg_id:225611 Wide ancient microbial DNAs Quaternary sediments holocene mud sediment clone K AB3000
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EU385763.1 gg_id:265942 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S EU3857
EU385870.1 gg_id:263318 Stratified microbes sediments Core MD05-2902 subseafloor sediment South China S EU3858
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EU037997.1 gg_id:241901 Episodic subaerial speleogenesis controlled mineralogy microbial colonization and cc EU0379
CU917587.1 gg_id:538628 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU9175
DQ513102.1 gg_id:160026 Microbial life fluids ridge flank crustal fluid clone FS274-70B-03 DQ513
EU385714.1 gg_id:274642 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S EU3857
AB241538.1 gg_id:143037 microbial structure Phragmites rhizosphere biofilm reed bed reactor laboratory clon AB2415
DQ513037.1 gg_id:160017 Microbial life fluids ridge flank crustal fluid clone FS142-4B-02 DQ513
AB189693.1 gg_id:113904 termite gut homogenate clone Tc-59 AB1896
AF407200.1 gg_id:31890 CB-contaminated groundwater clone GIF9 AF4072
FJ264678.1 gg_id:330913 Manganese and Iron Dependent Anaerobic Oxidation Methane methane seep sedim FJ2646
DQ463707.2 gg_id:167201 distinct Lake Tanganyika anoxic hypolimnion clone TK-SH11 DQ463
AM086125.1 gg_id:147104 Abundance and archaea mesotrophic Lake Kinneret lake profundal sediment clone AM086
FN396625.1 gg_id:554232 constant flux thermophilic cold seabed Arctic marine surface sediment clone s5_0_II FN3966
DQ394968.1 gg_id:155275 harbor sediment clone VHS-B3-87 DQ394
EU542435.1 gg_id:261089 Effects chemical structure concentration on pathways microbial during dechlorinatio EU5424
FJ901746.1 gg_id:512765 phreatic limestone sinkholes northeastern Mexico biomat 50m deep cenote La Palita FJ9017
EU386079.1 gg_id:267006 Biogeographical and microbes sediments on subseafloor sediment South China Sea EU3860
AY093456.1 gg_id:56382 deep marine sediment clone MB-A2-101 AY0934
EU385821.1 gg_id:273489 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S EU3858
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GQ259278.1 gg_id:563464 Microbial activities coastal marine sediments and water column Svalbard deep sedi GQ259
FJ873289.1 gg_id:549034 Vertical and archaea methane-rich cold seep located base sediments Okhotsk Sea clo FJ8732

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FJ901649.1 gg_id:570224 phreatic limestone sinkholes northeastern Mexico biomat 30m deep cenote La Palita FJ9016
EU181502.1 gg_id:253195 Prokaryotic enhanced organic matter remineralization continental margin marine se EU181
EU488464.1 gg_id:535141 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU488
FJ746280.1 gg_id:559658 Microbial oligotrophic marine sediments: South Pacific Gyre ocean sediment 5306 m FJ7462
DQ330175.1 gg_id:159156 Guerrero Negro hypersaline mat clone 08D2Z16 DQ330
AB525458.1 gg_id:552108 Segregated ANME-1 and -2 cold-seep marine sediments deep-sea methane seep sed AB525
GQ246424.1 gg_id:559475 Temporal and spatial China North Yel Sea sediments clone Ld1-29 GQ246
DQ811888.1 gg_id:163063 mangrove soil clone MSB-5B10 DQ811
FJ264593.1 gg_id:352084 Manganese and Iron Dependent Anaerobic Oxidation Methane methane seep sedim FJ2645
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GQ264467.1 gg_id:568917 Structure Simulated Level Waste Site simulated level waste site clone WW3_173 GQ264
EU386131.1 gg_id:273805 Biogeographical and microbes sediments on subseafloor sediment South China Sea c EU386
EU335161.1 gg_id:241504 Changes microbial metabolic and along hydrogeochemically variable profile saturate EU335
EF019820.1 gg_id:206654 aspen rhizosphere clone Elev_16S_1165 EF0198
EU287395.1 gg_id:249501 Pacific arctic surface sediment clone S26-95 EU287
GQ262892.1 gg_id:582010 Structure Simulated Level Waste Site simulated level waste site clone F1_52X2 GQ262
GQ264295.1 gg_id:571700 Structure Simulated Level Waste Site simulated level waste site clone WW2_113 GQ264
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GQ402693.1 gg_id:587291 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
DQ837236.1 gg_id:255513 Archaeal and pristine National Park Spain Donana coastal aquifer clone 49S1_2B_10 DQ837
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FJ746106.1 gg_id:543849 Microbial oligotrophic marine sediments: South Pacific Gyre ocean sediment 5306 m FJ7461
GQ264238.1 gg_id:577544 Structure Simulated Level Waste Site simulated level waste site clone WW1_b36 GQ264
FJ153023.1 gg_id:329203 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX4C FJ1530
EF157231.1 gg_id:239349 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon EF1572
FN545887.2 gg_id:567811 un 2 Rupi basin Bulgaria hot spring clone S2R-176 FN5458
EU043839.1 gg_id:246200 luences structure fosters richness subtropical Altamaha Ohopee River Valley inland c EU0438
EF516921.1 gg_id:222810 grassland soil clone FCPN634 EF5169
FJ466072.1 gg_id:513165 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea FJ4660
EF494362.1 gg_id:222240 Nunnock River granitic landscape clone NR.1.006 EF4943
AY425774.1 gg_id:104491 volcanic deposit 1790 clone 1790-6 AY4257
GU205279.1 gg_id:525657 unusual Microbial Venezuelan Tepui (Orthoquartzite) Cave: Dominance Chloroflexal GU205
DQ128986.2 gg_id:183422 old forest soil clone HSB OF53_F07 DQ128
EF492970.1 gg_id:250185 Iron-manganese Nodule and Its Surrounding Soil soil around iron-manganese nodule EF4929
EF516298.1 gg_id:226220 grassland soil clone FCPN436 EF5162
EU134194.1 gg_id:254105 tallgrass prarie soil clone FFCH12345 EU134
DQ450736.1 gg_id:161567 Microbial Alpine Tundra Wet Meadow Soil: Chloroflexi Cold Water-Saturated satura DQ450
FJ478503.1 gg_id:557636 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4785
EU881266.1 gg_id:321040 (long-term grazing and burned annual) Karst region serious disturbance field soil clor EU881

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EU134187.1 gg_id:238971 tallgrass prarie soil clone FFCH11515 EU134
EF516303.1 gg_id:217400 grassland soil clone FCPP610 EF5163
EF516607.1 gg_id:217959 grassland soil clone FCPS457 EF5166
EF516939.1 gg_id:226026 grassland soil clone FCPN516 EF5169
AY425786.1 gg_id:100895 volcanic deposit 1959 clone 1959-2 AY4257
FJ466064.1 gg_id:551596 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea FJ4660
AY425785.1 gg_id:100738 volcanic deposit 1959 clone 1959-1 AY4257
AM749770.1 gg_id:246345 Isolation ing candidate division soils New Zealand steam-affected geothermal soil AM749
EU117169.1 gg_id:257714 Scratching surface rare biosphere tag primers recent progress made toward microbi EU117
DQ395967.1 gg_id:154958 deep-sea octacoral clone ctg_CGOGA96 DQ395
FJ479460.1 gg_id:557444 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4794
EU133984.1 gg_id:241342 tallgrass prarie soil clone FFCH15563 EU1339
DQ450723.1 gg_id:160354 Microbial Alpine Tundra Wet Meadow Soil: Chloroflexi Cold Water-Saturated satura DQ450
AY425792.1 gg_id:105343 volcanic deposit 1959 clone 1959-8 AY4257
EF018760.1 gg_id:204816 aspen rhizosphere clone Amb_16S_1221 EF0187
DQ453119.1 gg_id:156599 acid mine drainage waste ore deposit clone S23 DQ453
FJ466045.1 gg_id:513135 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea FJ4660
EU881207.1 gg_id:316520 Karst region natural restoration land soil clone KNR200711-096 EU8812
EU133983.1 gg_id:240228 tallgrass prarie soil clone FFCH14125 EU1339
AM180156.1 gg_id:159894 Ktedobacter racemifer str. SOSP1-21 AM180
EF516615.1 gg_id:223797 grassland soil clone FCPT647 EF5166
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EF018870.1 gg_id:206963 aspen rhizosphere clone Amb_16S_1353 EF0188
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EF018513.1 gg_id:206278 aspen rhizosphere clone Amb_16S_768 EF0185
EF018442.1 gg_id:206890 aspen rhizosphere clone Amb_16S_1066 EF0184
GQ263112.1 gg_id:566107 Structure Simulated Level Waste Site simulated level waste site clone F2_63X2 GQ263
DQ067037.1 gg_id:134616 Lake Washington sediment clone pLW-95 DQ067
FJ478583.1 gg_id:541082 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4785
EU488103.1 gg_id:549321 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU488
GU444080.1 gg_id:522273 Effects amendments on fertility and microbial structure cucumber Cucumis sativus L GU444
DQ814518.1 gg_id:168875 zebrafish digestive tract clone aaa30c11 DQ814
EU644259.1 gg_id:282711 and Samoylov Island Lena active layer -centred polygon near surface horizon; Rim_T EU6442
EF516339.1 gg_id:218184 grassland soil clone FCPS580 EF5163
AM709744.1 gg_id:256904 symbiotic Ruegeria strains cuttlefish Sepia officinalis renal appendages clone B4SOA AM709
EU644199.1 gg_id:284171 and Samoylov Island Lena active layer -centred polygon near surface horizon; Rim_T EU6441
EF516912.1 gg_id:217746 grassland soil clone FCPU758 EF5169
EU488018.1 gg_id:534789 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU4880
GQ397072.1 gg_id:512939 Functional unvegetated perhumid recently-deglaciated soils do not correlate shifts s GQ397

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EU488088.1 gg_id:551024 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU488
EU245384.1 gg_id:256810 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M1-A0 EU245
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FJ894331.1 gg_id:566611 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B2E; ear pu FJ8943
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AY221598.1 gg_id:90766 lead-contaminated soil clone HN1-15 AY221
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FJ675508.1 gg_id:514898 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6755
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EU134180.1 gg_id:247448 tallgrass prarie soil clone FFCH3294 EU134
EU979025.1 gg_id:349986 Effects intercropping Rhizobium inoculation on microbial biomass and rhizosphere b EU979
AY921935.1 gg_id:113628 farm soil clone AKYG1722 AY921
FJ671223.1 gg_id:516459 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6712
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GQ263261.1 gg_id:583206 Structure Simulated Level Waste Site simulated level waste site clone F3_91X GQ263
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FJ481270.1 gg_id:582300 Microbes marine sponges sponge tissue clone XB1A10F FJ4812
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GU118592.1 gg_id:554992 Threatened Corals Provide Microbial Habitats clone Mfav_D06 GU118
EU035922.2 gg_id:353248 Insight microbial structure Norwegian deep-water Desmacidon sponge deep-sea cor EU035

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EF516466.1 gg_id:217784 grassland soil clone FCPS455 EF5164
DQ666683.2 gg_id:211216 Desulfurispirillum alkaliphilum str. SR 1 DQ666
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AY093470.1 gg_id:63113 deep marine sediment clone MB-B2-105 AY0934
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GQ389121.1 gg_id:542202 quality deterioration drinking system during serious red water outbreak clone S74 GQ389
CU927882.1 gg_id:549004 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU927
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AY328748.1 gg_id:88230 drinking water system simulator clone DSSD50 AY3287
EF516003.1 gg_id:227019 grassland soil clone FCPN395 EF5160
AY945890.1 gg_id:147415 Thauera and Azoarcus functionally important genera denitrifying quinoline-removal AY9458
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AY222299.1 gg_id:83349 silica sinter depositing geothermal power station discharge drain clone ST01-SN2C AY2222
AM991180.1 gg_id:278744 Microbial groundwater and their potential use biomonitoring karst spring water clo AM991
EF540417.1 gg_id:225363 oil-shale semi-coke solid waste clone MK42 EF5404
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EU881250.1 gg_id:328994 (long-term grazing and burned annual) Karst region serious disturbance field soil clo EU881
EU134279.1 gg_id:236597 tallgrass prarie soil clone FFCH18662 EU134
EU134280.1 gg_id:237637 tallgrass prarie soil clone FFCH2285 EU134
EU937941.1 gg_id:343561 Biogeochemistry Iron Oxidation Circumneutral Freshwater Habitat riparian iron oxidi EU937
EU134269.1 gg_id:249228 tallgrass prarie soil clone FFCH6070 EU134
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AF289160.1 gg_id:30917 freshwater clone PRD01a012B AF289
GU303847.1 gg_id:564895 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU303
EU871391.1 gg_id:342685 Genetic Bovine (Bos taurus) Rumen Thailand clone CF244 EU871
EF445288.1 gg_id:206256 dairy cow rumen clone NED4H4 EF4452
GQ448661.1 gg_id:589410 Microbiome neonatal calves: shedding microorganisms fecal clone calf784_10wks_g GQ448
EU474510.1 gg_id:301639 bighorn sheep feces clone BHSD_aaa02b04 EU474
FJ682976.1 gg_id:515041 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6829
GU304200.1 gg_id:588446 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU304
GU304110.1 gg_id:555951 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU304
FJ680800.1 gg_id:523621 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6808
AY992501.1 gg_id:135530 mouse cecum clone C23_g15 AY9925
EU622719.1 gg_id:277694 -feed administered sub-therapeutic chlorotetracycline alters structure and but not a EU622
EU459550.1 gg_id:301924 capybara feces clone CAP_aah99f10 EU459
FJ682880.1 gg_id:525341 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6828

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DQ394643.1 gg_id:151120 -Arctic peninsula Svalbard Norway determined genes and rumen isolates reindeer o DQ394
GU208308.1 gg_id:578358 Study on Sediment Dongping Lake sediment clone Ftt1-21 GU208
EU459480.1 gg_id:301614 capybara feces clone CAP_aah98b01 EU459
FJ683022.1 gg_id:525809 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6830
AB270013.1 gg_id:170218 Influence temperature and humidity on heifers rumen contents Holstein heifer (Bos AB270
FJ684721.1 gg_id:515243 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6847
EU871372.1 gg_id:310781 Genetic Bovine (Bos taurus) Rumen Thailand clone CF191 EU871
FJ683369.1 gg_id:526124 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6833
EU777280.1 gg_id:309344 Okapi feces clone OK2_d08_1 EU777
GU119744.1 gg_id:569143 Threatened Corals Provide Microbial Habitats chloroplast clone Gven_I13 GU119
DQ851108.1 gg_id:168769 Bigelowiella natans DQ851
FJ382004.1 gg_id:546960 Potentially pathogenic and air stem cell transplant winter hospital shower water BMT FJ3820
GU084820.1 gg_id:583906 Volvox carteri f. nagariensis str. UTEX 2908 GU084
FJ423446.1 gg_id:369386 Chlamydomonas reinhardtii str. CC-503 cw92 mt+ FJ4234
BK000554.2 gg_id:79762 Chlamydomonas reinhardtii BK000
EU258745.1 gg_id:256833 summer sea Dalian and Liaodong determined bay clone D0924 EU258
EU394542.1 gg_id:547628 Coccolithophore bloom dynamics shape (NE-Atl) northern Bay Biscay pelagic free-livi EU394
GU119877.1 gg_id:591283 Threatened Corals Provide Microbial Habitats reef water clone Reef_J10 GU119
GU061486.1 gg_id:539327 and function microbial mesoscale eddy perturbations South China Sea clone CE1-DC GU061
D11347.1 gg_id:70155 Chlorella vulgaris str. 211-1e D1134
EF516670.1 gg_id:225891 grassland soil clone FCPS712 EF5166
FJ968739.1 gg_id:545380 Oocystis solitaria FJ9687
GQ495399.1 gg_id:587227 terrestrial volcanic rocks Iceland Hnausahraun lava f clone Bas-7-41 GQ495
DQ059300.1 gg_id:130918 Prochlorales cyanobacterium str. EV-7 DQ059
FJ203496.1 gg_id:331291 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h FJ2034
GU119832.1 gg_id:591712 Threatened Corals Provide Microbial Habitats chloroplast clone Past_I24 GU119
FJ203477.1 gg_id:339585 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h FJ2034
FJ203311.1 gg_id:310472 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c FJ2033
FJ203366.1 gg_id:309870 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h FJ2033
FJ203504.1 gg_id:333836 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h FJ2035
FJ203472.1 gg_id:329853 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h FJ2034
FJ203458.1 gg_id:303580 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h FJ2034
U08345.1 gg_id:26799 Codium fragile U0834
FJ535833.1 gg_id:566475 Avrainvillea lacerata FJ5358
FJ535846.1 gg_id:538813 Rhipocephalus phoenix FJ5358
GU119661.1 gg_id:534254 Threatened Corals Provide Microbial Habitats chloroplast clone Dstr_C23 GU119
FJ203191.1 gg_id:354177 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c FJ2031
GU119692.1 gg_id:560647 Threatened Corals Provide Microbial Habitats chloroplast clone Dstr_D14 GU119
FJ535834.1 gg_id:544846 Avrainvillea nigricans FJ5358
GU119669.1 gg_id:586094 Threatened Corals Provide Microbial Habitats chloroplast clone Dstr_G10 GU119
FJ203461.1 gg_id:330936 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h FJ2034

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FJ203380.1 gg_id:352490 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h FJ2033
FJ203174.1 gg_id:336968 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c FJ2031
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FJ203465.1 gg_id:330199 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h FJ2034
FJ203376.1 gg_id:330464 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h FJ2033
GU119820.1 gg_id:585617 Threatened Corals Provide Microbial Habitats chloroplast clone Mfra_J19 GU119
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FJ203600.1 gg_id:305139 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h FJ2036
FN563093.1 gg_id:509525 Crustomastix stigmatica str. CCMP 2493 FN563
EF520512.1 gg_id:233592 structure lakes: what controls ? acid-impacted lake clone ADK-WYh02-15 EF5205
AY948038.1 gg_id:142412 Synchrony and seasonality two temperate rivers USA: Massachusetts Parker River cl AY948
AF534437.1 gg_id:85239 Toolik Lake main station at 3 m depth clone TLM13/TLMdgge20 AF5344
U70724.1 gg_id:25107 environmental sample Cape Hatteras picoplankton clone OM283 U7072
AY947987.1 gg_id:144486 Synchrony and seasonality two temperate rivers USA: Massachusetts Parker River cl AY947
AY947975.1 gg_id:142536 Synchrony and seasonality two temperate rivers USA: Massachusetts Ipswich River c AY947
AF530388.2 gg_id:155728 Dinophysis norvegica str. norvCC04 AF5303
AY948025.1 gg_id:141924 Synchrony and seasonality two temperate rivers USA: Massachusetts Parker River cl AY948
X55015.1 gg_id:3470 Pyrenomonas salina Pla. X55015
NC_000926.1 gg_id:51823 Guillardia theta NC_00
AB294341.1 gg_id:209603 Microbial structure deep coal seem groundwater stream clone SWB30 AB2943
AY948019.1 gg_id:142940 Synchrony and seasonality two temperate rivers USA: Massachusetts Parker River cl AY948
GQ358203.1 gg_id:588592 Cryptomonas paramecium str. CCAP977/2a GQ358
FJ719664.1 gg_id:525501 Euglena tristella str. Yeonhwaji091407B FJ7196
AY626053.1 gg_id:131617 Monomorphina pyrum str. ACOI 2778 AY6260
AF289248.1 gg_id:101247 Euglena viridis str. SAG 1224-17d AF2892
AY626043.1 gg_id:129536 Euglena deses str. SAG 1224-19b AY6260
EU750700.1 gg_id:443968 Monomorphina pseudopyrum str. CCAC 0093 EU750
EU750698.1 gg_id:378739 Euglena caudata str. ASW 08048 EU750
FJ719655.1 gg_id:530167 Euglena communis str. SAG1224-40 FJ7196
EU750701.1 gg_id:373273 Phacus applanatus str. ASW 08023 EU750
AY626050.1 gg_id:138007 Euglena proxima str. SAG 1224-11b AY6260
EU370511.1 gg_id:556321 Euglena granulata str. UTEX 2345 EU370
AY626056.1 gg_id:133071 Euglena limnophila str. ACOI 2674 AY6260
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AY158150.1 gg_id:102748 Euglena agilis str. UW Nowy_Targ k-1
AY158151.1 gg_id:102889 Euglena agilis str. UW Wawocko k-1
AF289254.1 gg_id:26708 Trachelomonas volvocina str. AICB 524
FJ719684.1 gg_id:521728 Phacus inflexus str. ACOI1336
FJ719695.1 gg_id:517906 Phacus trimarginatus str. Gungnamji052507B
AY626057.1 gg_id:134448 Phacus orbicularis str. AICB 502
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FJ719661.1 gg_id:520311 Euglena sp. str. MI67
EU221504.1 gg_id:340965 Phacus segretii str. ACOI 1337
EU221502.1 gg_id:354548 Phacus hamelii str. ACOI 1088
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FJ719707.1 gg_id:519272 Trachelomonas pertyi str. SAG1283-13
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EU221507.1 gg_id:337382 Trachelomonas abrupta str. NJ T801
FJ719647.1 gg_id:524613 Colacium sp. str. NJ
EU750706.1 gg_id:407237 Euglena adhaerens str. ASW 08138
EU370503.1 gg_id:545259 Euglena geniculata str. MI62
FJ719674.1 gg_id:524130 Lepocinclis fusca str. MI100
AY626046.1 gg_id:137790 Euglena viridis str. ACOI 2951
EU221510.1 gg_id:340082 Trachelomonas echinata str. SAG1283-22
EU221513.1 gg_id:355652 Trachelomonas hispida str. UTEX 539
EU221520.1 gg_id:324257 Trachelomonas volvocinopsis str. SAG1283-16
EU221497.1 gg_id:344325 Lepocinclis tripteris str. SAG1224-16
EU221509.1 gg_id:314485 Trachelomonas bernardinensis str. ACOI 1103
EU221521.1 gg_id:321537 Trachelomonas zorensis str. UTEX 1331
AY626060.1 gg_id:128298 Euglena spathirhyncha str. SAG 1224-42
EU221505.1 gg_id:338024 Phacus triqueter str. SAG1261-8
AY626044.1 gg_id:131844 Euglena mutabilis str. SAG 1224-9b
AY221726.1 gg_id:111684 Lepocinclis ovum str. SAG 1244-8
EU750704.1 gg_id:429842 Discoplastis adunca str. ASW 08095
EU221511.1 gg_id:332418 Trachelomonas ellipsoidalis str. NJ T1
NC_001675.1 gg_id:128892 Cyanophora paradoxa str. Pringsheim LB555
AM084275.1 gg_id:142111 Cyanoptyche gloeocystis str. SAG 34.90

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GQ348805.1 gg_id:535038 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ348
EF574942.1 gg_id:233349 site S25 near Coco's Island marine clone S25_1286 EF5749
FJ612356.1 gg_id:513373 and Biogeochemistry Dongping Lake Ecosystems lake water clone DP10.2.41 FJ6123
DQ513030.1 gg_id:160706 Microbial life fluids ridge flank crustal fluid clone FS142-30B-02 DQ513
EF520514.1 gg_id:234436 structure lakes: what controls ? acid-impacted lake clone ADK-WYh02-13 EF5205
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AY702175.1 gg_id:138411 biased towards marine algal plastids photosynthetic picoeukaryote open ocean site AY702
GU119867.1 gg_id:540713 Threatened Corals Provide Microbial Habitats reef water clone Reef_L05 GU119
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EF573807.1 gg_id:231663 site S25 near Coco's Island marine clone S25_151 EF5738
X99077.1 gg_id:72546 Ochrosphaera neapolitana str. CCMP593 X99077
EF574682.1 gg_id:233758 site S25 near Coco's Island marine clone S25_1026 EF5746
EF574443.1 gg_id:233591 site S25 near Coco's Island marine clone S25_787 EF5744
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NC_007288.1 gg_id:138642 Emiliania huxleyi str. CCMP 373 NC_00
DQ015781.1 gg_id:140203 Antarctic lake water clone ELB19-095 DQ015
AY706940.1 gg_id:110187 Pterocladia lucida AY706
FJ202832.1 gg_id:303559 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2028
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AM259754.1 gg_id:215148 Spatial sponge- Mediterranean sponge Tethya aurantium seawater clone TAU-7-68 AM259
DQ026698.1 gg_id:146905 Euptilota molle DQ026
DQ026685.1 gg_id:145086 Diapse ptilota DQ026
DQ026693.1 gg_id:148247 Sciurothamnion stegengae DQ026
DQ026692.1 gg_id:146233 Seirospora interrupta DQ026
AY706948.1 gg_id:111094 Gelidium pristoides AY706
AY706939.1 gg_id:110833 Gelidiella acerosa AY706
AY706941.1 gg_id:110867 Pterocladiella capillacea AY706
DQ026688.1 gg_id:146462 Callithamnion collabens DQ026
FJ203641.1 gg_id:305702 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h FJ2036
DQ269091.1 gg_id:187735 marine macro-alga surface clone DPC025 DQ269
DQ026682.1 gg_id:148404 Crouania elisiae DQ026
AY706944.1 gg_id:109889 Gelidium caulacantheum AY706
DQ026687.1 gg_id:147909 Proposal Euptiloteae trib. nov South Africa: Kommetjie Cape Peninsula DQ026
FJ202795.1 gg_id:344186 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2027
GU119563.1 gg_id:591956 Threatened Corals Provide Microbial Habitats chloroplast clone Apal_J16 GU119
U38804.1 gg_id:69121 Porphyra purpurea str. Avonport U3880
NC_007932.1 gg_id:154530 Porphyra yezoensis NC_00
U38804.1 gg_id:129267 Porphyra purpurea str. Avonport U3880
AM084277.1 gg_id:144620 Porphyridium aerugineum str. SAG 43.94 AM084

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AF170721.1 gg_id:19387 Thorea violacea str. SAG 51.94	AF1707
DQ269106.1 gg_id:188204 marine macro-alga surface clone DPC164	DQ269
X81903.1 gg_id:3476 Glaucosphaera vacuolata str. SAG B 13.82	X81903
Z29521.1 gg_id:3474 Chondrus crispus	Z29521
AF170713.1 gg_id:29775 Compsopogon coeruleus str. SAG B 36.94	AF1707
Z18289.1 gg_id:3475 Palmaria palmata -- chloroplast	Z18289
GU119866.1 gg_id:583758 Threatened Corals Provide Microbial Habitats reef water clone Reef_H15	GU119
AJ536459.1 gg_id:102607 Lauderia borealis str. P125 CCAP 1044/1	AJ5364
FJ002211.1 gg_id:306594 Thalassiosira gravida str. CCMP 986 C140	FJ0022
AF327029.1 gg_id:38733 algal bloom clone AWS98-19b	AF3270
AJ007876.1 gg_id:3438 cyanobacterium clone LD27	AJ0078
GU119608.1 gg_id:579531 Threatened Corals Provide Microbial Habitats chloroplast clone Dstr_I18	GU119
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AJ536452.1 gg_id:101506 Bacillaria paxillifer str. p73	AJ5364
AF418971.1 gg_id:30625 USA: Colorado Fort Collins Horsetooth Reservoir clone HT2A3	AF4189
FJ002215.1 gg_id:305627 Chaetoceros calcitrans str. PCC 537/nioz C07	FJ0022
FJ002196.1 gg_id:337513 Melosira cf. octogona str. CCMP 483 C122	FJ0021
FJ002179.1 gg_id:327536 Attheya septentrionalis str. CCMP 2083 C102	FJ0021
FJ002181.1 gg_id:340216 Aulacoseira granulata var. angustissima str. CCAP 1002/2 C104	FJ0021
FJ002221.1 gg_id:332808 Nitzschia closterium C14	FJ0022
FJ002188.1 gg_id:340298 Fragilaria pinnata str. CCAP 1029/2 C112	FJ0021
L10941.1 gg_id:3402 marine snow clone AGG56	L10941
DQ521489.1 gg_id:175452 Antarctic lake ice cover clone ANTLV1_E03	DQ521
AJ536456.1 gg_id:102146 Cymatosira belgica str. P189 CCAP 1018/1	AJ5364
EU841053.1 gg_id:317660 biofilm grown on benthic ovals 0.5 degrees C 0.8 m depth polluted river surface clon	EU8410
AF514852.1 gg_id:64743 Haslea ostrearia	AF5148
AM991155.1 gg_id:278448 Microbial groundwater and their potential use biomonitoring karst spring water clo	AM991
GU119856.1 gg_id:555672 Threatened Corals Provide Microbial Habitats reef water clone Reef_J18	GU119
AJ536466.1 gg_id:107146 Corethron pennatum str. P135	AJ5364
AY221720.1 gg_id:112272 Stephanodiscus minutulus str. SAG 49.91	AY2217
AF534438.1 gg_id:83959 Toolik Lake main station at 3 m depth clone TLM14	AF5344
EF573915.1 gg_id:227603 site S25 near Coco's Island marine clone S25_259	EF5739
AY948053.1 gg_id:143740 Synchrony and seasonality two temperate rivers USA: Massachusetts Parker River cl	AY9480
GU119861.1 gg_id:586764 Threatened Corals Provide Microbial Habitats reef water clone Reef_N20	GU119
X14873.1 gg_id:3448 Pylaiella littoralis Pla.	X14873
DQ307678.1 gg_id:149793 Fucus vesiculosus	DQ307
GQ231542.1 gg_id:563800 Aureoumbra lagunensis str. CCMP 1507	GQ231
EF419352.1 gg_id:212582 Substantial alterations cutaneous biota psoriatic lesions human skin clone 1PN75	EF4193
DQ513100.1 gg_id:159889 Microbial life fluids ridge flank crustal fluid clone FS274-44B-03	DQ513
EF574323.1 gg_id:228263 site S25 near Coco's Island marine clone S25_667	EF5743

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U24588.1 gg_id:3550 Lygodium japonicum U2458
AB197035.2 gg_id:141908 Selaginella uncinata AB197
EU017103.1 gg_id:243468 Passiflora biflora EU017
AY660566.1 gg_id:108861 Huperzia lucidula AY660
DQ478785.1 gg_id:221305 Dacrydium pierrei DQ478
DQ478783.1 gg_id:220978 Cephalotaxus fortunei DQ478
DQ000201.1 gg_id:123131 Trewia nudiflora DQ000
X07675.1 gg_id:3541 Glycine max str. Maple arrow X07675
GQ076398.1 gg_id:436938 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw36 GQ076
FJ755183.1 gg_id:559773 Selaginella moellendorffii FJ7551
DQ359689.1 gg_id:177315 Ranunculus macranthus DQ359
GQ997924.1 gg_id:518737 Ximenia americana GQ997
DQ417653.1 gg_id:155825 Trifolium repens DQ417
AF244555.1 gg_id:36243 Gnetum leyboldii AF244
DQ478789.1 gg_id:225032 Abies fabri DQ478
NC_008454.1 gg_id:192539 Pelargonium x hortorum NC_00
EF219137.1 gg_id:214073 microbial extremely acidic metal-rich stream massive sulfide (Huelva Spain) and their EF2191
U24595.1 gg_id:3525 Tmesipteris oblanceolata U2459
U24585.1 gg_id:3545 Isoetes melanopoda U2458
AJ007728.1 gg_id:53526 Orobanche minor AJ0077
AP009339.1 gg_id:245721 Cycas taitungensis AP009
GQ998717.1 gg_id:527256 Quercus nigra GQ998
EU016691.1 gg_id:239198 Yucca schidigera EU016
AJ401353.1 gg_id:18362 Cuscuta campestris AJ4013
NC_005973.1 gg_id:101027 Oryza nivara str. SL10 NC_00
AF244549.1 gg_id:34845 Adiantum pedatum AF244
AJ440719.1 gg_id:64370 putative agent rhinosporidiosis AJ4407
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NC_008407.1 gg_id:173745 Jasminum nudiflorum NC_00
X73670.1 gg_id:3546 Daucus carota -- chloroplast X7367
GQ000614.1 gg_id:469179 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ000
GQ043792.1 gg_id:439422 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw97 GQ043
NC_004543.1 gg_id:128955 Anthoceros formosae NC_00
U24596.1 gg_id:3536 Spirogyra maxima U2459
FJ901425.1 gg_id:578127 phreatic limestone sinkholes northeastern Mexico growth slide biofilm 1m deep ceno FJ9014
U47845.1 gg_id:29047 Cytinus ruber U4784
U24591.1 gg_id:3534 Selaginella apoda U2459
U67743.1 gg_id:35074 Cynomorium coccineum U6774

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U24579.1 gg_id:3556 Coleochaete orbicularis	U24579
U67740.1 gg_id:45967 Bdallophyton americanum	U67740
U67742.1 gg_id:72055 Mitrastema yamamotoi	U67742
EU799970.1 gg_id:303568 It's all ranking aquatic Newport Harbour RI clone 1C227648	EU799
AB355043.1 gg_id:242402 Monitoring and archaeal two heavy polluted areas lake Egypt based on surface wate	AB3550
AF289247.1 gg_id:30353 Eutreptia viridis str. SAG 1226-1c	AF2892
AF170711.1 gg_id:28521 Chroothece richteriana str. SAG B 104.79	AF1707
AF172715.1 gg_id:30150 Pavlova gyrans	AF1727
FJ719672.1 gg_id:530315 Eutreptiella gymnastica str. MCC-NIES381	FJ7196
FJ390400.1 gg_id:366238 Cyanidium sp. Atacama	FJ3904
DQ249873.1 gg_id:161126 Eutreptiella braarudii str. CCMP-1594	DQ249
EU586032.1 gg_id:258653 Cyanidium caldarium str. YSK-1	EU5860
EU750699.1 gg_id:385423 Eutreptiella pomquetensis str. CCMP 1491	EU7506
AB234298.1 gg_id:141161 Nephroselmis pyriformis	AB2342
GU062005.1 gg_id:577338 and function microbial mesoscale eddy perturbations South China Sea clone S-DCM-	GU062
FN563105.1 gg_id:512475 Mesostigma viride str. SAG 50-1	FN5631
AF132790.1 gg_id:3564 Gloeobacter violaceus str. PCC 7421	AF1327
EF583862.1 gg_id:237833 Anabaena sp. str. BECID31	EF5838
AJ630458.1 gg_id:108010 Anabaena augstumalis 'SCHMIDKE JAHNKE/4a' str. SCMIDKE JAHNKE/4a	AJ6304
X59559.1 gg_id:3092 Anabaena sp str. PCC 7120	X59559
AM711537.1 gg_id:258918 Nostoc sp. str. PCC 8112	AM711
GQ466520.1 gg_id:540733 analyses genus Anabaena soil rice field	GQ466
AF247593.1 gg_id:29130 Anabaena variabilis str. NIES23	AF2475
AF317631.1 gg_id:50880 Nostoc sp. str. PCC 7120	AF3176
DQ234828.1 gg_id:142226 Anabaena variabilis str. KCTC AG10273	DQ234
AB275346.1 gg_id:211084 Nostoc sp. str. Os1-C1	AB2753
AY218829.1 gg_id:81799 Anabaena flos-aquae str. UTCC 64	AY2188
AY742448.1 gg_id:101942 Nostoc sp. str. 8941	AY7424
AM773302.1 gg_id:296783 Anabaenopsis cf. abijatae str. AB2002/25	AM773
AM773306.1 gg_id:289237 Anabaenopsis elenkinii str. AB2002/37	AM773
AY038036.1 gg_id:29506 Cyanospira rippkae str. PCC 9501	AY0380
EU157977.1 gg_id:346176 Aphanizomenon issatschenkoi str. 1311	EU1579
AY196087.1 gg_id:88937 Aphanizomenon issatschenkoi str. TAC419	AY1960
FJ830579.1 gg_id:538751 Anabaena cf. fallax str. CENA208	FJ8305
AY196088.1 gg_id:88923 Aphanizomenon issatschenkoi str. LEMCYA31	AY1960
EU157982.1 gg_id:352387 Aphanizomenon issatschenkoi str. 473	EU1579
AB115471.1 gg_id:101333 Cylindrospermopsis raciborskii str. DMKU51006	AB1154
AY701569.1 gg_id:99710 Anabaena compacta str. 1403/24	AY7015
FJ830573.1 gg_id:573019 Anabaena crassa str. CENA196	FJ8305
AB271212.1 gg_id:173309 Anabaena spiroides	AB2712
AY701546.1 gg_id:107062 Anabaena planktonica str. TAC435	AY7015

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AJ630434.1 gg_id:107985 Anabaena sigmoidea str. 0tu36s7 AJ6304
AY701560.1 gg_id:107303 Anabaena ellipsoides str. AnaHB AY7015
AY701548.1 gg_id:107359 Anabaena planktonica str. 1403/27 AY7015
DQ023199.1 gg_id:128225 Anabaena lemmermannii 'BC 0005' BC Ana 0005 DQ023
AY196086.1 gg_id:88724 Aphanizomenon gracile 'Aph NH-5' str. Aph NH-5 AY1960
AJ630419.1 gg_id:107969 Anabaena flos-aquae str. 1tu31s11 AJ6304
AJ630443.1 gg_id:107992 Aphanizomenon flos-aquae str. 1tu26s2 AJ6304
EU157987.1 gg_id:348194 Aphanizomenon flos-aquae str. A8 EU1579
FJ830571.1 gg_id:575863 Anabaena circinalis str. CENA191 FJ8305
AF317632.1 gg_id:28360 Aphanizomenon flos-aquae str. NIES81 AF3176
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AJ630425.1 gg_id:107974 Anabaena mucosa str. 1tu35s5 AJ6304
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AF247573.1 gg_id:23978 Anabaena circinalis str. AWQC150A AF2475
AY354194.1 gg_id:101150 Aphanizomenon gracile str. LMECYA40 AY3541
AJ293118.1 gg_id:43523 Anabaena spiroides str. PMC9702 AJ2931
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FJ592868.1 gg_id:511684 Fumarole-supported islands biodiversity within hyperarid -elevation landscape on Pu FJ5928
AJ781148.1 gg_id:110881 Nodularia sphaerocarpa str. UTEX B 2093 AJ7811
AJ781144.1 gg_id:110114 Nodularia sphaerocarpa str. Fae19 AJ7811
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AF268006.2 gg_id:37800 Nodularia spumigena str. L575 AF2680
AY038034.1 gg_id:20340 Nodularia spumigena str. PCC 9350 AY0380
AF268009.1 gg_id:35491 Nodularia spumigena str. NSLA01 AF2680
AF268017.1 gg_id:74014 Nodularia spumigena str. NSPH05A14 AF2680
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DQ185257.1 gg_id:148513 Nostoc punctiforme str. SAG 69.79 DQ185
DQ185234.1 gg_id:149137 Nostoc sp. 'Lobaria hallii cyanobiont' DQ185
AB325714.1 gg_id:310463 Nostoc cf. commune str. KG-54 AB3257
AF027654.1 gg_id:3108 Nostoc sp. PCC 9709 str. PCC9709 AF0276
AJ630449.1 gg_id:108000 Nostoc edaphicum str. X AJ6304
AY328900.1 gg_id:103321 Nostoc sp. str. 119.7.2 AY3289
AJ630447.1 gg_id:107997 Nostoc calcicola str. III AJ6304

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AY328896.1 gg_id:99053 Nostoc sp. str. 9.4.22 AY328
DQ234824.1 gg_id:143784 Anabaena flos-aquae str. UTEX LB2391 DQ234
DQ185223.1 gg_id:148113 Nostoc commune '0'Brien 02011101' DQ185
EU178144.1 gg_id:256672 Nostoc sphaeroides str. HBHF0604 EU178
DQ234825.1 gg_id:142304 Anabaena flos-aquae str. UTEX LB2557 DQ234
FJ592873.1 gg_id:554414 Fumarole-supported islands biodiversity within hyperarid -elevation landscape on Pu FJ5928
DQ185226.1 gg_id:148337 Nostoc sp. 'Peltigera membranacea 1 cyanobiont' DQ185
DQ185256.1 gg_id:149796 Nostoc punctiforme str. SAG 68.79 DQ185
AY218833.1 gg_id:81294 Nostoc commune str. UTEX 584 AY218
AB251860.1 gg_id:327757 Nostoc commune AB251
EU178143.1 gg_id:250532 Nostoc flagelliforme str. IMGA0408 EU178
AY742447.1 gg_id:101785 Nostoc sp. str. 8916 AY7424
AF506239.1 gg_id:58861 Nostoc sp. 'Peltigera pruinosa cyanobiont 14' 'Peltigera AF5062
FJ815314.1 gg_id:534084 Microcystin Production Tripartite Cyanolichen Peltigera leucophlebia Finland clone A1 FJ8153
AB113666.1 gg_id:110233 Nostoc commune AB113
EF174207.1 gg_id:200545 Nostoc sp. 'Pannaria cyanobiont' sphinctrina 1b Ch EF1742
GU396093.1 gg_id:522456 Nostoc piscinale str. BF3 GU396
AF506243.1 gg_id:58858 Nostoc sp. 'Peltigera pruinosa cyanobiont 18' 'Peltigera AF5062
AB428654.1 gg_id:331170 Nostoc commune AB428
AF506247.1 gg_id:58854 Nostoc sp. 'Peltigera praetextata cyanobiont 22' 'Peltigera AF5062
FJ815321.1 gg_id:542307 Microcystin Production Tripartite Cyanolichen Peltigera leucophlebia Finland clone U FJ8153
AB275349.1 gg_id:205766 Nostoc sp. str. Ni4-C1 AB2753
EU282431.1 gg_id:253266 Nostoc sp. str. 195-A21 EU2824
FJ592874.1 gg_id:532880 Fumarole-supported islands biodiversity within hyperarid -elevation landscape on Pu FJ5928
FJ592872.1 gg_id:546107 Fumarole-supported islands biodiversity within hyperarid -elevation landscape on Pu FJ5928
AF506251.1 gg_id:58852 Nostoc sp. 'Nephroma parile cyanobiont 26' 'Nephroma AF5062
AJ344563.1 gg_id:35715 Nostoc sp. DM103 str. SAG 2028 AJ3445
AB098071.1 gg_id:110216 Nostoc commune str. SO-42 AB098
AY328897.1 gg_id:99213 Nostoc sp. str. 113.5 AY328
AB088405.2 gg_id:63340 Nostoc commune str. M-13 AB088
AF506240.1 gg_id:56511 Nostoc sp. 'Peltigera venosa cyanobiont 15' 'Peltigera AF5062
AB251862.1 gg_id:311353 Nostoc commune AB2518
AJ630450.1 gg_id:108003 Nostoc ellipsosporum str. V AJ6304
AY701573.1 gg_id:103881 Anabaena flos-aquae str. NIES73 AY7015
DQ234831.1 gg_id:141547 Trichormus variabilis str. KCTC AG10178 DQ234
EF088341.1 gg_id:199561 Nostoc sp. str. CENA 107 EF0883
AY218828.1 gg_id:82104 Nostoc muscorum str. CENA61 AY218
AF160256.1 gg_id:36477 Anabaena bergii str. 283A AF1602
AF247597.1 gg_id:48640 Anabaena flos-aquae str. NRC525-17 AF2475
AF268018.1 gg_id:50096 Nodularia sphaerocarpa str. CDAC1966/93-1 AF2680

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DQ364237.1 gg_id:157669 Anabaena sp. str. SSM-00 DQ364
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AM711529.1 gg_id:268782 Nostoc calcicola str. TH2S22 AM711
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AY785313.1 gg_id:108357 Stigonematales cyanobacterium str. AEL04-Oct-6-03 AY7853
AB074504.1 gg_id:80820 Calothrix brevissima str. IAM M-249 AB0745
AY642569.1 gg_id:150707 and carbonate precipitation giant microbialites ly alkaline Lake Van Turkey microbiali AY6425
AB093486.1 gg_id:83776 Tolypothrix sp. str. IAM M-259 AB0934
EU022706.1 gg_id:245919 Nostoc sp. SKS8 EU0227
AF425995.1 gg_id:56651 Aphanizomenon sp. str. NH-5 AF4259
AJ781143.1 gg_id:110879 Nodularia harveyana str. Bo53 AJ7811
AB187507.1 gg_id:111394 Nostoc sp. str. YK-01 AB1875
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AM711544.1 gg_id:258214 Nostoc sp. str. Mau15 AM711
GU434226.1 gg_id:527300 Wollea saccata str. ACCS 045 GU434
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AM711543.1 gg_id:267299 Nostoc sp. str. Cam2S01 AM711
FJ592869.1 gg_id:548891 Fumarole-supported islands biodiversity within hyperarid -elevation landscape on Pu FJ5928
DQ185231.1 gg_id:145091 Nodularia harveyana 'Huebel 1983/300' str. Huebel 1983/300 DQ185
AJ630426.1 gg_id:107976 Anabaena oscillarioides str. BECID22 AJ6304
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EU340174.1 gg_id:249819 on Aquatic Macrophytes Geothermally Active Area Sedge Bay Yellowstone Lake WY EU3401
AB325536.1 gg_id:318589 Rivularia sp. str. IAM M-261 AB3255
DQ532230.1 gg_id:166201 Geographical Variation Microbial Burden and Spacecraft Assembly Johnson Space C DQ532
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FJ192908.1 gg_id:312572 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior FJ1929

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AY069954.1 gg_id:44224 Scytonema sp. str. U-3-3 AY0699
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EU188123.1 gg_id:340419 Uncultivated oceanic unicellular N2-fixing cyanobacteria are picoplankton unusual 7(EU1881
AB119259.1 gg_id:93641 Aphanothece sacrum AB1192
AM258981.1 gg_id:226595 Cyanobacterium stanieri PCC 7202 str. SAG 88.79 AM258
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AB039001.1 gg_id:29085 Synechocystis sp. str. PCC 6308 AB0390
GU118753.1 gg_id:563811 Threatened Corals Provide Microbial Habitats clone Mfra_B24 GU118
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AJ000709.1 gg_id:3245 Euhalothece sp. 'MPI 95AH10' str. MPI 95AH10 'MPI AJ0007
AJ000708.1 gg_id:3244 Cyanothece sp. str. PCC 7418 AJ0007
AB067577.1 gg_id:67719 Gloeothece sp. str. KO11DG AB0675
DQ357946.1 gg_id:200320 Host specificity and phylogeography Prochlorophyte Prochloron sp. obligate symbio DQ357
EF126149.1 gg_id:175235 Polyphasic unicellular cyanobacteria Graneticolobacter lagoonensis gen. sp. nov. Mic EF1261
DQ058891.1 gg_id:160743 Halothece sp. str. PCyano42 DQ058
DQ289927.1 gg_id:165105 Microbial Carbon and Nitrogen Cycling Sediments South Atlantic Bight Permeable Sh DQ289
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AJ781040.1 gg_id:149911 Snowella litoralis str. 0TU37s04 AJ7810
BA000022.2 gg_id:137040 Synechocystis sp. str. PCC 6803 BA0000
GQ375043.1 gg_id:566848 Synechocystis sp. str. CCALA 700 GQ375
D89033.1 gg_id:3135 Microcystis viridis str. NIES102 D89033
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D89034.1 gg_id:3237 Microcystis wesenbergii str. NIES111 D89034
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AY845229.1 gg_id:110862 Synechocystis sp. clone 36P1 AY8452
AB003166.1 gg_id:3232 Spirulina subsalsa str. M-223 AB0031
AF329394.1 gg_id:56680 Spirulina subsalsa str. FACHB351 AF3293
AF445678.1 gg_id:74772 travertine hot spring clone SM1D12 AF4456
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DQ455751.1 gg_id:156826 Synechococcus sp. 'Salton Sea' str. Salton Sea DQ455
AB003164.1 gg_id:3125 Oscillatoria rosea str. M-220 AB0031
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AF132784.1 gg_id:136187 Gloeocapsa sp. str. PCC 73106 AF1327
GQ340127.1 gg_id:587573 Prokaryotic Marathonas Reservoir Greece water column clone B07-41-BAC GQ340
EF429517.2 gg_id:210875 Thermophilic microbial mats tropical geothermal location display pronounced season EF4295
AY493599.1 gg_id:190488 Chondrocystis sp. ANT.LH59B.1 AY4935
EU409845.1 gg_id:554144 microbial fouling painted and unpainted structures outdoor concrete surfaces clone EU4098
EF522288.1 gg_id:227059 Endolithic Microbial Ecosystems Rocky Mountain endolithic sandstone clone FQSS06 EF5222
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FJ595625.1 gg_id:536201 rock Black Canyon New Mexico: and Geochemistry varnish covered rocks clone V22_ FJ5956
DQ471449.1 gg_id:159374 unicellular thermophilic cyanobacterium tBTRCCn 23 DQ471
EU134272.1 gg_id:250650 tallgrass prarie soil clone FFCH11821 EU134
AJ344553.1 gg_id:34564 Chroococcidiopsis sp. BB82.3 str. SAG 2024 BB82.3 AJ3445
DQ471448.1 gg_id:159142 unicellular thermophilic cyanobacterium tBTRCCn 28 DQ471
DQ914865.2 gg_id:172573 Chroococcidiopsis sp. str. CC3 DQ914
DQ532182.1 gg_id:167334 Geographical Variation Microbial Burden and Spacecraft Assembly Johnson Space C DQ532
EF032781.1 gg_id:182352 cyanobacterial mat in lava cave clone HAVOmat11 EF0327
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FJ890996.1 gg_id:540977 Hypolithic structure hyperaird core Atacama Desert quartz clone AY1_7 FJ8909
AM746687.1 gg_id:241102 etiology rosy discoloration ancient wall paintings rosy-discoloured mural clone A9 AM746
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GQ214113.1 gg_id:583323 China loess clone P913 GQ214
DQ914863.2 gg_id:166256 Chroococcidiopsis sp. str. CC1 DQ914
GQ092934.1 gg_id:429375 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw407a02 GQ092
GQ087815.1 gg_id:386885 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw359a0 GQ087
AB177177.1 gg_id:129771 seafloor methane hydrate clone ODP1230B22.23 AB177
GQ002512.1 gg_id:507150 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbu GQ002
DQ451473.1 gg_id:156813 forest soil clone FAC34 DQ451
X78681.1 gg_id:3207 Pleurocapsa sp. PCC 7516 str. PCC7516 X78681
AB039009.1 gg_id:46080 Stanieria sp. str. PCC 7301 AB039
AJ344556.1 gg_id:24838 Chroococcidiopsis sp. str. CCMP1489 AJ3445
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AJ344562.1 gg_id:45178 Myxosarcina sp. str. SAG 30.84; PCC 7325 AJ3445
FJ358911.1 gg_id:534175 and redox-stratified sediments marine reef sandy sediment clone SO78 FJ3589
EF208682.1 gg_id:200249 Vertical and horizontal structure microbial sandy carbonate sediment clone CI5cm.B1 EF2086
AB115964.1 gg_id:244883 Crinalium epipsammum str. SAG 22.89 AB115
FJ356670.1 gg_id:535815 Lyngbya majuscula str. PNG6-221 FJ3566
GQ231522.1 gg_id:587135 Lyngbya majuscula str. PAL-8-17-08-2 GQ231
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FJ147304.1 gg_id:343887 Lyngbya polychroa str. PNG6-45 FJ1473

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FM995184.1 gg_id:574890 digestive gland QX infected and naive Sydney rock oysters Saccostrea glomerata cya FM995
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AB039013.1 gg_id:40937 Lyngbya aestuarii str. PCC 7419 AB039(
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DQ181680.1 gg_id:172516 Biogeographical and ecological ranges benthic cyanobacteria East Antarctic lakes mi DQ181
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EF522259.1 gg_id:223924 Endolithic Microbial Ecosystems Rocky Mountain endolithic sandstone clone FQSS03 EF5222
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EU753636.1 gg_id:348181 modern freshwater stromatolites Ruidera Pools Natural Park Spain dry stromatolite EU753
FJ230796.1 gg_id:353695 Microclimate and limits photosynthesis cyanobacteria Northern Australia hypolithic s FJ2307
AY493588.1 gg_id:193060 Leptolyngbya antarctica ANT.ACE.1 AY4935
AJ505942.1 gg_id:99196 Limnothrix redekei str. 165a AJ5059
GQ848190.1 gg_id:586119 Limnothrix sp. str. B15 GQ848
AF132792.1 gg_id:3301 Prochlorothrix hollandica AF1327
FJ612359.1 gg_id:567936 and Biogeochemistry Dongping Lake Ecosystems lake water clone DP10.2.87 FJ6123
DQ450184.1 gg_id:151457 (Uruguay) Atlantic coastal lagoon clone R1C7 DQ450
AJ007864.1 gg_id:3304 cyanobacterium clone LD7 AJ0078
AY493581.1 gg_id:184822 Phormidium pristleyi ANT.LH66.1 AY4935
AY493582.1 gg_id:187739 Phormidium pristleyi ANT.LH61.2 AY4935
EU340169.1 gg_id:241071 on Aquatic Macrophytes Geothermally Active Area Sedge Bay Yellowstone Lake WY EU340
AM709633.1 gg_id:218516 Pseudanabaena sp. str. PCC 7367 AM709
DQ181740.1 gg_id:170530 Biogeographical and ecological ranges benthic cyanobacteria East Antarctic lakes mi DQ181
EU196365.1 gg_id:359531 filamentous cyanobacterium str. 72-1 EU1963
EF126240.1 gg_id:274997 Phototrophic microbial build laminated Fe-formations on Sulawesi Indonesia mesoph EF1262
AF445691.1 gg_id:28685 travertine hot spring clone SM1F09 AF4456

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AB003165.1 gg_id:3386 Phormidium mucicola str. M-221 AB003
AM259268.1 gg_id:180764 Pseudanabaena sp. str. 0tu30s18 AM259
AB039016.1 gg_id:16700 Pseudanabaena sp. str. PCC 6802 AB039
GU117964.1 gg_id:563947 Threatened Corals Provide Microbial Habitats clone Acer_M19 GU117
EF032779.1 gg_id:189054 cyanobacterial mat in lava cave clone HAVOmat08 EF0327
AJ630648.1 gg_id:99912 Oscillatoriales cyanobacterium str. UVFP2 AJ6306
FJ444635.1 gg_id:567570 Cotton Rhizosphere cotton rhizosphere clone 2h-1 FJ4446
EU255708.1 gg_id:559534 serpentinized spring water freshwater mesophilic microbial mat clone Mat-CYANO-S EU255
AY493984.1 gg_id:136196 Fingerprinting aggregates soil clone 349 AY4939
GU118152.1 gg_id:577676 Threatened Corals Provide Microbial Habitats clone Dstr_B02 GU118
AY151728.1 gg_id:99678 microbial mat clone Fr121 AY1517
GQ487938.1 gg_id:554238 Microbial metal soil polluted heavy metals clone T7-132 GQ487
EF654073.1 gg_id:278028 Pseudanabaenaceae cyanobacterium PBP-U-KK1 EF6540
AB488091.1 gg_id:535035 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSSURO AB488
DQ431005.1 gg_id:190474 phototrophic microbial mats Arctic springs (Greenland) hot spring DQ431
FJ933259.1 gg_id:539884 Leptolyngbya sp. FYG FJ9332
AF448079.1 gg_id:62919 Synechococcus sp. str. IR11 AF448
FJ202607.1 gg_id:344914 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2026
NC_009925.1 gg_id:238741 Acaryochloris marina str. MBIC11017 NC_00
AB486797.1 gg_id:554203 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCORO AB486
FJ902633.1 gg_id:570149 phreatic limestone sinkholes northeastern Mexico biofilm 1m deep hydrothermal ver FJ9026
AM710386.1 gg_id:249359 Acaryochloris sp. str. JJ7-5 7-5 AM710
EU340178.1 gg_id:237480 on Aquatic Macrophytes Geothermally Active Area Sedge Bay Yellowstone Lake WY EU340
AF076162.1 gg_id:3261 Antarctic LB3-80 clone AF076
EU805341.1 gg_id:334597 It's all ranking aquatic 250 miles Panama City clone 6C233345 EU805
EU703363.1 gg_id:455236 lakes on Eastern Tin Plateau freshwater lake altitude 4298 masl clone XZTSH29 EU703
FJ999597.1 gg_id:426115 sponge Haliclona simulans South China Sea clone B16 FJ9995
FJ381976.1 gg_id:582549 Potentially pathogenic and air stem cell transplant winter hospital shower water BMT FJ3819
AF448063.1 gg_id:62935 Synechococcus sp. str. UBR AF448
EU703182.1 gg_id:558485 taxon richness -altitude lakes eastern tin plateau predominance Bacteroidetes and S EU703
EF574289.1 gg_id:232723 site S25 near Coco's Island marine clone S25_633 EF5742
GU061586.1 gg_id:557211 and function microbial mesoscale eddy perturbations South China Sea clone CE2-5m GU061
EF575274.1 gg_id:227868 site S25 near Coco's Island marine clone S25_1618 EF5752
EU237304.1 gg_id:236472 Genes transcripts Eastern and Western Equatorial North Atlantic Ocean microbial as EU237
FJ382039.1 gg_id:512103 Potentially pathogenic and air stem cell transplant winter hospital shower water BMT FJ3820
GU305759.1 gg_id:550168 Research on changes structure during algae outbreak oligotrophic lakes (YangHe res GU305
EF574827.1 gg_id:235076 site S25 near Coco's Island marine clone S25_1171 EF5748
EU237266.1 gg_id:250183 Genes transcripts Eastern and Western Equatorial North Atlantic Ocean microbial as EU237
FJ382047.1 gg_id:583334 Potentially pathogenic and air stem cell transplant winter hospital shower water BMT FJ3820
GU119261.1 gg_id:578434 Threatened Corals Provide Microbial Habitats reef water clone Reef_B17 GU119
FJ497746.1 gg_id:581946 Synechococcus sp. str. KORDI-36 FJ4977

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AM259804.1 gg_id:216449 Spatial sponge- Mediterranean Tethya aurantium sponge endosome clone TAI-8-74 AM259
EU802588.1 gg_id:351201 It's all ranking aquatic Northeast Colon Panama clone 4C229939 EU8025
EU802974.1 gg_id:355538 It's all ranking aquatic Northeast Colon Panama clone 4C230373 EU8029
AF448070.1 gg_id:62928 Synechococcus sp. str. PS845 AF4480
EU237323.1 gg_id:257932 Genes transcripts Eastern and Western Equatorial North Atlantic Ocean microbial as: EU2373
EU703496.1 gg_id:375870 lakes on Eastern Tin Plateau freshwater lake altitude 4279 masl clone XZZLH78 EU7034
EU802573.1 gg_id:342607 It's all ranking aquatic Northeast Colon Panama clone 4C229920 EU8025
EF574201.1 gg_id:233862 site S25 near Coco's Island marine clone S25_545 EF5742
EF574424.1 gg_id:229355 site S25 near Coco's Island marine clone S25_768 EF5744
GU118310.1 gg_id:581829 Threatened Corals Provide Microbial Habitats clone Dstr_D01 GU118
AF330250.1 gg_id:53206 Synechococcus sp. str. LBB3 AF3302
EU703334.1 gg_id:409409 lakes on Eastern Tin Plateau freshwater lake altitude 4298 masl clone XZTSH6 EU7033
EF573792.1 gg_id:234682 site S25 near Coco's Island marine clone S25_136 EF5737
AJ347056.1 gg_id:60158 sponge clone TK09 AJ3470
EU237326.1 gg_id:242635 Genes transcripts Eastern and Western Equatorial North Atlantic Ocean microbial as: EU2373
EF572237.1 gg_id:232120 Coco's Island site 23 marine clone S23_336 EF5722
AM710354.1 gg_id:227959 Cyanobium sp. str. JJ19B5 19-B5 AM710
EF574923.1 gg_id:232787 site S25 near Coco's Island marine clone S25_1267 EF5749
NC_008319.1 gg_id:161964 Synechococcus sp. str. CC9311 NC_00
EU703246.1 gg_id:398037 lakes on Eastern Tin Plateau oligosaline lake altitude 4718 masl clone XZNMC20 EU7032
FJ382144.1 gg_id:558480 Potentially pathogenic and air stem cell transplant summer hospital shower water BM FJ3821
AF053397.1 gg_id:3347 Prochlorococcus marinus MIT 9303 str. MIT9303 AF0533
EU802507.1 gg_id:339262 It's all ranking aquatic Northeast Colon Panama clone 4C229843 EU8025
EU802290.1 gg_id:335985 It's all ranking aquatic Northeast Colon Panama clone 4C229599 EU8022
GU119448.1 gg_id:558489 Threatened Corals Provide Microbial Habitats reef water clone Reef_I02 GU119
FJ999612.1 gg_id:467632 sponge Haliclona simulans South China Sea clone B132 FJ9996
EU805221.1 gg_id:321688 It's all ranking aquatic 250 miles Panama City clone 6C233218 EU8052
EU237285.1 gg_id:251143 Genes transcripts Eastern and Western Equatorial North Atlantic Ocean microbial as: EU2372
FJ437825.1 gg_id:566422 Benthic okenone production Fayetteville New York Green Lake chemocline 20.5 m wa FJ4378
EF571914.1 gg_id:228854 Coco's Island site 23 marine clone S23_13 EF5719
AY125385.1 gg_id:81638 Synechococcus sp. clone A315025 AY1253
X03538.1 gg_id:3299 Synechococcus elongatus X03538
AY884054.1 gg_id:140661 Synechococcus sp. str. TS-15 AY8840
AY884059.1 gg_id:140190 Synechococcus sp. str. TS-104 AY8840
AY884052.1 gg_id:139842 Synechococcus sp. str. JA-3-3Ab AY8840
AF132773.1 gg_id:3159 Synechococcus sp. str. C9 AF1327
EF205469.1 gg_id:216560 among geographically regions central Tibet geothermal spring mat clone YCB43 EF2054
DQ471441.1 gg_id:159447 filamentous thermophilic cyanobacterium tBTRCCn 301 DQ471
EU000446.1 gg_id:238052 unculutured clones (IW) Western Ghats region IRDE water clone IWENVB17 EU0004
EU091541.1 gg_id:246617 clones IRDE (IW) Western Ghats region India water clone IWENVC5 EU0915

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AF448081.1 gg_id:62920 Synechococcus sp. str. PCC 6312 AF448
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FJ425596.1 gg_id:361402 communnities healthy and diseased colonies Caribbean coral Montastrea faveolata c FJ4255
AF216946.1 gg_id:40082 Synechococcus sp. PCC 7902 str. PCC7902 AF216
EF438248.1 gg_id:215715 Temporal spatial variability epilithic Bacteroidetes and Cyanobacteria forested river c EF4382
FJ999729.1 gg_id:378810 Caldithrix sp. str. MC FJ9997
AF323775.1 gg_id:53652 benzoate-degrading consortium clone BA059 AF323
FJ484504.1 gg_id:550182 microbial autonomous rover world's deepest phreatic sinkhole wall biomat El Zacator FJ4845
EU487910.1 gg_id:565473 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU487
AB177153.1 gg_id:130950 seafloor methane hydrate clone ODP1230B14.21 AB177
DQ811935.1 gg_id:164927 mangrove soil clone MSB-4E9 DQ811
AF286031.1 gg_id:31738 saltmarsh clone LCP-26 AF286
EU592472.1 gg_id:543260 Seasonal changes Salton Sea hypersaline sediment clone SSS10A EU592
DQ811933.1 gg_id:171914 mangrove soil clone MSB-4A2 DQ811
AJ515882.1 gg_id:57548 Deferribacter abyssi str. JR AJ5158
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FN356326.1 gg_id:544906 Prokaryotic structure sulfate reducer activity -temperature reservoirs and without ni FN356
U75602.1 gg_id:1863 Deferribacter thermophilus str. BMA1 U7560
FN356319.1 gg_id:568730 Prokaryotic structure sulfate reducer activity -temperature reservoirs and without ni FN356
EU407777.1 gg_id:263407 Deferribacter sp. str. SL50 EU407
AB364234.1 gg_id:350097 Calditerrivibrio nitroreducens str. Yu37-1 (= NBRC 101217) AB364
AF220344.1 gg_id:74231 Flexistipes sp. vp180 AF2203
FJ901100.1 gg_id:563173 Polymorphism microbial reservoirs water cut stage oil field clone Z-47 FJ9011
FJ900968.1 gg_id:509886 Polymorphism microbial reservoirs water cut stage oil field clone G-6 FJ9009
AJ299402.1 gg_id:25709 Geovibrio agilis AJ2994
AY387671.1 gg_id:95739 Mucispirillum schaedleri str. UNSW I23 AY3876
EF097086.1 gg_id:186413 mouse cecum clone SWPT18_aaa01c01 EF0970
AF146526.1 gg_id:43329 Denitrovibrio acetiphilus AF1465
NR_029235.1 gg_id:549883 Dictyoglomus thermophilum str. H-6-12; DSM 3960 NR_02
CP001251.1 gg_id:526493 Dictyoglomus turgidum str. DSM 6724 CP0012
CP001055.1 gg_id:278168 Elusimicrobium minutum str. Pei191 CP0010
AB198564.1 gg_id:135579 termite gut wall fraction clone RsW02-112 AB1985
FJ879997.1 gg_id:447372 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8799
FJ879844.1 gg_id:406473 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8798
FJ825512.1 gg_id:552696 Microbial during start-up mesophilic biogas plant clone 2B_BS5_13 FJ8255
AJ583207.1 gg_id:94589 radioactive site ground water clone S15B-MN11 AJ5832
AB426236.1 gg_id:260316 -situ identification study benzene-degrading s under methanogenic condition anaerc AB426
DQ837258.1 gg_id:241732 Archaeal and pristine National Park Spain Donana coastal aquifer clone 49S1_2B_60 DQ837
AF407708.1 gg_id:60591 Great Artesian Basin clone G58 AF407

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o__Elusimicrobiales	f__unclassified
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g__Fibrobacter

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s__Fibrobacter succinogenes	53005

FJ810557.1 gg_id:417474 Subsurface ecosystem resilience: Long-term attenuation subsurface contaminants su FJ8105
AY622271.1 gg_id:104126 subsurface soil clone S-J147 AY6222
EF018546.1 gg_id:217004 aspen rhizosphere clone Amb_16S_807 EF0185
AB487935.1 gg_id:576679 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSSUR0 AB4879
EU861834.1 gg_id:312378 effects chronic fertilization on alpine tundra microbial implications carbon and nitrog EU8618
EU117172.1 gg_id:250278 Scratching surface rare biosphere tag primers recent progress made toward microbi EU1171
DQ451527.1 gg_id:156651 forest soil clone FAC88 DQ451
EF516402.1 gg_id:218152 grassland soil clone FCPS607 EF5164
EU134602.1 gg_id:248280 tallgrass prarie soil clone FFCH1966 EU1346
GQ402750.1 gg_id:509120 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
EU861853.1 gg_id:330280 effects chronic fertilization on alpine tundra microbial implications carbon and nitrog EU8618
EU589308.1 gg_id:276586 China Ningxia rice paddy field soil clone 2_E5 EU5893
AY921882.1 gg_id:114382 farm soil clone AKYG853 AY9218
EF515890.1 gg_id:220050 grassland soil clone FCPS480 EF5158
AB282960.1 gg_id:223649 candidate phylum 'Termite Group 1' and members various flagellated protists endos AB2829
AB282957.1 gg_id:223823 candidate phylum 'Termite Group 1' and members various flagellated protists endos AB2829
AB298058.1 gg_id:253597 'Endomicrobia' and their specific affiliation termite gut flagellates endosymbiont Dev AB2980
AB126236.1 gg_id:104704 termite gut clone Rs-E67 AB1262
AY512589.1 gg_id:110572 symbiont Pyrsonympha vertens Reticulitermes santonensis clone Pv-1 AY5125
AB192273.1 gg_id:141207 termite gut homogenate clone RPK-30 AB1922
AB298011.1 gg_id:251556 'Endomicrobia' and their specific affiliation termite gut flagellates endosymbiont Din AB2980
AB192274.1 gg_id:142490 termite gut homogenate clone RPK-57 AB1922
AY571459.1 gg_id:114701 termite gut clone RsaP150 AY5714
AB282959.1 gg_id:224561 candidate phylum 'Termite Group 1' and members various flagellated protists endos AB2829
AB282961.1 gg_id:223811 candidate phylum 'Termite Group 1' and members various flagellated protists endos AB2829
AB297999.1 gg_id:248629 'Endomicrobia' and their specific affiliation termite gut flagellates endosymbiont Tric AB2979
AB298082.1 gg_id:242418 'Endomicrobia' and their specific affiliation termite gut flagellates endosymbiont Oxy AB2980
AB299537.1 gg_id:253909 Motility Symbiont Termite Gut Flagellate Caduceia versatilis Member 'Synergistes' G AB2995
AB192270.1 gg_id:143184 termite gut homogenate clone RPK-45 AB1922
AB188146.1 gg_id:103702 endosymbiont Trichonympha agilis gut termite Reticulitermes speratus clone RsTG1 AB1881
AY571454.1 gg_id:114696 termite gut clone RsaP84 AY5714
AB282962.1 gg_id:220873 candidate phylum 'Termite Group 1' and members various flagellated protists endos AB2829
AB282964.1 gg_id:223647 candidate phylum 'Termite Group 1' and endosymbiont members various flagellated AB2829
FJ746265.1 gg_id:549436 Microbial oligotrophic marine sediments: South Pacific Gyre ocean sediment 5306 m FJ7462
EU386053.1 gg_id:260503 Biogeographical and microbes sediments on subseafloor sediment South China Sea c EU3860
AF352534.1 gg_id:35729 hot spring clone QL4-2 AF3525
EF198046.1 gg_id:182021 Microbial structures mesophilic and methanogenic consortia anaerobic thermophilic EF1980
EU924259.1 gg_id:340778 Microbiology and geochemistry Little Hot Creek hot spring sediment temperature 80 EU9242
GQ844336.1 gg_id:561611 Microbial full-scale produced water treatment plant biofilm anoxic tank clone BB-B4 GQ844
AJ496284.1 gg_id:100224 Fibrobacter intestinalis str. NR9 AJ4962
AB275494.1 gg_id:169977 Fibrobacter succinogenes str. AS226 AB2754

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g__Fibrobacter
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AB275500.1 gg_id:163075 Fibrobacter succinogenes str. OS118 AB2755
AB275485.1 gg_id:170693 Fibrobacter succinogenes str. AS211 AB2754
EU473538.1 gg_id:290276 Somali wild ass feces clone WA_aaa04b07 EU4735
AJ496186.1 gg_id:63459 Fibrobacter succinogenes str. HM2 AJ4961
EU459511.1 gg_id:288501 capybara feces clone CAP_aah98h04 EU4595
EU381839.1 gg_id:260857 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU3818
EU463562.1 gg_id:293363 domesticated horse feces clone horsem_aai96b08 EU4635
EU473558.1 gg_id:301021 Somali wild ass feces clone WA_aaa01h11 EU4735
AB275496.1 gg_id:165381 Fibrobacter succinogenes str. OS102 AB2754
AB275498.1 gg_id:164826 Fibrobacter succinogenes str. OS112 AB2754
AB275501.1 gg_id:173599 Fibrobacter succinogenes str. OS119 AB2755
EU473606.1 gg_id:289079 Somali wild ass feces clone WA_aaa01d09 EU4736
EU779396.1 gg_id:329327 Somali Wild Ass feces clone WA_aaa03d04 EU7793
GU303627.1 gg_id:576830 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU303
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AM982635.2 gg_id:278133 microbial and slurry pig saw dust spent bedding clone PISD-AJG03 AM982
EF190823.1 gg_id:242362 Evidence occurrence members genus Fibrobacter sites landfill clone Brom F10 EF1908
EF190825.1 gg_id:251106 Evidence occurrence members genus Fibrobacter sites landfill clone Brom F7 EF1908
AB192084.1 gg_id:141091 termite gut homogenate clone M1PT4-02 AB1920
EF454459.2 gg_id:219116 termite hindgut clone 290cost002-P3L-2166 EF4544
AB255935.1 gg_id:170934 Localization Cell Morphologies Members Candidate TG3 and Subphylum Phylum Fibr AB2559
AB255932.1 gg_id:172833 Localization Cell Morphologies Members Candidate TG3 and Subphylum Phylum Fibr AB2559
AB243279.1 gg_id:147943 acetone-preserved termite gut clone M2PB4a-059 AB2432
AB192090.1 gg_id:142085 termite gut homogenate clone M2PT2-85 AB1920
AB042056.1 gg_id:38100 Alicyclobacillus acidocaldarius str. ATCC 27009T AB0420
EU740980.1 gg_id:352119 Alicyclobacillus acidocaldarius str. DT-M7 EU7409
AY573797.1 gg_id:115084 Alicyclobacillus acidoterrestris str. ATCC 49025 AY5737
AB042058.1 gg_id:18608 Alicyclobacillus acidoterrestris str. DSM 3923 AB0420
X51928.1 gg_id:14346 Alicyclobacillus cycloheptanicus X51928
AB233323.1 gg_id:151272 Alicyclobacillus disulfidooxidans AB2333
AJ133633.1 gg_id:46515 Alicyclobacillus hesperidum str. FR-11 AJ1336
AJ564766.1 gg_id:102873 New record moss thermophilic species and physico-chemic al properties geothermal AJ5647
AB084128.1 gg_id:67142 Alicyclobacillus sendaiensis str. NTAP-1 AB0841
AJ133634.1 gg_id:30162 Alicyclobacillus sp. str. FR-3 AJ1336
AB059665.1 gg_id:38406 Alicyclobacillus acidocaldarius subsp. genomic species 1 str. DSM 455 AB0596
EU680819.1 gg_id:283968 Alicyclobacillus sp. str. AYTae-7 EU6808
AM749794.1 gg_id:235845 Alicyclobacillus sp. K1 AM749
EU680818.1 gg_id:284287 Alicyclobacillus sp. str. ATSae-10 EU6808
AB004581.1 gg_id:14337 Alicyclobacillus sp. str. KHA-31 AB0045
DQ838045.1 gg_id:170052 Alicyclobacillus acidocaldarius Tc-12-31 DQ838
AB004580.1 gg_id:14336 Alicyclobacillus sp. str. MIH-2 AB0045

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DQ464146.1 gg_id:158365 acid mine drainage clone D1-23 DQ464
EU571186.1 gg_id:258187 eubacterium sp. str. 23-2 EU571
EU282873.1 gg_id:236165 Alicyclobacillus sp. str. Talven1 EU282
AB264021.1 gg_id:219729 Alicyclobacillus sp. str. S-TAB AB264
AY911435.1 gg_id:122869 rock interior clone NEC02064 AY911
AM749773.1 gg_id:255809 Isolation ing candidate division soils New Zealand steam-affected geothermal soil AM749
AB264024.1 gg_id:218349 Alicyclobacillus sp. str. 4-A336 AB264
AB264025.1 gg_id:225783 Alicyclobacillus sp. str. 5A239-2O AB264
AJ617864.1 gg_id:110806 oxic-anoxic interphase flooded paddy soil clone D282111 AJ6178
DQ444975.2 gg_id:157680 Tumebacillus permanentifrigoris str. Eur1 9.5 DQ444
NR_028637.1 gg_id:571645 Alicyclobacillus acidiphilus str. TA-67; DSM 14558 NR_02
NR_024753.1 gg_id:534871 Alicyclobacillus herbarius str. CP-1; DSM 13609 NR_02
EU638395.1 gg_id:324634 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU638
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AM749772.1 gg_id:249259 Isolation ing candidate division soils New Zealand steam-affected geothermal soil AM749
EU137838.1 gg_id:247268 Alicyclobacillus ferrooxidans str. TC-34 EU137
AB369003.1 gg_id:559429 and microbial oils produced Asia petroleum crude oil (Arabian Extra light) clone PT-A AB369
DQ129298.1 gg_id:138337 microarray level air two cities Texas urban aerosol clone AKIW802 DQ129
AF137502.2 gg_id:71417 Alicyclobacillus tolerans str. K1 AF137
EU137837.1 gg_id:253241 Alicyclobacillus ferripilum str. TC-71 EU137
NR_024801.1 gg_id:558567 Alicyclobacillus pomorum str. 3A; DSM 14955 NR_02
DQ999995.1 gg_id:207114 Isolation microorganisms undisturbed argillaceous formation under evaluation repo DQ999
EU360507.1 gg_id:263805 pilot biological ferrous iron oxidation mine water treatment plant clone W-Z-135 EU360
AB487996.1 gg_id:579786 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSSUR0 AB487
FM179383.1 gg_id:306748 Alicyclobacillus sp. str. ZJ-6 FM179
AB052970.1 gg_id:29823 this relatively close relationship to Alicyclobacillus and Sulfobacillus. However there is AB052
AJ617865.1 gg_id:110321 oxic-anoxic interphase flooded paddy soil clone D02302 AJ6178
EU419142.1 gg_id:264263 Microbial and ecology selected andesitic hydrothermal acidic hydrothermally modifi EU419
EU282871.1 gg_id:252896 Alicyclobacillus sp. str. CLA EU282
GU001882.1 gg_id:564204 Alkalibacillus sp. str. PL203 GU001
AJ238041.1 gg_id:26016 Bacillus haloalkaliphilus str. DSM 5271T AJ238
EU874387.1 gg_id:350384 Alkalibacillus sp. str. ISL-17 EU874
X72876.1 gg_id:14602 Bacillus sp str. DSM5271 X72876
AB264528.1 gg_id:164233 Alkalibacillus silvaisolus str. BM2 AB264
GU083678.1 gg_id:579049 Microorganism Xiarinur soda lake sediment clone x95 GU083
AJ865469.1 gg_id:109033 Bacillus arseniciselenatis str. DSM 15340 AJ8654
EU143680.1 gg_id:239928 Bacillus alkalidiazotrophicus str. MS 6 EU143
FJ430064.1 gg_id:368030 Anoxybacillus sp. E243 FJ4300
AY770577.1 gg_id:108674 Anoxybacillus flavithermus str. KWF-1 AY770
FJ430004.1 gg_id:359437 Anoxybacillus sp. A402b FJ4300

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EF654664.1 gg_id:256759 Anoxybacillus mongoliensis str. T4
AY248707.1 gg_id:84072 Anoxybacillus gonensis str. A4
AY248708.1 gg_id:83767 Anoxybacillus gonensis str. A7
AY248706.1 gg_id:85315 Anoxybacillus gonensis str. A2
AY122325.1 gg_id:64346 Anoxybacillus gonensis str. G2T
AF004589.1 gg_id:14519 Anoxybacillus flavithermus str. DSM2641
AB234213.1 gg_id:154371 Anoxybacillus pushchinoensis str. -1
AY248709.1 gg_id:84979 Anoxybacillus kestanbolensis str. K1
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FJ808725.1 gg_id:523983 Anoxybacillus gonensis str. P39
FJ430059.1 gg_id:363871 Anoxybacillus sp. E184aa
NR_024690.1 gg_id:567725 Bacillus carboniphilus str. JCM9731
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AF140005.1 gg_id:14502 Bacillus sp. str. ML-172
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EU818841.1 gg_id:307283 Bacillus sp. str. FR
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EF601577.1 gg_id:229131 Bacillus licheniformis str. BL43
AY462196.1 gg_id:110378 Bacillus subtilis str. DF3
EF473134.1 gg_id:227033 Bacillus subtilis qd382
AB301017.1 gg_id:244529 Bacillus amyloliquefaciens str. GH14
EF666489.1 gg_id:253477 Bacillus subtilis str. 0G
AY867792.1 gg_id:110184 Bacillus subtilis str. C2

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EU586781.1 gg_id:275467 Bacillus amyloliquefaciens str. MZ-15
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FJ435222.1 gg_id:358462 Bacillus licheniformis str. 11
EU056571.1 gg_id:251864 Bacillus subtilis SK1
EF428249.2 gg_id:220863 Bacillus subtilis str. HDYM-25
EF523474.1 gg_id:225817 Bacillus subtilis str. BSD-2
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AY279207.1 gg_id:87398 Bacillus subtilis str. HA401
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AB115959.1 gg_id:91208 Bacillus subtilis str. KT1003
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EF101720.1 gg_id:194233 Bacillus subtilis str. HU83
EU056572.1 gg_id:244688 Bacillus subtilis K1
EU373438.1 gg_id:273306 Bacillus subtilis str. YRR10

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AB300807.1 gg_id:239288 Bacillus amyloliquefaciens str. TC4
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AB211023.1 gg_id:115299 Bacillus subtilis str. SSCS21-1
EU586780.1 gg_id:277086 Bacillus amyloliquefaciens str. MZ-40
GQ302520.1 gg_id:576407 Bacillus subtilis str. BP-5
EF488170.1 gg_id:301350 Bacillus subtilis str. SC2-4
DQ415893.3 gg_id:150939 Bacillus subtilis str. MA139

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EU884651.1 gg_id:319039 Bacillus subtilis str. HUSS-4AG
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NC_006274.1 gg_id:129290 Bacillus cereus E33L str. ZK
CP001283.1 gg_id:531130 Bacillus cereus str. AH820
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NC_005957.1 gg_id:128891 Bacillus thuringiensis serovar konkukian str. 97-27
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ABKF01000014.1 gg_id:266909 Bacillus anthracis str. A0193
CP000001.1 gg_id:128982 Bacillus cereus str. E33L
NC_003909.8 gg_id:128527 Bacillus cereus str. ATCC 10987
NZ_ABDK01000012.1 gg_id:263541 Bacillus cereus str. NVH0597-99

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NC_005957.1 gg_id:128895 Bacillus thuringiensis serovar konkukian str. 97-27	NC_005
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NR_024817.1 gg_id:536739 Bacillus asahii str. MA001; FERM BP-4493	NR_024
AJ605772.2 gg_id:162067 Bacillus sp. str. K1-10	AJ6057
AJ606036.2 gg_id:163130 Bacillus sp. str. B1-1	AJ6060
AJ605773.3 gg_id:191440 Bacillus sp. K1-5	AJ6057
AB211021.1 gg_id:115202 Bacillus subtilis str. SSCS22-1	AB2110
EU070356.1 gg_id:278527 Bacillus sp. str. B247Ydz-hn	EU0703
DQ870720.1 gg_id:224292 Bacillus badius str. LMtotJ2	DQ870
GQ497939.1 gg_id:545039 Bacillus badius str. KO_CM52	GQ497
X62178.1 gg_id:14618 Bacillus aminovorans str. NCIMB 8292	X62178
AB425362.1 gg_id:526725 Bacillus sp. str. S207	AB4253
EU169170.1 gg_id:246151 Bacillus badius str. B22	EU1691
AY505500.1 gg_id:99298 Bacillus baekryungensis str. GSP36	AY5055
FJ907965.1 gg_id:556964 Bacillus baekryungensis str. LY096	FJ9079
FJ999563.1 gg_id:400929 Bacillus arsenicus str. HLSB44	FJ9995
AJ422145.1 gg_id:103946 Bacillus barbaricus str. V2-BIII-A2	AJ4221
GQ200827.1 gg_id:545867 Bacillus barbaricus str. P2	GQ200
EU867386.1 gg_id:548056 Bacillus barbaricus str. CCGE2121	EU8673
EU373318.1 gg_id:272802 Bacillus clausii str. SSR06	EU3733
AY066000.1 gg_id:17073 Bacillus clausii str. za-w-3	AY0660
EU571192.1 gg_id:262229 Bacillus sp. str. 25-4	EU5711
AF329474.1 gg_id:71598 Bacillus clausii str. LMG 19610	AF3294
GU296472.1 gg_id:565057 Engineered heat treated methanogenic granules (EHTG): promising biotechnological	GU296
EF014452.1 gg_id:178543 Bacillus coahuilensis str. m4-4	EF0144
EF428124.1 gg_id:260802 Bacillus sp. str. LL2	EF4281
FJ973533.1 gg_id:409809 Bacillus cohnii str. NBPP99 B99	FJ9735
AB023412.1 gg_id:14683 Bacillus cohnii str. YN-2000	AB0234
AM747232.1 gg_id:242373 Bacillus cereus str. INRA AF2	AM747

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EU434504.1 gg_id:275759 Bacillus endophyticus str. b359 EU4345
DQ298363.1 gg_id:152512 studies on and nifH Lasiurus sindicus Sewan grass Thar Desert Rajasthan India rhizos DQ298
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EF514218.1 gg_id:223044 Bacillus endophyticus str. SP31 EF5142
EU434382.1 gg_id:267998 Bacillus endophyticus str. a107 EU4343
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AY443036.1 gg_id:101066 Bacillus farraginis str. R-6540 AY4430
GQ903403.1 gg_id:568117 Bacillus sp. str. XJSL3-4 GQ903
FJ950606.1 gg_id:439204 Bacillus sp. str. c69 FJ9506
AY739688.1 gg_id:114233 lubricant-contaminated soil clone KU65 AY7396
FJ897757.1 gg_id:593258 Bacillus firmus str. RKS160 FJ8977
EU867351.1 gg_id:591316 Bacillus firmus str. CCGE2067 EU8673
DQ298269.1 gg_id:152877 studies on and nifH Lasiurus sindicus Sewan grass Thar Desert Rajasthan India rhizos DQ298
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GQ903396.1 gg_id:578791 Bacillus firmus str. XJSL2-7 GQ903
GQ199760.1 gg_id:539360 Bacillus sp. str. 210_58 GQ199
FJ613615.1 gg_id:536913 Bacillus firmus str. 40 FJ6136
FJ974057.1 gg_id:390675 Bacillus firmus str. SK20 FJ9740
GU297606.1 gg_id:576952 Bacillus pumilus str. U4 GU297
AY180964.1 gg_id:107468 Bacillus megaterium str. BAC19 AY1809
DQ275180.1 gg_id:157508 Bacillus megaterium str. WN586 DQ275
DQ207561.1 gg_id:140380 Bacillus megaterium CECRIbio 04 DQ207
DQ870697.1 gg_id:223236 Bacillus megaterium str. KSC_SF2j DQ870
AY739901.1 gg_id:107305 Bacillus megaterium str. ALA2; NRRL B-21660 AY7399
AJ550461.1 gg_id:82893 Bacillus flexus AJ5504
AY422986.1 gg_id:97150 Bacillus flexus str. R-6558 AY4229
FJ944656.1 gg_id:532878 Bacillus megaterium str. KUDC1034 FJ9446
AB271139.1 gg_id:167801 Bacillus megaterium str. MX1-1 AB2711
FJ435231.1 gg_id:365270 Bacillus pumilus str. 20 FJ4352
FJ527662.1 gg_id:546932 Bacillus subtilis str. rif200882 FJ5276
FJ527637.1 gg_id:535676 Bacillus megaterium str. rif200893 FJ5276
FJ393316.1 gg_id:358958 Bacillus megaterium str. TCCC11368 FJ3933
GU434216.1 gg_id:522385 Bacillus thuringiensis str. CC7 GU434
DQ275179.1 gg_id:158919 Bacillus megaterium str. WN585 DQ275
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AJ550462.1 gg_id:83730 Bacillus megaterium AJ5504
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AJ563600.1 gg_id:87224 Bacillus flexus str. B14 AJ5636

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EU240391.1 gg_id:238627 Bacillus megaterium str. B110 EU2403
EU884649.1 gg_id:307261 Bacillus flexus str. XUZ-R EU8846
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EU880510.1 gg_id:347469 Bacillus megaterium str. PRE2 EU8805
EU256395.1 gg_id:249550 Bacillus megaterium str. FJ011 EU2563
EU977771.1 gg_id:550751 Bacillus flexus str. 1P03SB EU9777
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AM950294.1 gg_id:265711 Bacillus sp. BS29 HS-2008 AM950
DQ416793.1 gg_id:274123 Bacillus sp. G2DM-33 DQ416
AM749775.1 gg_id:252827 Isolation ing candidate division soils New Zealand steam-affected geothermal soil AM749
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AY169818.1 gg_id:76323 Bacillus funiculus str. NK1.2 AY1698
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AM747040.1 gg_id:257202 Bacillus longiquaesitum str. LMG 23781
AJ001222.1 gg_id:14628 grassland soil clone DA154
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AJ830709.1 gg_id:101734 Bacillus subtilis KCM-RG5
EU723824.1 gg_id:352888 Bacillus licheniformis str. HDDMM02
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EF634026.1 gg_id:254351 Paenibacillus polymyxa str. ISSDS-853
FJ263033.1 gg_id:361895 Bacillus simplex str. RC18
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EU647708.1 gg_id:273793 Bacillus muralis str. REG23
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DQ659140.1 gg_id:165620 Bacillus simplex str. L1
EU647709.1 gg_id:276019 Bacillus muralis str. REG52
EF154253.1 gg_id:189650 Bacillus simplex str. 13
GU339279.1 gg_id:548055 Bacillus nealsonii str. EH51

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FJ373036.1 gg_id:319978 Bacillus sp. str. S6-1 FJ3730
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AB121094.1 gg_id:97746 Bacillus thermoamylovorans str. BTa AB1210
GU125619.1 gg_id:576690 Bacillus thermoamylovorans str. IMAU80201 GU125
AJ586361.1 gg_id:103073 Bacillus thermoamylovorans str. R-19047 AJ5863
NR_026145.1 gg_id:574109 Bacillus pseudalcaliphilus str. DSM 8725 NR_02
AB434284.2 gg_id:274005 Bacillus trypoxylicola str. SU1 AB4342
FJ944648.1 gg_id:570600 Bacillus anthracis str. KUDC1024 FJ9446
FJ390462.1 gg_id:367534 Bacillus weihenstephanensis str. HY3 FJ3904
NC_010184.1 gg_id:247358 Bacillus weihenstephanensis str. KBAB4 NC_01
CP000903.1 gg_id:244782 Bacillus weihenstephanensis str. KBAB4 CP000
EU169187.1 gg_id:248122 Bacillus mycoides str. B1 EU169
AF144645.1 gg_id:14949 Bacillus mycoides str. DRC1 AF1446
Z84580.1 gg_id:14934 Bacillus cereus str. WSBC10210 Z84580
EF210282.1 gg_id:222605 Bacillus weihenstephanensis str. CCM 4965 EF2102
EU169143.1 gg_id:256275 Bacillus weihenstephanensis str. B28 EU169
Z84577.1 gg_id:14931 Bacillus cereus str. WSBC10201 Z84577
Z84578.1 gg_id:14932 Bacillus cereus str. WSBC10204 Z84578
AY277557.1 gg_id:90026 Bacillus weihenstephanensis str. P2-14 AY2775
Z84579.1 gg_id:14933 Bacillus cereus str. WSBC10206 Z84579
DQ289062.1 gg_id:143741 Bacillus cereus HKS 4-2 DQ289
NZ_ABDI01000038.1 gg_id:270703 Bacillus cereus str. B4264 NZ_AB
GQ375259.1 gg_id:591843 Bacillus cereus str. ANY GQ375
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AJ277907.1 gg_id:111676 Bacillus cereus str. Biosubtyl-Dalat AJ2779
AB363736.1 gg_id:243254 Bacillus mycoides str. NBRC 100169 AB3637
FJ435224.1 gg_id:364671 Bacillus megaterium str. 13 FJ4352
DQ078742.1 gg_id:131320 Bacillus thuringiensis str. LDC-9 DQ078
GU171377.1 gg_id:586881 Bacillus mycoides str. JS03-04 GU171
EF582416.1 gg_id:232949 Bacillus cereus str. HDYM-14 EF5824
GQ263498.1 gg_id:593429 Structure Simulated Level Waste Site simulated level waste site clone FW2_192B GQ263
EU661712.1 gg_id:282658 Bacillus cereus str. NBRAJATH9 EU6617
AY221057.1 gg_id:106573 sediments collected at Charon's Cascade near Echo River October 2000 clone CCM22 AY2210
FJ859684.2 gg_id:574826 Bacillus pseudomycoides str. BIHB 337 FJ8596
EU240443.1 gg_id:254608 Bacillus weihenstephanensis str. B164 EU2404
AY461750.2 gg_id:102293 Bacillus sp. str. H-09 AY4617
AY803744.1 gg_id:108980 Bacillus cereus str. PGS2 AY8037
AY373361.1 gg_id:95158 Bacillus cereus str. T1 AY3733
EF210302.1 gg_id:225543 Bacillus thuringiensis serovar graciosensis str. IEBC-T66 001 EF2103

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EF472264.1 gg_id:223125 Bacillus cereus str. LQ84 EF4722
EU861960.1 gg_id:314347 effects chronic fertilization on alpine tundra microbial implications carbon and cyclin EU861
EU240372.1 gg_id:256396 Bacillus thuringiensis str. B106 EU2403
AY461762.2 gg_id:112023 Bacillus thuringiensis serovar israelensis AY4617
DQ855661.1 gg_id:167765 Bacillus sp. str. KA-10 DQ855
DQ232746.1 gg_id:143250 Bacillus anthracis str. JH18 DQ232
EU240420.1 gg_id:235911 Bacillus cereus str. B170 EU2404
AJ577281.1 gg_id:88623 Bacillus cereus str. B 412 AJ5772
AF206326.1 gg_id:25668 Bacillus cereus AF2063
GU235995.1 gg_id:592408 Bacillus thuringiensis str. Bm-1 GU235
NZ_ABDJ01000017.1 gg_id:259649 Bacillus cereus str. G9842 NZ_AB
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EU429672.1 gg_id:538578 Bacillus thuringiensis serovar israelensis str. B6064 EU429
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EU624434.1 gg_id:284074 Bacillus cereus str. S6-10 EU624
AY148429.1 gg_id:71520 Bacillus hackensackii AY148
AB364962.1 gg_id:242335 Bacillus lentus str. S3 AB364
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EU977649.1 gg_id:534073 Bacillus thuringiensis str. 1P05AA EU977
EU647707.1 gg_id:277002 Bacillus mycoides str. REG65 EU647
AY373320.1 gg_id:94901 Bacillus thermoamylovorans str. R-7499 AY3733
ABLH01000020.1 gg_id:266008 Bacillus anthracis str. A0465 ABLH0
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EU240435.1 gg_id:249373 Bacillus cereus str. B151 EU240
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AJ577275.1 gg_id:89224 Bacillus cereus str. B 308
EU874877.1 gg_id:314756 Bacillus cereus W65
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EU834245.1 gg_id:336418 Bacillus cereus str. DS16
FJ784127.1 gg_id:547186 Bacillus thuringiensis str. L79
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DQ648274.1 gg_id:160122 Bacillus cereus str. EKS4-2
FM179770.1 gg_id:316755 Acetobacter pasteurianus str. BAC24
FJ194529.1 gg_id:309115 Bacillus sp. str. EC13
FM179769.1 gg_id:307651 Acetobacter pasteurianus str. AUC29
EF422071.1 gg_id:206243 Bacillus cereus str. 4.1.1.B
EU240432.1 gg_id:245763 Bacillus cereus str. B148
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EU037097.1 gg_id:252646 Bacillus thuringiensis str. AAJ18
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FJ601906.1 gg_id:517014 Bacillus thuringiensis str. INRS10
EU366384.1 gg_id:259344 Bacillus cereus str. IV12
FJ393303.1 gg_id:360120 Bacillus mycoides str. TCCC11292
EF210297.1 gg_id:221031 Bacillus cereus str. BGSC 6A17
NZ_ABDK01000016.1 gg_id:264203 Bacillus cereus str. NVH0597-99
DQ870694.1 gg_id:219738 Bacillus thuringiensis str. KSC_SF4d
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GQ421475.1 gg_id:567815 Bacillus anthracis str. B14
NZ_ABLB01000010.1 gg_id:267868 Bacillus anthracis str. A0389
DQ206989.1 gg_id:139967 Bacillus thuringiensis

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EU977819.1 gg_id:541219 Bacillus thuringiensis str. 1P03AC	EU9778
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EU867374.1 gg_id:576820 Bacillus thuringiensis str. CCGE2286	EU8673
FJ544356.1 gg_id:417757 Bacillus cereus str. ji16	FJ5443
EU624445.1 gg_id:283792 Bacillus cereus str. SS-07	EU6244

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EU429661.1 gg_id:539396 Bacillus thuringiensis serovar dendrolimus str. CB02
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AY279195.1 gg_id:86963 Bacillus cereus str. KNUC53
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EU862564.1 gg_id:345324 Bacillus cereus str. AB31
EU047593.1 gg_id:236591 Bacillus cereus str. JZ
EU429663.1 gg_id:552736 Bacillus thuringiensis serovar kurstaki str. B6066
EU652055.1 gg_id:277261 Bacillus thuringiensis str. me-2
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EU384285.1 gg_id:268205 Bacillus sp. B31(2008) str. B31
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AJ288157.1 gg_id:30826 Bacillus cereus Ki 2l
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EU874887.1 gg_id:324930 Bacillus thuringiensis W64
DQ350831.1 gg_id:146267 Geobacillus thermoglucosidasius str. MH403
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EF210294.1 gg_id:220824 Bacillus thuringiensis serovar tohokuensis str. IEBC-T17 001
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EF440289.1 gg_id:204295 Bacillus cereus str. 6.1.1.B
AY795568.1 gg_id:108985 Bacillus cereus str. ATCC 25621; NCIMB 10437
AY279191.1 gg_id:87400 Bacillus cereus str. KNUC55
EF528295.1 gg_id:225627 Bacillus cereus str. CICCHLJ Q93
CP000001.1 gg_id:128980 Bacillus cereus str. E33L
EF495116.1 gg_id:268827 Bacillus thuringiensis str. 19198

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FJ435220.1 gg_id:364047 Bacillus cereus str. 5
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AJ577282.1 gg_id:88453 Bacillus cereus str. RIVM BC00067
EU874878.1 gg_id:338180 Bacillus cereus W77
FJ393296.1 gg_id:364850 Bacillus cereus str. TCCC11197
GQ199759.1 gg_id:593828 Bacillus sp. str. 210_57
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EU240374.1 gg_id:238262 Bacillus cereus str. B79
EU240370.1 gg_id:248317 Bacillus thuringiensis str. B75
DQ286343.1 gg_id:143417 Bacillus thuringiensis
DQ870690.1 gg_id:223264 Bacillus cereus str. KSC_SF6e
GQ280107.1 gg_id:587574 Bacillus sp. str. JS-37
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EU915688.1 gg_id:337668 Bacillus cereus str. HY-4
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DQ104989.1 gg_id:136735 Bacillus cereus str. JS 18
EF428239.2 gg_id:221830 Bacillus cereus str. HDYM-09
AB020194.1 gg_id:49517 Bacillus sp. str. TGS337
DQ125836.1 gg_id:129649 uranium contaminated soil clone AKAU4062
GU011949.1 gg_id:580873 Bacillus cereus str. NBST4
EF173327.1 gg_id:189594 Bacillus cereus MKI13
FJ393301.1 gg_id:368881 Bacillus cereus str. TCCC11289
EU794727.1 gg_id:345174 Bacillus cereus str. FM-4
FJ644694.1 gg_id:537182 Bacillus weihenstephanensis str. MX13
FJ601904.1 gg_id:518441 Bacillus thuringiensis str. INRS8
FJ393312.1 gg_id:369175 Bacillus cereus str. TCCC11331
EU169144.1 gg_id:249918 Bacillus weihenstephanensis str. B27
FM178868.1 gg_id:331746 Acetobacter pasteurianus str. CCM 3614
EU435384.1 gg_id:262184 Bacillus thuringiensis str. AAJ17
GQ226038.1 gg_id:592770 Bacillus cereus str. S1
FJ263046.1 gg_id:369371 Bacillus cereus str. ZD19
EU118117.1 gg_id:238591 Bacillus cereus
EF126181.1 gg_id:186107 Bacillus cereus str. HCY02

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EU366375.1 gg_id:261809 Bacillus thuringiensis str. IV5 EU3663
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D78478.1 gg_id:14678 Bacillus simplex str. DSM1321 D78478
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DQ365564.1 gg_id:150246 Bacillus megaterium str. GH09 DQ365
GU306176.1 gg_id:550447 Bacillus subtilis str. SIV02 GU306
FJ373030.1 gg_id:350988 Bacillus selenatarsenatis str. S3-3 FJ3730
FJ665200.1 gg_id:559213 Study Prokarytic Selected Niches Western Ghats India ground swab mangrove forest FJ6652
AJ781029.2 gg_id:109258 Bacillus herbersteinii str. D-15a AJ7810
GQ284379.1 gg_id:588475 Bacillus sp. str. PCWCS14 GQ284
GU397390.1 gg_id:528465 Bacillus jeotgali str. B36 GU397
AM930284.1 gg_id:542223 gradual cooling stage mass and its spatial composting clone SMG26 AM930
DQ129523.1 gg_id:137611 urban aerosol clone AKIW936 DQ129
FM180514.1 gg_id:311881 Bacillus sp. ZZ-2208 str. A10 FM180
GQ129974.1 gg_id:405643 Genetic inventory 'JPL-SAF' during MSL mission spacecraft assembly clean room floc GQ129
AM888179.1 gg_id:256974 Bacillus sp. str. TSWCSN16 AM888
GQ918255.1 gg_id:563322 Bacillus aestuarii str. JP1 GQ918
EU660355.1 gg_id:295089 Bacillus horikoshii str. CT1 EU6603
GQ980238.1 gg_id:559130 Bacillus humi str. NBK2 GQ980
AF221061.1 gg_id:28181 Bacillus jeotgali str. YKJ-10 AF2210
DQ448759.1 gg_id:157767 Bacillus sp. str. CNJ748 PL04 DQ448
EU221357.1 gg_id:248557 Bacillus simplex str. J2S3 EU2213
AB245380.1 gg_id:145947 Bacillus panaciterrae str. Gsoil 1517 AB2453
EU623596.1 gg_id:292837 Bacillus pumilus str. B-15 EU6235
AM084896.1 gg_id:139148 airborne fungal spores boreal forests contrasting human disturbance soil uranium n AM084
EU723827.1 gg_id:343771 Bacillus megaterium str. HDDMM05 EU7238
GQ855295.1 gg_id:557777 Bacillus shandongensis str. YH221 GQ855
AB190040.2 gg_id:156768 Bacillus megaterium str. N-18-25-9 AB1900
GQ889251.1 gg_id:551677 Bacillus megaterium str. S13 GQ889
AJ550460.1 gg_id:83070 Bacillus horikoshii AJ5504
AB486733.1 gg_id:550115 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCOR(AB486
FJ527649.1 gg_id:554625 Bacillus megaterium str. rif200888 FJ5276
DQ298329.1 gg_id:152305 studies on and nifH Lasiurus sindicus Sewan grass Thar Desert Rajasthan India rhizos DQ298
AJ491841.1 gg_id:78046 Bacillus megaterium str. C1 AJ4918
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GQ355276.1 gg_id:576569 Bacillus sp. str. DL006 GQ355
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FJ544338.1 gg_id:457472 Bacillus boroniphilus str. 822 FJ5443
EF113321.1 gg_id:187551 Bacillus halmapalus LB 16 EF1133
AY493966.1 gg_id:136840 Fingerprinting aggregates soil clone 1469 AY4939
FJ009399.1 gg_id:303812 Bacillus megaterium str. F6 FJ0093
FJ435229.1 gg_id:368409 Bacillus pumilus str. 18 FJ4352
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AB488269.1 gg_id:541821 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSSUR0 AB488
FJ713099.1 gg_id:566717 Bacillus sp. str. EBL3-7 FJ7130
FJ527635.1 gg_id:553940 Bacillus megaterium str. rif200805 FJ5276
AF423304.1 gg_id:136610 oligonucleotide fingerprinting genes soil clone 48-1 AF4233
AM292611.1 gg_id:165187 Influence uranyl and sodium nitrate on natural soil uranium mining waste pile clone AM292
X64465.1 gg_id:14575 Bacillus methanolicus str. C1 X64465
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FJ435233.1 gg_id:368404 Bacillus subtilis str. 24 FJ4352
EF612335.1 gg_id:248729 Bacillus sp. str. OS-03 EF6123
AY167803.1 gg_id:77353 Bacillus megaterium str. SAFN-040 AY1678
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AY167809.1 gg_id:77431 Bacillus niacini str. SAFN-021 AY1678
EU621912.1 gg_id:279144 Bacillus sp. str. CCBAU 10711 EU6219
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EU221410.1 gg_id:257133 Bacillus megaterium str. A2P4 EU2214
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AY373358.1 gg_id:95154 Bacillus megaterium str. c5 AY3733
EU194337.1 gg_id:248142 Bacillus megaterium str. XJUHX-40 EU1943
EU257442.1 gg_id:242832 Bacillus subtilis C6-3 EU2574
DQ129455.1 gg_id:138279 microarray level air two cities Texas urban aerosol clone AKIW1087 DQ129
AJ315063.1 gg_id:73206 Bacillus sp. LMG 19495 AJ3150
AJ132749.1 gg_id:14644 Bacillus sp. IDA629 AJ1327
AY422985.1 gg_id:98079 Bacillus sp. str. R-7413 AY4229
AJ236893.1 gg_id:14638 Bacillus sp. IDA624 AJ2368
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DQ084539.1 gg_id:130986 Bacillus sp. GD0705	DQ084
EU427313.1 gg_id:265143 Bacillus drentensis str. MD	EU4273
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EU977669.1 gg_id:575144 Bacillus sp. str. 2P03AE	EU977
DQ079002.1 gg_id:157632 Bacillus sp. str. GB02-29	DQ079
DQ870699.1 gg_id:221727 Bacillus drentensis str. KSC_SF1a	DQ870
EU244583.1 gg_id:246332 Bacillus megaterium str. 39	EU2445
AB043862.1 gg_id:31425 Bacillus sp. str. KX6	AB0438
FJ897776.1 gg_id:554312 Bacillus sp. str. BH85161	FJ8977
FJ006895.1 gg_id:344390 Bacillus sp. str. WPCB111	FJ0068
AY559426.1 gg_id:100562 hot spring water clone LS8	AY5594
EU373355.1 gg_id:271561 Bacillus megaterium str. HNL16	EU3733
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EU124558.1 gg_id:238032 Bacillus sp. str. OSS 19	EU1245
FJ393314.1 gg_id:356703 Bacillus megaterium str. TCCC11353	FJ3933
EF451042.1 gg_id:211366 Bacillus aeris str. HIO-9	EF4510
EU652093.1 gg_id:276320 Bacillus megaterium str. ra-10	EU6520
GQ903460.1 gg_id:533975 Halobacillus sp. str. XJSL9-1	GQ903
EF428245.2 gg_id:227217 Bacillus megaterium str. HDYM-21	EF4282
GU395997.1 gg_id:523931 Bacillus flexus str. NT	GU395
EF688339.1 gg_id:236657 soil clone F1-249	EF6883
DQ129478.1 gg_id:137976 microarray level air two cities Texas urban aerosol clone AKIW717	DQ129
EU834243.1 gg_id:322164 Bacillus subtilis str. DS13	EU8342
EU867376.1 gg_id:578786 Bacillus herbersteinensis str. CCGE2319	EU8673
EU660347.1 gg_id:295408 Bacillus boroniphilus str. CM25	EU6603
AF218239.1 gg_id:111679 Bacillus sp	AF2182
AF227833.1 gg_id:49305 str. 31284	AF2278
AB331453.1 gg_id:241651 dynamics changes physicochemical parameters during aerobic treatment aerated pi	AB3314
AF423288.1 gg_id:52810 soil clone 720-1	AF4232
AF423299.1 gg_id:24269 soil clone 911-1	AF4232
FJ897758.1 gg_id:574270 Bacillus firmus str. RKS161	FJ8977

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GQ980245.1 gg_id:540946 Bacillus niacini str. NBK36	GQ980
EU221362.1 gg_id:253472 Bacillus licheniformis str. B2S1	EU2213
EU880507.1 gg_id:342033 Bacillus megaterium str. PRE6	EU8805
D16282.1 gg_id:14924 Sporolactobacillus dextrus str. IAM 12380	D16282
FJ644597.1 gg_id:562015 toxic marine dinoflagellates and Ostreopsis ovata malaysian waters benthic dinoflage	FJ6445
AY167861.1 gg_id:77319 Bacillus megaterium str. SAFR-040	AY1678
DQ523498.1 gg_id:161560 Bacillus megaterium str. B69	DQ523
X77791.1 gg_id:14626 Bacillus pseudomegaterium str. ATCC 49866	X77791
FJ227525.1 gg_id:353069 Identification unculturable species growing sludge methane reactor after methanoge	FJ2275
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GQ386842.1 gg_id:553886 Bacillus sp. str. GS2	GQ386
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DQ298356.1 gg_id:154482 studies on and nifH Lasiurus sindicus Sewan grass Thar Desert Rajasthan India rhizos	DQ298
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AJ971870.1 gg_id:133358 Bacillus sp. Bt 18	AJ9718
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GQ129958.1 gg_id:441209 Genetic inventory 'JPL-SAF' during MSL mission spacecraft assembly clean room floc	GQ129
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FJ527639.1 gg_id:537851 Bacillus megaterium str. rif200886	FJ5276
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GU434676.1 gg_id:520638 Bacillus sp. str. CCBAU 05776	GU434
EU169572.1 gg_id:248760 Bacillus sp. str. CRRI 5	EU1695

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EU465971.1 gg_id:291602 African elephant feces clone AFEL3_aao15a10	EU4659
AB111938.1 gg_id:100263 Bacillus halmapalus str. A64	AB1119
FJ527638.1 gg_id:558171 Bacillus megaterium str. rif200881	FJ5276
EF682888.1 gg_id:236521 Eastern Mediterranean atmosphere clone F11_11A_FL	EF6828
DQ129461.1 gg_id:137767 microarray level air two cities Texas urban aerosol clone AKIW398	DQ129
DQ129500.1 gg_id:137566 urban aerosol clone AKIW884	DQ129
EU071549.1 gg_id:248921 Bacillus flexus str. EHFS1_S05Hd	EU0715
DQ288677.1 gg_id:142195 Bacillus sp. str. GPTSA 8T	DQ288
AF423230.1 gg_id:30044 soil clone 1448-1	AF4232
DQ448791.1 gg_id:158400 Bacillus sp. str. CNJ843 PL04	DQ448
U20385.2 gg_id:14581 Bacillus infernus str. TH-23 (=SMCC/W 479)	U20385
EF636833.1 gg_id:277750 Metagenomic and Namib desert sand clone 5	EF6368
DQ248237.1 gg_id:142445 carbon tetrachloride contaminated soil clone UE5	DQ248
GU122960.1 gg_id:528670 Bacillus megaterium str. DBTBIG	GU122
AY603079.1 gg_id:99806 Bacillus sp. str. STB9	AY6030
EU647526.1 gg_id:283943 recovered Xidatan Tanggula and Yuzhufeng glaciers glacial snow glacier Tin Plateau c	EU6475
GQ284391.1 gg_id:544730 Bacillus sp. str. PCWCS41	GQ284
AM992181.1 gg_id:282014 Bacillus boroniphilus PC IW 34	AM992
EU221374.1 gg_id:245999 Bacillus niacini str. Y2S4	EU2213
EF512129.1 gg_id:221973 Bacillus megaterium str. CSQ-6	EF5121
DQ298328.1 gg_id:152419 studies on and nifH Lasiurus sindicus Sewan grass Thar Desert Rajasthan India rhizos	DQ298
EF581379.1 gg_id:231418 Bacillus sp. str. CRRI1	EF5813
EF516247.1 gg_id:220392 grassland soil clone FCPN527	EF5162
DQ167241.1 gg_id:139261 Bacillus sp. str. MRN493	DQ167
GQ903404.1 gg_id:593201 Bacillus sp. str. XJSL3-5	GQ903
FJ435232.1 gg_id:365453 Bacillus subtilis str. 23	FJ4352
AB486506.1 gg_id:554221 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC	AB4865
EU221387.1 gg_id:248883 Bacillus humi str. P2P3	EU2213
EF682884.1 gg_id:255979 Eastern Mediterranean atmosphere clone F11_4D_FL	EF6828
U20384.1 gg_id:14577 Bacillus infernus str. TH-22 (=SMCC/W 478)	U20384
EF528264.1 gg_id:226279 Bacillus megaterium str. CICCHLJ Q30	EF5282
EU879090.1 gg_id:331270 Bacillus megaterium str. HDDMN04	EU8790
EU571144.1 gg_id:275875 Bacillus sp. str. 7-3	EU5711
FJ527634.1 gg_id:564272 Bacillus megaterium str. rif200885	FJ5276
AY559417.1 gg_id:104622 hot spring water clone LW3	AY5594
EU589286.1 gg_id:261699 China Ningxia rice paddy field soil clone 2_B7	EU5892
AM419753.1 gg_id:181498 Bacillus sp. str. TDWCW7	AM419
EU221371.1 gg_id:255624 Bacillus vireti str. B2P6	EU2213
DQ365587.1 gg_id:145161 Bacillus flexus str. GS11	DQ365

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DQ462195.1 gg_id:158236 Bacillus megaterium str. MP-5 DQ462
AB034715.1 gg_id:28732 compost clone 4-57 AB0347
AB198720.1 gg_id:131715 Bacillus borophilicus str. T-17s AB1987
GQ479946.1 gg_id:549663 Bacillus megaterium str. L4 GQ479
FJ393317.1 gg_id:356944 Bacillus megaterium str. TCCC11370 FJ3933
AM411966.1 gg_id:244199 Bacillus sp. str. P-43 AM411
EU221360.1 gg_id:256079 Bacillus niacini str. J2S7 EU2213
DQ906820.1 gg_id:253527 Oman subsurface soil clone 5C-13 DQ906
EU834241.1 gg_id:342723 Bacillus vireti str. DS11 EU8342
EU571116.1 gg_id:264293 Paenibacillus sp. str. 1-2 EU5711
AM411965.1 gg_id:253372 Bacillus sp. str. P-30 AM411
EU004564.1 gg_id:235358 Bacillus sp. str. HM06-02 EU0045
AY509228.1 gg_id:104385 Bacillus niacini str. S154 AY5092
AY167813.1 gg_id:77415 Bacillus megaterium str. SAFN-017 AY1678
DQ079008.1 gg_id:157487 Bacillus sp. str. GB02-2A DQ079
DQ298264.1 gg_id:154068 studies on and nifH Lasiurus sindicus Sewan grass Thar Desert Rajasthan India rhizos DQ298
FJ435230.1 gg_id:367954 Bacillus pumilus str. 19 FJ4352
EU620419.1 gg_id:278318 Bacillus megaterium str. S8-12 EU6204
AY920317.1 gg_id:140024 Bacillus sp. str. KT-1 AY9203
FJ851432.1 gg_id:532099 Bacillus sp. str. 1NLA3E FJ8514
AF423214.1 gg_id:34585 soil clone 1200-1 AF4232
FJ416490.1 gg_id:370385 Bacillus sp. str. BL4-6 FJ4164
AB245377.1 gg_id:146955 Bacillus pocheonensis str. Gsoil 420 AB2453
FJ535471.1 gg_id:510800 Bacillus sp. B7(2008) str. B7 FJ5354
AB486217.1 gg_id:591208 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC AB4862
GQ304778.1 gg_id:592464 Bacillus horikoshii str. A2 GQ304
GQ083176.1 gg_id:392856 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ083
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EU465102.1 gg_id:300373 African elephant feces clone AFYEL_aaj68b02 EU4651
FJ222553.1 gg_id:314498 Bacillus subtilis str. WR-W2 FJ2225
EU870509.1 gg_id:312403 Bacillus pumilus str. Sua-BAC014 EU8705
EF101699.1 gg_id:182801 Bacillus subtilis str. HU75 EF1016
EU216752.1 gg_id:244321 Bacillus pumilus str. JH1-1 EU2167
EU221348.1 gg_id:248169 Bacillus subtilis str. AM1C4 EU2213
AY296812.1 gg_id:101635 Bacillus licheniformis str. IBT017 AY2968
AY905693.1 gg_id:112084 Bacillus subtilis str. CICC10265 AY9056
AB547219.1 gg_id:527595 Bacillus axarquiensis str. NCCP-51 AB5472
AB044748.1 gg_id:29235 Bacillus sp. KSM-K38 AB0447
EF646827.1 gg_id:241931 Bacillus licheniformis str. YS01 EF6468
AJ532701.1 gg_id:76003 uranium mill tailings clone Gitt-KF-76 AJ5327

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DQ298263.1 gg_id:151865 studies on and nifH Lasiurus sindicus Sewan grass Thar Desert Rajasthan India rhizos DQ298
AY907698.1 gg_id:112579 Bacillus subtilis str. CICC10080 AY9076
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EU660314.1 gg_id:300233 Bacillus subtilis str. CT17 EU6603
DQ129423.1 gg_id:138175 microarray level air two cities Texas urban aerosol clone AKIW703 DQ129
GQ865645.1 gg_id:543387 Bacillus subtilis str. DSVP25 GQ865
EU071555.1 gg_id:249702 Bacillus licheniformis str. EHFS2_S05Hd EU0715
EU742145.1 gg_id:346842 Bacillus licheniformis str. SKU 3 EU7421
EF173323.1 gg_id:175072 Bacillus licheniformis MKI9 EF1733
AY739691.1 gg_id:114611 lubricant-contaminated soil clone KUD46A AY7396
AY971360.1 gg_id:115295 Bacillus subtilis str. CICC10152 AY9713
AY667495.1 gg_id:102851 Bacillus sp. str. BH724 AY6674
EU672846.1 gg_id:289007 Bacillus licheniformis str. TS-01 EU6728
EF516409.1 gg_id:224115 grassland soil clone FCPP531 EF5164
EU042150.1 gg_id:245253 Bacillus subtilis str. Q47(1) EU0421
EU719191.1 gg_id:337655 Bacillus pumilus str. A1 EU7191
EU240965.1 gg_id:274648 Bacillus subtilis str. YC-12B EU2409
FJ687490.1 gg_id:545577 Bacillus aquimaris str. VITP4 FJ6874
GQ199593.1 gg_id:543593 Bacillus subtilis str. DL-3-4-3 GQ199
GQ983544.1 gg_id:593069 Bacillus amyloliquefaciens str. HYD-B17 GQ983
FJ937899.1 gg_id:567864 Bacillus sp. str. LS48 FJ9378
EU162839.1 gg_id:251156 Bacillus licheniformis str. 8-37-0-1 EU1628
EF633685.1 gg_id:242176 Bacillus sp. 'TS 33' str. TS IW 33 EF6336
EF101727.1 gg_id:191042 Bacillus subtilis str. GB12 EF1017
EU571103.1 gg_id:272881 Bacillus subtilis str. EM 11 EU5711
AY842874.1 gg_id:109651 Bacillus licheniformis str. CICC10093 AY8428
GQ375214.1 gg_id:571371 Bacillus amyloliquefaciens str. CICC 20164 GQ375
EU117278.1 gg_id:257156 Bacillus licheniformis str. B8 EU1172
FN395277.1 gg_id:428974 Bacillus sp. str. FR-W2C1 FN3952
AB301015.1 gg_id:253269 Bacillus pumilus str. GH56 AB3010
AY805232.1 gg_id:109012 Bacillus subtilis str. BSK AY8052
AB362273.1 gg_id:262094 Bacillus hwajinpoensis str. JAM-FM0801 AB3622
EU921229.1 gg_id:326750 Bacillus pumilus str. BM-F13 EU9212
EF513611.1 gg_id:220004 Bacillus subtilis str. A60 EF5136
DQ785743.1 gg_id:161720 Bacillus subtilis str. WSH-062 DQ785
NR_028709.1 gg_id:577421 Bacillus siralis str. 171544; DSM 13140 NR_028
EU826027.1 gg_id:317297 Bacillus subtilis str. CDB86 EU8260

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EF154418.1 gg_id:176669 Bacillus subtilis str. RP24 EF1544
FJ976612.1 gg_id:538157 Bacillus pumilus str. LCR103 FJ9766
FJ607434.1 gg_id:544209 Bacillus cibi str. 102 FJ6074
FJ263034.1 gg_id:368912 Bacillus subtilis str. RC22 FJ2630
FJ951435.1 gg_id:444096 Streptomyces indiaensis str. IF 5 FJ9514
FJ999559.1 gg_id:385478 Bacillus sp. str. HLSB39 FJ9995
AY296813.1 gg_id:101803 Bacillus licheniformis str. IBT018 AY2968
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GU143792.1 gg_id:583331 Bacillus subtilis str. SV10 GU143
AY867793.1 gg_id:110674 Bacillus subtilis str. 4-7 AY8677
EU627167.1 gg_id:277872 Bacillus subtilis str. NH.100 EU6271
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EU874880.1 gg_id:322338 Bacillus pumilus W93 EU8748
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DQ129544.1 gg_id:137539 urban aerosol clone AKIW616 DQ129
AB301024.1 gg_id:252338 Bacillus amyloliquefaciens str. GH58 AB3010
FJ392727.1 gg_id:362442 Bacillus subtilis str. H10-7 FJ3927
AY162128.1 gg_id:76767 Bacillus subtilis str. HAZ14 AY1621
AY995569.2 gg_id:122232 Bacillus subtilis str. IDCC1102 AY9955
FJ937907.1 gg_id:513315 Bacillus aquimaris str. LS71 FJ9379
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AJ880761.1 gg_id:112618 Bacillus subtilis SMF7 AJ8807
AY030326.1 gg_id:36519 Bacillus licheniformis str. KL-047 AY0303
AY920496.1 gg_id:112943 Bacillus subtilis str. Fds-1 AY9204
FJ907196.1 gg_id:574051 Bacillus licheniformis 13 FJ9071
AY462210.1 gg_id:110364 Bacillus pumilus str. DF39 AY4622
EU982438.1 gg_id:321882 Enrichment and detection moderate thermophilic microorganisms vents Lau Basin h EU9824
X76436.1 gg_id:14505 Bacillus alcalophilus X76436
AB020195.1 gg_id:46318 Bacillus sp. str. TGS437 AB0201
X60611.1 gg_id:14659 Bacillus benzoevorans str. NCIMB 12555 X60611
EU982547.1 gg_id:573697 Bacillus subtilis str. 1857 EU9825
AY971358.1 gg_id:115292 Bacillus subtilis str. CICC10148 AY9713
EU977781.1 gg_id:534273 Bacillus vallismortis str. 1P07SD EU9777
FN393828.1 gg_id:549949 Bacillus pumilus str. ES-215-1 FN3938
EU770587.1 gg_id:335963 Bacillus licheniformis str. SVD1 EU7705
DQ866803.1 gg_id:170213 Bacillus subtilis str. B-FS06 DQ866
FJ188306.1 gg_id:545376 Bacillus hwajinpoensis str. UST040801-008 FJ1883
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EU627169.1 gg_id:278386 Bacillus subtilis str. NH.160
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AY347312.1 gg_id:92087 Bacillus sp. str. -11
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EU123939.1 gg_id:318813 Bacillus subtilis 1975
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EU333893.1 gg_id:262062 Bacillus pumilus str. K22-10
AF489591.1 gg_id:68699 Bacillus amyloliquefaciens str. CMB01
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EU660366.1 gg_id:294422 Bacillus pumilus str. CT14
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EF032673.1 gg_id:178850 Bacillus subtilis str. AU14
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EU407552.1 gg_id:270598 Bacillus pumilus str. UFV-E34

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EU847237.1 gg_id:331448 Bacillus licheniformis str. TT2AG
EU594552.1 gg_id:276256 Bacillus pumilus str. 2-1
GQ284402.1 gg_id:555414 Bacillus sp. str. TSWCSN9
GQ280120.1 gg_id:540755 Bacillus sp. str. JS-50
AY800557.1 gg_id:108974 Bacillus subtilis str. N-6
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EF443161.1 gg_id:210305 Bacillus subtilis str. M2
EU870499.1 gg_id:328563 Bacillus licheniformis str. Sua-BAC002
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FJ348039.1 gg_id:349151 Bacillus sp. str. GGC-P3
EF433411.1 gg_id:204383 Bacillus sonorensis str. BCRC 17416
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EU221673.1 gg_id:240721 Bacillus subtilis FL
AY553096.1 gg_id:104097 Bacillus subtilis str. MO3
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EU882849.1 gg_id:332567 Bacillus subtilis str. F3-7
EF488088.1 gg_id:221995 Bacillus subtilis str. QD9
AB196351.1 gg_id:140945 Bacillus pumilus str. PS9
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EU236746.1 gg_id:245090 Bacillus mojavensis str. Z19
EF032676.1 gg_id:180275 Bacillus subtilis str. AU21
GU250447.1 gg_id:558795 Bacillus amyloliquefaciens str. BFE 5335
FJ493042.1 gg_id:564008 Bacillus licheniformis str. G2
GQ903425.1 gg_id:581826 Bacillus pumilus str. XJSL5-6
FJ263042.1 gg_id:357233 Bacillus pumilus str. ZA13
EU366373.1 gg_id:258739 Bacillus amyloliquefaciens str. IV3
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EU113216.1 gg_id:238662 Bacillus licheniformis str. IO21
EU146061.1 gg_id:245167 Streptomyces clavuligerus str. MTCC 7037; Mit-1
AY548949.1 gg_id:106026 Bacillus pumilus str. 8N-4
GQ375236.1 gg_id:509935 Bacillus licheniformis str. CICC 10182
DQ129874.2 gg_id:138024 Bacillus sp. LCKW-Isolate15N

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DQ071564.1 gg_id:132112 Bacillus licheniformis str. MKU 4
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DQ395958.1 gg_id:151652 deep-sea octacoral clone ctg_CGOGA60
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GQ284409.1 gg_id:572836 Bacillus barbaricus str. TSWCSN41
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AY859478.1 gg_id:110687 Bacillus licheniformis str. CICC 10180
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EF154254.1 gg_id:190953 Bacillus vallismortis str. 14
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AJ494727.1 gg_id:63747 Bacillus pumilus EI-24-10
DQ846632.1 gg_id:172881 Bacillus subtilis str. JK-1
X70312.1 gg_id:14666 Bacillus macroides str. NCDO 1661
AY833099.1 gg_id:110581 Bacillus simplex Ph18
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FJ999562.1 gg_id:398862 Bacillus arsenicus str. HLSB43
AY162129.1 gg_id:76813 Bacillus subtilis str. WP1-21
DQ129441.1 gg_id:138452 microarray level air two cities Texas urban aerosol clone AKIW750
DQ129494.1 gg_id:189584 microarray level air two cities Texas urban aerosol clone AKIW837
AM888178.1 gg_id:239470 Bacillus sp. str. TSWCSN2
GU397397.1 gg_id:523649 Bacillus pumilus str. H4
AJ494732.1 gg_id:63740 Bacillus pumilus EI-31-12
AB300800.1 gg_id:255945 Bacillus subtilis str. ND1
AJ494729.1 gg_id:63744 Bacillus pumilus EI-26-5
AY647307.1 gg_id:104302 Bacillus aquimaris str. MSU1110
EU231620.1 gg_id:257555 Bacillus subtilis str. TCCC11002
AB301016.1 gg_id:254047 Bacillus subtilis str. GHGH1
AB536966.1 gg_id:536973 Bacillus sp. str. MB142
AB547220.1 gg_id:517018 Bacillus nealsonii str. NCCP-28
GQ199594.1 gg_id:584451 Bacillus subtilis str. DMJS-2-1
AY740598.1 gg_id:100517 Bacillus pumilus str. 115b
EU620418.1 gg_id:279135 Bacillus pumilus str. S8-11
DQ005494.1 gg_id:122715 Bacillus subtilis str. CICC10156
GQ470396.1 gg_id:590065 Bacillus pumilus str. DQgbc1
EU071546.1 gg_id:236711 Bacillus atrophaeus str. EHFS1_S11Hb
FJ393319.1 gg_id:366264 Bacillus subtilis str. TCCC11377
AY030332.1 gg_id:40827 Bacillus subtilis str. KL-120
AB301012.1 gg_id:236191 Bacillus subtilis str. GH41
EU869232.1 gg_id:340981 Bacillus subtilis str. CM-B94
EU366372.1 gg_id:262423 Bacillus subtilis str. IV2
FJ999558.1 gg_id:416262 Bacillus pumilus str. HLSB33
FJ966221.1 gg_id:576226 Bacillus subtilis str. Bio AA3
EF101735.1 gg_id:187170 Bacillus licheniformis str. HU53
DQ351930.2 gg_id:147897 Bacillus licheniformis str. K10
AY219900.1 gg_id:83777 Bacillus subtilis
EF101707.1 gg_id:177700 Bacillus subtilis str. HU48
EU293872.1 gg_id:253939 Bacillus licheniformis str. ER-15
AY162126.1 gg_id:76500 Bacillus subtilis str. GA1-5
DQ187380.1 gg_id:140126 Brevibacterium halotolerans

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GQ199
AY7405
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FJ3933
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DQ187

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FN646073.1 gg_id:528869 Staphylococcus felis 302
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EF672040.1 gg_id:242290 Bacillus atrophaeus str. XJU
GU071204.1 gg_id:549335 Bacillus sp. str. DIT 16
DQ299293.1 gg_id:146304 Bacillus sp. str. Eg3
AJ277905.1 gg_id:17874 Bacillus subtilis str. Lactipan
GQ280079.1 gg_id:590719 Bacillus subtilis str. JS-9
GU549439.1 gg_id:521130 Bacillus amyloliquefaciens str. 5YN8
FJ577678.1 gg_id:542902 Bacillus safensis str. B1-2
EF032679.1 gg_id:177267 Bacillus pumilus str. AU39
GQ131307.1 gg_id:430388 Bacillus sp. str. DJ-1C
EU624438.1 gg_id:280180 Bacillus aquimaris str. S6-14
EU660369.1 gg_id:287551 Bacillus pumilus str. CT19
FJ897770.1 gg_id:577536 Bacillus sp. str. HU28.1
X76444.1 gg_id:14499 Bacillus species
EU336956.1 gg_id:241285 Bacillus subtilis str. LZ-70
DQ408586.1 gg_id:156458 Bacillus licheniformis str. DZ023
EU870498.1 gg_id:326932 Bacillus subtilis str. Sua-BAC001
FJ481961.1 gg_id:570763 Bacillus pumilus str. K12
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GQ303255.1 gg_id:589582 Bacillus subtilis str. ME-N11
FJ493055.1 gg_id:563925 Bacillus subtilis str. T-2
AB539824.1 gg_id:592862 Bacillus sp. str. SAD5-1
EU927408.1 gg_id:303436 Bacillus aquimaris str. 8-N60
EU430991.1 gg_id:262130 Bacillus sporothermodurans 19
AB305270.1 gg_id:234885 Bacillus subtilis str. YS1-4
AJ863174.1 gg_id:125463 poplar tree microcosm bulk soil unflooded clone 20BSU58
AB196350.1 gg_id:140905 Bacillus licheniformis str. PS2
EU656111.1 gg_id:281486 Bacillus nealsonii str. DSM 15077
EU466040.1 gg_id:289634 African elephant feces clone AFEL3_aao16e01
GQ214132.1 gg_id:580418 Bacillus subtilis str. C8K1
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EF528284.1 gg_id:225373 Bacillus pumilus str. CICCHLJ Q68
EU373428.1 gg_id:269485 Bacillus subtilis str. YRR03
EU379297.1 gg_id:266973 Bacillus pumilus str. 6J-4c
FJ686821.1 gg_id:559334 Bacillus pumilus str. LB4
AY897211.1 gg_id:111931 Bacillus subtilis str. ZJY-116
AJ628743.1 gg_id:100629 Bacillus simplex str. LMG 11160
EU231625.1 gg_id:251346 Bacillus pumilus str. TCCC11012

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DQ071567.1 gg_id:137349 Bacillus licheniformis str. MKU 6
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EU627588.1 gg_id:279531 Bacillus subtilis str. HU87.1
DQ988131.1 gg_id:195533 Bacillus subtilis str. BBDC1
AY462216.1 gg_id:110763 Bacillus subtilis str. DF60
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ABRX01000004.1 gg_id:319639 Bacillus pumilus str. ATCC 7061
EU231614.1 gg_id:254702 Bacillus subtilis str. TCCC17017

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EU780103.1 gg_id:330308 Bacillus pumilus str. DT83 EU780
EU869264.1 gg_id:339196 Bacillus subtilis str. BG-B81 EU869
EU873181.1 gg_id:342551 Bacillus pumilus str. BM-Y10 EU873
AY030324.1 gg_id:71264 Bacillus macroides str. KL-009 AY030
GQ903332.1 gg_id:574670 Bacillus licheniformis str. dhs-40 GQ903
AY603656.2 gg_id:106861 Bacillus malacitensis str. CR-95 AY603
EF528262.1 gg_id:221178 Bacillus subtilis str. CICCHLJ Q34 EF5282
EU624429.1 gg_id:281207 Bacillus pumilus str. S6-05 EU624
EU124559.1 gg_id:257350 Bacillus simplex str. OSS 24 EU124
FJ268976.1 gg_id:357376 unculturable unpolluted rhizospheric loamy soil Phragmites cummunis growing fresh FJ2689
X92161.1 gg_id:40983 Lake Elmenteita isolate WE4 X92161
EF187430.2 gg_id:190564 Bacillus sp. str. CP1 EF1874
FJ373271.1 gg_id:367322 Bacillus subtilis str. EH 37 FJ3732
EU302589.1 gg_id:250531 Bacillus subtilis str. HA Cheonggukjang EU302
EU240379.1 gg_id:244299 Bacillus simplex str. B76 EU240
EF427892.1 gg_id:203939 Bacillus subtilis str. JKC-16 EF4278
EU882846.1 gg_id:308994 Bacillus subtilis str. H10-5-5 EU8828
GU132507.1 gg_id:576641 Bacillus sp. str. JJM-1 GU132
DQ112221.1 gg_id:137047 Bacillus licheniformis str. CICC10266 DQ112
AJ250318.1 gg_id:69789 Bacillus shackletonii str. LMG 18435 AJ2503
EU620445.1 gg_id:275997 Aerobic Facultative Alkalitolerant and Halotolerant Endospore Formers Soil Alvord B EU620
AY373018.1 gg_id:94983 Bacillus sp. str. DIT030428 AY3730
EF528273.1 gg_id:227083 Bacillus pumilus str. CICCHLJ Q47 EF5282
EU870503.1 gg_id:345937 Bacillus licheniformis str. Sua-BAC006 EU870
AJ550463.1 gg_id:82717 Bacillus pumilus AJ5504
FJ380930.1 gg_id:360936 Bacillus sp. str. K-05 FJ3809
AY162136.1 gg_id:77146 Bacillus licheniformis str. GA8 AY162
AF142575.1 gg_id:14706 Bacillus sp. str. Biosubtyl AF1425
DQ906100.1 gg_id:171545 Bacillus subtilis str. N391 DQ906
AY913754.1 gg_id:112493 Bacillus subtilis str. CICC10082 AY913
EF433409.1 gg_id:210498 Bacillus atrophaeus str. BCRC 17123 EF4334
GU549438.1 gg_id:526750 Bacillus amyloliquefaciens str. 2YN11 GU549
EF032684.1 gg_id:190390 Bacillus subtilis str. AU55 EF0326
EU513395.1 gg_id:259992 Bacillus licheniformis str. TMPSB-D1 EU513
EU366229.1 gg_id:258954 Bacillus mojavensis str. A21 EU366
EF032680.1 gg_id:195409 Bacillus subtilis str. AU40 EF0326
EU257699.1 gg_id:256234 Bacillus subtilis str. G2 acidophilus milk EU257
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AJ880760.1 gg_id:112711 Bacillus subtilis SUF3 AJ8807
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EU046268.1 gg_id:251845 Bacillus yunchengensis str. YC1 EU0462
EU379253.1 gg_id:273917 Bacillus pumilus str. 1RN-3E EU3792
AJ494728.1 gg_id:63743 Bacillus pumilus EI-25-8 AJ4947
AB305265.1 gg_id:227636 Bacillus licheniformis str. L1 AB3052
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EU373425.1 gg_id:269350 Bacillus licheniformis str. YRR01 EU3734
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EU734179.1 gg_id:338610 Bacillus licheniformis str. X2 EU7341
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GQ203617.1 gg_id:561556 Bacillus pumilus str. KS-2 GQ203
EU365683.1 gg_id:266012 Bacillus subtilis str. M-11 EU3656
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DQ870737.1 gg_id:221052 Bacillus circulans str. JSC_SF51 DQ870
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AB536963.1 gg_id:574573 Bacillus sp. str. MB138 AB5369
FJ821596.1 gg_id:554302 Bacillus sp. str. DD1 FJ8215
AY842870.1 gg_id:111078 Bacillus licheniformis str. CICC10086 AY8428
EU935597.1 gg_id:346146 Bacillus licheniformis str. G1 ASIL EU9355
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GQ463619.1 gg_id:564988 Bacillus licheniformis str. XRK4 GQ463

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EU870502.1 gg_id:318100 Bacillus amyloliquefaciens str. Sua-BAC005 EU870
EU624418.1 gg_id:283388 Bacillus arsenicus str. S8-14 EU624
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AY456263.1 gg_id:105383 Bacillus pumilus str. DSMZ27 AY4562
AY995570.2 gg_id:125804 Bacillus subtilis str. IDCC1103 AY9955
EU586322.1 gg_id:265692 Bacillus licheniformis str. H*1 EU5863
GQ280082.1 gg_id:513749 Bacillus subtilis str. JS-12 GQ280
DQ232734.1 gg_id:142272 Bacillus pumilus str. JH4 DQ232
AY762058.1 gg_id:125815 Bacillus sp. str. M1 5-5 AY762
GQ280017.1 gg_id:580384 Bacillus licheniformis str. BJ-7 GQ280
GQ302521.1 gg_id:537803 Bacillus subtilis str. BP-13 GQ302
EU379284.1 gg_id:261753 Bacillus pumilus str. 4RS-5f EU379
EU557029.1 gg_id:269982 Bacillus subtilis str. KU3 EU557
DQ395976.1 gg_id:155560 deep-sea octacoral clone ctg_CGOGA03 DQ395
AY839858.1 gg_id:110561 Bacillus licheniformis str. CICC10098 AY8398
EF439667.1 gg_id:215811 Bacillus pumilus str. S2 EF4396
AY913756.1 gg_id:112580 Bacillus subtilis str. CICC10081 AY9137
EU008574.1 gg_id:236385 Bacillus licheniformis str. PS7 EU008
EU753616.1 gg_id:354902 modern freshwater stromatolites Ruidera Pools Natural Park Spain dry stromatolite EU753
AY913755.1 gg_id:112686 Bacillus subtilis str. CICC10078 AY9137
FJ514932.1 gg_id:557292 Bacillus sp. str. CAU 348 FJ5149
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DQ071560.1 gg_id:132973 Bacillus licheniformis str. MKU 1 DQ071
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DQ118379.1 gg_id:130032 Bacillus licheniformis str. CICC 10183 DQ118

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EU755382.1 gg_id:355623 Bacillus subtilis str. DSVP24
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AB508839.1 gg_id:588430 Bacillus licheniformis str. CMBL-Hg2 AB5088
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EU366369.1 gg_id:276519 Bacillus subtilis str. I1 EU3663
FM180523.1 gg_id:325682 Bacillus pumilus str. B9 FM180
AY929251.1 gg_id:113947 Bacillus subtilis str. CG-312 AY9292
FJ538256.1 gg_id:566024 Bacillus sp. str. DHVB1 FJ5382
FJ686818.1 gg_id:563067 Bacillus amyloliquefaciens str. LB1 FJ6868
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EU867370.1 gg_id:577641 Bacillus asahii str. CCGE2069 EU8673
FJ392725.1 gg_id:369758 Bacillus subtilis str. F1-5 FJ3927
AF157696.1 gg_id:14668 Bacillus macroides str. dhr2 AF1576
EU341173.1 gg_id:247284 Evaluation Rapid Technologies Estimate Microbial Burden and Commercial Airline Ca EU3411
EF474343.1 gg_id:218989 Bacillus subtilis str. DC10 EF4743
EU689157.1 gg_id:367096 Bacillus amyloliquefaciens str. ATCC 23842 EU6891
GQ305125.1 gg_id:582824 Bacillus subtilis str. xw-2 GQ305
EF101730.1 gg_id:190540 Bacillus firmus str. GB1 EF1017
DQ911347.1 gg_id:244447 Paenibacillus lautus str. DMT637 DQ911
GU385855.1 gg_id:514350 Bacillus simplex str. QT9 GU385
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GQ280087.1 gg_id:511562 Bacillus licheniformis str. JS-17 GQ280
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GQ871450.1 gg_id:542698 Bacillus licheniformis str. KK2 GQ871
FJ999555.1 gg_id:462822 Bacillus pumilus str. HLSB4 FJ9995
AM910583.1 gg_id:261115 Bacillus licheniformis str. 51.4 AM910
FN395272.1 gg_id:455038 Bacillus pumilus str. FR-S1Aa FN3952
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GU594321.1 gg_id:519610 Bacillus aquimaris str. AP.MSU5 GU594

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AY971363.1 gg_id:115327 Bacillus subtilis str. CICC10150 AY9713
FJ544350.1 gg_id:420591 Bacillus subtilis str. ji09 FJ5443
AY114158.1 gg_id:63981 Bacillus subtilis str. GL AY1141
DQ350833.1 gg_id:149060 Empedobacter brevis str. N1 DQ350
GQ503324.1 gg_id:584233 Bacillus licheniformis str. AsK03 GQ503
EF113324.1 gg_id:191576 Bacillus licheniformis LB 6C EF1133
FJ937901.1 gg_id:509065 Bacillus sp. str. LS52 FJ9379
GU392041.1 gg_id:575901 Bacillus licheniformis str. KBDL4 GU392
EU571194.1 gg_id:273050 Bacillus sp. str. 25-7 EU5711
EU586319.1 gg_id:270613 Bacillus subtilis str. P*46 EU5863
EF101708.1 gg_id:190005 Bacillus subtilis str. HU50 EF1017
FJ906822.1 gg_id:563243 Bacillus subtilis str. L520 FJ9068
GQ121033.1 gg_id:430149 Bacillus amyloliquefaciens str. TSWK1-1 GQ121
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FJ226762.1 gg_id:341035 Bacillus oshimensis str. OS4 FJ2267
EU240392.1 gg_id:249403 Bacillus megaterium str. B100 EU2403
GQ280014.1 gg_id:594063 Bacillus sp. str. BJ-4 GQ280
EF661579.1 gg_id:246165 strict anaerobic extreme thermophilic hydrogen-producing enriched digested lab-sca EF6615
AJ564608.1 gg_id:87915 Geobacillus debilis str. F10 AJ5646
FJ808721.1 gg_id:523365 Geobacillus pallidus str. P112 FJ8087
FJ808724.1 gg_id:529616 Geobacillus pallidus str. P161 FJ8087
EU935594.1 gg_id:317043 Geobacillus pallidus str. M71 EU9355
EU935598.1 gg_id:305020 Geobacillus pallidus str. AH23 EU9355
FJ417407.1 gg_id:365570 Geobacillus pallidus str. P86 FJ4174
EU935593.1 gg_id:315068 Geobacillus pallidus str. P45 EU9355
FJ808718.1 gg_id:520138 Geobacillus pallidus str. P66 FJ8087
FJ417405.1 gg_id:367668 Geobacillus pallidus str. P22 FJ4174
FJ808716.1 gg_id:523683 Geobacillus pallidus str. G19A FJ8087
EU935591.1 gg_id:340153 Geobacillus pallidus str. P26 EU9355
AY608982.1 gg_id:104271 Geobacillus toebii str. BGSC 99A1 AY6089
AJ005760.1 gg_id:14539 Geobacillus stearothermophilus str. K1041 AJ0057
EU271906.1 gg_id:244287 Geobacillus sp. str. LV-3 EU2719
AB116108.1 gg_id:91321 Geobacillus thermodenitrificans str. T1600 AB1161
AF114424.1 gg_id:14536 Geobacillus thermodenitrificans str. NS AF1144
GQ180112.1 gg_id:542840 Bacillus clausii str. DF3 GQ180
AY608984.1 gg_id:104580 Geobacillus thermoglucosidasius str. BGSC W9A15 AY6089
EU484349.1 gg_id:274601 Geobacillus vulcani str. BCRC 17563 EU4843
EU214622.1 gg_id:323684 Geobacillus stearothermophilus mt-22 EU2146

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GQ255948.1 gg_id:533915 Geobacillus toebii str. HBB-218 GQ255
EU381187.1 gg_id:352606 Geobacillus stearothermophilus str. GBPI-13 EU3811
AY466700.1 gg_id:104680 Anoxybacillus toebii str. NS1-1 AY4667
AY608945.1 gg_id:102443 Geobacillus lituanicus str. BGSC W9A89 AY6089
NR_025143.1 gg_id:563677 Geobacillus toebii str. SK-1; KCTC 0306BP NR_025
Z26930.1 gg_id:14542 Geobacillus pallidus str. DSM 3670* Z26930
AJ489330.1 gg_id:70432 Geobacillus thermoleovorans I80 AJ4893
AY312404.1 gg_id:88427 Geobacillus jurassicus str. DS1 AY3124
AJ489328.1 gg_id:70679 Geobacillus thermoleovorans T70 AJ4893
GQ112279.1 gg_id:374316 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ112
EU484350.1 gg_id:275411 Geobacillus lituanicus str. BCRC 17562 EU4843
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AB543491.1 gg_id:573601 Geobacillus pallidus str. NCCP-131 AB5434
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FJ808712.1 gg_id:524476 Geobacillus stearothermophilus str. Ah22 FJ8087
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AB210953.1 gg_id:115284 Geobacillus toebii str. SSCT84-3 AB2109
AY682097.1 gg_id:106402 Geobacillus stearothermophilus str. 49 AY6820
Z26922.1 gg_id:14568 Bacillus caldotenax str. DSM 406 Z26922
DQ355387.1 gg_id:147769 Solubilization and biodegradation polycyclic aromatic hydrocarbons under condition DQ355
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AY550104.1 gg_id:104797 Geobacillus thermocatenulatus hs6 AY5501
AF411064.1 gg_id:45180 Geobacillus anatolicus str. SB AF4110
EU214619.1 gg_id:309162 Geobacillus stearothermophilus ir-25 EU2146
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GQ487459.1 gg_id:590908 Geobacillus toebii str. HBB-247 GQ487
EU381193.1 gg_id:352145 Geobacillus stearothermophilus str. GBPI-12 EU381
AY608936.1 gg_id:106419 Geobacillus thermoleovorans str. BGSC 96A1 AY608
GQ096866.1 gg_id:406506 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw GQ096
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EU214620.1 gg_id:336321 Geobacillus stearothermophilus it-8 EU214
EU652071.1 gg_id:273513 Geobacillus stearothermophilus str. mm-19 EU652
EU381183.1 gg_id:325891 Geobacillus stearothermophilus str. GBPI-5 EU381
NC_006510.1 gg_id:128657 Geobacillus kaustophilus str. HTA426 NC_00
FN428682.1 gg_id:571762 Geobacillus pallidus str. R-35634 FN428
EU214627.1 gg_id:335894 Geobacillus toebii mc-12 EU214
FJ429998.1 gg_id:357811 Geobacillus sp. A364 FJ4299
X60618.1 gg_id:14567 Geobacillus kaustophilus str. NCIMB 8547 X60618
EF469734.1 gg_id:222519 Geobacillus vulgivagus str. CDZ 1 EF4697
EF025325.1 gg_id:186620 Geobacillus stearothermophilus str. ARM 1 EF0253
EU621361.1 gg_id:279618 Geobacillus pallidus str. DR03 EU6213
EU484353.1 gg_id:272744 Bacillus caldovelox str. BCRC 11957 EU4843
L09227.1 gg_id:14553 Saccharococcus thermophilus L09227
EF535794.1 gg_id:218748 Geobacillus toebii str. T85 EF5357
AY248718.1 gg_id:86077 Geobacillus caldoxylosilyticus str. TK4 AY2487
AY491497.1 gg_id:107338 Geobacillus stearothermophilus AY4914
M77488.1 gg_id:14564 Bacillus thermoleovorans M7748
EU484357.1 gg_id:268222 Geobacillus kaustophilus str. BCRC 11223 EU4843
AY248717.1 gg_id:85270 Geobacillus thermoleovorans str. G1 AY2487
EU884294.1 gg_id:338217 Geobacillus stearothermophilus str. BMSCE-1 EU884
AM947545.1 gg_id:260757 Minor changes detected microbial structure and after three week thermophilic dige AM947
X57309.1 gg_id:14552 Geobacillus stearothermophilus str. T10 X57309
EU652094.1 gg_id:276376 Geobacillus subterraneus str. ra-11 EU652
EU214626.1 gg_id:318116 Geobacillus toebii mc-9 EU214
AY952967.1 gg_id:114690 Bacillus caldotenax str. CCSD 3900 AY9529
AY297092.2 gg_id:88437 Geobacillus stearothermophilus str. BGSC 9A21; DSM 13240 AY2970
AY536054.1 gg_id:104537 Bacillus pallidus str. Row2A1 AY5360
GQ180111.1 gg_id:580954 Bacillus clausii str. DF2 GQ180
DQ923400.1 gg_id:197471 Geobacillus stearothermophilus str. 5 DQ923
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DQ452018.1 gg_id:219154 Bacillus sp. HT4 DQ452
FN428688.1 gg_id:541063 Geobacillus uzenensis str. R-35640 FN428
AY608938.1 gg_id:106733 Bacillus caldovelox str. BGSC 96A5 AY608
EU428777.1 gg_id:274145 Geobacillus toebii str. DPE7 EU428

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EU710557.1 gg_id:349122 Bacillus sp. str. TSSC-3 EU7105
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GU397404.1 gg_id:520933 Halobacillus dabanensis str. B1B GU397
GQ903455.1 gg_id:552668 Halobacillus dabanensis str. XJSL8-6 GQ903
FJ937910.1 gg_id:533869 Halobacillus litoralis str. LS93 FJ9379
AY190534.1 gg_id:80237 Halobacillus locisalis str. MSS-155 AY1905
NR_025244.1 gg_id:543606 Halobacillus salinus str. HSL-3; KCCM 41590 NR_025
FJ444962.1 gg_id:582194 Halobacillus trueperi str. whb16 FJ4449
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FJ444988.1 gg_id:567005 Halobacillus trueperi str. whb42 FJ4449
FJ999556.1 gg_id:379642 Halobacillus trueperi str. HLSB14 FJ9995
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FJ444991.1 gg_id:593188 Halobacillus trueperi str. whb45 FJ4449
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EF533970.1 gg_id:265846 Halobacillus sp. str. Y13 EF5339
DQ458839.1 gg_id:156629 Halobacillus sp. str. YT242 DQ458
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AB198758.1 gg_id:110746 Halobacillus sp. str. IS-Hb9 AB1987
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AM161501.1 gg_id:144741 Halobacillus virgiliensis str. S21 AM161
AB305176.1 gg_id:229439 Halobacillus sp. str. S19-3 AB3051
EU170130.1 gg_id:242105 Halobacillus sp. str. T15 EU1701
DQ089676.1 gg_id:128093 Halobacillus trueperi str. I101 DQ089
AB243865.1 gg_id:235317 Halobacillus faecis str. IGA7-4 AB2438
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AB539831.1 gg_id:554742 Halobacillus sp. str. SVT14 AB5398
GQ342530.1 gg_id:545041 Halobacillus mangrovi str. VKSJ-1 GQ342
X94558.1 gg_id:14614 Halobacillus litoralis str. SL-4 X94558
AM295006.1 gg_id:254422 Halobacillus sp. str. FP5 AM295
FJ746574.1 gg_id:537031 Halobacillus sp. str. H57B77 FJ7465
AM161506.1 gg_id:144979 Halobacillus styriensis str. I3A AM161
FJ999554.1 gg_id:439688 Halobacillus trueperi str. HLSB3 FJ9995
FJ386520.1 gg_id:552974 Halobacillus sp. str. IA-27 FJ3865

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EU602318.2 gg_id:587130 Halobacillus halophilus str. MMD047 EU602
EU868843.1 gg_id:309460 Halobacillus sp. str. S27-1 EU868
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AY881246.1 gg_id:111708 Halobacillus yeomjeoni str. MSS-402 AY881
DQ458838.1 gg_id:156924 Halobacillus sp. str. YT234 DQ458
AB362695.1 gg_id:237041 Halolactibacillus halophilus str. NRIC 0629 AB362
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AB362701.1 gg_id:239864 Halolactibacillus miurensis str. NRIC 0637 AB362
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AB362698.1 gg_id:254684 Halolactibacillus miurensis str. NRIC 0633 AB362
AB362694.1 gg_id:249393 Halolactibacillus halophilus str. NRIC 0628 AB362
AB196783.1 gg_id:132611 Halolactibacillus halophilus str. M2-2 AB196
AB231905.1 gg_id:137844 Lentibacillus kapialis str. PN7-6 AB231
AY762976.1 gg_id:102689 Salibacillus sp. str. BH113 AY762
AB191345.1 gg_id:100303 Lentibacillus halophilus str. PS11-2 AB191
AB365482.1 gg_id:235720 Virgibacillus siamensis str. MS3-4 AB365
AY667497.1 gg_id:103142 Virgibacillus sp. str. BH260 AY667
EU442366.1 gg_id:274948 Marinococcus sp. str. 05 EU442
X90835.1 gg_id:14475 Marinococcus halophilus str. DSM 20408 X90835
EU281853.2 gg_id:242528 Alkalilactibacillus ikkense str. GCM68 EU281
EU143688.1 gg_id:247337 Natronobacillus azotifixans str. ES 3 EU143
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AJ316297.1 gg_id:70179 Virgibacillus picturae str. LMG 20959 AJ316
AB539827.1 gg_id:542410 Oceanobacillus picturae str. SAD12-1 AB539
EF512732.1 gg_id:223472 Oceanobacillus picturae str. JL85 EF5127
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AJ309561.1 gg_id:47685 Bacillus litoralis str. IB-B4 AJ3095
AY647302.1 gg_id:103563 Oceanobacillus iheyensis str. MSU3110 AY6473
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EU583724.1 gg_id:263804 Pontibacillus sp. str. JSM 072002 EU5837
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GU001908.1 gg_id:575458 Salimicrobium halophilum str. PLF GU001
EU868872.1 gg_id:344756 Salimicrobium luteum str. M1-1 EU8688
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AM905297.1 gg_id:235359 Sediminibacillus halophilus str. EN8d AM905
FJ999948.1 gg_id:577242 Terribacillus saccharophilus str. EQH19 FJ9999
DQ519571.1 gg_id:161113 Goribacillus litoralis str. CL-GR16 DQ519
AY553068.1 gg_id:107125 Bacillus sp. str. GSP9 AY5530
GQ304893.1 gg_id:588713 Terribacillus sp. str. DB2 GQ304

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AB185150.1 gg_id:103731 Halobacillus sp. str. SR5-3	AB185
GQ903447.1 gg_id:584245 Thalassobacillus devorans str. XJSL7-8	GQ903
EU817571.1 gg_id:348471 Thalassobacillus sp. str. AD-1	EU817
EU308489.1 gg_id:369188 Thalassobacillus sp. str. FIB228	EU308
GU397401.1 gg_id:523161 Thalassobacillus devorans str. T1B	GU397
AY616012.1 gg_id:99851 Virgibacillus koreensis str. BH30097	AY616
AB243851.1 gg_id:252650 Virgibacillus halophilus str. 5B73C	AB243
EU191907.1 gg_id:241247 Salinibacillus sp. str. BH128	EU191
AJ618979.1 gg_id:101225 Geobacillus amylolyticus str. MR3C	AJ6189
FJ675088.1 gg_id:517206 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I	FJ6750
GQ903428.1 gg_id:558327 Bacillus pumilus str. XJSL5-9	GQ903
NR_027209.1 gg_id:561406 Filobacillus milosensis str. SH714; DSM 13259	NR_02
AY422987.1 gg_id:97903 Virgibacillus sp. str. R-7428	AY422
FJ543002.1 gg_id:524185 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone B	FJ5430
FJ425909.1 gg_id:586791 Virgibacillus litoralis str. JSM 089168	FJ4259
EU369158.1 gg_id:348666 libraries oyster shell clone MBHOS-09	EU369
NR_029096.1 gg_id:541374 Tenuibacillus multivorans str. 28-1; NBRC 100370	NR_02
AM930318.1 gg_id:538016 gradual cooling stage mass and its spatial composting clone SMQ1	AM930
AJ315056.1 gg_id:46172 Virgibacillus necropolis str. LMG 19488	AJ3150
EF600581.1 gg_id:296462 leaf litter clone E2-1	EF6005
EU009754.1 gg_id:256614 between classification and soils Ross Sea region Antarctic ornithogenic soil clone 11H	EU009
EU191908.1 gg_id:242845 Virgibacillus sp. str. BH258	EU191
AM409184.1 gg_id:184332 Anoxybacillus bogroviensis str. NBIMCC 8427=DSM 1795	AM409
EF205590.1 gg_id:207832 among geographically regions central Tibet geothermal spring mat clone TP80	EF2055
EF675742.1 gg_id:534570 Virgibacillus arcticus str. Hal 1	EF6757
AY121435.1 gg_id:63143 Amphibacillus sp. str. YIM-kkny10	AY1214
EF520006.1 gg_id:221367 Halobacillus sp. str. BH097	EF5200
AB034710.1 gg_id:27234 compost clone 4-28	AB034
FJ347755.1 gg_id:361710 Halalkalibacillus sp. str. B3A	FJ3477
DQ664537.1 gg_id:163144 Filobacillus sp. str. BH204	DQ664
AB533312.1 gg_id:579420 Amphibacillus sp. str. DA-19	AB5333
EF600597.1 gg_id:287481 leaf litter clone E1-38	EF6005
X90834.1 gg_id:14615 Marinococcus albus str. DSM 20748	X90834
X82436.1 gg_id:14603 Gracilibacillus dipsosauri str. DD1	X82436
AM114102.1 gg_id:145545 Paucisalibacillus globulus str. B22	AM114
FJ425900.1 gg_id:536206 Aquisalibacillus sp. str. JSM 078194	FJ4259
FJ380184.1 gg_id:367058 ornithogenic Ross Sea region Antarctica AB1 soil clone J9	FJ3801
EU417652.2 gg_id:273369 Virgibacillus sp. str. ZLC-17	EU417
EU213011.1 gg_id:244056 Virgibacillus sp. str. CC-YMP-6	EU213
AB189326.1 gg_id:103803 Gracilibacillus sp. str. SA-Gb1	AB189
EU868883.1 gg_id:319984 Halalkalibacillus halophilus str. M24-1	EU868

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EU249938.1 gg_id:246585 Polyphasic description Pocillopora seawater adjacent Pacillopora meandrina coral co EU249
EU430986.1 gg_id:260081 Paucisalibacillus globulus 5 EU430
FJ357159.1 gg_id:358728 Virgibacillus sp. str. ISL-24 FJ3571
EU369133.1 gg_id:325308 libraries oyster shell clone MBIOS-17 EU369
DQ842544.1 gg_id:173209 Application Glucose Glutamate Temperature Biotrickling Filtration Hydrogen Sulphic DQ842
AB197126.1 gg_id:129671 Gracilibacillus borotolerans str. T16X AB197
DQ346527.1 gg_id:156308 during composting libraries compost clone 3B13 DQ346
NR_028649.1 gg_id:587710 Cerasibacillus quisquiliarum str. BLx; DSM 15825 NR_02
AB189333.1 gg_id:99420 Filobacillus sp. str. SA-Fb1 AB189
FJ348416.1 gg_id:552637 Investigation microbial soil method saltern 15 cm be surface clone DGGE gel band ntu FJ3484
AM292417.2 gg_id:192309 Salirhabdus caputitis str. CVS14 AM292
FN428698.1 gg_id:574818 Geobacillus caldoproteolyticus str. R-35652 FN428
NR_028642.1 gg_id:569518 Paraliobacillus ryukyuensis str. O15-7; DSM 15140 NR_02
EU143689.1 gg_id:236513 Amphibacillus diazotrophicus str. 22KS-2 EU143
EU135676.1 gg_id:248158 Virgibacillus sp. str. YIM C834 EU135
AM400872.1 gg_id:244314 Bacillus sp. str. Jsl1 AM400
AB176374.1 gg_id:187575 Microbial Hydrothermal System Suiyo Seamount on Izu-Ogasawara Arc vent area wa AB176
DQ504377.1 gg_id:160666 Bacillus sp. str. 17-5 DQ504
AB176366.1 gg_id:178532 Microbial Hydrothermal System Suiyo Seamount on Izu-Ogasawara Arc vent area wa AB176
EF422411.1 gg_id:203680 Bacillus sp. str. ANL-iso4 EF4224
AY762977.1 gg_id:102843 Bacillus sp. str. BH164 AY762
GQ009179.1 gg_id:500487 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw GQ009
EU620444.1 gg_id:276370 Aerobic Facultative Alkalitolerant and Halotolerant Endospore Formers Soil Alvord B EU620
FM244839.1 gg_id:359288 Bacillus sp. str. HS-136 FM244
AM492160.1 gg_id:206482 Salsuginibacillus kocurii str. CH9d AM492
DQ115802.2 gg_id:133117 Bacillus sp. CM1 DQ115
FJ437873.1 gg_id:548924 Benthic okenone production Fayetteville New York Green Lake 25 m water depth clo FJ4378
GU217709.1 gg_id:590271 Bacillus sp. str. ljh-13 GU217
FJ380159.1 gg_id:363860 ornithogenic Ross Sea region Antarctica AB1 soil clone 9/4/2D FJ3801
AY376312.1 gg_id:105770 Bacillus bogoriensis str. LBB3 AY3763
EU620448.1 gg_id:276903 Aerobic Facultative Alkalitolerant and Halotolerant Endospore Formers Soil Alvord B EU620
AJ717379.1 gg_id:110222 Bacillus sp. AC6t AJ7173
FJ764775.1 gg_id:541211 Bacillus sp. str. E-172 FJ7647
EU491818.1 gg_id:267423 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU491
AY553128.1 gg_id:101804 Bacillus sp. str. GSP69 AY553
DQ344635.1 gg_id:147585 Sinococcus beijingensis str. IMBZ007 DQ344
AB002644.1 gg_id:14473 G+C gram-positive HTA454 AB002
EU091310.1 gg_id:255095 Bacillus halodurans str. C7 EU091
EF422410.1 gg_id:206803 Bacillus sp. str. ANL-isoa2 EF4224
AY753654.1 gg_id:99130 Bacillus sp. str. HA6 AY753
AM050346.1 gg_id:134015 Bacillus sp. str. BR AM050

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GQ007987.1 gg_id:501679 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw: GQ007
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GQ280018.1 gg_id:514033 Bacillus sp. str. BJ-8 GQ280
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FJ430003.1 gg_id:366859 Geobacillus sp. A394 FJ4300
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AB489108.1 gg_id:550082 Virgibacillus pantothenticus str. GL4-1 AB4891
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AY373323.1 gg_id:94551 Virgibacillus proomii str. R-6762 AY3733
GU339240.1 gg_id:551232 Virgibacillus proomii str. EH10 GU339
AY543017.1 gg_id:99017 Brochothrix thermosphacta MF 110 AY5430
AY543038.1 gg_id:100369 Brochothrix campestris DSMZ 4712 AY5430
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g__Listeria
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s__Listeria grayi	47198
s__Listeria marthii	47270
s__Listeria monocytogenes	46065
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s__Listeria monocytogenes	46917
s__Listeria seeligeri	46697
s__Listeria seeligeri	46823
s__Listeria welshimeri	47292
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s__Brevibacillus borstelensis	47447

X98526.1 gg_id:15034 Listeria grayi str. ATCC19120 X98526
EU545982.1 gg_id:343691 Listeria marthii str. NR-9579 EU5459
CP001604.1 gg_id:528087 Listeria monocytogenes str. 08-5923 CP0016
CP001604.1 gg_id:528088 Listeria monocytogenes str. 08-5923 CP0016
NC_002973.6 gg_id:108681 Listeria monocytogenes str. 4b F2365 NC_00
CP001175.1 gg_id:522930 Listeria monocytogenes str. HCC23 CP0011
DQ065845.1 gg_id:133743 Listeria seeligeri str. ATCC 35967 DQ065
DQ065844.1 gg_id:133797 Listeria seeligeri str. 2436KA DQ065
DQ065846.1 gg_id:130677 Listeria welshimeri str. ATCC 35897 DQ065
NC_003212.1 gg_id:128465 Listeria innocua str. Clip11262 NC_00
FJ774219.1 gg_id:566482 Listeria monocytogenes str. N9 FJ7742
CP001604.1 gg_id:528090 Listeria monocytogenes str. 08-5923 CP0016
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AJ535698.1 gg_id:100269 Listeria seeligeri 50 AJ5356
NC_008555.1 gg_id:196027 Listeria welshimeri serovar 6b str. SLCC5334 NC_00
X98532.1 gg_id:15046 Listeria welshimeri str. ATCC35897 X98532
FJ557241.1 gg_id:376496 Listeria sp. str. CIP 109804 FJ5572
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Y14579.1 gg_id:14469 Ammoniphilus oxalaticus str. RAOx-FF Y14579
Y14578.1 gg_id:14468 Ammoniphilus oxalaticus str. RAOx1 Y14578
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DQ378179.1 gg_id:155936 oil-polluted soil clone F14_Pitesti DQ378
GQ062548.1 gg_id:410410 Topographical and Temporal Human Skin Microbiome skin nare clone nbw12b03c1 GQ062
DQ129330.1 gg_id:138087 microarray level air two cities Texas urban aerosol clone AKIW1134 DQ129
AM930509.1 gg_id:252328 Mobilizing agents enhance fungal degradation polycyclic aromatic hydrocarbons an AM930
Y14581.1 gg_id:14466 Oxalophagus oxalicus str. DSM 5503T Y14581
AB271755.1 gg_id:166364 Aneurinibacillus aneurinilyticus str. NBRC 15521 AB2717
X77789.1 gg_id:14455 Bacillus acidovorans str. ATCC 51159 X77789
GU397386.1 gg_id:521475 Aneurinibacillus migulanus str. A72 GU397
D78462.1 gg_id:14454 Aneurinibacillus migulanus str. ATCC9999 D78462
AJ715385.1 gg_id:100842 Aneurinibacillus terranovensis str. LMG 22483 AJ7153
EF032876.1 gg_id:174619 Aneurinibacillus thermoaerophilus str. AFNA 1 EF0328
X94196.1 gg_id:14460 Aneurinibacillus thermoaerophilus str. DSM 10154 X94196
DQ890194.1 gg_id:162600 Aneurinibacillus thermoaerophilus str. HZ DQ890
X94197.1 gg_id:14461 Aneurinibacillus thermoaerophilus str. DSM 10155 X94197
AB112725.1 gg_id:99186 Aneurinibacillus danicus str. NCIMB 13288T AB1127
DQ350838.1 gg_id:146417 Aneurinibacillus migulanus str. U603 DQ350
AJ586382.1 gg_id:104351 Brevibacillus borstelensis str. R-16402 AJ5863
DQ350837.1 gg_id:146165 Brevibacillus borstelensis str. U404 DQ350
EU714903.1 gg_id:323091 Brevibacillus borstelensis str. SRDTh2 EU7149

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AF378231.1 gg_id:72419 Brevibacillus invocatus str. LMG 18167 AF3782
AY745239.1 gg_id:107154 Brevibacillus laterosporus AY7452
AJ715383.1 gg_id:100531 Brevibacillus levickii str. R-22010 AJ7153
D78464.1 gg_id:14444 Brevibacillus reuszeri str. NRRL NRS-1206 D78464
AY196006.1 gg_id:82008 Brevibacillus thermoruber str. WR-249 AY1960
DQ452016.1 gg_id:220136 Brevibacillus sp. FB2 DQ452
AB048253.1 gg_id:27343 Brevibacillus agri str. MC-C1 AB0482
EF690427.1 gg_id:242098 Brevibacillus formosus M13-7 EF6904
EU497965.1 gg_id:266742 Brevibacillus sp. str. P-6 EU4979
EU730932.1 gg_id:318433 Brevibacillus invocatus str. 176 EU7309
FJ009377.1 gg_id:349508 Brevibacillus brevis str. G14 FJ0093
GQ495662.1 gg_id:560159 Brevibacillus brevis str. L-25 GQ495
EF055990.1 gg_id:181337 Brevibacillus parabrevis str. LH1-1 EF0559
AJ457160.1 gg_id:67396 Brevibacillus sp. str. AV-Pb AJ4571
AY493971.1 gg_id:136682 Fingerprinting aggregates soil clone 1047 AY4939
EU605978.1 gg_id:271212 Brevibacillus brevis str. B12 EU6059
EU621907.1 gg_id:277682 Brevibacillus sp. str. CCBAU 10720 EU6219
EU730938.1 gg_id:335118 Brevibacillus centrosporus str. 218 EU7309
D78460.1 gg_id:14443 Brevibacillus formosus str. NRRL NRS-863 D78460
EU221377.1 gg_id:253356 Brevibacillus laterosporus str. Y2S9 EU2213
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FJ430060.1 gg_id:362530 Brevibacillus sp. E187 FJ4300
AP008955.1 gg_id:560716 Brevibacillus brevis str. NBRC 100599 (= 47) AP0089
AB112717.1 gg_id:103446 Brevibacillus limnophilus str. DSM 6472 AB1127
AY072721.1 gg_id:77296 Brevibacillus sp. str. SE004 AY0727
FJ592179.1 gg_id:556989 Brevibacillus agri str. Q6-2 FJ5921
EU638360.1 gg_id:307934 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU6383
FJ430048.1 gg_id:361257 Brevibacillus sp. D505a FJ4300
AJ971483.1 gg_id:130970 Cohnia thermotolerans str. CCUG 47242 AJ9714
AB362828.1 gg_id:251819 Paenibacillus sp. str. YT1101 AB3628
AF227835.1 gg_id:16553 str. 31295 AF2278
EF203083.2 gg_id:206849 Paenibacillus sp. str. HIO-4 EF2030
EU134631.1 gg_id:253479 tallgrass prarie soil clone FFCH11327 EU1346
DQ129381.1 gg_id:137918 microarray level air two cities Texas urban aerosol clone AKIW1107 DQ129
AM900791.1 gg_id:244571 Cohnella sp. PA228 AM900
EU284591.1 gg_id:253236 Microbacterium sp. str. sq5 EU2845
EF368009.1 gg_id:214536 Cohnella soli str. 5GH36-9 EF3680
NR_028674.1 gg_id:565706 Bacillus edaphicus str. T7; CIP 105814 NR_028
DQ898308.1 gg_id:173293 Bacillus mucilaginosus str. AS1.231 DQ898
AF182807.2 gg_id:17949 Paenibacillus velasolus str. P1 AF1828

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AJ320491.1 gg_id:28165 Paenibacillus alvei str. DSM 29 AJ3204
EF103205.1 gg_id:182312 Paenibacillus sp. str. MSCB-8 EF1032
EF690415.1 gg_id:252209 Paenibacillus amylolyticus M18-5 EF6904
AJ884854.1 gg_id:186123 Paenibacillus sp. DF4MM5 AJ8848
FJ006879.1 gg_id:313888 Paenibacillus sp. str. WPCB056 FJ0068
AJ884852.1 gg_id:199597 Paenibacillus sp. DF4MM1 AJ8848
FJ944661.1 gg_id:545044 Paenibacillus amylolyticus str. KUDC1039 FJ9446
AJ495806.1 gg_id:55541 Paenibacillus sp. p22D AJ4958
AJ884856.1 gg_id:174753 Paenibacillus sp. DF4SC1 AJ8848
AB073201.1 gg_id:77745 Paenibacillus apiarius str. DSM 5581 AB0732
GQ284360.1 gg_id:549779 Paenibacillus barengoltzii str. THWCSN11 GQ284
GQ284370.1 gg_id:559070 Paenibacillus barengoltzii str. THWCSN47 GQ284
DQ124699.1 gg_id:140775 Paenibacillus barengoltzii str. SAFN-125 DQ124
GQ284353.1 gg_id:577062 Paenibacillus barengoltzii str. THWCS6 GQ284
GQ284361.1 gg_id:547686 Paenibacillus barengoltzii str. THWCSN13 GQ284
GQ284355.1 gg_id:548873 Paenibacillus barengoltzii str. THWCS8 GQ284
EU888523.1 gg_id:314265 Paenibacillus barengoltzii str. ES_MS41c EU8885
GQ284369.1 gg_id:583230 Paenibacillus barengoltzii str. THWCSN46 GQ284
GQ284371.1 gg_id:567491 Paenibacillus barengoltzii str. THWCSN50 GQ284
AB073364.1 gg_id:78279 Paenibacillus borealis str. DSM 13118 AB0733
FJ266315.1 gg_id:513350 Paenibacillus borealis str. RFNB4 FJ2663
AJ011322.1 gg_id:14376 Paenibacillus borealis KK19 AJ0113
NR_024857.1 gg_id:555585 Paenibacillus campinasensis str. 324; KCTC 364BP NR_024
AF181573.1 gg_id:73805 Paenibacillus cf. polymyxa 6 AF1815
EF516124.1 gg_id:225551 grassland soil clone FCPP694 EF5161
EF492898.1 gg_id:243136 Iron-manganese Nodule and Its Surrounding Soil soil around iron-manganese nodule EF4928
DQ906781.1 gg_id:250537 Oman subsurface soil clone 2A-10 DQ906
EU240430.1 gg_id:245111 Paenibacillus chondroitinus str. B179 EU2404
AB245386.1 gg_id:150342 Paenibacillus pocheonensis str. Gsoil 1138 AB2453
AJ438302.1 gg_id:67648 Paenibacillus cookii str. R-11600 AJ4383
D78466.1 gg_id:14415 Paenibacillus curdlanolyticus str. IFO15724T D78466
FJ944652.1 gg_id:539755 Paenibacillus elgii str. KUDC1030 FJ9446
AY090110.1 gg_id:89996 Paenibacillus elgii str. SD17 AY0901
FJ189797.1 gg_id:571764 Paenibacillus illinoisensis str. CSB12 FJ1897
D85397.1 gg_id:14360 Paenibacillus illinoisensis str. NRRL NRS-1356T D85397
FJ973530.1 gg_id:465403 Paenibacillus lactis str. NBPP29 B29 FJ9735
AY257868.1 gg_id:84777 Paenibacillus lactis str. MB 1871 AY2578
AY257870.1 gg_id:101148 Paenibacillus lactis str. MB 2035 AY2578
EF415643.1 gg_id:207810 Paenibacillus larvae C EF4156

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EU834247.1 gg_id:330648 Paenibacillus lautus str. DS19 EU8342
EU236729.1 gg_id:247052 Paenibacillus lautus str. X6 EU2367
EU249589.1 gg_id:251174 Paenibacillus sp. str. TPSB9 EU2495
AJ491842.1 gg_id:78091 Paenibacillus lautus str. C2 AJ4918
AB363733.1 gg_id:252320 Paenibacillus lautus str. NBRC 15380 AB3637
FJ974058.1 gg_id:382810 Paenibacillus lautus str. SK21 FJ9740
EF190498.1 gg_id:246384 Paenibacillus lentimorbus str. NRRL B-2521 EF1904
EF190499.1 gg_id:241813 Paenibacillus lentimorbus str. DNG 10 EF1904
EF190503.1 gg_id:238399 Paenibacillus lentimorbus str. DNG 16 EF1905
EU071599.1 gg_id:237117 Paenibacillus macerans str. EHFS1_S05Ta EU0715
EF459546.1 gg_id:205051 Paenibacillus macquariensis KFC-81 EF4595
AY230766.1 gg_id:84901 Paenibacillus massiliensis str. Smarlab BioMol-2301065 AY2307
AF353681.1 gg_id:51767 Paenibacillus naphthalenovorans str. PR-N1; ATCC BAA-206; DSM14203 AF3536
AF480935.1 gg_id:84099 Paenibacillus nematophilus str. NEM1a AF4809
EF190490.1 gg_id:239823 Paenibacillus popilliae str. Dutky 1S EF1904
EF190489.1 gg_id:250407 Paenibacillus popilliae str. NRRL B-2524 EF1904
DQ338445.1 gg_id:147610 Paenibacillus sabina str. T67 DQ338
DQ338447.1 gg_id:149770 Paenibacillus sabina str. JD2 DQ338
DQ338446.1 gg_id:147466 Paenibacillus sabina str. T49 DQ338
FJ973543.1 gg_id:418246 Paenibacillus sp. str. NBPP40 B40 FJ9735
GU321990.1 gg_id:568880 Paenibacillus stellifer str. Hp92 GU321
AJ316013.1 gg_id:48149 Paenibacillus stellifer str. IS1 AJ3160
EF690404.1 gg_id:255964 Paenibacillus terrae M1-4 EF6904
AJ318910.2 gg_id:77277 Paenibacillus terrae str. MH72 AJ3189
AJ297714.1 gg_id:42642 Paenibacillus sp. P15-9 AJ2977
AB073203.1 gg_id:78225 Paenibacillus validus str. JCM 9077 AB0732
AM900793.1 gg_id:249211 Paenibacillus sp. PA231 AM900
EU867345.1 gg_id:553260 Paenibacillus sp. str. CCGE3112 EU8673
AY837734.1 gg_id:141548 -Based Identification Midgut Field-Caught Anopheles gambiae Sensu Lato and . funes AY8377
AB092351.1 gg_id:71025 Paenibacillus fujiensis str. Br1 AB0923
DQ338448.1 gg_id:146263 Paenibacillus sabina str. G18-7 DQ338
EU257517.1 gg_id:268656 Paenibacillus ourofinensis str. AC13MSD EU2575
NR_028886.1 gg_id:579344 Paenibacillus graminis str. RSA19; ATCC BAA-95 NR_028
AM162329.1 gg_id:141176 Paenibacillus sp. L47 AM162
FN563205.1 gg_id:564674 Impact changing HRT OLR on prokaryotes involved biomethanizitaion and fuzzy logic FN5632
EU391155.1 gg_id:410549 Paenibacillus pueri str. b13i-1 EU3911
EF194764.2 gg_id:187176 Paenibacillus sp. str. FH2071 EF1947
AB162693.1 gg_id:122657 Paenibacillus sp. str. SH-55 AB1626
EF165014.1 gg_id:192432 Bacillus sp. str. PML14 EF1650
AB377108.1 gg_id:263427 Paenibacillus alvei str. AUG6 AB3771

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AY328609.1 gg_id:88221 drinking water system simulator clone HOClCi60 AY3286
AM930274.1 gg_id:571641 gradual cooling stage mass and its spatial composting clone SMG8 AM930
DQ346513.1 gg_id:154742 during composting libraries compost clone 2B29 DQ346
DQ129556.1 gg_id:138658 microarray level air two cities Texas urban aerosol clone AKIW1130 DQ129
AJ251193.1 gg_id:21436 Paenibacillus sp. str. TRO4 (=LMG 19081) AJ2511
GQ249618.1 gg_id:589407 Microbial anaerobic sediments Bay Cadiz (Spain) marine sediment: 18-20 cm layer cl GQ249
AM492794.1 gg_id:555079 Paenibacillus darangshiensis str. DSL-01 = JBRI 2110 AM492
EU257201.2 gg_id:278281 Paenibacillus riograndensis str. SBR5 EU2572
EF452662.1 gg_id:214602 Paenibacillus sp. str. DCY16 EF4526
AM900790.1 gg_id:235287 Paenibacillus sp. PA227 AM900
DQ816106.1 gg_id:166366 mouse cecum clone aaa87h04 DQ816
FN395280.1 gg_id:421089 Paenibacillus sp. str. FR-W5cb FN3952
GU272267.1 gg_id:535255 library dichlorvos treatment rape phyllosphere clone TF178 GU272
EU730934.1 gg_id:312510 Paenibacillus validus str. 197 EU7309
X77792.1 gg_id:14409 Bacillus viscosus str. ATCC 51155 X77792
AB045094.1 gg_id:99679 Paenibacillus pabuli str. HSCC 492T (NRRL NRS-924T) AB0450
DQ338444.1 gg_id:146742 Paenibacillus sabina str. T27 DQ338
EU571156.1 gg_id:276668 Paenibacillus sp. str. 11-5 EU5711
EU798300.1 gg_id:350178 Paenibacillus favisporus str. GXN153 EU7983
AY728023.1 gg_id:163477 Paenibacillus sp. str. H3029 AY7280
EU464732.1 gg_id:302066 Hartmann's mountain zebra feces clone AFZEB_aaj69h02 EU4647
FJ544322.1 gg_id:461651 Paenibacillus graminis str. 801 FJ5443
AY279193.1 gg_id:86920 Paenibacillus favisporus str. KNUC56 AY2791
EU464951.1 gg_id:300927 African elephant feces clone AFYEL_aaj65f10 EU4649
EU570250.1 gg_id:275303 Paenibacillus sp. str. CJ25 EU5702
EU003588.1 gg_id:235578 Paenibacillus sp. str. NCCB 100172 EU0035
EF690429.1 gg_id:243542 Paenibacillus sp. M9-2 EF6904
EU571197.1 gg_id:269962 Paenibacillus sp. str. 25-14 EU5711
AJ318909.2 gg_id:77280 MH21 earthworm gut AJ3189
AY559427.1 gg_id:202319 Hot Springs Taiwan hot spring water clone LS35 AY5594
EU240395.1 gg_id:245141 Paenibacillus amylolyticus str. B87 EU2403
AY326632.1 gg_id:136867 Amazon soil clone 43-1 AY3266
EU240394.1 gg_id:239112 Paenibacillus sp. str. B113 EU2403
AM745263.1 gg_id:243849 Paenibacillus caespitis str. LMG 23879 AM745
AJ131119.1 gg_id:14368 Paenibacillus sp. vortex AJ1311
AY772704.1 gg_id:110061 Paenibacillus polymyxa str. CP7 AY7727
EF025575.1 gg_id:185569 Paenibacillus ehimensis str. IB5 EF0255
DQ129332.1 gg_id:137603 urban aerosol clone AKIW967 DQ129
DQ407277.1 gg_id:156397 Paenibacillus sp. str. PALXIL02 DQ407
AM906087.1 gg_id:252504 Paenibacillus sp. str. P117 AM906

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AB073189.1 gg_id:78298 Paenibacillus glucanolyticus str. DSM 5162 AB073
EU249588.1 gg_id:237405 Paenibacillus sp. str. DFVB13 EU249
GQ244430.1 gg_id:579358 Paenibacillus sp. str. R2 GQ244
GQ007872.1 gg_id:501793 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ007
DQ272469.1 gg_id:141630 Paenibacillus sp. str. ADC2 DQ272
EU134647.1 gg_id:252877 tallgrass prarie soil clone FFCH14175 EU134
DQ291142.1 gg_id:142876 Paenibacillus sepulcri str. CCM 7311; LMG 19508 DQ291
FJ432004.1 gg_id:366723 Paenibacillus chibensis str. ZYb3 FJ4320
EF690424.1 gg_id:240189 Paenibacillus sp. M10-6 EF6904
GQ476810.2 gg_id:578500 Paenibacillus sp. str. R172 GQ476
AF071860.1 gg_id:14395 Paenibacillus popilliae str. NRRL B-4081 AF071
AY592793.1 gg_id:103973 deep-sea mud volcano clone Napoli-4B-79; BC07-4B-79 AY592
AF130254.1 gg_id:42610 Paenibacillus koreensis str. YC300 AF130
AY302187.1 gg_id:90699 Paenibacillus polymyxa str. BS04 AY302
DQ816367.1 gg_id:168948 mouse cecum clone aab17b06 DQ816
EF620476.1 gg_id:247159 Paenibacillus polymyxa str. ISSDS-307 EF6204
AB042938.1 gg_id:43825 Paenibacillus glycanilyticus str. DS-1 AB042
AB294155.1 gg_id:210271 Paenibacillus sp. str. BS2 AB294
GU187433.1 gg_id:569728 Paenibacillus sp. str. CAU 9324 GU187
AY289501.2 gg_id:100104 Paenibacillus sp. IDA4508 AY289
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AJ576374.1 gg_id:99041 midgut homogenate Pachnoda ephippiata larva clone PeM01 AJ5763
GQ497919.1 gg_id:586156 Paenibacillus sp. str. KO_CM21 GQ497
AJ863291.1 gg_id:120989 poplar tree microcosm rhizosphere unflooded clone 4RHU38 AJ8632
AB073192.1 gg_id:78185 Paenibacillus illinoisensis str. JCM 9907 AB073
GQ202679.1 gg_id:577284 Paenibacillus sp. str. U4 STR GQ202
AM162295.1 gg_id:143576 Paenibacillus sp. 6M20 AM162
AF480934.1 gg_id:84499 Paenibacillus sp. str. NEM3 AF480
EU722403.1 gg_id:342726 Paenibacillus sp. str. 13-4-17 EU722
AB119649.2 gg_id:94822 Paenibacillus abekawaensis str. MG1 AB119
FJ542823.1 gg_id:520512 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone A FJ5428
AY382189.1 gg_id:98371 Paenibacillus sp. str. R-7652 AY382
EF212892.1 gg_id:272047 Paenibacillus urinalis str. 5402403 EF2128
AM745265.1 gg_id:258150 Paenibacillus telluris str. LMG 23881T AM745
AM162324.1 gg_id:143178 Paenibacillus sp. HO2-R17 AM162
GU080334.1 gg_id:539906 Paenibacillus sp. str. XP13 GU080
AY266990.1 gg_id:86275 Paenibacillus sp. str. 448-L5 AY266
AB179866.1 gg_id:99385 Paenibacillus sp. str. SG AB179
AF515611.1 gg_id:64883 Paenibacillus polymyxa str. GBR-1 AF5156

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DQ407283.1 gg_id:151967 Paenibacillus sp. str. PALXIL11 DQ407
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EU134664.1 gg_id:257557 tallgrass prarie soil clone FFCH7932 EU134
AF355463.1 gg_id:42808 Paenibacillus polymyxa AF355
DQ836314.1 gg_id:166697 Paenibacillus validus str. S3 DQ836
DQ890521.1 gg_id:163114 Paenibacillus taiwanensis str. BCRC 17411 DQ890
AF164345.1 gg_id:46987 Paenibacillus chinjuensis str. WN9 AF1643
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AB111937.2 gg_id:100108 Paenibacillus sp. str. A63 AB111
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EF079062.1 gg_id:179040 Paenibacillus donghaensis str. JH 8 EF079
AF395028.1 gg_id:38098 Paenibacillus sp. str. C15 AF395
AJ229199.1 gg_id:50002 anoxic bulk soil flooded rice microcosm clone BSV44 clone AJ2291
AF006077.1 gg_id:14405 Bacillus mucilaginosus str. 1480D AF006
AM162334.1 gg_id:141122 Paenibacillus sp. YN08-04 AM162
GQ058441.1 gg_id:430478 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1 GQ058
EU464831.1 gg_id:289481 Hartmann's mountain zebra feces clone AFZEB_aaj71f03 EU464
GQ476811.2 gg_id:546073 Paenibacillus sp. str. R12-2 GQ476
EF127602.1 gg_id:207635 Fossil Genes and Microbes Entombed Oldest Ice on Earth ice clone EME078 EF1276
EU571139.1 gg_id:263497 Paenibacillus sp. str. 3-1 EU571
EU888525.1 gg_id:334762 Paenibacillus sp. str. FR1_23 EU888
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AF468220.1 gg_id:110511 Paenibacillus sp. 1 AF468
NR_025754.1 gg_id:574476 Paenibacillus sanguinis str. 2301083; CCUG 48214 NR_02
DQ816668.1 gg_id:165977 mouse cecum clone aaa97a09 DQ816
AY167820.1 gg_id:77386 Paenibacillus sp. str. SAFN-007 AY167
NR_029109.1 gg_id:563078 Paenibacillus xylanilyticus str. XIL14; LMG 21957 NR_02
DQ085279.1 gg_id:137505 Paenibacillus ruminocola str. G22 DQ085
DQ125886.1 gg_id:134126 uranium contaminated soil clone AKAU4139 DQ125
FJ040809.1 gg_id:572351 Paenibacillus macerans str. HR13 FJ0408
AM162300.1 gg_id:143828 Paenibacillus sp. F11 AM162
X77846.1 gg_id:14423 Paenibacillus durus str. DSM 1735 X77846
AB362821.1 gg_id:241963 Paenibacillus sp. str. YT0003 AB362

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AJ011321.1 gg_id:14375 Paenibacillus borealis KM8 AJ0113
AY397766.1 gg_id:96549 Paenibacillus sp. str. R-6466 AY3977
EU464438.1 gg_id:288992 African elephant feces clone AFEL_aai29b10 EU4644
AB045097.1 gg_id:100154 Bacillus sp. str. HSCC 1649T (IK-5) AB0450
EF620469.1 gg_id:245314 Paenibacillus polymyxa str. ISSDS-795 EF6204
EU379277.1 gg_id:270084 Paenibacillus pabuli str. 4RS-1a EU3792
EU249590.1 gg_id:257331 Paenibacillus xylanilyticus str. DPBS5 EU2495
DQ338443.1 gg_id:145299 Paenibacillus forsythia str. T98 DQ338
GU328687.1 gg_id:566956 Paenibacillus sp. str. Nz32 GU328
GQ423056.1 gg_id:557058 Paenibacillus sp. str. S22 GQ423
AB073363.1 gg_id:77737 Paenibacillus kobensis str. DSM 10249 AB0733
GQ355278.1 gg_id:590264 Paenibacillus sp. str. GT-L27 GQ355
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AB482199.1 gg_id:553697 Paenibacillus abekawaensis str. MG1 (= DSM 16939 = NBRC 100733) AB4821
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EU134644.1 gg_id:257088 tallgrass prarie soil clone FFCH13623 EU1346
EF626690.1 gg_id:240072 Paenibacillus sp. str. CKOBP-6 EF6266
AJ000984.2 gg_id:14396 soil clone DA116 AJ0009
AB073197.1 gg_id:77646 Paenibacillus thiaminolyticus str. IFO 15656 AB0731
AB366401.1 gg_id:277860 Paenibacillus pabuli str. SW12 AB3664
AM162321.1 gg_id:141438 Paenibacillus sp. HS16-12 AM162
NR_025106.1 gg_id:548770 Paenibacillus brasilensis str. PB1 72; ATCC BAA-413 NR_025
GU213302.1 gg_id:588836 Paenibacillus sp. str. 4-10 GU213
AB362822.1 gg_id:248417 Paenibacillus sp. str. YT0011 AB3628
GQ284368.1 gg_id:573503 Paenibacillus barengoltzii str. THWCSN26 GQ284
FN673694.1 gg_id:517700 Paenibacillus anaericanus str. DSM 15890 FN6736
EU331367.1 gg_id:242588 Influence Nitrate on Microbial Reduction Pertechnetate nitrate microcosm sediment EU3313
FN293173.1 gg_id:543248 Paenibacillus sp. str. MC-246 FN2931
EU373421.1 gg_id:273400 Paenibacillus polymyxa str. YRL13 EU3734
DQ023221.2 gg_id:132196 Paenibacillus sp. str. GPTSA 19T DQ023
DQ309072.1 gg_id:150196 Paenibacillus soli str. DCY03 DQ309
EU497637.1 gg_id:259802 Paenibacillus sp. str. Dg-1009 EU4976
EF016794.1 gg_id:251102 Hyper-Arid Atacama Desert Soils soil clone A2B-E3-114 EF0167
GQ015526.1 gg_id:494140 Topographical and Temporal Human Skin Microbiome skin back clone nbw817f06c1 GQ015
AB045102.1 gg_id:104520 Paenibacillus ehimensis str. HSCC 594 (IFO 15658) AB0451
AF537343.3 gg_id:104054 Bacillus sp. str. MZLU AF5373
GU457786.1 gg_id:520530 Paenibacillus sp. str. R1-12-4 GU457
AM162305.1 gg_id:142343 Paenibacillus sp. A26 AM162
EU661711.1 gg_id:285693 Paenibacillus ehimensis str. NBRAJATH7 EU6617
EF125184.1 gg_id:188416 Paenibacillus sp. str. SA-7-6 EF1251

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AJ716019.1 gg_id:100354 Paenibacillus barcinonensis str. BP-23 AJ7160
AB245383.1 gg_id:146833 Paenibacillus ginsengagri str. Gsoil 3125 AB2453
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EU647520.1 gg_id:545572 Paenibacillus sp. str. TeW EU6475
FN563170.1 gg_id:582506 Impact changing HRT OLR on prokaryotes involved biomethanizitaion and fuzzy logic FN5631
AM162341.1 gg_id:141288 Paenibacillus sp. GR13-04 AM162
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EU571189.1 gg_id:260618 Paenibacillus sp. str. 23-13 EU5711
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AJ863305.1 gg_id:119660 poplar tree microcosm rhizosphere unflooded clone 16RHU11 AJ8633
AJ223990.1 gg_id:14384 Paenibacillus odorifer str. TOD45 AJ2239
AM162322.1 gg_id:141541 Paenibacillus sp. YO4-02 AM162
AF290916.1 gg_id:28736 Paenibacillus daejeonensis str. AP-20 AF2909
EU638756.1 gg_id:353899 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU6387
DQ444985.1 gg_id:158562 Paenibacillus sp. Eur1 9.25 DQ444
EF682937.1 gg_id:245965 Eastern Mediterranean atmosphere clone F12_5F_FL EF6829
FJ479476.1 gg_id:573137 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4794
AB369185.1 gg_id:240501 Microbiological Assessment Circulation Mud Fluids During First Operation Drilling De AB3691
GU214173.1 gg_id:534180 and biota slimes Canadian paper mills slime mill taken wet section around papermal GU214
EF208754.1 gg_id:200803 Paenibacillus sp. str. Ao3 EF2087
FJ859876.1 gg_id:574741 Paenibacillus sp. str. MSL-9 FJ8598
AF492843.1 gg_id:67227 Bacillus sp. str. NK395 AF4928
AB271758.1 gg_id:170195 Paenibacillus polymyxa str. NBRC 15309 AB2717
FJ999582.1 gg_id:410196 Paenibacillus sp. str. HLSBA1 FJ9995
AB362823.1 gg_id:246316 Paenibacillus sp. str. YT0039 AB3628
AF465647.1 gg_id:34110 Bacillus sp. str. YNPRH6P-1 AF4656
DQ816052.1 gg_id:163426 mouse cecum clone aaa86f09 DQ816
EF694702.1 gg_id:235485 Paenibacillus terrae EH23-5 EF6947
FN433032.1 gg_id:533274 Paenibacillus alvei CCM2B FN4330
GQ074220.1 gg_id:392310 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ074
AM991254.1 gg_id:277951 Microbial groundwater and their potential use biomonitoring karst spring water clo AM991
EU867347.1 gg_id:545107 Paenibacillus sp. str. CCGE3115 EU8673
GU214160.1 gg_id:587713 and biota slimes Canadian paper mills slime mill taken wet section around papermal GU214
AJ011327.1 gg_id:14381 Paenibacillus borealis HM31 AJ0113
AY493972.1 gg_id:136753 Fingerprinting aggregates soil clone 449 AY4939
EU465045.1 gg_id:296852 African elephant feces clone AFYEL_aaj67b11 EU4650

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EU046270.1 gg_id:236825 Paenibacillus xinjiangensis str. HR1 EU0462
AY839866.1 gg_id:110036 Paenibacillus sp. str. B518 AY8398
DQ346553.1 gg_id:154746 during composting libraries compost clone 2B39 DQ346
EU134635.1 gg_id:237941 tallgrass prarie soil clone FFCH12118 EU1346
AB041721.1 gg_id:50544 Paenibacillus koleovorans str. TK AB0417
GQ015112.1 gg_id:494553 Topographical and Temporal Human Skin Microbiome skin back clone nbw816b06c1 GQ015
DQ787687.1 gg_id:172955 holocene lake sediment clone SLB315 DQ787
DQ129261.1 gg_id:137642 urban aerosol clone AKIW887 DQ129
AJ005795.1 gg_id:14413 Thermobacillus xylanilyticus str. XE AJ0057
GQ471930.1 gg_id:551611 Toward Plant Cell Wall Degradation Under Thermophilic Condition: Unique Microbia GQ471
AB234269.1 gg_id:148244 Biotransformation Polychlorinated Dioxins Microbial Dynamics Sediment Microcosm AB2342
FJ478798.1 gg_id:590559 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4787
AF375881.1 gg_id:38647 Pasteuria penetrans AF3758
AF516396.1 gg_id:86730 Pasteuria nishizawae str. Tohoku AF5163
AJ878853.1 gg_id:111838 Pasteuria hartismerei AJ8788
AF254387.1 gg_id:44324 Candidatus Pasteuria usgae S-1 AF2543
AF515699.1 gg_id:87218 Pasteuria goettingianae AF5156
U34688.1 gg_id:14343 Daphnia endosymbiotic bacterium U34688
GQ448221.1 gg_id:589624 Microbiome neonatal calves: shedding microorganisms fecal clone calf32_10wks_gr GQ448
GU385871.1 gg_id:522968 Bacillus psychrodurans str. QT25 GU385
AM980508.1 gg_id:269916 Bacillus insolitus str. DSM 5T AM980
AY030325.1 gg_id:18100 Bacillus sp. str. KL-024 AY0303
EU240419.1 gg_id:254377 Bacillus psychrodurans str. B169 EU2404
EU778690.1 gg_id:345702 Springbok feces clone SBK_e12_1 EU7786
EF377312.1 gg_id:203909 Bacillus sp. str. CCBAU 10775 EF3773
EU458350.1 gg_id:292185 spotted hyena feces clone HY1_b04 EU4583
AB017538.1 gg_id:15018 Renibacterium salmoninarum AB0175
EU249570.1 gg_id:243498 Bacillus sp. str. TSG11 EU2495
EF377302.1 gg_id:204730 Bacillus sp. str. CCBAU 13244 EF3773
EU249572.1 gg_id:237395 Bacillus sp. str. DFVB3 EU2495
AY536564.1 gg_id:103433 Bacillus psychrodurans str. WED2.3 AY5365
X70321.1 gg_id:14997 Kurthia zopfii str. NCIMB 9878 X70321
AB271741.1 gg_id:172747 Kurthia sibirica str. NBRC 101530 AB2717
AB199593.2 gg_id:119659 Bacillus borotolerans str. T-12B AB1995
AF169518.1 gg_id:74854 Bacillus sp. str. BD-83 AF1695
FM178866.1 gg_id:330655 Acetobacter pasteurianus str. CCM 3612 FM178
GQ280058.1 gg_id:592898 Bacillus sp. str. BJ-48 GQ280
EU867354.1 gg_id:543461 Lysinibacillus fusiformis str. CCGE2086 EU8673
GQ496620.1 gg_id:592278 Lysinibacillus sphaericus str. DMT-7 GQ496
L14016.1 gg_id:14980 Bacillus sphaericus L14016

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EU187497.1 gg_id:257140 Lysinibacillus sphaericus str. X-17 EU187
EU252508.1 gg_id:238118 Bacillus sp. str. AM20 EU252
GU129144.1 gg_id:588459 Lysinibacillus sphaericus str. TMB5 GU129
AF169523.1 gg_id:42176 Bacillus sp. str. BD-94 AF169
GU385849.1 gg_id:522769 Acetobacter pasteurianus str. QT3 GU385
GQ501071.1 gg_id:549791 Lysinibacillus fusiformis str. Ma-Su CECRI 2 GQ501
GQ284348.1 gg_id:580342 Lysinibacillus fusiformis str. PCWCS3 GQ284
DQ289063.1 gg_id:144100 Bacillus macroides WST 1 DQ289
L38654.1 gg_id:14988 Bacillus sphaericus L38654
GU084135.1 gg_id:540739 Lysinibacillus fusiformis str. DB-1 GU084
GQ280094.1 gg_id:585121 Bacillus sp. str. JS-24 GQ280
FJ266320.1 gg_id:509099 Lysinibacillus sphaericus str. RFNB10 FJ2663
EU240383.1 gg_id:248547 Lysinibacillus sphaericus str. B85 EU240
EU647711.1 gg_id:273725 Lysinibacillus fusiformis str. REG60 EU647
EU855791.1 gg_id:346402 Lysinibacillus sphaericus Drngp EU855
GQ889259.1 gg_id:569561 Lysinibacillus sphaericus str. S8 GQ889
DQ990064.1 gg_id:195474 Microbial Profiling Some Heterotrophic isolates Waters and Shal Groundwater Wells DQ990
AB199591.2 gg_id:123207 Bacillus borotolerans str. T-10a AB199
GQ284508.1 gg_id:540272 Lysinibacillus sp. str. TSSAS2-47 GQ284
GU201856.1 gg_id:529798 Lysinibacillus fusiformis str. Zw-13-3 GU201
AJ237708.1 gg_id:14648 Marinibacillus marinus str. DSM 1297 AJ2377
EU812465.1 gg_id:326668 Bacillus sp. str. B-9987 EU812
AY190535.1 gg_id:79732 Marinibacillus campisalis str. SF-57 AY190
AF281158.1 gg_id:28627 Jeotgalibacillus alimentarius str. YKJ-13 AF281
FJ263020.1 gg_id:367827 Sporosarcina sp. str. ZD30 FJ2630
DQ444983.1 gg_id:157780 Sporosarcina sp. Eur1 9.21 DQ444
FJ999934.1 gg_id:562449 Paenisporosarcina macmurdoensis str. EQH5 FJ9999
AF237975.1 gg_id:73281 Planococcus citreus str. MS20 AF237
FJ373028.1 gg_id:354487 Planococcus citreus str. W2-3 FJ3730
NR_026090.1 gg_id:544445 Planococcus citreus str. NCIMB 1493 NR_02
AJ966515.2 gg_id:119206 Planococcus columbaii str. PgEx11 AJ9665
EF467308.1 gg_id:215171 Planococcus maitriensis str. Anita I EF4673
FJ675069.1 gg_id:518131 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6750
AJ544622.1 gg_id:81178 Planococcus maitriensis str. S1 AJ5446
AM412216.1 gg_id:178613 Planococcus rifietoensis Z19-1zhy AM412
GQ129917.1 gg_id:406391 Genetic inventory 'JPL-SAF' during MSL mission spacecraft assembly clean room floc GQ129
EU652853.1 gg_id:281832 Planococcus sp. str. ZY002 EU652
AM411996.1 gg_id:191228 Planococcus rifietoensis Z19-2zhy AM411
AJ314745.1 gg_id:29551 Planococcus antarcticus str. CMS 26or AJ3147
AJ314747.1 gg_id:37775 Planococcus antarcticus str. CMS 84or AJ3147

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DQ084464.1 gg_id:132599 Planomicrobium sp. str. CSS-3 DQ084
AM111009.1 gg_id:140923 Planococcus sp. str. 3059 AM111
DQ435614.1 gg_id:154002 Planococcus sp. str. L4 DQ435
EU362181.1 gg_id:324748 Paenibacillus sp. str. C8 EU362
FJ717184.1 gg_id:534668 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United Kingc FJ7171
AY771711.1 gg_id:108687 Planococcus psychrotoleratus str. S2-46 AY7717
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AY538695.1 gg_id:103548 Planococcus sp. str. Smarlab 3302355 AY5386
EU845048.1 gg_id:321091 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8450
AY437845.1 gg_id:101657 Planococcus stackebrandtii str. K22-03 AY4378
AJ697862.1 gg_id:103823 Planomicrobium novatatis str. 3-12 AJ6978
AY771727.1 gg_id:143378 Planococcus psychrotoleratus S3-21 AY7717
EU036220.1 gg_id:243814 Planomicrobium sp. str. 0423 EU0362
AY260168.1 gg_id:87474 Planococcus kazaiensis str. K01-30 AY2601
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AF169531.1 gg_id:39697 Bacillus pycnus str. NRS-1691 AF1695
GU001896.1 gg_id:590554 Rummeliibacillus stabekisii str. PL71 GU001
EU468086.1 gg_id:289850 cheetah feces clone CE2_e08_3 EU4680
FJ675233.1 gg_id:517131 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6752
EU773781.1 gg_id:324889 Cheetah feces clone CE2_f11_1 EU7737
EU467969.1 gg_id:289010 cheetah feces clone CE2_c09_1 EU4679
FJ671794.1 gg_id:515670 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6717
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EU266058.1 gg_id:279405 Bacillus sp. str. SL170 EU2660
AF169519.1 gg_id:35115 Bacillus sp. str. BD-85 AF1695
EU776120.1 gg_id:316126 Spotted hyena feces clone HY1_h08_1 EU7761
EU794212.1 gg_id:330402 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_R41 EU7942
EU867363.1 gg_id:574930 Solibacillus silvestris str. CCGE2032 EU8673
EU464938.1 gg_id:302898 African elephant feces clone AFYEL_aaj65e03 EU4649
EU366378.1 gg_id:273023 Bacillus silvestris str. IV13 EU3663
FJ379320.1 gg_id:555419 Bacillus sp. str. KHg2 FJ3793

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EU466752.1 gg_id:298191 African elephant feces clone AFEL2_aao29a02 EU466
EU467027.1 gg_id:298756 African elephant feces clone AFEL2_aao32h06 EU467
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EU464646.1 gg_id:297510 African elephant feces clone AFEL_aai32e01 EU464
EU466769.1 gg_id:291375 African elephant feces clone AFEL2_aao29c04 EU466
X70319.1 gg_id:14991 Caryophanon latum str. NCDO 2034 X70319
EU466938.1 gg_id:296817 African elephant feces clone AFEL2_aao31f02 EU466
GQ448631.1 gg_id:562030 Microbiome neonatal calves: shedding microorganisms fecal clone calf784_6wks_gr GQ448
FJ676958.1 gg_id:514467 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6769
EU458326.1 gg_id:295839 spotted hyena feces clone HY1_e04 EU458
EU466850.1 gg_id:300468 African elephant feces clone AFEL2_aao30d02 EU466
EU466880.1 gg_id:290915 African elephant feces clone AFEL2_aao30g07 EU466
EU464508.1 gg_id:289686 African elephant feces clone AFEL_aai30d01 EU464
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EU466764.1 gg_id:287843 African elephant feces clone AFEL2_aao29b09 EU466
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EU467023.1 gg_id:296178 African elephant feces clone AFEL2_aao32h01 EU467
EU458363.1 gg_id:303075 spotted hyena feces clone HY1_d11_1 EU458
FJ683349.1 gg_id:524261 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6833
EU466929.1 gg_id:300324 African elephant feces clone AFEL2_aao31e01 EU466
FJ683448.1 gg_id:526268 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6834
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EU466807.1 gg_id:297158 African elephant feces clone AFEL2_aao29g03 EU466
EU465903.1 gg_id:303066 African elephant feces clone AFEL3_aao13g06 EU465
EU465955.1 gg_id:302347 African elephant feces clone AFEL3_aao14g03 EU465
EU466959.1 gg_id:295052 African elephant feces clone AFEL2_aao31h03 EU466
EU466899.1 gg_id:291942 African elephant feces clone AFEL2_aao31a10 EU466
EU466051.1 gg_id:290668 African elephant feces clone AFEL3_aao16f08 EU466
AJ491302.1 gg_id:64192 Caryophanon latum str. DSM 14151 AJ4913
EU466806.1 gg_id:290595 African elephant feces clone AFEL2_aao29g02 EU466
EU466995.1 gg_id:294075 African elephant feces clone AFEL2_aao32d11 EU466
FJ227504.1 gg_id:304321 Identification unculturable species growing sugarcane molasses based distillery spent FJ2275
EU466017.1 gg_id:297626 African elephant feces clone AFEL3_aao15h09 EU466
AM934693.1 gg_id:274290 Bacillus sp. str. CL1.8 AM934

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EU466831.1 gg_id:290295 African elephant feces clone AFEL2_aao30a11	EU466
DQ824578.1 gg_id:194282 human fecal clone RL185_aaj69h06	DQ824
EF371373.1 gg_id:210245 Bacillus sp. str. ge09	EF3713
AB196468.1 gg_id:109827 Bacillus sp. str. FST-B30	AB196
FJ973540.1 gg_id:378451 Bacillus ginsengi str. NBPP103 B103	FJ9735
AY167819.1 gg_id:77326 Sporosarcina aquimarina str. SAFN-008	AY167
FJ944660.1 gg_id:579648 Sporosarcina aquimarina str. KUDC1038	FJ9446
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EU468034.1 gg_id:292404 cheetah feces clone CE2_f04_1	EU468
EF459543.1 gg_id:216487 Sporosarcina globispora KFC-52	EF4595
X54968.1 gg_id:15012 Sporosarcina psychrophila str. W16A	X54968
X54969.1 gg_id:15013 Sporosarcina psychrophila str. W5	X54969
EU939438.1 gg_id:356519 Fecal wild pygmy loris feces clone WF16S_292	EU939
DQ337594.1 gg_id:149329 Bacillus sp. CHNTR52	DQ337
D16277.1 gg_id:15015 Sporosarcina psychrophila str. IAM 12468	D1627
EU308121.1 gg_id:237733 Sporosarcina ginsengisoli str. FT7	EU308
AF548880.1 gg_id:55578 Bacillus sp. str. CPB 9	AF548
AM237400.1 gg_id:153553 Sporosarcina globispora OS-253	AM237
EU308120.1 gg_id:252542 Sporosarcina aquimarina str. FT1	EU308
AY167816.1 gg_id:77347 Filibacter limicola str. SAFN-012	AY167
AF548874.1 gg_id:57755 Bacillus sp. str. CPB 2	AF548
AJ831845.1 gg_id:107690 Bacillus sp. str. 41KF1	AJ8318
FJ894720.1 gg_id:574272 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota BME; ear p	FJ8947
X68415.1 gg_id:15008 Sporosarcina globispora str. DSM 4	X68415
AJ292316.1 gg_id:51589 Filibacter limicola str. DSM 13886T	AJ2923
EU369157.1 gg_id:330035 libraries oyster shell clone MBHOS-08	EU369
EU465852.1 gg_id:288698 African elephant feces clone AFEL3_aao13a02	EU465
EU464548.1 gg_id:289526 African elephant feces clone AFEL_aai30h06	EU464
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EU464560.1 gg_id:290883 African elephant feces clone AFEL_aai31a10	EU464
EU464504.1 gg_id:295722 African elephant feces clone AFEL_aai30c07	EU464
EU464652.1 gg_id:294019 African elephant feces clone AFEL_aai32e10	EU464
EU464510.1 gg_id:299366 African elephant feces clone AFEL_aai30d05	EU464
EU464562.1 gg_id:300541 African elephant feces clone AFEL_aai31a12	EU464
EU464545.1 gg_id:302644 African elephant feces clone AFEL_aai30h01	EU464
GU125639.1 gg_id:573715 Lysinibacillus sphaericus str. IMAU80223	GU125
EU464677.1 gg_id:296988 African elephant feces clone AFEL_aai32h12	EU464
AJ863177.1 gg_id:123425 poplar tree microcosm bulk soil unflooded clone 20BSU17	AJ8631
EU771773.1 gg_id:352179 African elephant feces clone AFYEL_aaj65e04	EU771

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AB547124.1 gg_id:523827 Bacillus sp. str. NCCP-36 AB5471
EU464503.1 gg_id:299250 African elephant feces clone AFEL_aai30c05 EU4645
EU465114.1 gg_id:291402 African elephant feces clone AFYEL_aaj68c06 EU4651
AM888194.1 gg_id:256287 Bacillus sp. str. TSWCSN5 AM888
EU464435.1 gg_id:289502 African elephant feces clone AFEL_aai29b05 EU4644
EU464428.1 gg_id:303291 African elephant feces clone AFEL_aai29a09 EU4644
EU464595.1 gg_id:294723 African elephant feces clone AFEL_aai31e08 EU4645
EU223959.1 gg_id:247009 -RFLP microbes Qinghai-Tin rail soil clone 142 EU2239
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EU464637.1 gg_id:290772 African elephant feces clone AFEL_aai32d01 EU4646
AB245381.1 gg_id:147870 Sporosarcina ginsengisoli str. Gsoil 1433 AB2453
EU464521.1 gg_id:293562 African elephant feces clone AFEL_aai30e07 EU4645
EU465008.1 gg_id:290826 African elephant feces clone AFYEL_aaj66f03 EU4650
AB243859.1 gg_id:252210 Sporosarcina saromensis str. HG645 AB2438
AY372918.1 gg_id:141968 Bacillus sp. str. PC2 AY3729
EU464628.1 gg_id:294015 African elephant feces clone AFEL_aai32b05 EU4646
EU464656.1 gg_id:298694 African elephant feces clone AFEL_aai32f04 EU4646
FJ681965.1 gg_id:530313 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6819
EU128488.1 gg_id:248552 Bacillus sp. str. CWBI B1434 EU1284
EU771617.1 gg_id:344433 African elephant feces clone AFEL2_aao31a11 EU7716
DQ125520.1 gg_id:134154 uranium contaminated soil clone AKAU3481 DQ125
EU464620.1 gg_id:290547 African elephant feces clone AFEL_aai32a04 EU4646
EU464601.1 gg_id:297706 African elephant feces clone AFEL_aai31f03 EU4646
AM180748.1 gg_id:147511 Planococcus citreus UC15 AM180
EU465860.1 gg_id:299202 African elephant feces clone AFEL3_aao13b02 EU4658
EU464657.1 gg_id:301998 African elephant feces clone AFEL_aai32f06 EU4646
AF500007.1 gg_id:66683 Planococcus maritimus str. TF-9 AF5000
DQ345467.1 gg_id:151317 during composting libraries compost clone 0B14 DQ345
EU458324.1 gg_id:300849 spotted hyena feces clone HY1_d11 EU4583
AY677116.1 gg_id:138589 Bacillus massiliensis str. 4400831 AY6771
EU464967.1 gg_id:302579 African elephant feces clone AFYEL_aaj65h11 EU4649
EU778726.1 gg_id:306956 Springbok feces clone SBK_g04_1 EU7787
EU771809.1 gg_id:313253 African elephant feces clone AFEL3_aao14a04 EU7718
FJ348029.1 gg_id:324182 Bacillus sp. str. GGC-P15A2b FJ3480
EU465862.1 gg_id:299731 African elephant feces clone AFEL3_aao13b04 EU4658
EU771667.1 gg_id:318825 African elephant feces clone AFEL_aai30b08 EU7716
EU466815.1 gg_id:301287 African elephant feces clone AFEL2_aao29g12 EU4668
EF675626.1 gg_id:247834 Bacillus sp. str. RM1A EF6756
EU464648.1 gg_id:287337 African elephant feces clone AFEL_aai32e03 EU4646

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EU771613.1 gg_id:319678 African elephant feces clone AFEL_aai31g11 EU7716
EU775992.1 gg_id:323455 Spotted hyena feces clone HY1_h06_3 EU7759
EU469346.1 gg_id:303364 springbok feces clone SBK_b03 EU4693
EU465873.1 gg_id:295003 African elephant feces clone AFEL3_aao13d02 EU4658
EU465924.1 gg_id:294077 African elephant feces clone AFEL3_aao14b11 EU4659
EU467924.1 gg_id:300689 cheetah feces clone CE2_c04 EU4679
DQ350822.1 gg_id:147600 Bacillus massiliensis str. 625 DQ350
DQ350820.1 gg_id:149022 Bacillus sphaericus str. 601 DQ350
FJ373039.2 gg_id:328019 Bacillus sp. str. S7-3 FJ3730
EU464583.1 gg_id:288939 African elephant feces clone AFEL_aai31d02 EU4645
EU464640.1 gg_id:291198 African elephant feces clone AFEL_aai32d04 EU4646
EF503617.1 gg_id:223021 Bacillus sp. str. ge12 EF5036
EU464615.1 gg_id:302384 African elephant feces clone AFEL_aai31h04 EU4646
AF506059.1 gg_id:66290 Sporosarcina sp. LCSAOTU9 AF5060
GU457789.1 gg_id:520283 Bacillus sp. str. 5M55 GU457
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EU464579.1 gg_id:290738 African elephant feces clone AFEL_aai31c09 EU4645
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EU464447.1 gg_id:302696 African elephant feces clone AFEL_aai29c10 EU4644
FJ681317.1 gg_id:520320 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6813
FJ682537.1 gg_id:515638 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6825
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DQ351921.1 gg_id:168183 manganese oxidation soil clone JH-GY13 DQ351
AM295339.1 gg_id:323201 Crocinobacterium jejui str. SW2G-14 AM295
EU464457.1 gg_id:293528 African elephant feces clone AFEL_aai29d11 EU4644
EF061442.1 gg_id:193195 Bacillus sp. NJSN49 EF0614
DQ346545.1 gg_id:156055 during composting libraries compost clone 2B31 DQ346
AM888182.1 gg_id:240670 Bacillus sp. str. TSWCSN8 AM888
AB170018.1 gg_id:104224 Ureibacillus sp. MM122 AB1700
AM932266.1 gg_id:272689 Ureibacillus sp. str. S22-30 AM932
AB375754.1 gg_id:340308 Bacillus sp. str. 50LAy-1 AB3757
NR_025394.1 gg_id:533566 Ureibacillus terrenus str. DSM 12654 TH9A NR_025
DQ348072.1 gg_id:149858 Ureibacillus koreensis str. HC 148 DQ348
DQ348071.1 gg_id:148390 Ureibacillus rudaensis str. HC 145 DQ348
AJ002154.1 gg_id:15001 Bacillus sp. str. TP-84 AJ0021
AY850379.1 gg_id:112646 Ureibacillus sp. 6T19 AY8503
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EF690414.1 gg_id:245684 Bacillus arenosi M18-3 EF6904
EU741070.1 gg_id:548314 Viridibacillus arenosi str. 13630P EU741
NR_025628.1 gg_id:542641 Viridibacillus arenosi str. LMG 22166 NR_02
AJ627211.1 gg_id:101984 Bacillus arvi str. LMG 22165 AJ6272
AF169520.1 gg_id:48079 Bacillus neidei str. BD-87 AF1695
AJ535733.1 gg_id:91416 Bacillus sp. str. US149 AJ5357
AB021193.1 gg_id:26043 Bacillus naganoensis str. ATCC53909 AB021
D16288.1 gg_id:14489 Sporolactobacillus inulinus str. IAM 12384 D16288
D16287.1 gg_id:14484 Sporolactobacillus kofuensis str. M18 D16287
D16285.1 gg_id:14478 Sporolactobacillus laevis str. IAM 12387 D16285
AB374522.1 gg_id:269392 Sporolactobacillus sp. str. QC81-06 AB3745
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D16290.1 gg_id:14491 Sporolactobacillus terrae str. IAM 12395 D16290
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AB231785.1 gg_id:154718 Tuberibacillus calidus str. 606b AB2317
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FJ674640.1 gg_id:526461 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6746
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EU194336.1 gg_id:243071 Jeotgalicoccus psychrophilus str. XJUHX-36 EU1943
EU583727.1 gg_id:266449 Jeotgalicoccus sp. str. JSM 076033 EU5837
AY028925.1 gg_id:44574 Jeotgalicoccus halotolerans str. YKJ-101 AY0289
FJ675373.1 gg_id:525451 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6753
FJ674485.1 gg_id:528297 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6744
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Y15711.1 gg_id:14905 Macrococcus caseolyticus str. ATCC 13548 Y15711
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Y15714.1 gg_id:14908 Macrococcus bovicus str. L2F4 Y15714
AM237362.1 gg_id:154444 Macrococcus equipercicus OS-58.a2 AM237
AB079788.1 gg_id:61797 Micrococcus luteus B-P 26 AB0797
AY119685.1 gg_id:64394 Macrococcus hajekii str. CCM 4809 AY1196
Y15713.1 gg_id:14912 Macrococcus carouselicus str. H8b16 Y15713
EU432572.1 gg_id:265732 Salinicoccus sp. str. 10093 EU4325
DQ989633.1 gg_id:192272 Salinicoccus sp. str. W24 DQ989
DQ093353.1 gg_id:134112 Salinicoccus roseus str. Iii10 DQ093

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o__Bacillales	f__Staphylococcaceae
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s__Salinicoccus roseus	43946
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GU397406.1 gg_id:517923 Salinicoccus roseus str. G0B GU397
DQ352839.2 gg_id:145617 Salinicoccus aurantium str. YIM 70202 DQ352
EF177689.1 gg_id:198961 Salinicoccus sp. str. Y22 EF1776
AF275710.1 gg_id:37750 Salinicoccus alkaliphilus str. T8 AF2757
EU534791.1 gg_id:282310 profile human skin microbiota ear punch biopsy female C57BL/6J mouse clone nbt21 EU5347
EF397606.1 gg_id:215022 Salinicoccus siamensis str. PN7-1 EF3976
AY028927.1 gg_id:26423 Salinicoccus hispanicus str. DSM 5352 AY0289
DQ767692.2 gg_id:164495 Salinicoccus sp. str. QW6 DQ767
FJ182049.2 gg_id:332643 Salinicoccus sp. str. Crm FJ1820
GQ280080.1 gg_id:549014 Staphylococcus gallinarum str. JS-10 GQ280
DQ355389.1 gg_id:158047 Staphylococcus saprophyticus DQ355
EU660331.1 gg_id:301632 Staphylococcus arlettae str. CM18 EU6603
AF015929.1 gg_id:14788 Staphylococcus aureus str. ATCC 29740 AF0159
AF146368.1 gg_id:14885 Staphylococcus aureus str. 71382 AF1463
EF510513.1 gg_id:220229 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aerug EF5105
DQ226212.1 gg_id:144797 Staphylococcus aureus DR.Y11 DQ226
DQ630753.1 gg_id:160169 Staphylococcus aureus DQ630
L36472.1 gg_id:138458 Staphylococcus aureus L36472
EF463060.1 gg_id:223814 Staphylococcus aureus str. RKA6 EF4630
X70648.1 gg_id:14825 Staphylococcus aureus str. NCDO 949 X70648
NC_007622.1 gg_id:150528 Staphylococcus aureus str. RF122 NC_007
AJ938182.1 gg_id:144650 Staphylococcus aureus str. RF122 AJ9381
DQ997836.1 gg_id:196205 Staphylococcus aureus str. F155 DQ997
EF463058.1 gg_id:224473 Staphylococcus aureus str. RKA4 EF4630
Y15856.1 gg_id:14889 Staphylococcus aureus str. M2 3 Y15856
FJ609418.1 gg_id:534669 Staphylococcus aureus str. PRSR-4 FJ6094
EU604543.1 gg_id:278032 Staphylococcus aureus str. 185060 (VRSA) EU6045
GQ919290.1 gg_id:567156 Staphylococcus aureus str. SGC801 GQ919
EU604544.1 gg_id:279269 Staphylococcus aureus str. 185100 EU6045
AY727530.2 gg_id:122846 Staphylococcus simiae str. CCM 7213 AY7275
GU213356.1 gg_id:561986 Staphylococcus aureus str. 44 GU213
EU807758.1 gg_id:305525 Staphylococcus aureus str. X13 EU8077
EU730931.1 gg_id:338529 Staphylococcus cohnii str. 175 EU7309
NR_028996.1 gg_id:581219 Staphylococcus nepalensis str. CW1; DSM 15150 NR_028
EF173930.1 gg_id:177509 Staphylococcus cohnii str. COL4 EF1739
GQ052971.1 gg_id:380781 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbu GQ052
GQ073909.1 gg_id:466553 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor GQ073
GQ053940.1 gg_id:412476 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1(GQ053
GQ103291.1 gg_id:413254 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw698f01 GQ103
GU354324.1 gg_id:528574 Staphylococcus epidermidis str. DGC-1 GU354
GQ069570.1 gg_id:421820 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1 GQ069

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GQ040672.1 gg_id:379296 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw957d07(GQ040
GQ025280.1 gg_id:459414 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor GQ025
GQ054930.1 gg_id:424474 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv GQ054
GQ063021.1 gg_id:433497 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw96f11c GQ063
GQ039744.1 gg_id:414390 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu427g05 GQ039
FN393796.1 gg_id:549256 Staphylococcus epidermidis str. ES-5a1 FN393
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GQ080181.1 gg_id:459819 Topographical and Temporal Human Skin Microbiome skin alar crease clone nbw113 GQ080
GQ055927.1 gg_id:408408 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw1040f(GQ055
GQ002213.1 gg_id:507448 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbu1(GQ002
GQ002082.1 gg_id:507580 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbu1(GQ002
GQ104186.1 gg_id:377635 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw564e0 GQ104
CP000029.1 gg_id:151979 Staphylococcus epidermidis str. RP62A CP000
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GQ021875.1 gg_id:487793 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ021
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GQ053159.1 gg_id:450808 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1 GQ053
GQ053281.1 gg_id:456798 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1 GQ053
GQ103944.1 gg_id:405855 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ103
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GQ035691.1 gg_id:449623 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbu3 GQ035
GQ001890.1 gg_id:507772 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbu1(GQ001
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GQ042909.1 gg_id:393511 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor GQ042
GQ004633.1 gg_id:505026 Topographical and Temporal Human Skin Microbiome skin nare clone nbu60g03c1 GQ004
GQ041706.1 gg_id:396889 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw931e0 GQ041
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GQ047106.1 gg_id:435044 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw GQ047

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AE015929.1 gg_id:146872 Staphylococcus epidermidis str. ATCC 12228 AE015
GQ110220.1 gg_id:374978 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw61 GQ110
GQ047495.1 gg_id:432278 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor GQ047
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AE015929.1 gg_id:146882 Staphylococcus epidermidis str. ATCC 12228 AE015
GQ073870.1 gg_id:455859 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor GQ073
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GQ039665.1 gg_id:377224 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu425h07 GQ039
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EU513396.1 gg_id:267848 Staphylococcus epidermidis str. TMPSB-D10 EU513
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EU861981.1 gg_id:330001 Staphylococcus capitis str. ICIRC102 EU861
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GQ051876.1 gg_id:420220 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ051
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GQ065910.1 gg_id:468242 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw94d05 GQ065
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GQ058791.1 gg_id:380540 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ058
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GQ053924.1 gg_id:422156 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1 GQ053
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GQ114233.1 gg_id:453143 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw59 GQ114
GQ039944.1 gg_id:392066 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor GQ039
GQ055749.1 gg_id:370903 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw1039a GQ055
GQ058773.1 gg_id:421285 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ058
GQ107890.1 gg_id:442266 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw555g0 GQ107
X68417.1 gg_id:14794 Staphylococcus aureus str. ATCC 12600 X68417
AY308046.1 gg_id:89118 Staphylococcus epidermidis str. AZ22L3 AY308
GQ073456.1 gg_id:452171 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor GQ073
GQ081939.1 gg_id:376646 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor GQ081
X75944.1 gg_id:14817 Staphylococcus epidermidis str. GH 654 X75944
EU855190.1 gg_id:346511 Staphylococcus equorum str. CTSP8 EU855
EF061907.1 gg_id:181589 Staphylococcus sp. str. M210 EF0619
GQ304781.1 gg_id:592590 Staphylococcus haemolyticus str. A5 GQ304
GQ045534.1 gg_id:459324 Topographical and Temporal Human Skin Microbiome skin interdigital web space cl GQ045
L37600.1 gg_id:14857 Staphylococcus haemolyticus L37600
X86640.1 gg_id:14867 Staphylococcus sp str. 1F-23 X86640
FN393802.1 gg_id:575037 Staphylococcus haemolyticus str. ES-263-1 FN3938
EU071616.1 gg_id:256023 Staphylococcus haemolyticus str. EHFS1_AU1Ha EU071
EU379304.1 gg_id:262934 Staphylococcus haemolyticus str. 6R-J-5 EU3793
EF522132.1 gg_id:225987 Staphylococcus haemolyticus str. CU37-21 EF5221
GQ037885.1 gg_id:385469 Topographical and Temporal Human Skin Microbiome skin interdigital web space cl GQ037
X86636.1 gg_id:14837 Staphylococcus sp str. 1F-09 X86636
X86650.1 gg_id:14838 Staphylococcus sp str. S5-96 X86650
AY903256.1 gg_id:111564 Staphylococcus lugdunensis str. Inje L2 AY9032
AF322002.2 gg_id:26685 Staphylococcus pettenkoferi str. B3117 AF3220
GQ104965.1 gg_id:448537 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ104
GQ038197.1 gg_id:427149 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbu GQ038
GQ038333.1 gg_id:432252 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbu GQ038
AJ780978.1 gg_id:137754 Staphylococcus pseudintermedius str. LMG 22221 AJ7809
GQ261178.1 gg_id:573127 Staphylococcus sciuri str. YL081101 GQ261
AY820254.1 gg_id:141666 Staphylococcus sciuri str. SCBM1 AY8202
AB523707.1 gg_id:471521 Staphylococcus sciuri str. -S05-2 AB5237
AB212276.1 gg_id:148758 Staphylococcus sciuri AB2122
FJ573173.1 gg_id:550011 Staphylococcus sciuri str. E9-3 FJ5731
GU140036.1 gg_id:549509 Staphylococcus sciuri str. HBSD GU140
AJ320272.1 gg_id:21472 Staphylococcus succinus str. SB72 AJ3202
GU143799.1 gg_id:539557 Staphylococcus succinus str. SV17 GU143
AB009942.1 gg_id:14879 Staphylococcus pulvereri str. ATCC 51698T AB0099
EU428955.1 gg_id:549555 Staphylococcus epidermidis str. BP/SU1 EU4289
GQ068053.1 gg_id:393219 Topographical and Temporal Human Skin Microbiome skin alar crease clone nbw14 GQ068

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GQ078527.1 gg_id:381886 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ078
GQ054452.1 gg_id:447357 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbu58 GQ054
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GQ058299.1 gg_id:454227 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1 GQ058
NC_007168.1 gg_id:130949 Staphylococcus haemolyticus str. JCSC1435 NC_00
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GQ046433.1 gg_id:380303 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ046
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GQ044635.1 gg_id:437606 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ044
FJ189773.1 gg_id:553926 Staphylococcus pasteuri str. NSB07 FJ1897
GQ039946.1 gg_id:412114 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor GQ039
GQ035710.1 gg_id:392562 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbu GQ035
DQ818408.1 gg_id:170545 mouse cecal microbiota-colonized zebrafish digestive tract clone aaa38g12 DQ818
GQ058878.1 gg_id:426011 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ058
GQ067668.1 gg_id:409194 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw141c1 GQ067
GQ022439.1 gg_id:487232 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbu31 GQ022
GQ099306.1 gg_id:392601 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw50 GQ099
Z22778.1 gg_id:14903 Spirochaeta sp str. human intestinal spirochaete oman strain 26 Z22778
GQ058415.1 gg_id:382697 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1 GQ058
GQ112722.1 gg_id:395866 Topographical and Temporal Human Skin Microbiome skin nare clone nbw587b05c1 GQ112
GQ053104.1 gg_id:443823 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1 GQ053

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EU861984.1 gg_id:330679 Staphylococcus epidermidis str. ICIRC142 EU861
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GQ110998.1 gg_id:446128 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw GQ110
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EU660348.1 gg_id:296554 Staphylococcus sciuri str. CM26 EU660
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NR_024667.1 gg_id:555928 Staphylococcus kloosii str. ATCC 43959 NR_02
GQ022602.1 gg_id:487068 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbu31 GQ022
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S83569.1 gg_id:14880 Staphylococcus sciuri S83569
GQ058681.1 gg_id:437545 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbu58 GQ058
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EU434592.1 gg_id:269729 Staphylococcus saprophyticus str. e35 EU434

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GQ031964.1 gg_id:375035 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw: GQ031
GQ038516.1 gg_id:373056 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu4 GQ038
GQ384358.1 gg_id:578611 Staphylococcus saprophyticus str. V GQ384
D83364.1 gg_id:14898 Staphylococcus felis str. ATCC49168T D8336
GQ042042.1 gg_id:388539 Topographical and Temporal Human Skin Microbiome skin alar crease clone nbw935 GQ042
GQ078746.1 gg_id:407621 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ078
FN646072.1 gg_id:526427 Staphylococcus gallinarum 205 FN646
X66100.1 gg_id:14771 Staphylococcus haemolyticus str. CCM2737 X6610
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GQ087014.1 gg_id:421924 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw3 GQ087
GQ022382.1 gg_id:487287 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbu31 GQ022
EF053370.1 gg_id:244892 Staphylococcus pseudolugdunensis str. B006 EF0533
GQ039739.1 gg_id:401413 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu427f07 GQ039
GQ109945.1 gg_id:446550 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw6 GQ109
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AM062696.1 gg_id:254131 Staphylococcus sciuri 11PP2C AM062
FN393800.1 gg_id:537866 Staphylococcus haemolyticus str. ES-230-1b FN3938
GU197539.1 gg_id:572188 Staphylococcus saprophyticus str. YSY1-8 GU197
GQ045709.1 gg_id:396437 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ045
GQ110243.1 gg_id:451900 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw61 GQ110
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GQ038366.1 gg_id:414478 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbu GQ038
GQ058751.1 gg_id:391994 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ058
GQ080676.1 gg_id:395347 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1 GQ080
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GQ056646.1 gg_id:407100 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw10 GQ056
GQ081926.1 gg_id:460583 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor GQ081
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L37598.1 gg_id:14763 Staphylococcus aureus L37598
GQ111528.1 gg_id:377601 Topographical and Temporal Human Skin Microbiome skin alar crease clone nbw581 GQ111
GQ056331.1 gg_id:430501 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor GQ056
GQ037007.1 gg_id:379870 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu387c11 GQ037
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GQ045883.1 gg_id:419749 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ045
GQ109824.1 gg_id:437550 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw6 GQ109
EU834242.1 gg_id:331162 Staphylococcus epidermidis str. DS12 EU834

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GQ082837.1 gg_id:436172 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ082
FJ481960.1 gg_id:509619 Staphylococcus epidermidis str. KZ5 FJ4819
GQ022494.1 gg_id:487173 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbu31 GQ022
DQ350835.1 gg_id:147170 Staphylococcus gallinarum str. S1004 DQ350
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GQ056225.1 gg_id:374799 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl GQ056
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GQ056435.1 gg_id:426976 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor GQ056
AB009943.1 gg_id:14779 Staphylococcus piscifermentans str. ATCC51136T AB009
EU652069.1 gg_id:275202 Staphylococcus epidermidis str. mm-17 EU652
GQ110094.1 gg_id:446609 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw61 GQ110
GQ022492.1 gg_id:487174 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbu31 GQ022
GQ022384.1 gg_id:487285 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbu31 GQ022
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S83566.1 gg_id:14834 Staphylococcus muscae str. MB4 = CCM 4175 S83566
GQ045749.1 gg_id:408256 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ045
GQ053856.1 gg_id:461179 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1 GQ053
EU798945.1 gg_id:330915 Staphylococcus sp. str. JY04 EU798
GQ062951.1 gg_id:374892 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw95g07c GQ062
GQ000155.1 gg_id:468720 Topographical and Temporal Human Skin Microbiome skin palm clone nbu103b07c1 GQ000
GQ021520.1 gg_id:488148 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbu27 GQ021
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GQ099584.1 gg_id:439243 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw51 GQ099
GU084442.1 gg_id:550096 Staphylococcus succinus str. AT4 GU084
AY167864.1 gg_id:77340 Staphylococcus epidermidis str. SAFR-016 AY1678
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FJ832086.1 gg_id:537678 Staphylococcus sp. str. MRC5-7-5 FJ8320
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GQ005789.1 gg_id:503874 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl GQ005
GQ041809.1 gg_id:414467 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw932h0 GQ041
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EU379296.1 gg_id:258529 Staphylococcus hominis str. 6J-4b EU379
GQ041958.1 gg_id:404670 Topographical and Temporal Human Skin Microbiome skin alar crease clone nbw934 GQ041
GQ042504.1 gg_id:449327 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl GQ042
GQ039994.1 gg_id:452485 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor GQ039

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GQ023137.1 gg_id:486532 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbu3(GQ023
GQ040897.1 gg_id:380127 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw959h07(GQ040
AY592222.1 gg_id:101489 marine ANAMMOX sediment clone AY592222 AY592
GQ081762.1 gg_id:373850 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor GQ081
GQ046325.1 gg_id:436031 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ046

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FJ389203.1 gg_id:553809 Staphylococcus devriesei str. KS-SP_27 FJ3892
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GQ041565.1 gg_id:370904 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw929f11 GQ041
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EF512729.1 gg_id:220295 Staphylococcus cohnii str. JL812 EF5127
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GQ013974.1 gg_id:495694 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw8 GQ013
GQ058842.1 gg_id:451616 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ058
GQ043595.1 gg_id:390563 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1016b GQ043
FJ380980.1 gg_id:576172 Staphylococcus haemolyticus str. BQN2T-01d FJ3809
DQ116003.1 gg_id:129388 bovine teat canal clone D-22 DQ116
DQ069223.1 gg_id:128398 sbsrfc mcrrgnsms mfc sll: implctns SLME's SA A mn cln SRB36 DQ069
DQ115992.1 gg_id:132839 bovine teat canal clone B-63 DQ115
DQ069205.1 gg_id:128067 gold mine clone MAB24 DQ069
FM872548.1 gg_id:369705 occupant source house floor dust clone FA03A04 FM872
EU373366.1 gg_id:262857 Macrococcus brunensis str. TPL01 EU3733
EU240887.1 gg_id:252685 Nosocomiicoccus ampullae str. TC-9 EU2408
AY167812.1 gg_id:77365 Bacillus sp. str. SAFN-018 AY1678
GQ153851.1 gg_id:396595 Laceyella sacchari str. T11-7 GQ153
NR_025007.1 gg_id:559489 Laceyella putida str. KCTC 3666 NR_025
AB239530.1 gg_id:144022 Thermoactinomyces sp. MBIC08001 str. YM3-653 (= MBIC08001) AB2395
AM940019.1 gg_id:266782 Desmospora activa str. IMMIB L-1269 AM940
AJ251778.1 gg_id:41281 Thermoactinomyces sanguinis str. CCUG 38657T AJ2517
GQ163470.1 gg_id:593230 Trigonala elaeagnus str. HBUM2132 GQ163
AB088363.1 gg_id:78838 Thermoactinomyces sp. str. C0170 AB0883
DQ119659.1 gg_id:133383 Thermoactinomyces sp. str. LA5 DQ119
AB088364.1 gg_id:78806 Thermoactinomyces sp. str. H0165 AB0883
GU002061.1 gg_id:565318 Shimazuella sp. str. FXJ7.246 GU002
AF138732.1 gg_id:111744 Thermoactinomyces vulgaris str. KCTC 9557 () AF1387
AF138734.1 gg_id:112113 Thermoactinomyces intermedius str. KCTC 9646 () AF1387
AB362275.1 gg_id:272839 Thermoactinomyces sp. str. JAM-FM1001 AB3622
AB002650.1 gg_id:14561 G+C gram-positive HTA1420 AB0026
GQ015481.1 gg_id:494185 Topographical and Temporal Human Skin Microbiome skin back clone nbw817b04c1 GQ015
AF138735.1 gg_id:22975 Thermoactinomyces peptonophilus str. KCTC 9740 () AF1387
EU779111.1 gg_id:321618 Takin feces clone TAK_aaa01d06 EU7791
EF371926.1 gg_id:212584 Planococcus pelagicus str. /HsP6(II) EF3719
EU465810.1 gg_id:289883 argali sheep feces clone AS2_aao35h09 EU4658
EU466486.1 gg_id:297742 bighorn sheep feces clone BH2_aao24e06 EU4664
Y07580.2 gg_id:14632 Drentse grassland soil clone DA011 Y07580
EU778808.1 gg_id:328205 Springbok feces clone SBK_h08_1_1 EU7788
EU773972.1 gg_id:327895 Cheetah feces clone CE2_e08_1 EU7739
EU466699.1 gg_id:295198 argali sheep feces clone AS3_aao20b04 EU4666
EU467930.1 gg_id:293972 cheetah feces clone CE2_d10 EU4679
EU469351.1 gg_id:290034 springbok feces clone SBK_f02_1 EU4693
EU467981.1 gg_id:301629 cheetah feces clone CE2_e05_1 EU4679
EF636829.1 gg_id:277855 Metagenomic and Namib desert sand clone 1 EF6368

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D16279.1 gg_id:14492 Bacillus racemilacticus str. IAM12319 D16279
EF590060.2 gg_id:228248 changes structure sediments Songhua River contaminated nitrobenzene -DGGE cloni EF5900
AY642582.1 gg_id:202831 and carbonate precipitation giant microbialites ly alkaline Lake Van Turkey microbiali AY6425
AM711118.1 gg_id:265604 Scopulibacillus darangshiensis str. DLS-06 AM711
DQ083102.1 gg_id:131214 soil clone X17 DQ083
EF515940.1 gg_id:224822 grassland soil clone FCPN728 EF5159
DQ448756.1 gg_id:157711 Bacillus sp. str. CNJ775 PL04 DQ448
FJ478789.1 gg_id:591482 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4787
EU134633.1 gg_id:246398 tallgrass prarie soil clone FFCH11580 EU1346
EU571191.1 gg_id:268803 Bacillus sp. str. 25-3 EU5711
FJ671330.1 gg_id:523662 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6713
AB002648.1 gg_id:14559 G+C gram-positive HTA1422 AB0026
NR_025005.1 gg_id:562523 Thermoflavimicrobium dichotomicum str. KCTC 3667 NR_025
AF332545.1 gg_id:40011 Bacillus thuringiensis B73 AF3325
AY597525.2 gg_id:150661 Photorhabdus luminescens PDBC EPN6.71 AY5975
AF332544.1 gg_id:41058 Bacillus megaterium B70 AF3325
EU365680.1 gg_id:269842 Bacillus cereus str. M-7 EU3656
DQ351341.1 gg_id:155340 Exiguobacterium homiense str. H1-R8 DQ351
AF227839.1 gg_id:40417 str. 61610 AF2278
DQ235551.1 gg_id:143456 biofilm water pipeline biofilms steel pipelines Gulf Mexico DQ235
X70316.1 gg_id:14691 Exiguobacterium aurantiacum str. NCDO 2321 X70316
X70313.1 gg_id:14688 Exiguobacterium acetylicum str. NCIMB 9889 X70313
GQ284484.1 gg_id:570858 Exiguobacterium indicum str. TDWCW4 GQ284
GQ284470.1 gg_id:590797 Exiguobacterium indicum str. PCWCW1 GQ284
CP001022.1 gg_id:267150 Exiguobacterium sibiricum str. 255-15 CP0010
DQ019165.1 gg_id:153908 Exiguobacterium undae str. DSM 14481 DQ019
D55730.1 gg_id:14687 Exiguobacterium acetylicum str. IFO12146 D55730
FJ970034.1 gg_id:374212 Exiguobacterium acetylicum str. QD-3 FJ9700
DQ019164.1 gg_id:154203 Exiguobacterium antarcticum str. DSM 14480 DQ019
GQ284483.1 gg_id:584187 Exiguobacterium indicum str. TDWCW3 GQ284
EF100862.1 gg_id:190839 Exiguobacterium sp. CON-C-8 EF1008
FJ821599.1 gg_id:552284 Exiguobacterium sp. str. TPS3 FJ8215
AB334767.1 gg_id:253456 Exiguobacterium undae str. 5 AB3347
GQ284346.1 gg_id:566992 Exiguobacterium acetylicum str. THWCSN38 GQ284
AB105164.1 gg_id:93416 Exiguobacterium oxidotolerans str. T-2-2 AB1051
FJ210797.1 gg_id:339135 Exiguobacterium sp. str. QDHT-01 FJ2107
X86600.1 gg_id:14694 Bacillus sp str. S2-97 X86600
GQ284477.1 gg_id:587191 Exiguobacterium indicum str. PCWCW8 GQ284
EU847143.1 gg_id:311208 Exiguobacterium aestuarii str. SR 101 EU8471
AJ344151.1 gg_id:72912 Exiguobacterium undae str. L2 AJ3441
Y13364.1 gg_id:14922 Gemella sanguinis str. 2045-94 Y13364

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FM873785.1 gg_id:370109 occupant source house mattress dust clone MA04F09 FM873
GQ087754.1 gg_id:423895 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ087
AJ251987.1 gg_id:45265 Gemella sp. str. M60449/99/1 T AJ2519
GQ006874.1 gg_id:502790 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu88g11c GQ006
GQ023356.1 gg_id:486313 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu317d07 GQ023
EU427463.1 gg_id:258882 Gemella sp. str. WAL 1945J EU4274
GQ006635.1 gg_id:503029 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu85h02c GQ006
Y13365.1 gg_id:14920 Gemella bergeri str. 617-93 Y13365
DQ113771.1 gg_id:129485 dog jejunum clone J5-76 DQ113
AM420049.1 gg_id:236798 Noma subgingival plaque clone 202F06(oral) AM420
EF999972.1 gg_id:278692 Haloplasma contractile str. SSD-17B EF9999
EF586062.1 gg_id:245842 Methanol-assimilating anaerobic solid waste digester fed methanol clone M55_D21_ EF5860
EF585995.1 gg_id:240344 Methanol-assimilating anaerobic solid waste digester fed methanol clone B55_K_B_F EF5859
GU455254.1 gg_id:519748 Understanding short-chain fatty acids accumulation enhanced alkaline digestion: kir GU455
EF586039.1 gg_id:248439 Methanol-assimilating anaerobic solid waste digester fed methanol clone M55_D15_ EF5860
DQ431898.1 gg_id:204684 microorganisms catalyzing nitrogen removal and organic matter metabolism perme DQ431
NZ_ACIL02000016.1 gg_id:469920 Catonella morbi str. ATCC 51271 NZ_AC
DQ113697.1 gg_id:129773 dog duodenum clone D5-23 DQ113
DQ113716.1 gg_id:130850 dog jejunum clone J1-18 DQ113
AF318316.1 gg_id:35088 Aerococcus sanguinicola str. BBMML 01 AF3183
U64456.1 gg_id:15070 Aerococcus urinae str. F1-84 U6445
U64457.1 gg_id:15071 Aerococcus urinae str. G1-84 U6445
U64460.1 gg_id:15074 Aerococcus urinae str. 998-93 U6446
AY707773.1 gg_id:136245 Aerococcus viridans str. 37R AY707
EU289060.1 gg_id:254233 microbiome cloacal openings urogenital and anal tracts tammar wallaby Macropus e EU289
EU289078.1 gg_id:237214 microbiome cloacal openings urogenital and anal tracts tammar wallaby Macropus e EU289
Y17318.1 gg_id:15076 Aerococcus christensenii str. CCUG 28826 Y17318
AJ278341.2 gg_id:23513 Aerococcus urinaehominis str. CCUG 42038b AJ2783
EU075039.1 gg_id:238621 Aerococcus viridans str. 15MS EU075
AM230658.1 gg_id:196766 Aerococcus suis str. 1821-02 AM230
AM292063.1 gg_id:250567 Aerococcus viridans zf-68-I AM292
GQ161096.1 gg_id:412780 Aerococcus viridans str. GDQY-1 GQ161
NR_029351.1 gg_id:593109 Facklamia sourekii str. SS 1019; CCUG 28783; ATCC 700629 NR_02
Y15716.1 gg_id:52354 Facklamia ignava Y15716
GQ071953.1 gg_id:425055 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw190d0 GQ071
Y18053.1 gg_id:15053 Facklamia languida str. 1144-97 Y18053
FM873282.1 gg_id:366119 occupant source house floor dust clone FD01A09 FM873
GQ497941.1 gg_id:561734 Facklamia sp. str. KO_PS21 GQ497
Y16426.1 gg_id:15060 Ignavigranum ruoffiae str. CCUG 37658 Y16426

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FJ674961.1 gg_id:517319 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6749
GQ002938.1 gg_id:506724 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu182e09 GQ002
GQ060659.1 gg_id:463917 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw03g08 GQ060
FM873468.1 gg_id:369668 occupant source house floor dust clone FD04B03 FM873
EU341289.1 gg_id:240694 Evaluation Rapid Technologies Estimate Microbial Burden and Commercial Airline Ca EU341
FJ672272.1 gg_id:515704 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6722
Y17780.1 gg_id:74511 Eremococcus coleocola str. M1832/95/2 Y17780
GQ068237.1 gg_id:399188 Topographical and Temporal Human Skin Microbiome skin alar crease clone nbw148 GQ068
AJ279038.1 gg_id:16600 Aerosphaera taetra str. CCUG 43036T AJ2790
AY959019.1 gg_id:132717 Microbes on human vaginal epithelium clone rRNA246 AY9590
GQ020706.1 gg_id:488962 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ020
FJ672416.1 gg_id:527548 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6724
GQ024094.1 gg_id:485575 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw GQ024
FJ672485.1 gg_id:531811 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6724
AF124041.1 gg_id:15240 sheep scab mite clone #1 AF1240
AB188091.1 gg_id:104418 Alkalibacterium iburiensis str. M3 AB1880
AB268550.1 gg_id:186973 Alkalibacterium polygonumreducens str. F11 AB2685
AB294173.1 gg_id:368743 Alkalibacterium kapii str. T82-5-1 AB2941
EU845714.1 gg_id:349078 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8457
GQ351352.1 gg_id:542881 Alkalibacterium sp. str. G4 GQ351
AF143512.2 gg_id:15252 Alkalibacterium olivapovliticus str. WW2-SN4c AF1435
AB294176.1 gg_id:361292 Alkalibacterium psychrotolerans str. JCM 12281 AB2941
AB294169.1 gg_id:364463 Alkalibacterium putridalgicola str. O26-12-2 AB2941
X92169.1 gg_id:27088 Lake Nakuru isolate WN16 X92169
GQ848212.1 gg_id:556700 and Archaeal Xiarinur Soda Lake Water-sediment Interface water-sediment interfac GQ848
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AY543031.1 gg_id:99269 Carnobacterium maltaromaticum MF 204 AY5430
GQ304934.1 gg_id:568366 Carnobacterium maltaromaticum str. MMF-26 GQ304
GQ304938.1 gg_id:581552 Carnobacterium maltaromaticum str. MMF-30 GQ304
GQ304920.1 gg_id:559437 Carnobacterium maltaromaticum str. MMF-12 GQ304
AM179873.1 gg_id:150460 Carnobacterium maltaromaticum B26 AM179
DQ027061.1 gg_id:134675 Carnobacterium sp. str. AT7 DQ027
EU845619.1 gg_id:312732 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8456
EU845247.1 gg_id:313812 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8457
L08623.1 gg_id:15257 Carnobacterium alterfunditum L08623
EU845677.1 gg_id:309286 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8456

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AM111051.1 gg_id:140940 Carnobacterium sp. str. 7196 AM111
DQ778093.1 gg_id:166840 Carnobacterium sp. str. LIV10 DQ778
EU817500.1 gg_id:332765 Carnobacterium sp. str. MS3 EU817
EU845027.1 gg_id:353898 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU845
AF184247.1 gg_id:36062 Carnobacterium maltaromaticum str. BA AF184
S86170.1 gg_id:15243 Carnobacterium funditum str. pf3 (DSM 5970) S86170
AJ387905.1 gg_id:16452 Carnobacterium gallinarum str. DSM 4847(T) NCFB 2766(T) AJ3879
AM179875.1 gg_id:146934 Carnobacterium divergens B33 AM179
GQ008057.1 gg_id:501608 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ008
EU773383.1 gg_id:326100 BigHorn sheep feces clone BH2_aao23f01 EU773
GQ008163.1 gg_id:501503 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ008
FJ674675.1 gg_id:522048 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface FJ6746
Y17300.1 gg_id:15259 Desemzia incerta str. DSM 20581 Y17300
FJ674414.1 gg_id:512638 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface FJ6744
FJ674411.1 gg_id:522459 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface FJ6744
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FJ675581.1 gg_id:530569 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface FJ6755
FJ675028.1 gg_id:509443 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface FJ6750
FJ671781.1 gg_id:525552 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface FJ6717
FJ674863.1 gg_id:520714 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface FJ6748
FJ674821.1 gg_id:525603 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface FJ6748
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FJ672402.1 gg_id:516922 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface FJ6724
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FJ674634.1 gg_id:527071 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface FJ6746
FJ194014.1 gg_id:353870 Genetic inventory 'KSC-Astrotek' spacecraft assembly clean room during DAWN missi FJ1940
AY879299.1 gg_id:141939 Granulicatella adiacens str. 03252090 AY879
AF016390.1 gg_id:15054 Granulicatella elegans str. DSM 11693; B1333 AF016
AB022026.1 gg_id:15057 Granulicatella elegans str. HHC5 AB022
AB252689.1 gg_id:216513 Granulicatella elegans str. PAGU 792 AB252
AJ312375.1 gg_id:70105 Granulicatella adiacens str. 10/833 AJ3123
AY879298.1 gg_id:143622 Granulicatella paradiacens str. 04401102 AY879
Y15408.1 gg_id:15055 Granulicatella elegans str. 2640-91 Y15408
FJ558447.1 gg_id:521851 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5584
GU374018.1 gg_id:532021 normal teeth clone SRC_DSC5 GU374
AB247277.1 gg_id:147894 Marinilactibacillus piezotolerans str. JCM 12337 AB247
AB159717.1 gg_id:103175 Marinilactibacillus psychrotolerans str. INCT119 AB159
AY485792.1 gg_id:99434 Marinilactibacillus piezotolerans str. LT20 AY485

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EU434512.1 gg_id:264683 Trichococcus collinsii str. b239 EU4345
EU434551.1 gg_id:268210 Trichococcus collinsii str. b140 EU4345
EU434537.1 gg_id:275949 Trichococcus collinsii str. b253 EU4345
EU434536.1 gg_id:274539 Trichococcus collinsii str. b255 EU4345
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EU434495.1 gg_id:277597 Trichococcus collinsii str. b362 EU4344
EU434510.1 gg_id:266846 Trichococcus collinsii str. b237 EU4345
NR_025435.1 gg_id:572224 Trichococcus palustris str. DSM 9172 NR_025
EU434478.1 gg_id:265112 Trichococcus collinsii str. b279 EU4344
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AJ306612.1 gg_id:47658 Trichococcus collinsii str. 37AN3 AJ3066
AB186878.1 gg_id:101202 polychlorinated dioxin dechlorinating microcosm clone TSBX03 AB1868
L76599.1 gg_id:15246 Trichococcus pasteurii str. ATCC 35945 L76599
EU844884.1 gg_id:327706 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8448
EU434522.1 gg_id:263346 Trichococcus flocculiformis str. b328 EU4345
FJ675543.1 gg_id:509026 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6755
Y17301.1 gg_id:15254 Trichococcus flocculiformis str. DSM 2094 Y17301
FJ672105.1 gg_id:527794 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6721
DQ337518.1 gg_id:145184 tetracycline and tylosin resistance genes impacted swine effluent holding pit DQ337
EU434437.1 gg_id:272157 Trichococcus flocculiformis str. a209 EU4344
FJ674344.1 gg_id:527737 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6743
FJ672700.1 gg_id:527399 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6727
EU434501.1 gg_id:265834 Trichococcus flocculiformis str. b319 EU4345
FJ671856.1 gg_id:511164 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6718
FJ671301.1 gg_id:526709 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6713
GQ080732.1 gg_id:409174 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1 GQ080
NR_026454.1 gg_id:552567 Granulicatella balaenopterae str. M1975/96/1; CCUG 37380 NR_026
FJ764779.1 gg_id:565642 Marinilactibacillus sp. str. E-109 FJ7647
FJ671733.1 gg_id:514230 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6717
FJ671721.1 gg_id:518863 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6717
FJ672820.1 gg_id:513562 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6728
FJ671872.1 gg_id:532281 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6718
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FJ670957.1 gg_id:516363 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6709
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FJ672927.1 gg_id:514848 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6729
FJ893130.1 gg_id:545089 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota HM3; ear p FJ8931
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FJ672013.1 gg_id:509420 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6720
FJ671894.1 gg_id:523062 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6718
FJ671904.1 gg_id:530966 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6719
FJ674889.1 gg_id:511294 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6748
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AY581816.1 gg_id:106773 feces clone 1D3 AY5818
AJ302648.1 gg_id:20210 Isobaculum melis CCUG 37660T AJ3026
FM875568.1 gg_id:365920 occupant source house dust skin surface swab clone SD01E05 FM875
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GU166170.1 gg_id:561594 intestinal tract larvae (Musca domestica) direct cloning and sequencing genes whea GU166
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NR_028748.1 gg_id:586815 Enterococcus avium str. E6844; CIP 103019 NR_02
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EF199997.1 gg_id:183702 Enterococcus casseliflavus str. ELS3 EF1999
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GQ337020.1 gg_id:544389 Enterococcus casseliflavus str. SS1229 GQ337
AJ420804.1 gg_id:42419 Enterococcus casseliflavus str. CECT969T AJ4208
AB547326.1 gg_id:515778 Enterococcus casseliflavus str. NCCP-53 AB5473
DQ395285.1 gg_id:156436 Enterococcus casseliflavus F00186 DQ395
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AJ301837.1 gg_id:40545 Enterococcus pseudoavium str. LMG 11426 AJ3018
EF591816.1 gg_id:232955 Enterococcus mundtii str. CWBI-B1431\(A2-17) EF5918
GU213907.1 gg_id:564647 Enterococcus hirae str. -12 GU213
GU255468.1 gg_id:583493 Enterococcus hirae str. ST3 GU255
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EU857635.1 gg_id:367979 Enterococcus faecium EU8576
EF533988.1 gg_id:222834 Enterococcus faecium str. IDCC 2102 EF5339
AY692451.1 gg_id:100464 Enterococcus faecium str. SL2 AY6924
EU857636.1 gg_id:366313 Enterococcus lactis EU8576
EU717965.1 gg_id:327400 Enterococcus faecalis str. Zy05 EU7179
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FJ982664.1 gg_id:429448 Enterococcus faecium str. JBE0015 FJ9826
EU887827.1 gg_id:341145 Enterococcus faecalis str. H13 EU8878
GQ337034.1 gg_id:533020 Enterococcus phoeniculicola str. SS1721 GQ337
AJ301839.1 gg_id:43998 Enterococcus saccharolyticus str. LMG 11427 AJ3018
Y18341.1 gg_id:15283 Enterococcus sulfureus str. NCIMB 13117T Y18341
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AF070223.1 gg_id:15287 Enterococcus faecium str. GUCR AF0702
Y18294.1 gg_id:15290 Enterococcus faecium str. NCFB 942T Y18294
AJ459875.1 gg_id:62639 larval intestine clone E AJ4598
AJ301838.1 gg_id:20443 Enterococcus raffinosus str. LMG 12999 AJ3018
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EU560859.1 gg_id:557059 Assessment genetic Apriona germari (Hope) larvae normalization techniques intestir EU5608
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AJ877015.1 gg_id:139088 Enterococcus aquimarinus str. LMG 16607 AJ8770
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FJ870986.1 gg_id:555272 Enterococcus faecium str. EF1 FJ8709
GQ156077.1 gg_id:578964 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
FN600541.1 gg_id:554755 Enterococcus raffinosus Raj FN6005

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AJ420800.1 gg_id:50018 Enterococcus faecium str. CECT410T
AY953149.1 gg_id:114861 anaerobic swine lagoon clone B-1A
Y18274.1 gg_id:15332 Enterococcus avium str. NCFB 2369T
FJ378672.1 gg_id:359990 Enterococcus faecium str. HN-N17
AY971749.1 gg_id:115294 Enterococcus faecium
EU081012.1 gg_id:238193 Enterococcus devriesei str. BMG 128
EU074827.1 gg_id:256245 Enterococcus mundtii str. MC6
AM157434.1 gg_id:141429 Enterococcus faecium mother C4
FJ378686.1 gg_id:357324 Enterococcus faecium str. HN-N31
AB012213.1 gg_id:15286 Enterococcus faecium str. JCM 5804
GQ337035.1 gg_id:584752 Enterococcus raffinosus str. SS1278
FJ378682.1 gg_id:367316 Enterococcus faecium str. HN-N27
AY057055.1 gg_id:49707 Enterococcus faecium str. ID9201
FJ749344.1 gg_id:539586 Enterococcus durans str. IMAU40069; QH27-4
AJ301826.1 gg_id:44126 Enterococcus casseliflavus str. LMG 10745
EU459193.1 gg_id:294816 hedgehog feces clone HH_aai33f05
AF335596.2 gg_id:74276 Enterococcus villorum str. ATCC 700913
AY098492.1 gg_id:72595 Enterococcus sp. AK61
FJ378693.1 gg_id:366369 Enterococcus faecium str. HN-N38
EU714899.1 gg_id:322682 Enterococcus mundtii str. SRDIPC3
FJ378706.1 gg_id:361210 Enterococcus faecium str. HN-F21
DQ295038.1 gg_id:141350 Enterococcus faecium str. MMA2
AY653231.1 gg_id:111218 Enterococcus faecium str. MLG856-2
FJ861091.1 gg_id:554398 Enterococcus faecium str. KLDS 6.0640
AJ874342.1 gg_id:133685 Enterococcus faecium str. RJ16
AF326472.1 gg_id:57509 Enterococcus ratti
FJ915701.1 gg_id:569577 Enterococcus faecium str. IMAU40164; QH25-2
EU977721.1 gg_id:534595 Enterococcus faecium str. 1P10AnC
FJ378689.1 gg_id:363778 Enterococcus faecium str. HN-N34
FJ378673.1 gg_id:362932 Enterococcus faecium str. HN-N18
EF533987.1 gg_id:220746 Enterococcus faecium str. IDCC 2101
GU084441.1 gg_id:562832 Enterococcus mundtii str. AT6
EF428252.2 gg_id:221584 Enterococcus mundtii str. HDYM-33
EU878169.1 gg_id:346951 Enterococcus faecium str. SH 528
GQ337037.1 gg_id:592016 Enterococcus termitis str. SS1793
DQ223885.1 gg_id:169662 Enterococcus raffinosus str. P6
GU384204.1 gg_id:516700 Enterococcus sp. str. CJ-1
EU428012.1 gg_id:263573 Enterococcus faecium str. SM21
FJ378676.1 gg_id:361678 Enterococcus faecium str. HN-N21

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FJ751788.1 gg_id:553011 Enterococcus hirae str. DSPV 346T FJ7517
AB066266.1 gg_id:62895 Enterococcus mundtii str. NFRI 7393 AB066
EU888524.1 gg_id:313899 Enterococcus faecium str. ES_MS1c EU888
FJ378683.1 gg_id:366505 Enterococcus faecium str. HN-N28 FJ3786
FJ917737.1 gg_id:556893 Enterococcus durans str. IMAU60186; ZLG7-1 FJ9177
GQ155710.1 gg_id:581919 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ155106.1 gg_id:572042 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
FJ378691.1 gg_id:359087 Enterococcus faecium str. HN-N36 FJ3786
GU139738.1 gg_id:590537 Enterococcus durans str. 2-4 GU139
AM039967.1 gg_id:146606 Enterococcus silesiacus str. LMG 23084 = R-23708 AM039
EU418442.1 gg_id:558319 Enterococcus faecium str. 133 EU418
FJ378678.1 gg_id:362310 Enterococcus faecium str. HN-N23 FJ3786
FJ378669.1 gg_id:366456 Enterococcus faecium str. HN-N14 FJ3786
AF395325.1 gg_id:37654 isopod gut clone RKPsBA AF3953
AJ276352.1 gg_id:30497 Enterococcus rottae str. CCM4629 AJ2763
FJ378681.1 gg_id:362734 Enterococcus faecium str. HN-N26 FJ3786
NZ_ACIY01000209.1 gg_id:470292 Enterococcus faecium str. DO NZ_AC
GQ337018.1 gg_id:582529 Enterococcus canintestini str. SS1787 GQ337
AB470234.1 gg_id:367959 Enterococcus pseudoavium str. h50 AB470
DQ985159.1 gg_id:223992 Enterococcus faecium str. R0026 DQ985
AJ301830.1 gg_id:39621 Enterococcus faecium str. LMG 11423 AJ3018
EU003448.1 gg_id:241772 Enterococcus faecium str. IDCC 2104 EU003
GQ155230.1 gg_id:549024 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
FJ378670.1 gg_id:368923 Enterococcus faecium str. HN-N15 FJ3786
EU528257.1 gg_id:287252 Seasonal Dynamics Mudflat Mouth Major Kentucky Lake Reservoir Tributary sedime EU528
FJ378668.1 gg_id:359756 Enterococcus faecium str. HN-N13 FJ3786
EU717963.1 gg_id:309491 Enterococcus faecium str. Lyws05 EU717
FJ378661.2 gg_id:362596 Enterococcus faecium str. HN-N6 FJ3786
GU369800.1 gg_id:529160 Enterococcus faecalis str. YH-10-3 GU369
FJ378692.1 gg_id:362577 Enterococcus faecium str. HN-N37 FJ3786
AJ301836.1 gg_id:74813 Enterococcus mundtii str. LMG 10748 AJ3018
EU845466.1 gg_id:316840 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU845
FJ378675.1 gg_id:361670 Enterococcus faecium str. HN-N20 FJ3786
AJ271856.1 gg_id:73318 Enterococcus faecalis str. UK873 traditional fermented milk AJ2718
FJ378707.1 gg_id:369245 Enterococcus faecium str. HN-F22 FJ3787
GQ155748.1 gg_id:557151 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
DQ199665.1 gg_id:140065 Enterococcus durans DQ199
FJ672209.1 gg_id:515601 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6722
FJ845008.1 gg_id:559785 Enterococcus faecium str. IMAU20109; ML11-2-2 FJ8450
EU459323.1 gg_id:294649 hedgehog feces clone HH_aai36d01 EU459

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FJ015055.1 gg_id:350606 Enterococcus lactis str. GA4 FJ0150
GQ131184.1 gg_id:424771 Enterococcus italicus str. IMAU70068; HS2301 GQ131
AF349930.1 gg_id:67810 Enterococcus sp. str. CR-303S AF3499
EU717957.1 gg_id:355438 Enterococcus faecium str. Yl05 EU7179
GU255467.1 gg_id:555823 Enterococcus faecium str. ST2 GU255
EU789396.1 gg_id:325104 Enterococcus faecium str. M0138 EU7893
FJ378697.1 gg_id:357775 Enterococcus faecium str. HN-N42 FJ3786
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AJ301832.1 gg_id:28797 Enterococcus flavescens str. LMG 13518 AJ3018
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EU459175.1 gg_id:288293 hedgehog feces clone HH_aai33c04 EU4591
FJ378674.1 gg_id:361558 Enterococcus faecium str. HN-N19 FJ3786
EU844974.1 gg_id:352189 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8449
AJ420806.1 gg_id:44890 Enterococcus mundtii str. CECT972T AJ4208
AJ301835.1 gg_id:48898 Enterococcus malodoratus str. LMG 10747 AJ3018
EU807757.1 gg_id:322616 Enterococcus faecalis str. NR1 EU8077
EU878170.1 gg_id:315043 Enterococcus faecium str. SH 632 EU8781
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EU689058.1 gg_id:352407 Tetragenococcus halophilus str. JCM 2015; T19 EU6890
EU522084.1 gg_id:305691 Tetragenococcus halophilus str. T2 EU5220
EU522090.1 gg_id:315186 Tetragenococcus halophilus str. T9 EU5220
D88824.1 gg_id:15292 Tetragenococcus muriaticus D88824
AJ301840.1 gg_id:20568 Enterococcus solitarius str. DSM 5634 AJ3018
Y18338.1 gg_id:15294 Enterococcus solitarius str. NCIMB 12902T Y18338
AY690334.1 gg_id:106000 Tetragenococcus koreensis str. Wan-Taek Im AY6903
GQ502552.1 gg_id:553330 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf4- GQ502
FJ675076.1 gg_id:519677 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6750
AJ576414.1 gg_id:101516 midgut homogenate Pachnoda ephippiata larva clone PeM56 AJ5764
AJ854484.1 gg_id:145696 Catellicoccus marimammalium str. M34/04/3 AJ8544
GQ156063.1 gg_id:565384 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
AJ576356.1 gg_id:107176 hindgut homogenate Pachnoda ephippiata larva clone PeH40 AJ5763
FJ672320.1 gg_id:512239 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6723
FJ675223.1 gg_id:524674 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6752
FJ192638.1 gg_id:330592 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior FJ1926
AJ576341.1 gg_id:101355 hindgut homogenate Pachnoda ephippiata larva clone PeH24 AJ5763
AY571409.1 gg_id:114659 termite gut clone RsaHf388 AY5714
Y16546.1 gg_id:43965 Atopobacter phocae str. m1590/94/2 Y16546
EU560817.1 gg_id:571665 Assessment genetic Apriona germari (Hope) larvae normalization techniques intestir EU5608

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EU147304.1 gg_id:236581 Lactobacillus brevis str. BFE 8359 EU1473
EU626007.1 gg_id:277794 Lactobacillus brevis str. KLDS 1.0722 EU6260
FJ532360.1 gg_id:562473 Lactobacillus brevis str. 14G FJ5323
EF412982.1 gg_id:204678 Lactobacillus brevis str. I211 EF4129
EU194344.1 gg_id:335435 Lactobacillus brevis str. LMG 11992 EU1943

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EU626006.1 gg_id:277822 Lactobacillus brevis str. KLDS 1.0721 EU6260
EF412980.1 gg_id:205080 Lactobacillus brevis str. I23 EF4129
FJ377713.1 gg_id:368916 Lactobacillus brevis str. RSD42 FJ3777
GU220024.1 gg_id:581930 Lactobacillus brevis str. SC2A GU220
CP000416.1 gg_id:187895 Lactobacillus brevis str. ATCC 367 CP0004
AB365977.1 gg_id:351825 Lactobacillus capillatus str. YIT 11317 AB3659
AB425925.1 gg_id:580392 Lactobacillus coleohominis str. TB-C19 AB4259
AJ292530.2 gg_id:23477 Lactobacillus coleohominis AJ2925
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GQ070874.1 gg_id:455412 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw GQ070
GQ074133.1 gg_id:371731 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ074
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GQ011573.1 gg_id:498091 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw793f10 GQ011
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DQ317604.1 gg_id:149002 Lactobacillus crispatus str. 15L08 DQ317
GQ070816.1 gg_id:441240 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw GQ070
DQ057450.1 gg_id:133039 str. ii1269 DQ057
DQ057440.1 gg_id:131154 str. ii1225 DQ057
AF243171.1 gg_id:33386 Lactobacillus crispatus str. TL23a AF2431
GQ010914.1 gg_id:498752 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ010
GQ078614.1 gg_id:422527 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ078
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AY204891.1 gg_id:81329 Lactobacillus curvatus str. YMRS3a AY2048
AY204890.1 gg_id:82190 Lactobacillus curvatus str. PSTJA3a AY2048
AF349922.1 gg_id:67818 derived cheese sample clone 51CR AF3499
EU722745.1 gg_id:326330 Lactobacillus delbrueckii str. L4 EU7227
FJ749581.1 gg_id:548624 Lactobacillus diolivorans str. IMAU10018; SY5-2 FJ7495
AB262731.1 gg_id:180597 Lactobacillus farraginis str. NRIC 0676 AB2627
AM266587.1 gg_id:161232 Lactobacillus faeni str. TMW 1.1303 = DSM 180 AM266
EU419594.1 gg_id:260994 Lactobacillus fermentum str. KLDS 1.0617 EU4195
EF535257.1 gg_id:220122 Lactobacillus fermentum str. KLB 261 EF5352
AF302116.1 gg_id:52471 Lactobacillus fermentum str. KLD AF3021
EU547297.1 gg_id:557918 Lactobacillus fermentum str. BCS25 EU5472
EU469860.1 gg_id:302890 western lowland gorilla feces clone GOR_aag72g08 EU4698
U62624.1 gg_id:15140 Lactobacillus fermentum str. KRM U62624
EF460496.1 gg_id:214156 Lactobacillus fermentum str. SR2 EF4604

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s__Lactobacillus lindneri	72028
s__Lactobacillus mali	73021
s__Lactobacillus manihotivorans	72716
s__Lactobacillus manihotivorans	72756

EF535258.1 gg_id:222909 Lactobacillus fermentum str. KLB 231 EF5352
AB370875.1 gg_id:276599 Lactobacillus fuchuensis str. B5M10 (=JCM 11249 =DSM 14340) AB3708
Y17361.1 gg_id:15125 Lactobacillus amylolyticus str. LA 5 Y17361
AB368915.1 gg_id:281310 Lactobacillus harbinensis str. T9-8 AB3689
AB196123.1 gg_id:140719 Lactobacillus harbinensis str. SBT10908 AB1961
FJ749416.1 gg_id:588829 Lactobacillus helveticus str. IMAU50013; YN15-4-1-2 FJ7494
FJ749434.1 gg_id:562265 Lactobacillus helveticus str. IMAU50033; YN17-1-2-3-1 FJ7494
EF533989.1 gg_id:225190 Lactobacillus suntoryeus str. IDCC 3101 EF5339
FJ749689.1 gg_id:556337 Lactobacillus helveticus str. IMAU30123; F1402 FJ7496
EU419585.1 gg_id:267753 Lactobacillus helveticus str. KLDS 1.0601 EU4195
FJ861099.1 gg_id:548478 Lactobacillus helveticus str. KLDS 1.0356 FJ8610
FJ749644.1 gg_id:549081 Lactobacillus helveticus str. IMAU30052; C6203 FJ7496
FJ861108.1 gg_id:541176 Lactobacillus helveticus str. KLDS 1.0647 FJ8611
AY675248.1 gg_id:105631 Lactobacillus suntoryeus str. LH AY6752
FJ861102.1 gg_id:540215 Lactobacillus helveticus str. KLDS 1.0635 FJ8611
FJ861100.1 gg_id:568817 Lactobacillus helveticus str. KLDS 1.0633 FJ8611
EU124655.1 gg_id:242121 Lactobacillus helveticus str. C7303 EU1246
FJ749412.1 gg_id:564090 Lactobacillus helveticus str. IMAU50009; YN1-4-2 FJ7494
GQ155447.1 gg_id:580616 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ155579.1 gg_id:572925 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GU138582.1 gg_id:544201 Lactobacillus helveticus str. LSYM7-1 GU138
AY763429.1 gg_id:100251 Lactobacillus acidophilus str. LH4 AY7634
FJ749714.1 gg_id:568800 Lactobacillus helveticus str. IMAU30155; XC1-2 FJ7497
AB368911.1 gg_id:285740 Lactobacillus hilgardii str. T3-12 AB3689
EU177634.1 gg_id:336162 Lactobacillus hilgardii str. NS13 EU1776
NZ_ACLN01000018.1 gg_id:470599 Lactobacillus iners str. DSM 13335 NZ_AC
AF333975.1 gg_id:52162 Lactobacillus ingluviei str. KR3 AF3339
AF317703.1 gg_id:40447 Lactobacillus thermotolerans str. G 43 AF3177
AF317702.1 gg_id:44614 Lactobacillus thermotolerans str. G 35 AF3177
EU510751.1 gg_id:266445 cecal contents Mus musculus strain C57BL/6J; WD5 clone WD5_aak40f06 EU5107
DQ015194.1 gg_id:202045 Obesity alters gut microbial ecology mouse cecum clone M2_g10_2 DQ015
AF243143.1 gg_id:31979 Lactobacillus jensenii str. BLB1a AF2431
EU559597.1 gg_id:265038 Lactobacillus jensenii str. ZDY46a EU5595
FJ749487.1 gg_id:553705 Lactobacillus kefiranofaciens subsp. kefirgranum str. IMAU50089; YN37-1-1 FJ7494
AJ575259.1 gg_id:95575 Lactobacillus subsp. kefiranofaciens str. LMG 19149 AJ5752
AB362681.1 gg_id:239687 Lactobacillus kefiri str. NRIC 0586 AB3626
EU688976.1 gg_id:286983 Lactobacillus kefiri str. F3201 EU6889
D37784.1 gg_id:15194 Lactobacillus lindneri DA1 D37784
FM878596.1 gg_id:550949 Lactobacillus mali str. LA214 FM878
EU460788.1 gg_id:294550 short-beaked echidna feces clone ECH_aai38b03 EU4607
AF000163.1 gg_id:15212 Lactobacillus manihotivorans str. YAM I; LMG 18011 AF0001

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GU138543.1 gg_id:569931 Lactobacillus mindensis str. LSWM2-4 GU138
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EU821350.1 gg_id:538942 Lactobacillus oeni str. 103 EU8213
AY733083.1 gg_id:104517 Lactobacillus oligofermentans str. MARL13 AY733
X94230.1 gg_id:15148 Lactobacillus panis str. DSM 6035T X94230
AB257867.1 gg_id:158349 Lactobacillus pantheris FP37-1 AB2578
NR_025189.1 gg_id:573944 Lactobacillus pantheris str. LMG 21017 NR_02
AB512779.1 gg_id:580959 Lactobacillus parabrevis str. YIT 12113 AB512
AB297927.1 gg_id:253940 Lactobacillus senmaizukensis str. L13 AB2979
AB473626.1 gg_id:528967 Lactobacillus paracollinoides str. JCM 15729 AB473
NR_029039.1 gg_id:566740 Lactobacillus parakefiri str. GCL 1731; LMG 15133 NR_02
NR_025045.1 gg_id:550403 Lactobacillus kimchii str. MT-1077; AP1077; JCM 10707 NR_02
AB191250.1 gg_id:107631 Lactobacillus paraplantarum str. II 32 AB191
AY383631.1 gg_id:95489 Lactobacillus plantarum str. MiLAB14 AY383
DQ486145.1 gg_id:158659 Lactobacillus plantarum str. SFCB2-7c DQ486
GU138564.1 gg_id:557831 Lactobacillus plantarum str. LSBM6-5 GU138
AB362711.1 gg_id:249730 Lactobacillus pentosus str. NRIC 1554 AB362
AB362739.1 gg_id:238712 Lactobacillus plantarum str. NRIC 1739 AB362
EU559599.1 gg_id:264917 Lactobacillus plantarum str. ZDY128 EU5595
AB326363.1 gg_id:588823 Lactobacillus pobuzihi str. NBRC 103224 E100326 AB3263
X76329.1 gg_id:15142 Lactobacillus pontis str. LTH 2587 X76329
AJ422032.1 gg_id:76876 Lactobacillus pontis str. LMG 14187T = R-1465 AJ4220
GQ155597.1 gg_id:511199 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
CP000705.1 gg_id:231242 Lactobacillus reuteri F275 str. DSM 20016 CP000
CP000705.1 gg_id:231245 Lactobacillus reuteri F275 str. DSM 20016 CP000
EF412975.1 gg_id:214229 Lactobacillus reuteri str. C1 EF4129
GQ155514.1 gg_id:510643 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ156435.1 gg_id:591239 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
GQ155466.1 gg_id:556287 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EF412977.1 gg_id:203814 Lactobacillus reuteri str. C16 EF4129
EF097168.1 gg_id:185432 mouse cecum clone SWPT18_aaa02d05 EF0971
GQ155469.1 gg_id:585860 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ155455.1 gg_id:575693 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ155615.1 gg_id:579207 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ155669.1 gg_id:558815 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EF412976.1 gg_id:216761 Lactobacillus reuteri str. C10 EF4129
GQ155573.1 gg_id:538440 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
AY735406.1 gg_id:108135 Lactobacillus reuteri str. LU3 AY7354
GQ448922.1 gg_id:585264 Microbiome neonatal calves: shedding microorganisms fecal clone calf783_2wks_gr GQ448
GQ155509.1 gg_id:540888 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155

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AB425927.1 gg_id:555024 Lactobacillus reuteri str. TB-D21 AB425
AB370880.1 gg_id:268385 Lactobacillus rossiae str. DSM 15814 AB370
EU180606.1 gg_id:307389 Lactobacillus reuteri str. NS98 EU180
GU138515.1 gg_id:587018 Lactobacillus rossiae str. LSWM2-5 GU138
GU138561.1 gg_id:544158 Lactobacillus rossiae str. LSAM1-2 GU138
AB034088.1 gg_id:26075 rumen clone 3C3d-2 AB034
AB425942.1 gg_id:551940 Lactobacillus saerimneri str. TB-I37 AB425
AB186340.1 gg_id:137150 Lactobacillus salivarius str. DLS 0811 AB186
FJ751781.1 gg_id:593337 Lactobacillus salivarius str. 325T FJ7517
AJ422037.1 gg_id:76839 Lactobacillus sanfranciscensis str. C57 = R-15351 AJ4220
NR_028658.1 gg_id:585770 Lactobacillus satsumensis str. NRIC 0604 NR_02
AB370882.1 gg_id:276238 Lactobacillus siligionis str. NBRC 101315 AB370
AB458681.1 gg_id:591269 Lactobacillus sucicola str. NRIC 0735 AB458
AJ621556.2 gg_id:132461 Lactobacillus vaccinostercus str. LMG 9215 AJ6215
AB218799.1 gg_id:159914 Lactobacillus vaccinostercus str. YIT 10316 AB218
AJ315640.1 gg_id:74107 Lactobacillus durianis str. LMG 19193 AJ3156
AB218797.1 gg_id:160167 Lactobacillus vaccinostercus str. YIT 10300 AB218
EF460497.1 gg_id:215674 Lactobacillus vaginalis str. SR8 EF4604
NR_025371.1 gg_id:536754 Lactobacillus frumenti str. TMW 1.666; DSM 13145 NR_02
AB242320.1 gg_id:142448 Lactobacillus mobilis str. SIID2227-1-3b AB2423
AY699577.1 gg_id:106143 Lactobacillus casei str. LC2 AY6995
AF243146.1 gg_id:48136 Lactobacillus rhamnosus str. F11 AF2431
AY735405.2 gg_id:108112 Lactobacillus paracasei str. LPC4 AY7354
EU825659.1 gg_id:445624 Lactobacillus rhamnosus EU8256
AY852248.1 gg_id:110589 Lactobacillus rhamnosus str. P15 AY8522
AJ558112.1 gg_id:83495 Lactobacillus casei str. CWBI-B623 AJ5581
EF495247.1 gg_id:218969 Lactobacillus rhamnosus str. L60 EF4952
AY773957.1 gg_id:107860 Lactobacillus rhamnosus 5D AY7739
AB362692.1 gg_id:249164 Lactobacillus paracasei str. NRIC 0625 AB3626
AY773945.1 gg_id:108736 Lactobacillus casei str. BCRC10697 AY7739
AY773958.1 gg_id:107861 Lactobacillus rhamnosus 11D AY7739
AY675253.1 gg_id:100985 Lactobacillus rhamnosus str. LR3 AY6752
NZ_ABWJ01000068.1 gg_id:335393 Lactobacillus rhamnosus str. HN001 NZ_AB
EU456340.1 gg_id:329446 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H74 EU4563
EU454546.1 gg_id:325815 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU4545
EU453007.1 gg_id:331646 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75 EU4530
EF097456.1 gg_id:181526 mouse cecum clone SWPT19_aaa02h04 EF0974
EF096822.1 gg_id:181275 mouse cecum clone SWPT13_aaa01c03 EF0968
EU621849.1 gg_id:278869 Lactobacillus plantarum str. K2 EU6218
GU125607.1 gg_id:563127 Lactobacillus alimentarius str. IMAU80187 GU125

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FJ480209.1 gg_id:582919 Lactobacillus plantarum str. WCP931 FJ4802
EU453133.1 gg_id:323257 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H80N EU453
EF614861.1 gg_id:232078 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o EF6148
EU456847.1 gg_id:316572 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU4568
EU453072.1 gg_id:330003 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H78S EU453
EF097553.1 gg_id:182410 mouse cecum clone SWPT19_aaa04c08 EF0975
EU450981.1 gg_id:310929 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU450
AB362726.1 gg_id:250627 Lactobacillus plantarum str. NRIC 1592 AB3627
EU455101.1 gg_id:304585 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU455
AY445127.1 gg_id:107784 Lactobacillus sp. str. RA2113 AY445
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EU526815.1 gg_id:263646 Lactobacillus paracasei str. L7 EU5268
EU509472.1 gg_id:261492 cecal contents Mus musculus strain C57BL/6J; MD9 clone MD9_aap58h09 EU5094
GQ155657.1 gg_id:583427 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
AB186322.1 gg_id:136262 Lactobacillus johnsonii str. DLM 1701 AB1863
AM113780.1 gg_id:140659 Lactobacillus homohiochii str. DSM 20571 AM113
AY667698.1 gg_id:112026 Lactobacillus alvei str. 1G2 AY6676
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AB008209.1 gg_id:257632 Lactobacillus gasseri DSM 20243 AB0082
AY590777.1 gg_id:106640 Lactobacillus plantarum str. lp-onlly AY5907
AM113785.1 gg_id:139929 Lactobacillus suebicus str. DSM 5007 AM113
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EU456268.1 gg_id:336900 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K79S EU4562
EU455863.1 gg_id:318335 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83N EU4558
EU457595.1 gg_id:352447 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83N EU4575
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EU455929.1 gg_id:333597 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H79S EU4559
EU722746.1 gg_id:322818 Lactobacillus reuteri str. L7 EU7227
EU451068.1 gg_id:324226 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU451
EU773885.1 gg_id:320037 Cheetah feces clone CE2_b07 EU7738
EU455600.1 gg_id:353888 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N EU4556
EU463871.1 gg_id:293298 Seba's short-tailed bat feces clone bat_aaj06b09 EU4638
EU468211.1 gg_id:300202 lion feces clone LI1_f05_1 EU4682
DQ399354.1 gg_id:153558 Lactobacillus paracasei str. SFCB2-5 DQ399
AB366389.1 gg_id:553644 Lactobacillus rapi str. YIT 11204 (= NRIC 0743 = JCM 15 AB3663
EU457577.1 gg_id:320463 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU4575
FJ749595.1 gg_id:561759 Lactobacillus reuteri str. IMAU10037; ZL12-1-1 FJ7495
AB257866.1 gg_id:157489 Lactobacillus suebicus MCH2-2 AB2578

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EU081010.1 gg_id:246945 Lactobacillus plantarum str. BMG 114 EU081
EU456750.1 gg_id:334574 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N EU456
FJ975803.1 gg_id:509149 Human gut microbiome adopts alternative state bowel transplantation ileum effluent FJ9758
EU006413.1 gg_id:251090 Salmonella enterica serovar typhimurium exploits inflammation compete intestinal r EU006
AY675252.1 gg_id:100824 Lactobacillus casei str. LC3 AY675
NZ_ACGU01000081.1 gg_id:470670 Lactobacillus ultunensis str. DSM 16047 NZ_AC
AY253659.1 gg_id:85511 Lactobacillus antri str. Kx146A4; LMG 22111T; DSM 16041T; CCUG 48456T AY253
GU138587.1 gg_id:568871 Lactobacillus plantarum str. LSYM4-5 GU138
EF098449.1 gg_id:187083 mouse cecum clone SWPT15_aaa03c12 EF0984
DQ057469.1 gg_id:137125 str. ii1348 DQ057
AB366391.1 gg_id:565657 Lactobacillus otakiensis str. YIT 11452 AB366
EU455899.1 gg_id:319136 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU455
FJ645924.1 gg_id:536462 Lactobacillus crustorum str. 90 FJ6459
DQ141558.2 gg_id:138504 Lactobacillus plantarum str. HDRS1 DQ141
EU456125.1 gg_id:315311 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU456
GU292563.1 gg_id:569336 Lactobacillus reuteri str. Probio-16 GU292
EU074833.1 gg_id:238687 Lactobacillus plantarum str. TC110 EU074
AB326356.1 gg_id:236816 Lactobacillus acidipiscis str. NBRC 102163 AB326
EU452791.1 gg_id:345369 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H74N EU452
GQ900607.1 gg_id:549064 Lactobacillus plantarum str. F35 GQ900
EU510744.1 gg_id:272882 cecal contents Mus musculus strain C57BL/6J; WD5 clone WD5_aak40e08 EU510
EU509523.1 gg_id:265707 cecal contents Mus musculus strain C57BL/6J; MD9 clone MD9_aap60b05 EU509
EU474981.1 gg_id:302975 red river hog feces clone RRH_aaa01h07 EU474
AB267406.1 gg_id:257071 Lactobacillus hayakitensis KBL13 AB267
AM113777.1 gg_id:140651 Lactobacillus curvatus str. DSM 20019 AM113
DQ837634.1 gg_id:170784 structures honeybee intestines and their response insecticidal proteins gut clone HB DQ837
DQ837632.1 gg_id:166998 structures honeybee intestines and their response insecticidal proteins gut clone HB DQ837
FJ861114.1 gg_id:545513 Lactobacillus plantarum str. KLDS 1.0630 FJ8611
EF412984.1 gg_id:210733 Lactobacillus gallinarum str. I16 EF4129
EU457730.1 gg_id:356383 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU457
EU504703.1 gg_id:259372 cecal contents Mus musculus strain C57BL/6J; myd1 clone myd1_aaa04g05 EU504
EU454829.1 gg_id:346005 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H74N EU454
AY992212.1 gg_id:130575 mouse cecum clone C16_F15 AY992
EU452351.1 gg_id:356305 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU452
GQ900605.1 gg_id:583868 Lactobacillus plantarum str. F33 GQ900
EU510741.1 gg_id:272748 cecal contents Mus musculus strain C57BL/6J; WD5 clone WD5_aak40e01 EU510
EU510975.1 gg_id:266415 cecal contents Mus musculus strain C57BL/6J; WD6 clone WD6_aak52f08 EU510
Y19167.1 gg_id:15232 Lactobacillus perolens str. L532 Y19167
EF097249.1 gg_id:198443 mouse cecum clone SWPT18_aaa03g06 EF0972
GQ289389.1 gg_id:561949 Lactobacillus brevis str. YJ10 GQ289
EU505416.1 gg_id:274138 cecal contents Mus musculus strain C57BL/6J; myd4 clone myd4_aaa04b07 EU505

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AY253657.1 gg_id:84126 Lactobacillus kalixensis str. Kx127A2; LMG 22115T; DSM 16043T; CCUG 48459T AY2536
GQ156506.1 gg_id:536680 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
EU453934.1 gg_id:312564 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU4539
EU460844.1 gg_id:300935 short-beaked echidna feces clone ECH_aai39b05 EU4608
NC_009513.1 gg_id:232292 Lactobacillus reuteri F275 str. DSM 20016 NC_009
FM177140.1 gg_id:338587 Lactobacillus casei str. BL23 FM177
AM113783.1 gg_id:140595 Lactobacillus malefermentans str. DSM 5705 AM113
AB425933.1 gg_id:576004 Lactobacillus equigenerosi str. TB-F27 AB4259
AB330933.1 gg_id:240133 Lactobacillus paracasei str. 1532 AB3309
FJ532361.1 gg_id:585123 Lactobacillus plantarum str. 14W FJ5323
AJ272031.1 gg_id:73879 Lactobacillus plantarum str. HSW36 AJ2720
GQ900597.1 gg_id:590725 Lactobacillus plantarum str. A15 GQ900
AJ417499.1 gg_id:70957 Lactobacillus farciminis str. DSM 20185 AJ4174
AB018528.1 gg_id:18684 Lactobacillus paralimentarius str. TB 1 AB0185
EU457235.1 gg_id:336661 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H78S EU4572
EU453395.1 gg_id:326168 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU4533
GU177629.1 gg_id:582937 Lactobacillus casei str. 3-2 GU177
EU776515.1 gg_id:314385 Lion feces clone LI1_d02 EU7765
EU460828.1 gg_id:288584 short-beaked echidna feces clone ECH_aai38h04 EU4608
EF187245.1 gg_id:348593 Lactobacillus sp. str. Bin4 EF1872
EU504694.1 gg_id:259726 cecal contents Mus musculus strain C57BL/6J; myd1 clone myd1_aaa04f04 EU5046
AF243163.1 gg_id:43142 Lactobacillus sp. str. KC45a AF2431
GQ030443.1 gg_id:446566 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw878c09c GQ030
GQ155448.1 gg_id:591100 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
AB268119.1 gg_id:192776 Lactobacillus composti str. NRIC 0690 AB2681
EU454159.1 gg_id:323205 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU4541
EU510722.1 gg_id:265346 cecal contents Mus musculus strain C57BL/6J; WD5 clone WD5_aak40a07 EU5107
EU454340.1 gg_id:323666 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H79S EU4543
EU505289.1 gg_id:263903 cecal contents Mus musculus strain C57BL/6J; myd4 clone myd4_aaa01h10 EU5052
EU460768.1 gg_id:301085 short-beaked echidna feces clone ECH_aai37g02 EU4607
DQ815603.1 gg_id:171781 mouse cecum clone aab43d12 DQ815
EF097628.1 gg_id:177863 mouse cecum clone SWPT20_aaa01e05 EF0976
FN185731.1 gg_id:578837 Lactobacillus sp. 1.1424 FN1857
EU453153.1 gg_id:324998 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N EU4531
EU454019.1 gg_id:313356 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75N EU4540
AM500777.1 gg_id:534519 proof spatial heterogeneity hot composting clone E12 AM500
FJ751792.1 gg_id:568482 Lactobacillus farciminis str. DSPV 353T FJ7517
AB512778.1 gg_id:559510 Lactobacillus lindneri str. YIT 10387 AB5127
EU505411.1 gg_id:271014 cecal contents Mus musculus strain C57BL/6J; myd4 clone myd4_aaa04a08 EU5054
GQ131124.1 gg_id:436188 Lactobacillus casei str. IMAU70007; BM2302 GQ131

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AB048833.1 gg_id:74053 Lactobacillus equi str. YIT 0455 AB048
DQ014569.1 gg_id:133995 mouse cecum clone M1_b08 DQ014
EU776667.1 gg_id:351922 Lion feces clone LI2_aae47g12 EU776
EU728754.1 gg_id:340933 Lactobacillus reuteri str. DJF_RP45 EU728
FJ192637.1 gg_id:356529 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior FJ1926
EF098373.1 gg_id:192635 mouse cecum clone SWPT15_aaa01g09 EF0983
EF096254.1 gg_id:189201 mouse cecum clone obob1_aaa03e05 EF0962
AM279150.1 gg_id:185189 Lactobacillus secaliphilus str. TMW 1.1309 AM279
EU457030.1 gg_id:353708 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU457
Y11374.1 gg_id:15179 Lactobacillus kunkeei str. YH-15 Y11374
EU454221.1 gg_id:326198 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H80N EU454
AF197125.1 gg_id:15202 Lactobacillus sp. str. C33LV5 AF197
EU419599.1 gg_id:275265 Lactobacillus plantarum str. KLDS 1.0623 EU419
EU463024.1 gg_id:297096 southern three-banded armadillo feces clone arma_aaj56f06 EU463
AB284944.1 gg_id:177366 Lactobacillus sp. str. TS1 AB284
DQ015596.1 gg_id:130744 mouse cecum clone M3_a03_3 DQ015
GQ202837.1 gg_id:551236 Lactobacillus plantarum str. C06 GQ202
EF096361.1 gg_id:174939 mouse cecum clone obob2_aaa01f01 EF0963
EU504983.1 gg_id:260003 cecal contents Mus musculus strain C57BL/6J; myd3 clone myd3_aaa01b10 EU504
AY281292.1 gg_id:105149 Lactobacillus curvatus str. KNUC04 AY281
X76330.1 gg_id:15190 Lactobacillus fructivorans str. DSM 20203 T X7633
AAPZ02000002.1 gg_id:325109 Lactobacillus reuteri str. 100-23 AAPZ0
AY735409.1 gg_id:108246 Lactobacillus plantarum str. LP2 AY735
EU507666.1 gg_id:270372 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_aaa02g07 EU507
EU451014.1 gg_id:316980 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU451
DQ239699.1 gg_id:144704 Lactobacillus plantarum str. L6 DQ239
EU460890.1 gg_id:302821 short-beaked echidna feces clone ECH_aai40a07 EU460
EU455582.1 gg_id:335842 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU455
GQ155531.1 gg_id:594070 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EU453262.1 gg_id:311179 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU453
AB498046.1 gg_id:590362 Lactobacillus sp. str. F9-2 AB498
EF096134.1 gg_id:191524 mouse cecum clone obob1_aaa01b04 EF0961
AJ417738.1 gg_id:56512 Lactobacillus letivazi str. JCL3994 AJ4177
EU453171.1 gg_id:337918 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K77S EU453
NC_009513.1 gg_id:232290 Lactobacillus reuteri F275 str. DSM 20016 NC_00
NR_028617.1 gg_id:577716 Lactobacillus algidus str. M 6 A9; JCM 10491 NR_02
DQ015578.1 gg_id:133239 mouse cecum clone M3_g04_2 DQ015
EU451147.1 gg_id:340145 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75N EU451

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0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0