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AF043742.1 gg_id:22902 Pseudoalteromonas distincta str. KMM 638T; ATCC700518 AF0437
FJ202088.1 gg_id:326316 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2020
EU050781.1 gg_id:246147 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_02_66 EU0507
FJ403097.1 gg_id:359108 Disease- changes healthy and diseased colonies Caribbean coral Montastrea faveolat FJ4030
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EF101548.1 gg_id:192719 Psychromonas arctica str. KOPRI24930 EF1015
AB365349.1 gg_id:275002 Psychromonas heitensis str. 04HE-4-40 (= MBIC 08331) AB3653
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U14582.1 gg_id:9115 gas vacuolate str.90-P<gv>1 U14582
AJ969456.1 gg_id:157483 Microbial black smoker s Mid Atlantic Ridge ecological implications rock fragments ch AJ9694
AF374385.1 gg_id:38990 Psychromonas arctica str. Pull 5.3 AF3743
AY548987.2 gg_id:99098 marine bone clone sacC3D3 AY5489
U85849.1 gg_id:9117 Psychromonas sp. str. IC004 U85849
AB304804.1 gg_id:236309 Psychromonas sp. str. JAMM 0394 AB3048
DQ009471.1 gg_id:126016 bacterioplankton clone SPOTSMAY03_890m29 DQ009
AB374544.1 gg_id:264272 Psychromonas sp. str. J42-3A AB3745
U73722.1 gg_id:9120 gas vacuolate str. 174 U73722
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AB304807.1 gg_id:252707 Psychromonas sp. str. JAMM 0700 AB3048
AY167326.1 gg_id:81340 Psychromonas sp. str. ANT9265 AY1673
AJ519627.1 gg_id:76528 uranium mill tailings soil clone Sh765B-TzT-48 AJ5196
AF235108.1 gg_id:71948 Alteromonas sp. str. KT1114 AF2351
DQ530480.1 gg_id:166114 Psychromonas sp. str. gape-82 DQ530
AJ416756.1 gg_id:25724 Psychromonas profunda str. 2825 AJ4167
FM994680.1 gg_id:561093 gill and deep-sea limpet Pectinodonta sp. digestive tract host on sunken wood deptl FM994
EF542799.1 gg_id:224364 Shewanella algae str. YJ06114 EF5427

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CP000302.1 gg_id:156979 Shewanella denitrificans str. OS217
AY771713.1 gg_id:137368 Shewanella frigidimarina str. S2-60
CP000447.1 gg_id:170610 Shewanella frigidimarina str. NCIMB 400
CP000931.1 gg_id:270485 Shewanella halifaxensis str. HAW-EB4
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NC_009092.1 gg_id:212572 Shewanella loihica str. PV-4
AB081762.1 gg_id:55880 Shewanella sairae str. SM2-1
NC_004347.1 gg_id:141355 Shewanella oneidensis str. MR-1
NC_004347.1 gg_id:141641 Shewanella oneidensis str. MR-1
AF145921.1 gg_id:9077 Shewanella japonica str. KMM 3299
CP000851.1 gg_id:249615 Shewanella pealeana str. ATCC 700345
NC_011566.1 gg_id:360003 Shewanella piezotolerans str. WP3
NC_011566.1 gg_id:360008 Shewanella piezotolerans str. WP3
AB081761.1 gg_id:60926 Shewanella schlegeliana str. HRKC24
CP000821.1 gg_id:253801 Shewanella sediminis str. HAW-EB3
NC_009831.1 gg_id:246709 Shewanella sediminis str. HAW-EB3
AF136392.1 gg_id:137029 Shewanella sp. str. ANA-3
NZ_AAUO01000015.1 gg_id:183742 Shewanella woodyi str. ATCC 51908

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AF005255.1 gg_id:9108 Shewanella putrefaciens str. MR-30 AF005
AF170300.1 gg_id:70300 Shewanella putrefaciens str. IR-1 AF170
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FJ952791.1 gg_id:372983 Shewanella sp. str. 3tb16 FJ9527
AF039055.1 gg_id:9060 Shewanella oneidensis str. SP-22 AF039
AY902211.1 gg_id:113783 Shewanella sp. str. BR2 AY902
AM269901.1 gg_id:159850 Shewanella sp. str. ES-5 AM269
AM180742.1 gg_id:146524 Shewanella gaetbuli UL19 AM180
DQ537513.1 gg_id:161502 Shewanella frigidimarina str. BSi20544 DQ537
NR_025794.1 gg_id:561965 Shewanella aquimarina str. SW-120; KCCM 41821 NR_02
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DQ325517.1 gg_id:148004 Shewanella sp. str. 62 DQ325
EF105398.1 gg_id:175874 Shewanella sp. str. IE9-3 EF1053
AF022402.1 gg_id:9027 Shewanella sp. ANG.209 str. ANG.strain 209 ANG.209 AF0224
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DQ665797.1 gg_id:173544 Shewanella frigidimarina str. BSi20542 DQ665
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DQ307731.1 gg_id:147165 Shewanella putrefaciens str. Hac411 DQ307
AF387347.1 gg_id:33931 Shewanella oneidensis str. DML7 AF3873
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AB205567.1 gg_id:114271 Shewanella colwelliana str. Q-06 AB205
AB205578.1 gg_id:114304 Shewanella baltica str. W145 AB205
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NZ_AATK01000145.1 gg_id:166958 Shewanella baltica str. OS195 NZ_AA
NR_029070.1 gg_id:575480 Shewanella gaetbuli str. TF-27; JCM 11814 NR_02
FJ210800.1 gg_id:328373 Shewanella algae str. QDHT-04 FJ2108
AF132874.1 gg_id:113095 Shewanella frigidimarina str. ACAM 517 AF1328
AY485224.1 gg_id:106352 Shewanella marisflavi str. SW-117 AY485
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AB204519.1 gg_id:137352 Shewanella pneumatophori str. SCRC-2738	AB204
AF132878.1 gg_id:38945 Shewanella frigidimarina str. ACAM 557	AF1328
EU290154.1 gg_id:256999 Shewanella marinus str. C4	EU290
DQ167234.1 gg_id:139040 Shewanella sp. str. HJ039	DQ167
DQ520894.1 gg_id:159825 Shewanella frigidimarina str. BSi20531	DQ520
EF105397.1 gg_id:179131 Shewanella sp. str. IE9-1	EF1053
AJ288152.1 gg_id:22553 Shewanella sp. Bok-1-30-2	AJ2881
DQ351772.1 gg_id:147472 Microbial Adherent Sediment Particles Heavy Metal Contaminated North Sea Surfac	DQ351
EU427307.1 gg_id:265579 Shewanella sp. MSI04	EU4273
FJ169987.1 gg_id:323759 Shewanella sp. str. E505-14	FJ1699
CP001252.1 gg_id:527693 Shewanella baltica str. OS223	CP0012
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AF011335.1 gg_id:9032 Shewanella pealeana str. ANG-SQ1	AF0113
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AB306516.1 gg_id:247972 Shewanella sp. str. MIB015	AB3065
AM990834.1 gg_id:278789 Shewanella sp. MOLA 59	AM990
AY170366.1 gg_id:69757 Shewanella waksmanii str. KMM 3823	AY1703
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AB094597.1 gg_id:83672 Shewanella surugaensis str. c959 AB094
AY445591.1 gg_id:103376 Shewanella profunda str. LT13a AY445
NC_009665.1 gg_id:255224 Shewanella baltica str. OS185 NC_00
AF132873.1 gg_id:37061 Shewanella frigidimarina str. ACAM 516 AF132
Y13699.1 gg_id:9053 Shewanella frigidimarina str. NCIMB 400 Y13699
AY351983.1 gg_id:92948 Shewanella affinis str. KMM 3587 AY351
GQ869534.1 gg_id:569132 Shewanella sp. str. KCCM 42936 GQ869
NC_009831.1 gg_id:246705 Shewanella sediminis str. HAW-EB3 NC_00
AB013839.1 gg_id:9017 Shewanella sp. 3-8.C AB013
NR_025934.1 gg_id:540854 Cardiobacterium hominis str. 6573; ATCC 15826 NR_02
AY596470.1 gg_id:104981 Cardiobacterium valvarum str. CCUG12990 AY596
DQ645464.1 gg_id:160756 Cardiobacterium valvarum VA1941 DQ645
CP000513.1 gg_id:226003 Dichelobacter nodosus str. VCS1703A CP000
AJ717394.1 gg_id:149350 Suttonella ornithocola str. B6/99/2 AJ717
X92131.1 gg_id:46026 Lake Elmenteita isolate 2E1 X92131
AF384209.1 gg_id:25151 Chromatium sp. str. NZ AF384
AM712619.1 gg_id:237043 Allochromatium phaeobacterium str. JA144 AM712
FJ716332.1 gg_id:508808 Chlorobi dominate shal chemocline Bahamas Sawmill Sink column 10.3 m water dept FJ7163
AF384208.1 gg_id:22729 Chromatium sp. str. NM2 AF384
NR_025315.1 gg_id:559119 Chromatium okenii str. DSM 169 NR_02
FJ437816.1 gg_id:541203 Benthic okenone production Fayetteville New York Green Lake chemocline 20.5 m wa FJ4378
AB478662.1 gg_id:548000 SSU sequences Alps Cadagno di Fuori submerged biofilm mats montane wetland clo AB478
DQ330802.1 gg_id:159452 Guerrero Negro hypersaline microbial mat clone 02D2Z45 DQ330
AJ223235.1 gg_id:7564 Lamprocystis purpurea str. DSM 4197 AJ2232
AM941378.1 gg_id:344367 Marichromatium indicum str. JA122 AM941
AM941379.1 gg_id:304631 Marichromatium indicum str. JA210 AM941
AM179449.1 gg_id:190862 Marichromatium imhoffii str. JA120 1 AM179
AM941377.1 gg_id:325577 Marichromatium indicum str. JA214 AM941
AM941046.1 gg_id:369706 Marichromatium indicum JA347 AM941
AJ889020.1 gg_id:112951 Marichromatium chilcum str. CH8 AJ889
FJ376391.1 gg_id:360805 Marichromatium purpuratum str. DSM 1711 FJ3763
FM177512.1 gg_id:344391 Marichromatium indicum str. JA290 FM177
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AF294030.1 gg_id:135580 Marichromatium purpuratum str. TAR AF294
FM177510.1 gg_id:333563 Marichromatium bheemlicum str. JA284 FM177
EU850807.1 gg_id:342759 Marichromatium purpuratum str. DSM 1591 EU850
AM180952.1 gg_id:148217 Marichromatium bheemlicum str. JA124 AM180
AJ543328.1 gg_id:111805 Marichromatium indicum str. JA100 AJ5433
AF508991.1 gg_id:71278 Nitrosococcus oceani str. SWC19 AF508

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AF508992.1 gg_id:56278 Nitrosococcus oceani str. AFC3 AF5089
AJ298748.1 gg_id:77717 Nitrosococcus halophilus AJ2987
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AM779060.1 gg_id:261543 Thiocapsa subramanianii str. JA146 AM779
AJ581994.1 gg_id:141744 Thiocapsa marina str. BM-3 AJ5819
AF112998.1 gg_id:7532 Thiocapsa roseopersicina str. 5811 AF1129
EF581005.1 gg_id:278653 Thiocapsa roseopersicina str. KS1 EF5810
AJ277022.1 gg_id:71426 Thiococcus sp. str. A31 AJ2770
Y12373.3 gg_id:71248 Thiococcus pfennigii str. 4250 Y12373
FN293055.1 gg_id:570678 Thiococcus pfennigii str. 4252 = DSM 228 FN2930
FN293058.1 gg_id:536936 Thiocystis gelatinosa str. 4310 = DSM 215 FN2930
D50655.1 gg_id:7517 Thiocystis gelatinosa D50655
AJ224438.1 gg_id:7518 Thiocystis violascens str. DSM 168T AJ2244
EF149014.1 gg_id:188673 Thiocystis sp. str. Mog3 EF1490
AM086640.1 gg_id:139588 Thiocystis sp. str. 448.10 AM086
AJ971090.1 gg_id:172979 Thiorhodococcus mannitophagus str. WS AJ9710
Y11316.1 gg_id:7526 Thiorhodococcus minor str. CE2203 Y11316
AM748925.1 gg_id:245986 Thiophaeococcus mangrovi str. JA304 AM748
AB016986.1 gg_id:7570 Thiorhodovibrio winogradskyi str. MBIC2776T AB0169
AB294924.1 gg_id:225518 -dependent & analyses hydrothermal system off Taketomi Island Japan microbial ma AB2949
DQ867045.1 gg_id:196530 Microbial and methanogenic potential temperature water Japan natural gas field clo DQ867
FJ535065.1 gg_id:545461 microbial colonizing walls Karstic Slovenia cave wall biofilm clone 2PJM13 FJ5350
AF420353.1 gg_id:55790 hydrothermal sediment clone AF420353 AF4203
DQ811841.1 gg_id:166871 mangrove soil clone MSB-4C11 DQ811
DQ395021.1 gg_id:152376 harbor sediment clone VHS-B5-48 DQ395
FJ712412.1 gg_id:516020 and Archaea Gas Hydrate Sediments (East Sea) Kazan Mud Volcano Anaximander Mo FJ7124
AY225634.1 gg_id:95183 Mid-Atlantic Ridge hydrothermal sediment clone AT-s26 AY2256
EU373841.1 gg_id:265007 southern Cretan margin (eastern Mediterranean Sea) canyon and slope sediment clo EU3738
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GU369919.1 gg_id:524281 and mats vents Arc white microbial film on pebble aphotic zone shal hydrothermal v GU369
FJ203535.1 gg_id:340951 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h FJ2035
EU617747.1 gg_id:337743 Seasonal variation microbial Yel Sea sediment clone C13S-68 EU617
FM877665.1 gg_id:362822 Microbial several mining wastes Bulgaria vicinity uranium mine Sliven clone Sliv-109 FM877
DQ499304.1 gg_id:159535 acidic cave snottite biofilm clone CV55 DQ499
EU050785.1 gg_id:254811 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_01_66 EU050
GU061986.1 gg_id:593500 and function microbial mesoscale eddy perturbations South China Sea clone S-DCM- GU061
AY225631.1 gg_id:96909 Mid-Atlantic Ridge hydrothermal sediment clone AT-s2-13 AY2256
EU652572.1 gg_id:278349 Seasonal variation microbial Yel Sea sediment clone B8S-132 EU6525
DQ269059.1 gg_id:182899 marine macro-alga surface clone UA09 DQ269

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

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EU246808.1 gg_id:241908 polyphasic description Pocillopora meandrina Palmyra Atoll Calcinus obscurus abdon EU246
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GU230383.1 gg_id:561498 Multilevel approach along Rio de la Plata-South Atlantic Ocean coastal water clone A GU230
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EU700176.1 gg_id:296708 Study on Shantou Bay Marine Sediments Microorganisms sediment clone STU34 EU700
EU800034.1 gg_id:307663 It's all ranking aquatic Newport Harbour RI clone 1C227721 EU800
GU118033.1 gg_id:579643 Threatened Corals Provide Microbial Habitats clone Apal_F02 GU118
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EF076070.1 gg_id:256660 Sponge- microorganisms: ecology and biotechnological potential Bahamas: Little San EF076
AB426192.1 gg_id:267544 -situ identification study benzene-degrading s under methanogenic condition anaerc AB426
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GQ406158.1 gg_id:593544 Benthic submerged sinkhole ecosystems sediment clone TS-45-9 GQ406
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DQ408758.1 gg_id:241921 endosymbionts gutless marine nematode Astomonema sp. sediments coral reef sed DQ408
EU555131.1 gg_id:265444 Microbial Sulfide Hydrothermal Vent Field Juan de Fuca Ridge Dudley hydrothermal EU555
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AM882566.1 gg_id:314376 Structure along hydrocarbon contamination coastal sediment oil polluted water pet AM882
EU050809.1 gg_id:253074 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_01_83 EU0508
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EU491139.1 gg_id:272596 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak EU491
AB294972.1 gg_id:225408 -dependent & analyses hydrothermal system off Taketomi Island Japan microbial ma AB2949
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AM282561.1 gg_id:193170 Thiorhodococcus kakinadaii str. JA130 AM282
AACY01032263.1 gg_id:105207 Sargasso Sea AACY0
EU491349.1 gg_id:260349 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X3 clone EU491
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AM997970.1 gg_id:541611 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A AM997
EU491101.1 gg_id:271612 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak EU491
EF208706.1 gg_id:202468 Vertical and horizontal structure microbial sandy carbonate sediment clone CI75cm.2 EF2087
EU617749.1 gg_id:332804 Seasonal variation microbial Yel Sea sediment clone D13S-16 EU617
NR_029333.1 gg_id:589849 Thiocystis violacea str. N. Pfennig 2711; DSM 207 NR_02
DQ676383.1 gg_id:219789 Archaeal sediment and plankton freshwater pond suboxic freshwater-pond clone M DQ676
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AJ002796.2 gg_id:7556 Thiohalocapsa halophila str. SG3202 AJ0027
DQ330805.1 gg_id:159272 Guerrero Negro hypersaline microbial mat clone 02D2Z63 DQ330
EU236358.1 gg_id:295840 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg91C2 EU2363
FM242313.1 gg_id:328728 sequences sediment clone 25 T9d-oil FM242
FJ264656.1 gg_id:346479 Manganese and Iron Dependent Anaerobic Oxidation Methane methane seep sedime FJ2646
AF328856.1 gg_id:43810 Olavius algarvensis sulfur-oxidizing endosymbiont sulfur-oxidizing AF3288
AJ620507.1 gg_id:108086 Olavius crassitunicatus endosymbiont AJ6205
AM934861.1 gg_id:560973 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM934
AY953181.1 gg_id:114439 anaerobic swine lagoon clone B-1O AY953

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AJ404006.1 gg_id:67655 Thiobaca trueperi str. BCH AJ4040
AF468306.1 gg_id:80943 Arctic sea ice; northern Fram Strait clone ARKICE-74 AF4683
EU035919.2 gg_id:305967 Insight microbial structure Norwegian deep-water Desmacidon sponge deep-sea cor EU0359
FM242312.1 gg_id:323358 sequences sediment clone 62 T9d-oil FM242
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DQ834966.1 gg_id:239144 Methylohalomonas lacustra DQ834
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EU617748.1 gg_id:327160 Seasonal variation microbial Yel Sea sediment clone D13S-78 EU617
FJ971740.1 gg_id:437967 microbial autrotrophic denitrification granular sludge clone R2-B11 FJ9717
EF999974.1 gg_id:245668 Thiodictyon bacillosum str. DSM 234T EF9999
FJ712507.1 gg_id:529626 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) K FJ7125
EF999973.1 gg_id:257959 Thiodictyon elegans str. DSM 232T EF9999
AB186842.1 gg_id:103037 polychlorinated dioxin dechlorinating microcosm clone TSBX13 AB1868
GQ249599.1 gg_id:509542 Microbial anaerobic sediments Bay Cadiz (Spain) marine sediment: 12-14 cm layer cl GQ249
GQ347493.1 gg_id:540052 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ347
AF223299.1 gg_id:31454 marine sediment clone B2M60 AF2232
EU652571.1 gg_id:279434 Seasonal variation microbial Yel Sea sediment clone A8S-46 EU6525
FJ358866.1 gg_id:580890 and redox-stratified sediments marine reef sandy sediment clone OX79 FJ3588
FJ264672.1 gg_id:348014 Manganese and Iron Dependent Anaerobic Oxidation Methane methane seep sedim FJ2646
DQ867047.1 gg_id:186089 Microbial and methanogenic potential temperature water Japan natural gas field cl DQ867
GQ246364.1 gg_id:593033 Temporal and spatial China North Yel Sea sediments clone Cm1-27 GQ246
GU056102.1 gg_id:571289 Biologic Techniques Applied Microbial Prospecting China: Ban 876 Gas Oil Field Bein GU056
AB530206.1 gg_id:586045 Monitoring Suez and Tokyo bays based on analyses marine sediment clone Tokyo..B AB5302
AB530192.1 gg_id:549648 Monitoring Suez and Tokyo bays based on analyses marine sediment clone Suez..Ba AB5301
DQ269062.1 gg_id:190822 marine macro-alga surface clone DPC061 DQ269
EU134786.1 gg_id:243086 tallgrass prarie soil clone FFCH2627 EU1347

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AJ853601.1 gg_id:110147 landfill leachate clone GZKB108 AJ8536
EU236373.1 gg_id:297512 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg91G3 EU2363
AY225627.1 gg_id:96329 Mid-Atlantic Ridge hydrothermal sediment clone AT-s68 AY2256
FJ497388.1 gg_id:579158 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun FJ4973
EF632940.1 gg_id:242102 Unique microbial contrasting aquatic altitude Andean Altiplano (northern Chile) fresh EF6329
EU491429.1 gg_id:261838 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X4 clone EU4914
DQ811847.1 gg_id:164335 mangrove soil clone MSB-5C2 DQ811
DQ811843.1 gg_id:172303 mangrove soil clone MSB-4E4 DQ811
EF203207.1 gg_id:207236 phylotypes sediments Lake Kastoria Greece sediment clone Kas176B EF2032
FM877666.1 gg_id:366930 Microbial several mining wastes Bulgaria vicinity uranium mine Sliven clone Sliv-112 FM877
AY225635.1 gg_id:98613 Mid-Atlantic Ridge hydrothermal sediment clone AT-s80 AY2256
DQ811842.1 gg_id:171222 mangrove soil clone MSB-4D7 DQ811
AY328773.1 gg_id:88634 drinking water system simulator clone DSSD75 AY3287
DQ351776.1 gg_id:146277 Microbial Adherent Sediment Particles Heavy Metal Contaminated North Sea Surfac DQ351
FJ937836.1 gg_id:397082 Marine Sponge Gelliodes carnosa coastal waters Lingshui Bay Hainan Island South Ch FJ9378
EU236293.1 gg_id:290042 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg9Co20 EU2362
GU208274.1 gg_id:568003 Study on Sediment Dongping Lake sediment clone 6F3-6 GU208
GU118056.1 gg_id:580801 Threatened Corals Provide Microbial Habitats clone Apal_E11 GU118
AB188772.1 gg_id:114044 cold seep sediment clone SB1-7 AB1887
FJ205206.1 gg_id:559269 Prokaryotic deep-sea region East Lau Spreading Centre inactive hydrothermal field se FJ2052
GQ356981.1 gg_id:557781 Metal Dependent Marine Methane Oxidation methane seep sediment clone FeSO4_ GQ356
GU369933.1 gg_id:527507 and mats vents Arc white microbial film on pebble aphotic zone shal hydrothermal v GU369
EF612432.1 gg_id:244758 historic semiarid lead-zinc site mine tailings clone Fe-K6-C35 EF6124
EU491147.1 gg_id:261461 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak EU4911
DQ823153.1 gg_id:167115 Techniques Microbial Studies Oregon Caves National Monument Quad 3 off trail clo DQ823
AB189342.1 gg_id:113899 cold seep sediment clone JT58-17 AB1893
CP000453.1 gg_id:171890 Alkalilimnicola ehrlichei str. MLHE-1 CP0004
AJ404972.1 gg_id:46869 Alkalilimnicola halodurans 34Alc AJ4049
DQ217918.1 gg_id:142576 Alkalispirillum sp. str. AGDZ DQ217
DQ217919.1 gg_id:142198 Alkalispirillum sp. str. ALPs 2 DQ217
EU308278.1 gg_id:358039 Arhodomonas sp. str. 50B226a_1 EU3082
EU653291.1 gg_id:280943 Thiobacillus prosperus str. DSM 5130 EU6532
EU653290.1 gg_id:282074 Thiobacillus prosperus str. V6 EU6532
AY298904.1 gg_id:89646 Ectothiorhodosinus mongolicum str. M9 AY2989
EU590916.1 gg_id:265489 Ectothiorhodospira sp. str. PHS-1 EU5909
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AM902494.1 gg_id:571311 Ectothiorhodospira imhoffii str. JA319 AM902
FN293051.1 gg_id:562547 Halorhodospira halophila str. 9622 FN2930
AJ318525.1 gg_id:62637 Halorhodospira neutrophila str. SG 3301 AJ3185
FJ153016.1 gg_id:323860 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX4CI FJ1530
NZ_ABYM01000001.1 gg_id:349593 Thioalkalivibrio sp. str. HL-EbGR7 NZ_AB

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

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AM935364.1 gg_id:548480 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM935
EF157150.1 gg_id:245575 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon EF1571
AM936329.1 gg_id:560668 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM936
DQ378188.1 gg_id:153768 oil-polluted soil clone F24_Pitesti DQ378
M90662.1 gg_id:7758 Halothiobacillus hydrothermalis str. r3 M9066
AJ294337.1 gg_id:76987 Halothiobacillus hydrothermalis HY-66 AJ2943
AF170419.1 gg_id:19288 Halothiobacillus kellyi str. BII-1 AF1704
EU124668.1 gg_id:242036 Thioalkalibacter halophilus str. ALCO1 EU124
AF173169.1 gg_id:44985 Halothiobacillus neapolitanus str. DSM 581 AF1731
EU196318.1 gg_id:239328 Halothiobacillus sp. NP37 EU1963
EU245085.1 gg_id:256790 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-H1-G02 EU245
EU101029.1 gg_id:246599 Sulfide/oxygen supply ratio predicts outcome competition among sulfur-oxidizing wa EU101
EU101026.1 gg_id:246095 Sulfide/oxygen supply ratio predicts outcome competition among sulfur-oxidizing wa EU101
EU101090.1 gg_id:239627 Sulfide/oxygen supply ratio predicts outcome competition among sulfur-oxidizing wa EU101
AF154088.1 gg_id:7760 hydrocarbon seep clone BPC028 AF154
EU101065.1 gg_id:238117 Sulfide/oxygen supply ratio predicts outcome competition among sulfur-oxidizing wa EU101
EU101080.1 gg_id:251622 Sulfide/oxygen supply ratio predicts outcome competition among sulfur-oxidizing wa EU101
GU196195.1 gg_id:587626 Bioaugmentation improved recovery digesters after toxicant exposure lab-scale ana GU196
AM950234.1 gg_id:554439 Sulphide oxidation elemental sulphur membrane bioreactor: Performance and selec AM950
AB473891.1 gg_id:549132 sequences Cadagno di Fuori biofilm mat alpine wetland varying conductivities clone AB4738
EU037214.1 gg_id:252299 Hot Spring Microbial Mat Khir Ganga India hot spring microbial mat clone MO20 EU0372
GU390833.1 gg_id:530086 Dark hot springs: structure biofilms caves Acquasanta Terme (Italy) sulfidic cave stre GU390
GU390794.1 gg_id:519254 Dark hot springs: structure biofilms caves Acquasanta Terme (Italy) sulfidic cave stre GU390
GU390789.1 gg_id:517389 Dark hot springs: structure biofilms caves Acquasanta Terme (Italy) sulfidic cave stre GU390
GU196237.1 gg_id:577717 Bioaugmentation improved recovery digesters after toxicant exposure lab-scale ana GU196
EU101158.1 gg_id:236588 Sulfide/oxygen supply ratio predicts outcome competition among sulfur-oxidizing wa EU1011
GU390879.1 gg_id:515900 Dark hot springs: structure biofilms caves Acquasanta Terme (Italy) sulfidic cave stre GU390
DQ354745.1 gg_id:154107 subsurface water clone MS149BH1062003_5 DQ354
EU101063.1 gg_id:237262 Sulfide/oxygen supply ratio predicts outcome competition among sulfur-oxidizing wa EU101
EF467492.1 gg_id:214022 situ microelectrode voltammetry sulfur-oxidizing biofilms Frasassi sulfidic cave strear EF4674
DQ459215.1 gg_id:160856 Microbial consortia involved anaerobic degradation unsaturated and saturated LCFA DQ459
EU101162.1 gg_id:245464 Sulfide/oxygen supply ratio predicts outcome competition among sulfur-oxidizing wa EU1011
AY493939.1 gg_id:136667 Fingerprinting aggregates soil clone 455 AY4939
EU134704.1 gg_id:248771 tallgrass prarie soil clone FFCH11229 EU1347
GQ264259.1 gg_id:513055 Structure Simulated Level Waste Site simulated level waste site clone WW1_b62 GQ264
FJ535077.1 gg_id:584489 microbial colonizing walls Karstic Slovenia cave wall biofilm clone 3PJM60 FJ5350
DQ123669.1 gg_id:137171 'Division Labor' Degradation Polycyclic Aromatic Hydrocarbons Bioreactor Treating C DQ123
EU449562.1 gg_id:568421 Soil are Changed Agricultural Practices agricultural soil clone Plot4-D11 EU4495
EF605262.1 gg_id:262257 Steroidobacter denitrificans str. FS EF6052
EU202849.1 gg_id:313985 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo EU2028

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EF688386.1 gg_id:254180 soil clone F6-105 EF6883
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EU150278.1 gg_id:277979 acidobacteria and soil Niwot Ridge LTER clone Ni_D05_SFDN EU150
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EU150274.1 gg_id:278484 acidobacteria and soil Niwot Ridge LTER clone Ni_H9P1 EU150
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FJ672005.1 gg_id:516961 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6720
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EU193057.1 gg_id:366851 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo EU1930
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FJ545453.1 gg_id:513570 Diveristy Seawater and Sediment Northern North Yel Sea sediment clone S1-23 FJ5454
EU491448.1 gg_id:261579 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X4 clone EU4914

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EU491127.1 gg_id:276781 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak EU491
DQ351813.1 gg_id:146081 Microbial Adherent Sediment Particles Heavy Metal Contaminated North Sea Surfac DQ351
FJ202756.1 gg_id:338034 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2027
AJ567537.1 gg_id:90195 deep-sea sediment clone MBMPE11 AJ5675
DQ270631.1 gg_id:142048 hydrothermal carbonate chimney clone LC1446B-88 DQ270
EF125454.1 gg_id:175214 mangrove soil clone MSB-2F9 EF1254
EU617769.1 gg_id:336977 Seasonal variation microbial Yel Sea sediment clone C13S-11 EU617
EU491671.1 gg_id:269207 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU491
EU373852.1 gg_id:265200 southern Cretan margin (eastern Mediterranean Sea) canyon and slope sediment clc EU3738
EU617762.1 gg_id:339270 Seasonal variation microbial Yel Sea sediment clone D13S-135 EU617
AB015576.1 gg_id:7632 deep-sea sediment clone BD6-6 AB015
EU617760.1 gg_id:353103 Seasonal variation microbial Yel Sea sediment clone D13S-8 EU617
FM242213.1 gg_id:305299 sequences sediment clone 305 T0h-oil FM242
FJ203584.1 gg_id:324521 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h FJ2035
DQ351767.1 gg_id:145747 Microbial Adherent Sediment Particles Heavy Metal Contaminated North Sea Surfac DQ351
FJ416135.1 gg_id:366945 sediments sediment station NEC5 Northern Bering Sea clone 140J34 FJ4161
EU491722.1 gg_id:259776 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU491
EF174279.1 gg_id:181525 direct activated sludge compost maturation stage clone H49-814 EF1742
EF125451.1 gg_id:188380 mangrove soil clone MSB-2F4 EF1254
DQ334616.1 gg_id:175390 Impact metals on sediments heavy metal polluted marine sediment clone HB1-41-8 DQ334
EU287293.1 gg_id:239219 Pacific arctic surface sediment clone S11-110 EU287
FJ902650.1 gg_id:558486 phreatic limestone sinkholes northeastern Mexico biofilm 1m deep hydrothermal ver FJ9026
GQ259229.1 gg_id:512555 Microbial activities coastal marine sediments and column Svalbard deep water clone GQ259
EF061959.1 gg_id:194499 Xiamen China mangrove sediment clone XME27 EF0619
AY592131.1 gg_id:100439 marine ANAMMOX sediment clone AY592131 AY592
EF612422.1 gg_id:241321 historic semiarid lead-zinc mine tailings site soil clone OS-C47 EF6124
DQ395002.1 gg_id:155659 harbor sediment clone VHS-B4-54 DQ395
EU491622.1 gg_id:276755 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU491
FJ628326.1 gg_id:587067 transition and zone within near-shore basin: brackish water anoxic fjord Nitinat Lake (FJ6283
GU369930.1 gg_id:522232 and mats vents Arc white microbial film on pebble aphotic zone shal hydrothermal v GU369
EU925888.1 gg_id:327055 sediments sediment station DBS1 northern Bering Sea clone 099G35 EU9258
FJ202726.1 gg_id:304768 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2027
FJ545563.1 gg_id:553394 Diveristy Seawater and Sediment Northern North Yel Sea sediment clone S2-30 FJ5455
FJ479452.1 gg_id:564382 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4794
EF208680.1 gg_id:201369 Vertical and horizontal structure microbial sandy carbonate sediment clone CI5cm.BC EF2086
EU290675.1 gg_id:243727 microbial structure biogeochemical contrasting shelf sediments Namibian upwelling EU2906
GQ261760.1 gg_id:550306 shifts taxa and response localized organic loading deep sea sediment whale falls clo GQ261
AJ567539.1 gg_id:88336 deep-sea sediment clone MBMPE13 AJ5675
EU491447.1 gg_id:277437 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X4 clone EU491

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AM176878.1 gg_id:160646 Recovery mangrove sediment clone SZB50 AM176
DQ395393.1 gg_id:154568 deep-sea octacoral clone ctg_BRRAA68 DQ395
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GQ472813.1 gg_id:581306 Biodiversity planktonic Northern surface water northern Bering Sea clone b44 GQ472
AM997308.1 gg_id:575214 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A AM997
AY225636.1 gg_id:97007 Mid-Atlantic Ridge hydrothermal sediment clone AT-s2-59 AY2256
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AJ633957.1 gg_id:114452 host's accessory nidamental gland clone 30ANG2 AJ6339
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EU488042.1 gg_id:574507 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU488(
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EU652513.1 gg_id:277629 Seasonal variation microbial Yel Sea sediment clone C8S-5 EU652
EU488031.1 gg_id:572374 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU488(
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EU287183.1 gg_id:239964 Pacific arctic surface sediment clone P13-90 EU287
GQ246393.1 gg_id:593413 Temporal and spatial China North Yel Sea sediments clone Cm1-56 GQ246
EF540428.1 gg_id:227143 oil-shale semi-coke solid waste clone MK6 EF5404
EF208690.1 gg_id:202816 Vertical and horizontal structure microbial sandy carbonate sediment clone CI5cm.FC EF2086
EF597713.1 gg_id:247624 Metagenomics deep mediterranean warm bathypelagic habitat 3010m depth Ionian EF5977
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U91786.1 gg_id:10204 Candidatus Arsenophonus triatominarum U9178
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DQ158206.1 gg_id:140266 Averyella dalhousiensis str. 9501-97 1 DQ158
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DQ481464.1 gg_id:157163 Averyella dalhousiensis str. VTan-2 DQ481
DQ068917.1 gg_id:139129 microbiota antlions (Myrmeleon mobilis) whole animal laboratory starved antlion O DQ068
EU438866.1 gg_id:297157 Enterobacter amnigenus 2 EU438
EU741245.1 gg_id:335722 Enterobacter sp. str. KB3 EU741
AB291632.1 gg_id:241040 Insecticidal predatory antlion species (Neuroptera: Myrmeleontidae) larvae Myrmel AB291
EU879089.1 gg_id:305870 Pantoea agglomerans str. HDDMN03 EU879
AM184285.1 gg_id:161053 Enterobacter ludwigii str. WAB1946 AM184
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AY676878.1 gg_id:135960 Baumannia cicadellinicola B14 AY6768
AY676887.1 gg_id:136270 Baumannia cicadellinicola B34 AY6768
AF465797.1 gg_id:79588 Baumannia cicadellinicola AF4657
AY676896.1 gg_id:136019 Baumannia cicadellinicola B47 AY6768
AY676895.1 gg_id:137136 Baumannia cicadellinicola F02 AY6768
AF465795.1 gg_id:79106 Baumannia cicadellinicola AF4657
AY676877.1 gg_id:135411 Baumannia cicadellinicola B13 AY6768
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AJ233418.1 gg_id:51229 Brenneria rubrifaciens str. DSM 4483 AJ2334
U80207.1 gg_id:10197 Brenneria rubrifaciens str. ATCC 29291 U80207
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AB033773.1 gg_id:20966 Buchnera sp AB0337
AJ296755.1 gg_id:50183 Buchnera aphidicola (Maculolachnus submacula) (Maculolachnus AJ2967
FJ655495.1 gg_id:579584 Buchnera aphidicola (Stomaphis aphananthae) FJ6554
M63251.1 gg_id:9645 Buchnera aphidicola M6325
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FJ655509.1 gg_id:587576 Buchnera aphidicola (Lachnus tropicalis) FJ6555

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EU334777.1 gg_id:308536 Buchnera aphidicola (Cinara cedri) str. BCce2-1 EU334
AJ296753.1 gg_id:36645 Buchnera aphidicola (Stomaphis quercus) AJ2967
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AJ296758.1 gg_id:23853 Buchnera aphidicola (Panaphis juglandis) AJ2967
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Z19056.1 gg_id:9651 Buchnera aphidicola Z19056
AJ296750.1 gg_id:53693 Buchnera aphidicola (Pemphigus populi) AJ2967
AB064508.1 gg_id:40406 Buchnera aphidicola (Yamatocallis tokyoensis) #317 (Yamatocallis AB064
DQ418492.1 gg_id:171684 Buchnera aphidicola (Eriosoma lanigerum) str. Zhaotong DQ418
EU334773.1 gg_id:308102 Buchnera aphidicola (Cinara tujafilina) str. BCtu-1 EU334
M63255.1 gg_id:9653 Buchnera aphidicola M6325
AJ296754.1 gg_id:24924 Buchnera aphidicola (Tuberolachnus salignus) (Tuberolachnus AJ2967
FJ655507.1 gg_id:577120 Buchnera aphidicola (Lachnus roboris) FJ6555
Y11972.1 gg_id:202061 Buchnera aphidicola Y11972
L81121.1 gg_id:111650 Buchnera aphidicola L81121
AE016826.1 gg_id:146724 Buchnera aphidicola str. Bp (Baizongia pistaciae) AE016
FJ655512.1 gg_id:510297 Buchnera aphidicola (Nippolachnus piri) FJ6555
Y11973.1 gg_id:9652 Buchnera aphidicola Y11973
AY518294.1 gg_id:105511 Buchnera aphidicola (Aphis fabae fabae) AY518
FJ655500.1 gg_id:560641 Buchnera aphidicola (Stomaphis takahashii) FJ6555
DQ223869.1 gg_id:165272 Buttiauxella agrestis str. RT1 DQ223
DQ223870.1 gg_id:172544 Buttiauxella noackiae str. RT7 DQ223
DQ440549.1 gg_id:153634 Buttiauxella agrestis str. HS-39 DQ440
AF227860.1 gg_id:73465 Pantoea sp. str. 57916 AF227
DQ223871.1 gg_id:167300 Buttiauxella agrestis str. P1 DQ223
AJ293684.1 gg_id:69815 Buttiauxella agrestis str. S3/3-203 AJ2936
AJ233402.1 gg_id:10052 Buttiauxella ferragutiae str. DSM 9390 AJ2334
FJ716025.1 gg_id:513551 Diet- gut microbiota Lumbricus rubellus fingerprinting technique and cloning intestina FJ7160
AJ233406.1 gg_id:10056 Buttiauxella warmboldiae str. DSM 9404 AJ2334
NR_025328.1 gg_id:575201 Buttiauxella brennerae str. S1/6-571; DSM 9396 NR_02
AJ293687.1 gg_id:69978 Buttiauxella noackiae str. BR 626 AJ2936
AJ233403.1 gg_id:10053 Buttiauxella gaviniae str. DSM 9393 AJ2334
AJ233400.1 gg_id:10050 Buttiauxella agrestis str. DSM 4586 AJ2334
X92552.1 gg_id:9961 "Candidatus camponotii" X92552
AY334368.1 gg_id:106321 Camponotus sansabeanus symbiont AY3343
AJ245598.1 gg_id:20928 USA clone 14/7 AJ2455
AJ245592.1 gg_id:17213 Peru clone 5-5 AJ2455

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AY136152.1 gg_id:105167 Macrosiphum rosae symbiont AY136
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DQ228285.1 gg_id:150888 Acyrthosiphon pisum symbiont DQ228
AF493976.1 gg_id:82917 Cedecea davisae str. DSM 4568 AF493
DQ481466.1 gg_id:203232 Citrobacter freundii str. VTan-4 DQ481
DQ481470.1 gg_id:201655 Citrobacter freundii str. VTan-9 DQ481
EU468094.1 gg_id:299301 cheetah feces clone CE2_g02_2 EU468
GQ154806.1 gg_id:534457 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
GQ155543.1 gg_id:588290 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
DQ816142.1 gg_id:168998 mouse cecum clone aaa88f07 DQ816
GQ155506.1 gg_id:511336 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EU467996.1 gg_id:301223 cheetah feces clone CE2_g10 EU467
EU468053.1 gg_id:297805 cheetah feces clone CE2_a06_2 EU468
GQ155565.1 gg_id:556376 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EU540206.1 gg_id:283179 profile human microbiota antecubital fossa (inner elbow) skin clone nbt247b06 EU540
FJ658620.1 gg_id:509207 Metalworking Fluids and Aerosols Metallurgy Plant metalworking aerosol clone Sumn FJ6586
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DQ816132.1 gg_id:167280 mouse cecum clone aaa88d04 DQ816
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AB548827.1 gg_id:530232 Citrobacter freundii str. JCM 24062 AB548
GQ154694.1 gg_id:510488 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
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DQ192060.1 gg_id:166668 Citrobacter sp. I91-10 DQ192
EU528229.1 gg_id:280706 Seasonal Dynamics Mudflat Mouth Major Kentucky Lake Reservoir Tributary sedime EU528
DQ816596.1 gg_id:167950 mouse cecum clone aab20b03 DQ816
DQ816998.1 gg_id:169360 mouse cecum clone aaa94d12 DQ816
DQ294285.1 gg_id:141265 Citrobacter freundii str. 7 DQ294
EU365679.1 gg_id:258785 Citrobacter freundii str. M-8 EU365
FJ975807.1 gg_id:547342 Human gut microbiome adopts alternative state bowel transplantation ileum effluent FJ9758

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

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s__Enterobacter cowanii	4657

EU348325.1 gg_id:353216 symbiont
EU072500.1 gg_id:246330 pentatomid symbionts host gut clone Mh1
CP001836.1 gg_id:520563 Dickeya dadantii str. Ech586
EF530560.1 gg_id:226472 Erwinia chrysanthemi str. ICMP 4649
EU526397.1 gg_id:263449 Erwinia chrysanthemi
AF520709.2 gg_id:61200 Erwinia chrysanthemi str. CFBP 1270
AF520712.1 gg_id:61196 Dickeya dieffenbachiae str. CFBP 2051
EU821584.1 gg_id:366934 Erwinia chrysanthemi str. A5307
AF520711.2 gg_id:61197 Dickeya zeae str. CFBP 2052
AF373199.1 gg_id:66727 Erwinia chrysanthemi str. 571
AB453281.1 gg_id:328862 Edwardsiella ictaluri str. PH-0744
GU176612.1 gg_id:588536 Edwardsiella ictaluri str. HSA-1
FJ405295.1 gg_id:358862 Edwardsiella tarda str. K6
FJ405305.1 gg_id:358984 Edwardsiella tarda str. K16
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EU259317.1 gg_id:244611 Edwardsiella tarda str. WY28
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GQ337957.1 gg_id:540452 Edwardsiella tarda str. TsLt
AF015259.1 gg_id:9737 Edwardsiella tarda str. CDC 4411-68
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EU231639.1 gg_id:256624 Edwardsiella ictaluri str. TCCC11053
FJ405308.1 gg_id:364288 Edwardsiella tarda str. K19
FJ405302.1 gg_id:359327 Edwardsiella tarda str. K13
EF467289.1 gg_id:227142 Edwardsiella tarda str. CD
EU181369.1 gg_id:248470 Rahnella sp. str. LR113
DQ645479.1 gg_id:159919 Escherichia coli str. F4-2
GQ264499.1 gg_id:586406 Structure Simulated Level Waste Site simulated level waste site clone WW3_48

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EU072
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EU526
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EU821
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EF025326.1 gg_id:176468 Enterobacter cloacae str. SREPS1 EF0253
EU855207.1 gg_id:355066 Enterobacter sp. str. CTSP29 EU855
DQ855282.1 gg_id:216257 Enterobacter sp. str. FMB-1 DQ855
GQ260085.1 gg_id:561327 Enterobacter cloacae str. ICIRC107 GQ260
EU047701.1 gg_id:251565 Enterobacter aerogenes str. HC050612-1 EU047
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EU047556.1 gg_id:249130 Enterobacter hormaechei str. TMPSB-T10 EU047
GU071202.1 gg_id:587429 Enterobacter sp. str. DIT 14 GU071
GQ260087.1 gg_id:564431 Enterobacter cloacae str. ICIRC10 GQ260
AJ508302.1 gg_id:80575 Enterobacter hormaechei str. CIP 103441 AJ5083
AY335554.1 gg_id:129942 Enterobacter aerogenes str. CBNU-20-1 AY335
DQ202394.1 gg_id:140607 Enterobacter cloacae str. B5 DQ202
GQ260081.1 gg_id:587124 Enterobacter cloacae str. ICIRC91 GQ260
EF210100.1 gg_id:203409 Enterobacter hormaechei str. Z2-7 EF2101
FJ868805.1 gg_id:541119 Enterobacter sp. str. BSRA1 FJ8688
EF446901.1 gg_id:214586 Enterobacter cloacae str. GW4 EF4469
AF130914.1 gg_id:10081 Pantoea endophytica str. A42 AF1309
GQ179978.1 gg_id:575168 Enterobacter hormaechei str. FS11 GQ179
AY995561.1 gg_id:115488 Enterobacter hormaechei AY995
AJ854063.3 gg_id:108298 Enterobacter nickellidurans str. NiVas 114 AJ8540
GQ260075.1 gg_id:512914 Enterobacter hormaechei str. ICIRC82 GQ260
FJ976545.1 gg_id:556584 Enterobacter sp. str. LCR36 FJ9765
EU073021.1 gg_id:254448 Enterobacter cloacae HQ040619-1 EU073
CU915026.1 gg_id:448667 and dynamics adapted microbiota during degradation Tunisian zarzatine enriched se CU915
DQ837566.1 gg_id:172044 Enterobacter sp. XIV DQ837
AB244457.1 gg_id:257506 Enterobacter cloacae str. An20-1 AB244
FJ976587.1 gg_id:545162 Enterobacter aerogenes str. LCR78 FJ9765
FJ999766.1 gg_id:385869 Enterobacter hormaechei str. SP FJ9997
EF179825.1 gg_id:258793 sequences adult Anopheles darlingi (Diptera: Culicidae) mosquitoes clone 4.2 EF1798
Y17665.1 gg_id:10077 Enterobacter cloacae Nr. 3 Y17665
EF059890.1 gg_id:218876 Enterobacter hormaechei str. E904 EF0598
DQ273684.1 gg_id:144399 Evaluation two chromogenic media glucosidase and commercial oligonucleotide pro DQ273
AY217654.1 gg_id:84190 Escherichia senegalensis str. F1p AY217
EU302833.1 gg_id:240810 Salmonella sp. str. DAP8 EU302
GQ478377.1 gg_id:551552 olive endosymbiont 'Candidatus Erwinia dacicola' switches intracellular extracellular GQ478
GQ131582.1 gg_id:460735 Erwinia rhapontici str. 1OP1 GQ131
Z96087.1 gg_id:9805 Erwinia rhapontici str. LMG 2688 Z96087
GQ131583.1 gg_id:451112 Erwinia rhapontici str. 1OP6 GQ131
GQ131584.1 gg_id:410468 Erwinia rhapontici str. 3OP1 GQ131
U80206.1 gg_id:9811 Erwinia rhapontici str. ATCC 29283 U8020

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s__Erwinia toletana	5774
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EF540891.1 gg_id:219853 Erwinia soli str. Ew02 EF5408
AM292080.1 gg_id:179624 Erwinia tasmaniensis str. Et2/99 AM292
AM055715.2 gg_id:149797 Erwinia pyrifoliae str. Ejp557 AM055
FJ594367.1 gg_id:569261 Erwinia amylovora str. EA312 FJ5943
FJ594360.1 gg_id:566379 Erwinia pyrifoliae str. WT19 FJ5943
AF130965.1 gg_id:9820 Erwinia toletana str. A89 AF1309
AF130964.1 gg_id:9814 Erwinia toletana str. A82 AF1309
GQ884173.1 gg_id:582459 Escherichia hermannii str. SH-2 GQ884
EF059889.1 gg_id:226692 Escherichia hermannii str. E895 EF0598
EF059869.1 gg_id:223949 Escherichia hermannii str. E757 EF0598
EU931561.1 gg_id:337373 Pantoea agglomerans str. ZFJ-6 EU9315
AB297966.1 gg_id:209376 Erwinia sp. str. AC81a (=SUPP41) AB2979
GQ024698.1 gg_id:484972 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ024
GU339282.1 gg_id:563485 Pantoea ananatis str. EH55 GU339
DQ273680.1 gg_id:141117 Evaluation two chromogenic media glucosidase and commercial oligonucleotide pro DQ273
U80201.1 gg_id:9861 Pectobacterium cypripedii str. ATCC 29267 U80201
EU289448.1 gg_id:253617 metagenomic approach biosynthesis ansamycin endophytes or symbionts enriched s EU2894
EU681952.1 gg_id:281980 Erwinia persicina str. WD1608 EU6819
FM163487.1 gg_id:289103 Achromobacter xylosoxidans str. RE1 FM163
AM055711.1 gg_id:149811 Erwinia billingiae str. Eb661 AM055
GQ024758.1 gg_id:484912 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ024
AF024607.1 gg_id:9823 Pantoea agglomerans str. TAC.I.94.1 AF0246
GQ043420.1 gg_id:423241 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw96 GQ043
GQ024848.1 gg_id:484822 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ024
AF141893.1 gg_id:71250 Erwinia amylovora str. BC202(=Ea491) AF1418
GQ024907.1 gg_id:484762 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ024
EU072495.1 gg_id:239362 pentatomid symbionts host gut clone Ah1 EU0724
EU362176.1 gg_id:351023 Erwinia sp. str. C3(2008) EU3621
FJ595863.1 gg_id:543943 Erwinia pyrifoliae str. WT36 FJ5958
AY373829.2 gg_id:101634 Salmonella subterranea str. FRC1 AY3738
GU124495.1 gg_id:582297 endosymbiotic (Stal) (rice brown planthopper) Enterobacteriales endosymbiont Nila GU124
GQ024853.1 gg_id:484817 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ024
GQ024769.1 gg_id:484901 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ024
AJ233417.1 gg_id:9810 Erwinia rhapontici str. DSM 4484 AJ2334
EF469631.1 gg_id:221786 Dioxyna bidentis ex Bidens tripartita symbiont EF4696
AB480771.1 gg_id:539151 Erwinia tasmaniensis str. Acj 205 AB4807
GQ024837.1 gg_id:484833 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ024
AM294946.1 gg_id:174382 Erwinia persicina str. LPPA 408 AM294
EU336938.2 gg_id:537651 Flavobacterium sp. str. AG13 EU3369
AF289542.1 gg_id:20321 Erwinia amylovora EA G-5 AF2895
AF024613.1 gg_id:9827 Pantoea agglomerans str. TAC.XII.93.2 AF0246

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AY702662.1 gg_id:169365 Margalefia venezuelensis str. MS12 AY702
DQ532292.1 gg_id:171458 Geographical Variation Microbial Burden and Spacecraft Assembly Kennedy Space C DQ532
AB480775.1 gg_id:575074 Erwinia tasmaniensis str. Acj 211 AB480
FJ595871.1 gg_id:573072 Erwinia amylovora str. LMG2068 FJ5958
GQ097550.1 gg_id:395052 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw GQ097
EU926632.1 gg_id:350789 Escherichia albertii str. 1297-05-19 EU926
NC_010498.1 gg_id:263846 Escherichia coli str. SECEC SMS-3-5 NC_01
AE014073.1 gg_id:146636 Shigella flexneri 2a str. 2457T AE014
DQ411026.1 gg_id:151002 Escherichia coli str. FR-2 DQ411
CP000038.1 gg_id:138890 Shigella sonnei str. Ss046 CP000
CU928163.2 gg_id:544923 Escherichia coli str. UMN026 CU928
AP010953.1 gg_id:568499 Escherichia coli O26:H11 str. 11368 AP010
CP000800.1 gg_id:257376 Escherichia coli str. E24377A CP000
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NC_010498.1 gg_id:263843 Escherichia coli str. SECEC SMS-3-5 NC_01
AAJV02000011.1 gg_id:314537 Escherichia coli str. E22 AAJV0
AAJV02000007.1 gg_id:340407 Escherichia coli str. E22 AAJV0
CP000819.1 gg_id:520568 Escherichia coli B str. REL606 CP000
CP000800.1 gg_id:257373 Escherichia coli str. E24377A CP000
FM180568.1 gg_id:369791 Escherichia coli 0127:H6 str. E2348/69 FM180
CP000948.1 gg_id:270792 Escherichia coli substr. DH10B str. K-12 CP000
CU928158.2 gg_id:554727 Escherichia fergusonii 35469 str. ATCC 35469T CU928
AAKB02000001.1 gg_id:281891 Escherichia coli str. 53638 AAKB0
CU928163.2 gg_id:544920 Escherichia coli str. UMN026 CU928
CU928161.2 gg_id:563144 Escherichia coli str. S88 CU928
EU009185.1 gg_id:238337 Shigella dysenteriae str. FBD014 EU009
AF233451.1 gg_id:17857 Escherichia coli AF2334
EF620924.1 gg_id:255332 Escherichia coli str. SYW003 EF6209
CU928161.2 gg_id:563145 Escherichia coli str. S88 CU928
CU928164.2 gg_id:536217 Escherichia coli str. IAI39 CU928
EU470924.1 gg_id:291766 red panda feces clone RP_2aaa03c06 EU470
EU470476.1 gg_id:301376 red panda feces clone RP_1aaa02h07 EU470
FJ950549.1 gg_id:428533 Escherichia coli str. c247 FJ9505
EU472923.1 gg_id:288465 red panda feces clone RPSD_1aaa04h11 EU472
GQ025583.1 gg_id:437123 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ025
EU472692.1 gg_id:303108 red panda feces clone RPSD_1aaa01c04 EU472
GQ008742.1 gg_id:500918 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ008
EU471177.1 gg_id:302439 red panda feces clone RP_3aaa04d05 EU471
EU472680.1 gg_id:288712 red panda feces clone RPSD_1aaa01d01 EU472
EU472729.1 gg_id:290328 red panda feces clone RPSD_1aaa02g10 EU472

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EU471295.1 gg_id:298340 red panda feces clone RP_3aaa03g05 EU471
EU470739.1 gg_id:289190 red panda feces clone RP_2aaa02e12 EU470
EU468348.1 gg_id:293649 lion feces clone LI2_aae47f10 EU468
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EU470710.1 gg_id:290311 red panda feces clone RP_1aaa04a05 EU470
EU470675.1 gg_id:301701 red panda feces clone RP_1aaa02e06 EU470
NC_011740.1 gg_id:471437 Escherichia fergusonii str. ATCC 35469 NC_01
EU471997.1 gg_id:292359 francois langur feces clone FL_1aaa02b11 EU471
EU472874.1 gg_id:298984 red panda feces clone RPSD_1aaa03c12 EU472
EU472807.1 gg_id:293337 red panda feces clone RPSD_1aaa03c08 EU472
EU471134.1 gg_id:290740 red panda feces clone RP_3aaa04h08 EU471
EU472693.1 gg_id:293094 red panda feces clone RPSD_1aaa04d06 EU472
EF620921.1 gg_id:238636 Escherichia coli str. SYW001 EF6209
EU471242.1 gg_id:293815 red panda feces clone RP_3aaa04h04 EU471
EU471056.1 gg_id:302667 red panda feces clone RP_3aaa04h09 EU471
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AF527826.1 gg_id:71573 Escherichia coli str. RREC II AF5278
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EU470517.1 gg_id:297922 red panda feces clone RP_1aaa02g03 EU470
EU458385.1 gg_id:291249 spotted hyena feces clone HY1_a06_1 EU458
EU472805.1 gg_id:295661 red panda feces clone RPSD_1aaa01d08 EU472
EU472917.1 gg_id:288548 red panda feces clone RPSD_1aaa03c05 EU472
GQ047930.1 gg_id:391527 Topographical and Temporal Human Skin Microbiome skin palm clone nbw139b10c GQ047
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EU778485.1 gg_id:305760 Red Panda feces clone RP_1aaa01h12 EU778
EU470629.1 gg_id:290610 red panda feces clone RP_1aaa01b03 EU470
NC_009800.1 gg_id:245367 Escherichia coli str. HS NC_00
FJ950548.1 gg_id:401252 Escherichia coli str. c249 FJ9505
EU470620.1 gg_id:300756 red panda feces clone RP_1aaa02h01 EU470
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EU471158.1 gg_id:289812 red panda feces clone RP_3aaa02c10 EU471
GU065251.1 gg_id:535199 Escherichia coli str. BDS3 GU065
X80733.1 gg_id:9684 Escherichia X80733
EU472760.1 gg_id:298347 red panda feces clone RPSD_1aaa03e07 EU472
GQ008489.1 gg_id:501176 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ008
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EU471245.1 gg_id:288664 red panda feces clone RP_3aaa03f02 EU471

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AF527827.1 gg_id:62512 Escherichia coli str. RREC I AF527
EU472717.1 gg_id:301245 red panda feces clone RPSD_1aaa04f12 EU472
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EU470705.1 gg_id:298055 red panda feces clone RP_1aaa03b10 EU470
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NC_011740.1 gg_id:471438 Escherichia fergusonii str. ATCC 35469 NC_01
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GQ025520.1 gg_id:413814 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ025
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GQ069064.1 gg_id:438768 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ069
EU470553.1 gg_id:302025 red panda feces clone RP_1aaa04b03 EU470
EU708318.1 gg_id:348648 Ewingella americana str. CH6 EU708
EU678359.1 gg_id:284672 Ewingella americana str. CH5 EU678
U29438.1 gg_id:10324 Ewingella americana str. NCPPB 3905 U2943
AY581130.1 gg_id:101409 Ewingella americana B791 AY581
EU196321.1 gg_id:246905 Aranicola sp. NP34 EU196
AF010251.1 gg_id:10139 Klebsiella granulomatis str. KH 22 d peripheral blood monocytes AF010
AY369139.1 gg_id:94946 Klebsiella pneumoniae AY369
GQ098970.1 gg_id:467551 Topographical and Temporal Human Skin Microbiome skin palm clone nbw504e12c1 GQ098

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AB353046.1 gg_id:257803 Klebsiella oxytoca str. No.6 AB3530
FJ816026.1 gg_id:577013 Klebsiella oxytoca str. GS-4-08 FJ8160
EF633998.1 gg_id:255739 Klebsiella pneumoniae str. M-4 EF6339
GU361112.1 gg_id:515224 Klebsiella oxytoca str. SHD-1 GU361
GQ075941.1 gg_id:461429 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ075
GU119910.1 gg_id:539869 Klebsiella oxytoca str. Bx-LA-0908 GU119
GQ098941.1 gg_id:392581 Topographical and Temporal Human Skin Microbiome skin palm clone nbw504b09c1 GQ098
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AF543283.1 gg_id:58294 Klebsiella oxytoca str. ChDC OS31 AF5432
AJ871861.1 gg_id:113052 Klebsiella oxytoca str. SB73 AJ8718
AB004754.1 gg_id:10108 Klebsiella oxytoca str. JCM1665 AB0047
AF319525.3 gg_id:71572 Klebsiella oxytoca AF3195
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AJ871860.1 gg_id:113819 Klebsiella oxytoca str. SB2942 AJ8718
CP000964.1 gg_id:355056 Klebsiella pneumoniae str. 342 CP0009
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GQ166862.1 gg_id:585007 Klebsiella pneumoniae str. EB6-THQ GQ166
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EU240959.1 gg_id:273616 Klebsiella pneumoniae str. YC-A42 EU2409
FJ593858.1 gg_id:514856 Klebsiella sp. str. AL060225_04 FJ5938
GQ214541.1 gg_id:554914 Klebsiella pneumoniae str. HDMB-X GQ214
EU723828.1 gg_id:306451 Klebsiella pneumoniae str. HDDMM07 EU7238
AF394537.1 gg_id:64272 Klebsiella pneumoniae str. 342 AF3945
CP001891.1 gg_id:527918 Klebsiella variicola str. -22 CP0018
FJ593855.1 gg_id:516172 Klebsiella sp. str. MNS_801a FJ5938
CP001891.1 gg_id:527914 Klebsiella variicola str. -22 CP0018
EF608176.1 gg_id:552087 Klebsiella pneumoniae str. HT24 EF6081
GQ155813.1 gg_id:559700 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
DQ185604.1 gg_id:140302 Klebsiella pneumoniae str. Ac01 DQ185
GQ156091.1 gg_id:550532 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
DQ379507.1 gg_id:153149 Klebsiella pneumoniae str. TSL-4 DQ379
GQ156048.1 gg_id:578617 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
GU594298.1 gg_id:514480 Klebsiella pneumoniae str. B16 GU594

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

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

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GQ156192.1 gg_id:575548 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
NC_012731.1 gg_id:375665 Klebsiella pneumoniae str. NTUH-K2044 NC_01
GQ154748.1 gg_id:556070 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
GQ155398.1 gg_id:579246 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
DQ837568.1 gg_id:168382 Klebsiella sp. III DQ837
EU734822.1 gg_id:349243 Pseudomonas aeruginosa str. NBRAJG90 EU7348
GQ155863.1 gg_id:539970 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ155396.1 gg_id:509168 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EF091148.1 gg_id:213635 Klebsiella pneumoniae str. 99 EF0911
EF566882.1 gg_id:273896 Klebsiella pneumoniae EF5668
FJ947063.1 gg_id:512541 Klebsiella pneumoniae str. fJ1 FJ9470
GQ155406.1 gg_id:572306 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
AY660026.2 gg_id:123487 Xenorhabdus poinarii AY660
NC_012731.1 gg_id:375668 Klebsiella pneumoniae str. NTUH-K2044 NC_01
CP001891.1 gg_id:527919 Klebsiella variicola str. -22 CP0018
GQ154942.1 gg_id:575251 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
GQ155346.1 gg_id:542868 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
FJ975804.1 gg_id:548574 Human gut microbiome adopts alternative state bowel transplantation ileum effluent FJ9758
EU078621.1 gg_id:251954 Klebsiella pneumoniae str. HR16 EU078
FJ593857.1 gg_id:532313 Klebsiella sp. str. AL060224_03 FJ5938
EU360793.1 gg_id:262483 Klebsiella pneumoniae str. ECU-21 EU360
GQ155955.1 gg_id:536479 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
FJ975797.1 gg_id:593596 Human gut microbiome adopts alternative state bowel transplantation ileum effluent FJ9757
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GQ155800.1 gg_id:537085 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ155680.1 gg_id:590210 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ155924.1 gg_id:590080 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
NC_012731.1 gg_id:375671 Klebsiella pneumoniae str. NTUH-K2044 NC_01
GQ154887.1 gg_id:511908 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
EF127829.1 gg_id:197404 Klebsiella oxytoca str. LF-1 EF1278
GQ155740.1 gg_id:512312 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
FJ436718.1 gg_id:358763 Klebsiella pneumoniae str. FIUMS1 FJ4367
GQ155340.1 gg_id:511148 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ155822.1 gg_id:513383 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
AJ233420.1 gg_id:27939 Klebsiella pneumoniae str. DSM 30104 AJ2334
DQ223868.1 gg_id:166493 Kluyvera intermedia str. P3 DQ223
NR_028802.1 gg_id:564215 Kluyvera intermedia str. 256; ATCC 33110 NR_02
NR_028803.1 gg_id:573005 Kluyvera cryocrescens str. 12993; ATCC 33435 NR_02
AJ277978.1 gg_id:22764 Leclercia adecarboxylata str. WG 162 AJ2779
AY451327.1 gg_id:99716 Leclercia adecarboxylata str. TERIPS4040 AY4513

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AJ853891.1 gg_id:108534 Enterobacter ludwigii str. EN-119 = DSMZ 16688 AJ8538
AF157695.1 gg_id:10087 Enterobacter cloacae str. drh3 AF1576
AY335552.1 gg_id:137221 Pantoea agglomerans str. CBNU-14-1 AY3355
AJ232240.1 gg_id:10085 isolate: SS-Unknown-1129 clone AJ2322
FJ592988.1 gg_id:432552 Pantoea agglomerans str. SB-2 FJ5929
EU302838.1 gg_id:247855 Pantoea sp. str. DAP13 EU3028
AJ276393.1 gg_id:71494 Leclercia adecarboxylata str. LBV 449 AJ2763
DQ011248.1 gg_id:136462 genes Da Qing Oil field microbial indicates presence variety sulfate-reducing fermen DQ011
AM184263.1 gg_id:161505 Pantoea agglomerans str. WAB1924 AM184
FJ587505.1 gg_id:586247 Pantoea sp. str. C-4-1 FJ5875
FJ593002.1 gg_id:447010 Pantoea agglomerans str. ST-1 FJ5930
GQ337696.1 gg_id:568247 Enterobacter aerogenes str. S18 GQ337
AF511434.1 gg_id:65397 Enterobacter cloacae CCCO10 AF5114
FN555402.1 gg_id:509744 Pantoea sp. I-Bh20-21 FN5554
FM210031.1 gg_id:334606 Enterobacter cancerogenus str. T2P18 FM210
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AY691545.1 gg_id:103577 Pantoea agglomerans str. ChDC YP3 AY6915
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EU590682.1 gg_id:258931 Pantoea agglomerans str. BH-18 EU5906
AM184264.1 gg_id:161559 Pantoea agglomerans str. WAB1925 AM184
AB004691.1 gg_id:10075 Pantoea agglomerans str. JCM1236 AB0046
AY488028.1 gg_id:99221 Enterobacter sp. str. BL-2 AY4880
EU557027.1 gg_id:266569 Enterobacter ludwigii str. KU201-3 EU5570
GQ070505.1 gg_id:376025 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw. GQ070
EF011164.1 gg_id:192215 Enterobacter hormaechei str. PT4 EF0111
DQ011253.1 gg_id:132962 stratum sewage clone 6 DQ011
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FM210030.1 gg_id:306906 Enterobacter cancerogenus str. R27c FM210
EF429005.1 gg_id:211593 Pantoea agglomerans str. GIST-Out2 EF4290
GQ374474.1 gg_id:533493 Pantoea agglomerans str. GS2 GQ374
AY792266.1 gg_id:123510 Humic Lake clone CrystalBog5A11 AY7922
AM184254.1 gg_id:160936 Pantoea agglomerans str. WAB1913 AM184
AM184266.1 gg_id:161444 Pantoea agglomerans str. WAB1927 AM184
EU884395.1 gg_id:368993 Enterobacter cloacae str. XA-2 EU8843
GQ478022.1 gg_id:570352 Enterobacter cloacae str. ham3 GQ478
EU164545.1 gg_id:239199 Enterobacter hormaechei 4 EU1645
AY900169.1 gg_id:142410 Pantoea agglomerans str. PCA0067 AY9001
AF199029.1 gg_id:27763 Pantoea agglomerans str. SP1 AF1990
GQ284566.1 gg_id:547400 Enterobacter ludwigii str. AR1.22 GQ284

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GQ374471.1 gg_id:570229 Pantoea agglomerans str. XJ1 GQ374
GQ856082.1 gg_id:556086 Leclercia adecarboxylata str. LMG 2803 GQ856
EF446899.1 gg_id:205646 Pantoea agglomerans str. AT2 EF4468
DQ392984.1 gg_id:156431 Pantoea agglomerans str. e DQ392
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DQ358125.1 gg_id:163102 Morganella morganii str. AP28 DQ358
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AB099401.1 gg_id:85614 Proteus vulgaris str. AU34 AB0994
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GU338400.1 gg_id:544871 Pantoea ananatis str. E-1-4 GU338
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GQ332198.1 gg_id:534397 Pantoea ananatis str. M408 GQ332
AB033602.1 gg_id:9868 Pantoea agglomerans AB0336
GQ383918.1 gg_id:592050 Pantoea ananatis str. 4CBJ1 GQ383
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GU324264.1 gg_id:591038 Pantoea ananatis str. M471 GU324
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FJ611812.1 gg_id:585566 Pantoea ananatis str. ATCC 27995 FJ6118
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AF130918.1 gg_id:9921 Pantoea agglomerans str. new*47con AF1309
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EU849107.1 gg_id:351329 Pantoea agglomerans str. PSB-UJ2-21 EU8491
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FJ611831.1 gg_id:537318 Pantoea agglomerans str. P9QLB FJ6118
AY941838.1 gg_id:114491 Pantoea agglomerans str. XW123 AY9418
EF516970.1 gg_id:218720 grassland soil clone FCPS402 EF5169
AF130932.1 gg_id:9887 Pantoea agglomerans str. A62 AF1309
GQ367483.1 gg_id:557905 Pantoea sp. str. A18/07 GQ367

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AF130899.1 gg_id:9913 Pantoea agglomerans str. A21	AF1308
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GQ169378.1 gg_id:537971 Pantoea eucalypti str. IEXa	GQ169
FJ999950.1 gg_id:561323 Pantoea agglomerans str. EQH21	FJ9999
AF130935.1 gg_id:9890 Pantoea agglomerans str. A67	AF1309
FM202484.1 gg_id:345858 Pantoea agglomerans str. EV2	FM202
AF130933.1 gg_id:9888 Pantoea agglomerans str. A63	AF1309
EU598802.1 gg_id:267618 Pantoea agglomerans	EU5988
GQ225111.1 gg_id:584259 Pantoea agglomerans str. NBRISRM	GQ225
AF130942.1 gg_id:9933 Pantoea agglomerans str. A74	AF1309
GQ130025.1 gg_id:463204 Genetic inventory 'JPL-SAF' during MSL mission spacecraft assembly clean room floc	GQ130
AM184091.1 gg_id:155126 Pantoea agglomerans str. 45	AM184
FM202485.1 gg_id:322033 Pantoea agglomerans str. EV3	FM202
NC_004547.2 gg_id:471486 Pectobacterium atrosepticum str. SCRI1043	NC_004
NC_004547.2 gg_id:471485 Pectobacterium atrosepticum str. SCRI1043	NC_004
EF530546.1 gg_id:221979 Pectobacterium wasabiae str. NZEC8974	EF5305
EF178667.1 gg_id:178973 Pectobacterium wasabiae str. NZEC12	EF1786
EF178665.1 gg_id:193423 Pectobacterium wasabiae str. NZEC9	EF1786

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NR_026047.1 gg_id:559459 Pectobacterium wasabiae str. SR91; ATCC 43316
CP001790.1 gg_id:523636 Pectobacterium wasabiae str. WPP163
EF530558.1 gg_id:218029 Pectobacterium wasabiae str. ICMP 9121
EF530556.1 gg_id:225898 Pectobacterium vasculorum str. ICMP 4226
Z96090.1 gg_id:9790 Pectobacterium carotovorum str. LMG 2386
EF178668.1 gg_id:182325 Pectobacterium atrosepticum str. NZEC20
AY278669.1 gg_id:87761 Photorhabdus sp. str. MOL
Z76750.1 gg_id:10266 Photorhabdus temperata str. Mge1
AY296252.1 gg_id:88447 Photorhabdus temperata
AY280573.1 gg_id:91820 Photorhabdus asymbiotica subsp. australis str. MB
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Z76749.1 gg_id:10224 Photorhabdus luminescens str. Q614
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EU930345.1 gg_id:323175 Photorhabdus luminescens str. HG29
EU136627.1 gg_id:238203 Photorhabdus sp. 3240
FJ006729.1 gg_id:356553 Photorhabdus luminescens str. SRK8
Z76744.1 gg_id:10222 Photorhabdus luminescens str. Brecon
Z76740.1 gg_id:10217 Photorhabdus luminescens str. Tn-5*2
FJ006727.1 gg_id:307512 Photorhabdus luminescens str. SRK6
AY216500.1 gg_id:85814 Photorhabdus sp. str. Q614
GQ359965.1 gg_id:579651 Plesiomonas shigelloides str. PIM23
AJ301682.1 gg_id:19524 Proteus mirabilis str. CIP103181T (ATCC29906T)
AJ634474.1 gg_id:105166 Proteus penneri str. ENT229
DQ453959.1 gg_id:154694 Proteus vulgaris str. T-6
DQ826507.1 gg_id:164105 Proteus vulgaris
EF194105.1 gg_id:203330 Proteus mirabilis D3
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DQ512963.1 gg_id:161130 Proteus sp. str. HS7514
AB079370.1 gg_id:19687 Proteus mirabilis str. U1-2
DQ449631.1 gg_id:156998 Proteus mirabilis str. O
AY820623.1 gg_id:108937 Proteus mirabilis
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EF626945.1 gg_id:238632 Proteus mirabilis str. TMPSB2
FJ581028.1 gg_id:560629 Proteus mirabilis str. IITRM5
GQ292550.1 gg_id:541537 Proteus vulgaris str. TEM11
NZ_ABVP01000020.1 gg_id:470878 Proteus penneri str. ATCC 35198
J01874.1 gg_id:37204 Proteus vulgaris
DQ885258.1 gg_id:170701 Proteus penneri str. NCTC 12737
DQ885257.1 gg_id:172390 Proteus vulgaris str. ATCC 29905

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EF528263.1 gg_id:225923 Proteus vulgaris str. CICCHLJ Q33
DQ499636.1 gg_id:170332 Proteus vulgaris
DQ205432.1 gg_id:139753 Proteus vulgaris str. knp3
DQ885259.1 gg_id:170436 Proteus myxofaciens str. NCIMB 13273
AJ301684.1 gg_id:36854 Providencia alcalifaciens str. CIP8290T (ATCC9886T)
DQ885261.1 gg_id:162080 Providencia alcalifaciens str. NCTC 10286
FJ418572.1 gg_id:360427 Providencia alcalifaciens str. Sam130-1A
DQ885265.1 gg_id:168679 Providencia heimbachae str. NCTC 12003
AF008581.1 gg_id:45337 Providencia stuartii str. ATCC 29914T
ABJD02000003.1 gg_id:286806 Providencia stuartii str. ATCC 25827
ABJD02000097.1 gg_id:280258 Providencia stuartii str. ATCC 25827
DQ885263.1 gg_id:162918 Providencia rettgeri str. NCTC 11801
AM040754.1 gg_id:130404 Moellerella wisconsensis str. DSM 5676
AM040492.1 gg_id:128082 Providencia rettgeri str. DSM 4542
EU464842.1 gg_id:294417 Hartmann's mountain zebra feces clone AFZEB_aaj71g06
AY803746.1 gg_id:108983 Providencia stuartii str. PGS13
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AB161460.1 gg_id:155411 Providencia sp. str. WW2
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DQ824750.1 gg_id:194664 human fecal clone RL185_aaj72f10
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FM209488.1 gg_id:309913 Rahnella aquatilis str. TS18
FJ222589.1 gg_id:315615 Rahnella sp. str. N2-2
FJ811859.1 gg_id:587642 Rahnella aquatilis str. 2B-CDF
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EF685273.1 gg_id:239195 Hepialus gonggaensis sequencing libraries larva guts clone Hg09
U88437.1 gg_id:10312 Rahnella sp. 'CDC 658-79' str. CDC 658-79
FJ811853.1 gg_id:551657 Rahnella aquatilis str. 9-BCH
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EU294414.1 gg_id:255855 Raoultella ornithinolytica str. cl40 sullage
AB099407.1 gg_id:86680 Raoultella planticola str. 8433
EF057396.1 gg_id:199546 Raoultella ornithinolytica str. D70
EF515335.1 gg_id:223344 Electricigen Enrichment MFC upf microbial fuel cell anode clone 23a10
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AB099400.1 gg_id:84971 Raoultella planticola str. 4131
EF515418.1 gg_id:220845 Electricigen Enrichment MFC upf microbial fuel cell anode clone 24b10
EU545405.1 gg_id:542722 Raoultella planticola str. XW10
FJ823046.1 gg_id:563810 Raoultella ornithinolytica str. gx-110

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EF515264.1 gg_id:225880 Electricigen Enrichment MFC upf microbial fuel cell anode clone 22b06 EF5152
EU294412.1 gg_id:257519 Raoultella ornithinolytica str. 38 sullage EU294
EF433545.1 gg_id:211783 Klebsiella sp. str. WW2 EF4335
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EF515440.1 gg_id:217863 Electricigen Enrichment MFC upf microbial fuel cell anode clone 24d09 EF5154
EF515404.1 gg_id:224329 Electricigen Enrichment MFC upf microbial fuel cell anode clone 24a05 EF5154
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FJ975862.1 gg_id:511415 Human gut microbiome adopts alternative state bowel transplantation ileum effluent FJ9758
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Y17663.1 gg_id:10129 Raoultella planticola str. 7444 Y17663
GQ154930.1 gg_id:511427 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
EU256396.1 gg_id:243243 Bacillus megaterium str. SZN4 EU256
FJ975841.1 gg_id:562152 Human gut microbiome adopts alternative state bowel transplantation ileum effluent FJ9758
AF129444.1 gg_id:42955 Raoultella planticola str. ATCC 33558T AF129
GQ154871.1 gg_id:583590 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
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AF511435.1 gg_id:65398 Serratia fonticola CCCO11b AF511
GQ156035.1 gg_id:545206 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
X93215.1 gg_id:10127 Raoultella planticola str. DSM 3069 T X93215
FJ975867.1 gg_id:569459 Human gut microbiome adopts alternative state bowel transplantation ileum effluent FJ9758
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EU704230.1 gg_id:296868 human biliary stents clone KLONE12 EU704
GQ156448.1 gg_id:593522 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
EU560831.1 gg_id:565501 Assessment genetic Apriona germari (Hope) larvae normalization techniques intestir EU5608
DQ223874.1 gg_id:170406 Obesumbacterium proteus str. RT6 DQ223
EU939439.1 gg_id:329096 Fecal wild pygmy loris feces clone WF16S_295 EU939

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GQ154719.1 gg_id:542496 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
DQ133596.1 gg_id:138380 Pantoea agglomerans str. B1 DQ133
FJ823007.1 gg_id:533363 Raoultella ornithinolytica str. gx-49 FJ8230
GQ154944.1 gg_id:578463 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
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EU560759.1 gg_id:538000 Assessment genetic intestinal flora Apriona germari (Hope) larvae -RFLP techniques EU560
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GQ156483.1 gg_id:540487 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
GQ156476.1 gg_id:579281 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
GQ154749.1 gg_id:536503 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
GQ154730.1 gg_id:575117 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
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GQ156507.1 gg_id:535104 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
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AB364958.1 gg_id:235818 Raoultella ornithinolytica str. R1 AB3649
GQ154797.1 gg_id:540793 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
AJ508301.1 gg_id:80910 Enterobacter kobei str. CIP 105566 AJ5083
EU870376.1 gg_id:315511 Enterobacter sp. str. SZDA EU8703
AF029226.1 gg_id:9779 Salmonella bongori str. JEO 4162 AF0292
EU014682.1 gg_id:241394 Salmonella bongori str. DSM 13772 EU0146
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EF604025.1 gg_id:232625 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040
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DQ344536.1 gg_id:148570 Salmonella paratyphi DQ344
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EF604076.1 gg_id:234402 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040
EF604396.1 gg_id:229998 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6043

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FJ609417.1 gg_id:572114 Salmonella enterica str. PRSC-1 FJ6094
EF604238.1 gg_id:233123 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6042
AF227869.1 gg_id:40959 Salmonella subsp. enterica serovar Typhimurium str. 65946 subsp. AF2278
NC_003197.1 gg_id:128871 Salmonella typhimurium LT2 str. LT2; SGSC 1412; ATCC 700720 NC_00
FJ377885.1 gg_id:363910 Salmonella typhi str. MR9 FJ3778
EF604017.1 gg_id:235063 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040
EF604089.1 gg_id:227942 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040
EF605240.1 gg_id:230644 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6052
EF604062.1 gg_id:230359 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040
EF604030.1 gg_id:232928 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040
EF604003.1 gg_id:233622 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040
EF604016.1 gg_id:227916 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040
EF604423.1 gg_id:234837 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6044

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EF604394.1 gg_id:229717 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6043
EF604064.1 gg_id:232978 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040
Z47544.1 gg_id:9756 Salmonella typhi str. Ty2 ATCC 19430 Z47544
EF604385.1 gg_id:233497 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6043
EF604103.1 gg_id:232094 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6041
EF604429.1 gg_id:229314 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6044
EF604416.1 gg_id:231885 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6044
AB273736.1 gg_id:248512 Salmonella enterica subsp. arizonae str. GTC 1732 AB2737
AE008820.1 gg_id:34689 Salmonella typhimurium LT2 str. LT2; SGSC 1412; ATCC 700720 LT2 AE0088
EF604012.1 gg_id:228028 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040
EF605229.1 gg_id:234498 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6052
EF605238.1 gg_id:232278 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6052
EF604380.1 gg_id:227822 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6043
EF604124.1 gg_id:232989 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6041
EF604049.1 gg_id:229879 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040
EU118106.1 gg_id:241765 Salmonella enteritidis str. E6 EU1181
EF604278.1 gg_id:229337 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6042
EF604417.1 gg_id:234591 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6044
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EF604382.1 gg_id:227996 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6043
EF604042.1 gg_id:234592 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040
EF605236.1 gg_id:231367 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6052
EF604252.1 gg_id:228883 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6042
AF008580.1 gg_id:52635 Salmonella enterica arizonae subsp. IIIa str. ATCC 13314T AF0085
EU118080.1 gg_id:247476 Salmonella paratyphi str. A5 EU1180
EU118113.1 gg_id:249809 Salmonella typhi str. T6 EU1181
EU118101.1 gg_id:251997 Salmonella enteritidis str. E2 EU1181
EF604366.1 gg_id:233919 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6043
AB273735.1 gg_id:255286 Salmonella enterica subsp. diarizonae str. GTC 1733 AB2737
EF604389.1 gg_id:228797 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6043
EF604006.1 gg_id:230459 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040
EF604041.1 gg_id:234900 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040

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EF604368.1 gg_id:229317 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6043
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EF604229.1 gg_id:230785 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6042
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EF603990.1 gg_id:229961 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6039
FN555100.1 gg_id:557204 Salmonella enterica str. 22/M185/01/98 FN555
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GU370899.1 gg_id:560434 Serratia entomophila str. AB2 GU370
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AM696771.1 gg_id:221173 sequencing libraries indoor dust clone BF0001A058 AM696
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AJ288155.1 gg_id:22004 Serratia proteamaculans 182
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EU554429.1 gg_id:275241 Pseudomonas fluorescens str. Ag03	EU5544
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U93263.1 gg_id:10181 Aranicola proteolyticus	U93263
AJ279002.1 gg_id:33276 Serratia fonticola str. IB4	AJ2790
DQ321559.1 gg_id:146025 gut- microorganisms larvae and adults southern pine beetle Dendroctonus frontalis	DQ321
AY253924.1 gg_id:83887 Serratia liquefaciens k 100	AY2539
FJ811865.1 gg_id:546427 Serratia liquefaciens str. 1-BCH	FJ8118
EU266583.1 gg_id:256972 Serratia plymuthica str. RG 6	EU2665
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DQ103512.1 gg_id:131626 Serratia sp. F2	DQ103
GU292825.1 gg_id:541724 Serratia sp. str. L5	GU292
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EU236755.1 gg_id:250856 Serratia plymuthica str. R1	EU2367
EU031768.1 gg_id:249473 Serratia sp. str. BS18	EU0317
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AJ233429.1 gg_id:10169 Serratia fonticola str. DSM 4576	AJ2334
AJ279044.1 gg_id:27304 Serratia quinivorans subsp. quinovora str. CP6	AJ2790
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AM157437.1 gg_id:142918 Serratia proteamaculans mother C4	AM157

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DQ833334.1 gg_id:166089 Title: Anaerobic Reductive Dechlorination Vinyl Chloride ly Enriched AuSable River S DQ833
DQ123840.1 gg_id:148321 Serratia liquefaciens str. JF-1116 DQ123
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AY573038.1 gg_id:101976 Yersinia sp. str. ARCTIC-P11 AY573
AJ233436.1 gg_id:10189 Serratia rubidaea str. DSM 4480 AJ2334
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FJ405353.1 gg_id:365131 Escherichia coli str. 4097 FJ4053
NC_004337.1 gg_id:140570 Shigella flexneri 2a str. 301 NC_00

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s__Sodalis glossinidius	6210
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s__unclassified	6272

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

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

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GQ047715.1 gg_id:441491 Topographical and Temporal Human Skin Microbiome skin palm clone nbw138d06c GQ047
GQ155218.1 gg_id:561972 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EU723822.1 gg_id:345487 Shigella sonnei str. HDDMG06 EU723
AB479110.1 gg_id:561984 Escherichia hermannii str. YS-11 AB479
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EU472797.1 gg_id:295950 red panda feces clone RPSD_1aaa03d01 EU472
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EF179843.1 gg_id:271664 sequences adult Anopheles darlingi (Diptera: Culicidae) mosquitoes clone 1.1 EF1798
GQ047641.1 gg_id:385282 Topographical and Temporal Human Skin Microbiome skin palm clone nbw137b10c GQ047
GQ491694.1 gg_id:593660 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
AY689045.1 gg_id:105300 Enterobacter sp. str. 6B_5 AY689
EF189919.1 gg_id:365055 Pantoea stewartii 40G RT2A EF1899
EU466029.1 gg_id:295053 African elephant feces clone AFEL3_aao16b08 EU466
FN433049.1 gg_id:547245 Citrobacter braakii CCM33B FN433
EU460308.1 gg_id:299829 polar bear feces clone PB1_aai26c12 EU460
GQ155101.1 gg_id:565925 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ047977.1 gg_id:445372 Topographical and Temporal Human Skin Microbiome skin palm clone nbw139g10c GQ047
EU472889.1 gg_id:293518 red panda feces clone RPSD_1aaa03f04 EU472
EU471175.1 gg_id:293468 red panda feces clone RP_3aaa01g02 EU471
AY792270.1 gg_id:122049 Humic Lake clone CrystalBog1E3 AY792
FJ364672.1 gg_id:370240 feces adult twins and mothers; TS19 clone TS19_a01f10 FJ3646
EU460405.1 gg_id:294051 polar bear feces clone PB1_aai28b07 EU460
DQ818978.1 gg_id:168683 mouse cecal microbiota-colonized zebrafish digestive tract clone aab40d10 DQ818
DQ133536.1 gg_id:138463 Citrobacter freundii str. GM1 DQ133
EU470874.1 gg_id:300686 red panda feces clone RP_2aaa01h11 EU470
AJ223409.1 gg_id:9789 Pectobacterium cacticida AJ2234
EF608524.1 gg_id:228556 predatory Poecilus chalcites their response lab rearing and antibiotic treatment diges EF6085
AY227805.1 gg_id:100736 Pantoea dispersa UQ68J AY2278
GQ155135.1 gg_id:578405 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EF551364.1 gg_id:223793 Enterobacter cloacae str. Rs-35 EF5513
GQ156545.1 gg_id:510870 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
GQ025567.1 gg_id:419206 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ025
GQ031700.1 gg_id:436114 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ031
EF643377.1 gg_id:236811 Mangroveibacter plantisponsor str. MSSRF40 EF6433

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GQ099252.1 gg_id:408166 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ099
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EU472888.1 gg_id:287425 red panda feces clone RPSD_1aaa01a08 EU472
GQ280089.1 gg_id:564812 Enterobacter sp. str. JS-19 GQ280
EU470635.1 gg_id:289750 red panda feces clone RP_1aaa02f04 EU470
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AF273037.1 gg_id:25611 Samsonia erythrinae AF273
EU459221.1 gg_id:292667 hedgehog feces clone HH_aai34c03 EU459
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GQ155237.1 gg_id:576536 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EU471097.1 gg_id:288710 red panda feces clone RP_3aaa04h05 EU471
GQ492914.1 gg_id:574632 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
GQ032083.1 gg_id:402097 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ032
EU471321.1 gg_id:301319 red panda feces clone RP_3aaa04c11 EU471
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GQ102003.1 gg_id:443904 Topographical and Temporal Human Skin Microbiome skin palm clone nbw502d01c1 GQ102
EU468008.1 gg_id:294204 cheetah feces clone CE2_b02_1 EU468
EU762556.1 gg_id:321515 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A> EU762
GQ493642.1 gg_id:551110 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
GQ155290.1 gg_id:561147 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ155055.1 gg_id:509758 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ492249.1 gg_id:536894 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
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EU472809.1 gg_id:299738 red panda feces clone RPSD_1aaa02d05 EU472
EU596536.1 gg_id:273327 Pantoea agglomerans str. SZ009 EU596
EU289465.1 gg_id:240399 metagenomic approach biosynthesis ansamycin endophytes or symbionts enriched s EU289
AB548574.1 gg_id:531505 Escherichia coli str. JCM 24001 AB548
EU466771.1 gg_id:289838 African elephant feces clone AFEL2_aao29c08 EU466
EU472860.1 gg_id:295962 red panda feces clone RPSD_1aaa02g08 EU472
GQ155181.1 gg_id:512375 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ114745.1 gg_id:385051 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ114
EU472794.1 gg_id:294989 red panda feces clone RPSD_1aaa03a08 EU472
FJ683754.1 gg_id:530543 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6837
DQ248277.1 gg_id:142545 carbon tetrachloride contaminated soil clone TA2 DQ248
EU772604.1 gg_id:322410 North American Black Bear feces clone BB1_h09 EU772
GU166291.1 gg_id:588020 Pantoea sp. str. Y1 GU166
E05133.1 gg_id:28107 Escherichia coli E05133

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GU223214.1 gg_id:581700 Enterobacter cloacae str. SK_C-2 GU223
U92195.1 gg_id:9714 Salmonella enterica subsp. houtenae serovar Houten str. Sh1 subsp. U92195
GQ102010.1 gg_id:386695 Topographical and Temporal Human Skin Microbiome skin palm clone nbw502d08c1 GQ102
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FJ009375.1 gg_id:338379 Enterobacter cancerogenus str. H3 FJ0093
AJ605115.1 gg_id:112171 Escherichia coli str. BL21 AJ6051
AB548825.1 gg_id:514639 Citrobacter freundii str. JCM 24060 AB5488
DQ392983.1 gg_id:156485 Pantoea agglomerans str. d DQ392
GQ154854.1 gg_id:511626 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154

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CP001790.1 gg_id:523633 Pectobacterium wasabiae str. WPP163 CP0017
GQ025498.1 gg_id:405896 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ025
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FJ611867.1 gg_id:538150 Enterobacter cancerogenus str. LMG 2693 FJ6118
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EU466945.1 gg_id:296544 African elephant feces clone AFEL2_aao31f11 EU4669
GQ155259.1 gg_id:553265 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
CP000247.1 gg_id:169669 Escherichia coli str. 536 CP0002
EU464454.1 gg_id:293609 African elephant feces clone AFEL_aai29d08 EU4644
GU171376.1 gg_id:580156 Rahnella aquatilis str. 5YN04-01 GU171
AM157447.1 gg_id:141508 Escherichia coli mother V4 AM157
FJ906795.1 gg_id:568033 Erwinia chrysanthemi str. Lichuan2 FJ9067
FJ997269.1 gg_id:430317 Escherichia coli str. DSPV 247T FJ9972
GQ155006.1 gg_id:568846 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
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EU780667.1 gg_id:307587 Pantoea sp. str. CWB304 EU7806
GQ031664.1 gg_id:465153 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ031
GQ155195.1 gg_id:582588 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EF446900.1 gg_id:210269 Enterobacter cloacae str. AW3 EF4469
GQ101953.1 gg_id:441943 Topographical and Temporal Human Skin Microbiome skin palm clone nbw501f08c1 GQ101
EF560774.1 gg_id:233520 Escherichia coli str. 228 EF5607
AM184220.1 gg_id:159834 Enterobacter cloacae str. WAB1878 AM184
EU937744.1 gg_id:329159 Enterobacter sakazakii str. JG 09 Iti 7 EU9377
DQ444288.1 gg_id:154803 Klebsiella oxytoca str. 17 DQ444
GQ047998.1 gg_id:430834 Topographical and Temporal Human Skin Microbiome skin palm clone nbw140a11c1 GQ047
GQ156028.1 gg_id:566205 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
EF102835.1 gg_id:257820 Pectobacterium carotovorum str. G-1-7 EF1028
EU470480.1 gg_id:291647 red panda feces clone RP_1aaa02b02 EU4704
DQ068852.1 gg_id:139468 microbiota antlions (Myrmeleon mobilis) GI tract freshly caught antlion OTU9 clone DQ068
EU470518.1 gg_id:288607 red panda feces clone RP_1aaa01b06 EU4705
CU915024.1 gg_id:449170 and dynamics adapted microbiota during degradation Tunisian zarzatine enriched se CU9150
CP001637.1 gg_id:524975 Escherichia coli str. DH1 CP0016
EU472906.1 gg_id:298938 red panda feces clone RPSD_1aaa02d07 EU4729
GQ155318.1 gg_id:509391 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
AY690711.1 gg_id:101221 Erwinia sp. str. MK01 AY6907
GQ048037.1 gg_id:462729 Topographical and Temporal Human Skin Microbiome skin palm clone nbw140f06c1 GQ048

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CU928161.2 gg_id:563140 Escherichia coli str. S88 CU928
AY834756.1 gg_id:110694 Rhodopseudomonas palustris str. 2c AY8347
GQ099129.1 gg_id:380807 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ099
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EU471308.1 gg_id:294785 red panda feces clone RP_3aaa03b08 EU4713
GQ155251.1 gg_id:594208 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
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GQ102051.1 gg_id:394557 Topographical and Temporal Human Skin Microbiome skin palm clone nbw502h07c1 GQ102
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CP000948.1 gg_id:270797 Escherichia coli substr. DH10B str. K-12 CP0009
EU468003.1 gg_id:290774 cheetah feces clone CE2_a06_1 EU4680
AE005174.2 gg_id:128878 Escherichia coli O157:H7 str. EDL933 AE0051
GQ155038.1 gg_id:554226 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ492044.1 gg_id:572998 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
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EU430750.1 gg_id:260369 Enterobacter sp. str. ZJUPD6 EU4307
NZ_ACGN01000123.1 gg_id:470367 Escherichia coli str. 83972 NZ_AC
DQ068760.1 gg_id:172586 Salmonella sp. str. Co9936 DQ068
AF395913.1 gg_id:38659 Enterobacter aerogenes AF3959
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GQ047665.1 gg_id:449134 Topographical and Temporal Human Skin Microbiome skin palm clone nbw137e10c1 GQ047
EU471071.1 gg_id:297139 red panda feces clone RP_3aaa03f12 EU4710
AB286558.1 gg_id:217008 Reducing production and domination comamonadaceae reducing oxygen supply was AB2865

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AF520708.1 gg_id:61203 Dickeya dianthicola str. CFBP 1200 AF5207
EF489443.1 gg_id:219392 Pantoea agglomerans str. GIST-NKst1 EF4894
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EF560782.1 gg_id:233200 Escherichia coli str. BE33 EF5607
U90758.1 gg_id:10315 Rahnella genosp. 3 str. DSM 30078 U90758
AJ233409.1 gg_id:10306 Brenneria alni str. DSM 11811 AJ2334
EU761873.1 gg_id:346129 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1 EU7618
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EU430753.1 gg_id:270355 Enterobacter sp. str. ZJUPD3 EU4307
DQ223881.1 gg_id:168597 Citrobacter gillenii str. P9 DQ223
NC_004431.1 gg_id:128802 Escherichia coli str. CFT073 NC_004
EU471669.1 gg_id:297637 Asiatic elephant feces clone AE1_aaa03f11 EU4716
DQ112330.1 gg_id:136199 Pantoea agglomerans str. RS-18 DQ112
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AM062693.1 gg_id:249744 Enterobacter amnigenus p412 AM062
EU471187.1 gg_id:291079 red panda feces clone RP_3aaa04e11 EU4711
GU185862.1 gg_id:587224 Enterobacter ludwigii str. HSBN1 GU185
GQ155216.1 gg_id:583212 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
AM491468.1 gg_id:213014 Aranicola sp. str. Nj-67 AM491
GQ101988.1 gg_id:430225 Topographical and Temporal Human Skin Microbiome skin palm clone nbw502b08c GQ101
GQ155035.1 gg_id:587112 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
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GQ047705.1 gg_id:399615 Topographical and Temporal Human Skin Microbiome skin palm clone nbw138b11c GQ047
DQ298156.1 gg_id:142765 Escherichia sp. SWM_Isolation_4 DQ298
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U88545.1 gg_id:9669 Salmonella typhi str. St111 U88545
EU472820.1 gg_id:294893 red panda feces clone RPSD_1aaa03c03 EU4728

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GQ155878.1 gg_id:549556 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ155057.1 gg_id:568864 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
FJ975887.1 gg_id:534463 Human gut microbiome adopts alternative state bowel transplantation ileum effluent FJ9758
FJ593037.1 gg_id:572846 Pectobacterium wasabiae str. JU-1 FJ5930
GQ155094.1 gg_id:593339 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
CU928162.2 gg_id:547290 Escherichia coli str. ED1a CU928
EF620926.1 gg_id:254200 Escherichia coli str. WD02 EF6209
EF620923.1 gg_id:254591 Escherichia coli str. SYW004 EF6209
GQ047692.1 gg_id:449355 Topographical and Temporal Human Skin Microbiome skin palm clone nbw138a03c GQ047
FJ906925.1 gg_id:562225 Cronobacter sakazakii str. Jor204 FJ9069
NR_024706.1 gg_id:562424 Pseudomonas flectens str. ATCC 12775 NR_02
FJ581031.1 gg_id:568374 Cronobacter sakazakii str. IITRM16 FJ5810
GQ165811.1 gg_id:548859 Enterobacter aerogenes str. IEY GQ165
FJ949577.1 gg_id:373419 Escherichia coli str. H1 FJ9495
EU778499.1 gg_id:325455 Red Panda feces clone RPSD_1aaa03f09 EU778
GQ099209.1 gg_id:452629 Topographical and Temporal Human Skin Microbiome skin interdigital web space cl GQ099
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EU537173.1 gg_id:285808 profile human microbiota antecubital fossa (inner elbow) skin clone nbt67h04 EU537
EU470953.1 gg_id:293383 red panda feces clone RP_2aaa01e06 EU470
EF604173.1 gg_id:233448 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6041
EF102834.1 gg_id:242926 Pantoea agglomerans str. G-4-13-2 EF1028
GU374071.1 gg_id:516475 soil East Calcutta wetland clone SRC_NBB14 GU374
EF515452.1 gg_id:224577 Electricigen Enrichment MFC upf microbial fuel cell anode clone 24e12 EF5154

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AY501386.1 gg_id:99525 Pantoea sp. str. PPE7 AY501
GQ155204.1 gg_id:509434 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ155021.1 gg_id:544405 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
AM184290.1 gg_id:160595 Pantoea agglomerans str. WAB1951 AM184
AF015258.1 gg_id:10180 Aquamonas haywardensis str. CDC 2404-94 EG121 AF015
EU471256.1 gg_id:291269 red panda feces clone RP_3aaa02b01 EU471
AM157425.1 gg_id:141026 Escherichia coli mother C3 AM157
EU078564.1 gg_id:236821 Enterobacter sp. str. R11-2 EU078
AJ871857.1 gg_id:113218 Klebsiella oxytoca str. SB136=ATCC 49131 AJ8718
AF130958.2 gg_id:10082 Pantoea endophytica str. A6 AF130
GQ155121.1 gg_id:575470 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EU471089.1 gg_id:292812 red panda feces clone RP_3aaa04g10 EU471
EU472826.1 gg_id:300494 red panda feces clone RPSD_1aaa02e07 EU472
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EU555536.1 gg_id:266023 Escherichia coli str. CNM 477-02 EU555
EU239468.1 gg_id:255707 Enterobacter asburiae str. XJUHX-5 EU239
FN433037.1 gg_id:543947 Escherichia fergusonii CCM27B FN433
EU778487.1 gg_id:305294 Red Panda feces clone RPSD_1aaa03c07 EU778
AF373173.1 gg_id:66748 Erwinia chrysanthemi str. 340 AF373
EU471241.1 gg_id:297916 red panda feces clone RP_3aaa01a04 EU471
AM933759.1 gg_id:330563 Kluyvera ascorbata 1919 AM933
FJ811870.1 gg_id:578058 Pantoea sp. str. 1-CDF FJ8118
AJ971890.1 gg_id:136113 Erwinia sp. Ob 05 AJ9718
EU470487.1 gg_id:302808 red panda feces clone RP_1aaa04c12 EU470
EF560781.1 gg_id:230035 Escherichia coli str. BE30 EF5607
AM184235.1 gg_id:160492 Enterobacter ludwigii str. WAB1894 AM184
EU535068.1 gg_id:283165 profile human skin microbiota ear punch biopsy female C57BL/6J mouse clone nbt18 EU535
GQ479959.1 gg_id:561718 Enterobacter aerogenes str. MZQ-HZ01 GQ479
DQ086778.1 gg_id:136046 Enterobacter cloacae str. I5 DQ086
AE005674.2 gg_id:128438 Shigella flexneri 2a str. 301 AE005
FJ405334.1 gg_id:366426 Escherichia coli str. 4061 FJ4053
EU470595.1 gg_id:289857 red panda feces clone RP_1aaa04h08 EU470
AJ233414.1 gg_id:9838 Erwinia mallotivora str. DSM 4565 AJ2334
GQ048031.1 gg_id:436643 Topographical and Temporal Human Skin Microbiome skin palm clone nbw140e09c1 GQ048
AJ308467.1 gg_id:34327 Enterobacter sp. 22 AJ3084
AJ309974.1 gg_id:45848 enterobacterium str. dtb112 AJ3099
AY825036.1 gg_id:109467 Enterobacter aerogenes str. NTG-01 AY825
GQ493841.1 gg_id:580139 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493

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GQ155178.1 gg_id:539032 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ156080.1 gg_id:588129 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
EU472802.1 gg_id:290812 red panda feces clone RPSD_1aaa04f09 EU472
AB273732.1 gg_id:243322 Shigella sonnei str. GTC 781 AB273
FJ906921.1 gg_id:542455 Cronobacter sakazakii str. Jor176 FJ9069
EU472837.1 gg_id:295363 red panda feces clone RPSD_1aaa02h08 EU472
GQ155060.1 gg_id:509438 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ031670.1 gg_id:381600 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ031
AB273742.1 gg_id:245432 Cedecea lapagei str. GTC 346 AB273
FJ405361.1 gg_id:358229 Rahnella aquatilis str. SPb FJ4053
EU471082.1 gg_id:295799 red panda feces clone RP_3aaa04g04 EU471
FJ366024.1 gg_id:361492 feces adult twins and mothers; TS25 clone TS25_a01g12 FJ3660
EU472850.1 gg_id:301348 red panda feces clone RPSD_1aaa03d12 EU472
FJ975869.1 gg_id:513372 Human gut microbiome adopts alternative state bowel transplantation ileum effluent FJ9758
ABHO01000013.1 gg_id:286158 Escherichia coli O157:H7 str. EC4196 ABHO
DQ347522.1 gg_id:147724 Paracoccus sp. B-1012 DQ347
DQ124676.1 gg_id:136582 Enterobacter aerogenes str. S2-1 DQ124
U90314.1 gg_id:9706 Salmonella subsp. enterica serovar Blockley str. Sb1 subsp. U90314
X80725.1 gg_id:9741 Escherichia coli str. ATCC 11775T X80725
FM180568.1 gg_id:369788 Escherichia coli 0127:H6 str. E2348/69 FM180
DQ068864.1 gg_id:139117 microbiota antlions (Myrmeleon mobilis) whole animal freshly caught antlion OTU1 DQ068
GQ493963.1 gg_id:583626 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
EU834264.1 gg_id:332053 Raoultella ornithinolytica str. DS44 EU834
EF178670.1 gg_id:180411 Erwinia chrysanthemi str. NZEC135 EF1786
EU857633.1 gg_id:366089 Shigella flexneri EU857
AM933754.1 gg_id:340632 Kluyvera cryocrescens 169 AM933
EU472757.1 gg_id:301762 red panda feces clone RPSD_1aaa02d04 EU472
EF560786.1 gg_id:231669 Escherichia coli str. BE45 EF5607
GQ025603.1 gg_id:416339 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ025
FJ811871.1 gg_id:552136 Enterobacter aerogenes str. 7-WCH FJ8118
EU773798.1 gg_id:346813 Cheetah feces clone CE2_e03 EU773
GQ047918.1 gg_id:402513 Topographical and Temporal Human Skin Microbiome skin palm clone nbw139a08c1 GQ047
EU778388.1 gg_id:354647 Red Panda feces clone RP_1aaa02f05 EU778
EU471154.1 gg_id:297213 red panda feces clone RP_3aaa03f09 EU471
AF024608.1 gg_id:9727 Pantoea agglomerans str. TAC.III.94.1 AF0246
GQ155244.1 gg_id:571288 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ025550.1 gg_id:382453 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ025
GU186121.1 gg_id:584341 Pantoea agglomerans str. IHB B 1383 GU186
EU460458.1 gg_id:293981 polar bear feces clone PB2_aai21b06 EU460

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GQ024535.1 gg_id:485135 Topographical and Temporal Human Skin Microbiome skin palm clone nbw123e03c1 GQ024
Z96089.1 gg_id:9989 Pectobacterium carotovorum str. LMG 2404-T Z96089
GQ154883.1 gg_id:547125 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
GQ025585.1 gg_id:403646 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ025
EU684953.1 gg_id:295125 Erwinia chrysanthemi str. E353 EU684
AB244472.1 gg_id:248467 Enterobacter aerogenes str. NC4211 AB244
GU594308.1 gg_id:531073 Escherichia coli str. AC3 GU594
EU470599.1 gg_id:303181 red panda feces clone RP_1aaa01f04 EU470
GQ101940.1 gg_id:429707 Topographical and Temporal Human Skin Microbiome skin palm clone nbw501b10c1 GQ101
FJ906923.1 gg_id:548205 Cronobacter sakazakii str. Jor183 FJ9069
GQ416891.1 gg_id:572750 Temporal succession biological degreasing systems clone F1jun.25 GQ416
FJ192752.1 gg_id:308904 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior FJ1927
EF515391.1 gg_id:220037 Electricigen Enrichment MFC upf microbial fuel cell anode clone 23g08 EF5153
GQ492620.1 gg_id:561719 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
GQ155307.1 gg_id:553345 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ493735.1 gg_id:590258 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
AM184247.1 gg_id:161342 Enterobacter aerogenes str. WAB1906 AM184
FJ405332.1 gg_id:367948 Escherichia coli str. 4059 FJ4053
EF560785.1 gg_id:232471 Escherichia coli str. BE42 EF5607
GQ155160.1 gg_id:585374 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ114876.1 gg_id:466445 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ114
AB273737.1 gg_id:236285 Trabulsiella guamensis str. GTC 1379 AB273
EU240950.1 gg_id:272583 Enterobacter hormaechei str. YO-B EU240
GQ085256.1 gg_id:409792 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw273b02c GQ085
AB548824.1 gg_id:529730 Citrobacter freundii str. JCM 24059 AB548
GQ031696.1 gg_id:454885 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ031
GQ155185.1 gg_id:582498 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
AJ233421.1 gg_id:9796 Leminorella grimontii str. DSM 5078 AJ2334
FJ364615.1 gg_id:362183 feces adult twins and mothers; TS19 clone TS19_a01a10 FJ3646
EU471104.1 gg_id:297764 red panda feces clone RP_3aaa03f01 EU471
FJ611877.1 gg_id:582578 Enterobacter sp. str. ATCC 27981 FJ6118
FJ404760.1 gg_id:368274 Mangroveibacter sp. str. WG-1 FJ4047
NZ_ABHL02000001.1 gg_id:316857 Escherichia coli O157:H7 str. EC4045 NZ_AB
NC_002655.2 gg_id:150516 Escherichia coli O157:H7 str. EDL933 NC_00
GQ155256.1 gg_id:545159 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
FJ608656.1 gg_id:566084 Klebsiella pneumoniae str. EP4 FJ6086
EU468018.1 gg_id:301955 cheetah feces clone CE2_c10_2 EU468
FJ178002.1 gg_id:333293 Escherichia coli str. AC 521 FJ1780
EU430751.1 gg_id:272055 Enterobacter sp. str. ZJUPD5 EU430
GQ492150.1 gg_id:537226 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492

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EU472682.1 gg_id:302297 red panda feces clone RPSD_1aaa01b01 EU472
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NC_002655.2 gg_id:150515 Escherichia coli O157:H7 str. EDL933 NC_00
FJ976591.1 gg_id:586643 Enterobacter cloacae str. LCR82 FJ9765
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EU470963.1 gg_id:291712 red panda feces clone RP_2aaa01f10 EU470
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GQ416550.1 gg_id:543441 Temporal succession biological degreasing systems clone F7jun.28 GQ416
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EU470754.1 gg_id:298335 red panda feces clone RP_2aaa03f01 EU470
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FJ975788.1 gg_id:589157 Human gut microbiome adopts alternative state bowel transplantation ileum effluent FJ9757
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GQ155197.1 gg_id:585037 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EU472785.1 gg_id:299402 red panda feces clone RPSD_1aaa01c08 EU472
Z83204.1 gg_id:9679 Escherichia coli Z83204
FJ364841.1 gg_id:365623 feces adult twins and mothers; TS19 clone TS19_a03g09 FJ3648
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EU130557.1 gg_id:244222 Escherichia coli str. LR09 EU1305
Z96093.1 gg_id:9800 Erwinia chrysanthemi str. LMG 2804 Z96093
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GQ259886.1 gg_id:582624 Shigella sonnei str. 136 GQ259
EU554428.1 gg_id:273485 Enterobacter cloacae str. Ag02 EU5544
GQ155046.1 gg_id:538073 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EU535123.1 gg_id:280193 profile human microbiota antecubital fossa (inner elbow) skin clone nbt171c02 EU5351
EU464506.1 gg_id:297762 African elephant feces clone AFEL_aai30c11 EU4645
GQ048005.1 gg_id:385167 Topographical and Temporal Human Skin Microbiome skin palm clone nbw140b08c1 GQ048
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GQ154843.1 gg_id:553840 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
EU470615.1 gg_id:291008 red panda feces clone RP_1aaa04d04 EU4706
GQ025492.1 gg_id:441988 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ025
GQ026798.1 gg_id:457125 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ026
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EU470573.1 gg_id:301959 red panda feces clone RP_1aaa03e03 EU4705
GQ154857.1 gg_id:580141 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
GQ047689.1 gg_id:449074 Topographical and Temporal Human Skin Microbiome skin palm clone nbw137h10c1 GQ047
CU928161.2 gg_id:563141 Escherichia coli str. S88 CU928
EF059842.1 gg_id:224891 Enterobacter asburiae str. E531 EF0598
EU467838.1 gg_id:297319 North American black bear feces clone BB1_b07_2 EU4678
GQ492166.1 gg_id:590121 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
GQ492874.1 gg_id:535252 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
FJ405333.1 gg_id:369236 Escherichia coli str. 4060 FJ4053
AY373830.1 gg_id:105259 Trabulsiella guamensis AY3738
AB198445.1 gg_id:135844 termite gut wall fraction clone RsW01-004 AB1984
GQ025599.1 gg_id:389061 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ025
GQ114854.1 gg_id:415761 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ114
U90316.1 gg_id:9661 Salmonella typhimurium str. Stm1 U90316
DQ068855.1 gg_id:138975 microbiota antlions (Myrmeleon mobilis) GI tract freshly caught antlion OTU6 clone DQ068
EU470655.1 gg_id:297290 red panda feces clone RP_1aaa04h06 EU4706
GQ031692.1 gg_id:383643 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ031

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EF515376.1 gg_id:225183 Electricigen Enrichment MFC upf microbial fuel cell anode clone 23e11 EF5153
GQ155116.1 gg_id:511824 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
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EF428236.2 gg_id:218527 Enterobacter hormaechei str. HDYM-06 EF4282
GQ155942.1 gg_id:574837 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
DQ818881.1 gg_id:164892 mouse cecal microbiota-colonized zebrafish digestive tract clone aab39b09 DQ818
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FJ975865.1 gg_id:554433 Human gut microbiome adopts alternative state bowel transplantation ileum effluent FJ9758
FJ368169.1 gg_id:362886 feces adult twins and mothers; TS3 clone TS3_a01a10 FJ3681
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GQ155100.1 gg_id:539752 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ047953.1 gg_id:434609 Topographical and Temporal Human Skin Microbiome skin palm clone nbw139e07c1 GQ047
EU472801.1 gg_id:295032 red panda feces clone RPSD_1aaa04g01 EU472
AF373203.1 gg_id:66723 Erwinia chrysanthemi str. GSPB 1406 AF3732
EU723875.1 gg_id:349834 Shigella sp. str. 121405 EU7238
GQ033388.1 gg_id:388657 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw1 GQ033
AY360397.1 gg_id:93777 Erwinia chrysanthemi str. S3-1 AY3603
EU275357.1 gg_id:250107 Pantoea agglomerans str. CONC7 EU2753
EU560857.1 gg_id:562063 Assessment genetic Apriona germari (Hope) larvae normalization techniques intestir EU5608
EU471032.1 gg_id:295686 red panda feces clone RP_2aaa01c11 EU4710
AB288903.1 gg_id:201514 termite gut homogenate clone BOf5-16 AB2889
GU594301.1 gg_id:516250 Escherichia coli str. A5 GU594
EF515211.1 gg_id:217868 Electricigen Enrichment MFC upf microbial fuel cell anode clone 21d06 EF5152
GQ155921.1 gg_id:548341 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EU009178.1 gg_id:250393 Shigella boydii str. FBD007 EU0091
GQ491471.1 gg_id:588423 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
EF608546.1 gg_id:230213 predatory Poecilus chalcites their response lab rearing and antibiotic treatment diges EF6085

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AB368994.1 gg_id:569024 and microbial oils produced Asia petroleum crude oil (Arabian Extra light) clone PT-A AB368
CP001637.1 gg_id:524976 Escherichia coli str. DH1 CP001
AM184214.1 gg_id:161150 Pantoea agglomerans str. WAB1872 AM184
EU472148.1 gg_id:288731 francois langur feces clone FL_2aaa02a09 EU472
EF515321.1 gg_id:219651 Electricigen Enrichment MFC upf microbial fuel cell anode clone 22h03 EF5153
EF011116.1 gg_id:199506 Enterobacter cancerogenus str. EBD EF0111
EF471230.1 gg_id:226404 Enterobacter sp. str. BBTR105 EF4712
CP001790.1 gg_id:523631 Pectobacterium wasabiae str. WPP163 CP001
AM157436.1 gg_id:141413 Escherichia coli mother C4 AM157
CP000247.1 gg_id:169667 Escherichia coli str. 536 CP000
EU470717.1 gg_id:302020 red panda feces clone RP_1aaa02h08 EU470
FJ368186.1 gg_id:366961 feces adult twins and mothers; TS3 clone TS3_a01c05 FJ3681
EU778424.1 gg_id:326151 Red Panda feces clone RPSD_1aaa01b11 EU778
AY804014.1 gg_id:112448 Escherichia coli str. T10 AY804
EU471322.1 gg_id:303145 red panda feces clone RP_3aaa04b03 EU471
GQ029738.1 gg_id:413180 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw926f08 GQ029
EU554433.1 gg_id:273281 Shigella boydii str. Ag07 EU554
EU472761.1 gg_id:301142 red panda feces clone RPSD_1aaa02f12 EU472
L10328.1 gg_id:9702 Escherichia coli L10328
EF560776.1 gg_id:232981 Escherichia coli str. BE14 EF5607
EF676101.1 gg_id:257345 Klebsiella oxytoca str. XJU-1 EF6761
GQ102000.1 gg_id:409168 Topographical and Temporal Human Skin Microbiome skin palm clone nbw502c09c1 GQ102
AJ854062.1 gg_id:108296 Serratia ureolytica str. NiVa 51 AJ854
GQ099091.1 gg_id:389986 Topographical and Temporal Human Skin Microbiome skin interdigital web space cl GQ099
GQ031106.1 gg_id:395646 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ031
FJ368221.1 gg_id:369163 feces adult twins and mothers; TS3 clone TS3_a01f08 FJ3682
CP000247.1 gg_id:169665 Escherichia coli str. 536 CP000
EU470534.1 gg_id:296475 red panda feces clone RP_1aaa04e05 EU470
EU471185.1 gg_id:290380 red panda feces clone RP_3aaa03b07 EU471
GQ927306.1 gg_id:540402 Enterobacter sp. str. M6 GQ927
EU761952.1 gg_id:316329 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1 EU761
FJ364654.1 gg_id:368156 feces adult twins and mothers; TS19 clone TS19_a01e03 FJ3646
GU186117.1 gg_id:593155 Enterobacter cloacae str. IHB B 1374 GU186
GU594309.1 gg_id:521580 Escherichia coli str. AB6 GU594
U88435.1 gg_id:10311 Rahnella sp. 'CDC 21234' str. CDC 21234 U88435
EU470575.1 gg_id:302778 red panda feces clone RP_1aaa03a07 EU470
EU999992.2 gg_id:343920 Enterobacter ludwigii str. T4384 EU999
EU240200.1 gg_id:236031 interfering detection phytoplasma universal phytoplasmic primers Mexico EU240
EU460602.1 gg_id:298145 polar bear feces clone PB2_aai23c03 EU460
EU472738.1 gg_id:302314 red panda feces clone RPSD_1aaa03d08 EU472
NZ_AAJU02000035.1 gg_id:318422 Escherichia coli str. F11 NZ_AA

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GQ099081.1 gg_id:403628 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ099
GQ155052.1 gg_id:574054 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
AF511430.1 gg_id:65406 Escherichia coli CCCO4 AF5114
AY344368.2 gg_id:91670 Lake Kauhako 30 m clone K2-30-35 AY3443
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FJ976582.1 gg_id:592530 Enterobacter cancerogenus str. LCR73 FJ9765
CP000247.1 gg_id:169666 Escherichia coli str. 536 CP000
EF102825.1 gg_id:257388 Enterobacter sp. str. G-226-1 EF1028
GQ154770.1 gg_id:589091 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
GQ025541.1 gg_id:431917 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ025
EF219421.2 gg_id:441069 Enterobacter cloacae str. ATCC 43560 EF2194
U92197.1 gg_id:9711 Salmonella subsp. enterica serovar Agona str. Sa1 subsp. U9219
GQ154820.1 gg_id:535230 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
GQ031713.1 gg_id:452836 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ031
NZ_ABHM02000001.1 gg_id:317271 Escherichia coli O157:H7 str. EC4042 NZ_AB
GQ155096.1 gg_id:594320 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
FJ859683.1 gg_id:573410 Enterobacter ludwigii str. BIHB 336 FJ8596
GQ155198.1 gg_id:586724 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
CP000468.1 gg_id:175186 Escherichia coli str. APEC O1 CP000
NC_008563.1 gg_id:176527 Escherichia coli str. APEC O1 NC_00
GQ155253.1 gg_id:582117 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
FJ976590.1 gg_id:581741 Enterobacter sp. str. LCR81 FJ9765
FJ811874.1 gg_id:593519 Enterobacter aerogenes str. 5-WCH FJ8118
ABHS01000007.1 gg_id:302893 Escherichia coli O157:H7 str. EC4486 ABHS0
X80726.1 gg_id:9698 Shigella sonnei X80726
FJ364922.1 gg_id:363434 feces adult twins and mothers; TS19 clone TS19_a04g07 FJ3649
FM180568.1 gg_id:369792 Escherichia coli 0127:H6 str. E2348/69 FM180
AAMJ02000006.1 gg_id:342676 Shigella dysenteriae str. 1012 AAMJ0
EU778390.1 gg_id:333367 Red Panda feces clone RPSD_1aaa01b09 EU778
EU554431.1 gg_id:273912 Shigella flexneri str. Ag05 EU554
AF400480.1 gg_id:18267 Secondary endosymbiont Bemisia tabaci clone TANZ3-2 of AF4004
DQ837613.1 gg_id:164437 structures honeybee intestines and their response insecticidal proteins gut clone HB DQ837
DQ026512.1 gg_id:134671 Xenorhabdus sp. str. PDBC SCX7 DQ026
GU480985.1 gg_id:521599 Xenorhabdus hominickii GU480
AB030020.1 gg_id:32418 Antonina crawii (Insecta Homoptera Pseudooccidae) symbiont AB030
AF286129.1 gg_id:21132 eubacterium Aleurodicus dugesii AF286
AF476107.1 gg_id:63935 Planococcus citri symbiont AF476
AY676889.1 gg_id:136328 Baumannia cicadellinicola B37 AY6768
AF400474.1 gg_id:50143 Secondary endosymbiont Bemisia tabaci clone IND34 AF4004

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AY660027.2 gg_id:119010 Xenorhabdus bovienii str. PDBC SCX6	AY660
AB064513.1 gg_id:49541 Buchnera aphidicola (Yamatocallis tokyoensis) #207 (Yamatocallis	AB0645
DQ068832.1 gg_id:139463 microbiota antlions (Myrmeleon mobilis) GI tract freshly caught antlion OTU7 clone	DQ068
AF476104.1 gg_id:63945 Dysmicoccus neobrevipes symbiont	AF4761
GU374099.1 gg_id:531978 soil East Calcutta wetland clone SRC_NBB4	GU374
AY676885.1 gg_id:136092 Baumannia cicadellinicola B30	AY6768
FJ655533.1 gg_id:592467 symbiont	FJ6555
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FJ655532.1 gg_id:542044 symbiont	FJ6555
EU348312.1 gg_id:348059 symbiont	EU3483
GQ154740.1 gg_id:534965 Human gut microbiome adopts alternative state bowel transplantation ileum intesti	GQ154
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AB083058.1 gg_id:60304 Placobdelloides siamensis symbiont	AB083
AF263559.1 gg_id:54656 Cacopsylla myrthi symbiont	AF2635
AF077608.1 gg_id:9978 symbiont	AF0776
AF286128.1 gg_id:27576 symbiont	AF2861
AF400478.1 gg_id:52003 Secondary endosymbiont Bemisia tabaci clone TANZ15 of	AF4004
AY167945.1 gg_id:76905 Isolation and identification hyper-ammonia producing swine storage pits manure	AY1679
AY676882.1 gg_id:136397 Baumannia cicadellinicola B23	AY6768
AF476110.1 gg_id:63934 Vryburgia amaryllidis symbiont	AF4761
AY999971.1 gg_id:200690 Placobdelloides jaegerskioeldi symbiont	AY9999
AF476101.1 gg_id:63942 Antonina pretiosa symbiont	AF4761
AF286127.1 gg_id:20298 symbiont	AF2861
NC_004344.2 gg_id:141977 Wigglesworthia glossinidia endosymbiont Glossina brevipalpis	NC_004
EF153305.1 gg_id:192342 identification gut red imported fire ant (Solenopsis Buren) GI tract Solenopsis invicta	EF1533
AB083059.1 gg_id:55799 Parabdella sp. symbiont	AB083
DQ211709.1 gg_id:164016 Xenorhabdus sp. str. FRM16	DQ211
D78008.1 gg_id:10301 Xenorhabdus japonica str. SK-1T (=IAM14265T)	D78008
GU480979.1 gg_id:529286 Xenorhabdus griffiniae str. T87	GU480
GQ923884.1 gg_id:589696 Xenorhabdus sp. str. KB-3	GQ923
DQ205450.1 gg_id:173648 Xenorhabdus sp. str. USNJ01	DQ205
GU480982.1 gg_id:526425 Xenorhabdus sp. str. R00I-293	GU480
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AY286478.1 gg_id:87839 Xenorhabdus nematophila	AY2864
FN667741.1 gg_id:524496 Xenorhabdus bovienii str. SS-2004	FN6677
AB243427.1 gg_id:160641 Xenorhabdus sp. str. MY8 IkWj136	AB2434
GU480989.1 gg_id:517099 Xenorhabdus szentirmaii	GU480

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AY278675.1 gg_id:86906 Xenorhabdus beddingii str. DSM4764
D78006.1 gg_id:10299 Xenorhabdus beddingii str. DSM4764
AY317154.1 gg_id:89531 Xenorhabdus bovienii str. CB54
GU480981.1 gg_id:527534 Xenorhabdus bovienii str. Monsanto
GU480988.1 gg_id:515326 Xenorhabdus bovienii str. Li6
DQ208305.1 gg_id:167325 Xenorhabdus bovienii str. TB20
DQ205453.1 gg_id:163330 Xenorhabdus bovienii str. USNY95
D78007.1 gg_id:10244 Xenorhabdus bovienii str. ATCC35271T
FJ860885.1 gg_id:545382 Xenorhabdus bovienii str. USAR01
X82252.1 gg_id:10246 Xenorhabdus bovienii str. DSM 4766
DQ329379.1 gg_id:146743 Xenorhabdus budapestensis str. CB43
GU480990.1 gg_id:529536 Xenorhabdus cabanillasii
GU480992.1 gg_id:520060 Xenorhabdus innexi
EU190977.1 gg_id:266440 Xenorhabdus kozodoii str. FR48
FJ860884.1 gg_id:591393 Xenorhabdus nematophila str. K97
AY278674.1 gg_id:87960 Xenorhabdus nematophila str. DSM3370
EU513180.1 gg_id:264777 Xenorhabdus poinarii str. SRK 1
DQ211703.1 gg_id:169069 Xenorhabdus poinarii str. AZ26
EU250472.1 gg_id:246846 Xenorhabdus poinarii str. Iran2
GU480993.1 gg_id:527414 Xenorhabdus stockiae str. T9
DQ646382.1 gg_id:161501 Yersinia kristensenii str. 03
AAYR01000001.1 gg_id:261186 Yersinia pestis biovar Antiqua str. UG05-0454
AF365943.1 gg_id:30561 Yersinia pseudotuberculosis str. 204
EU434476.1 gg_id:274633 Yersinia kristensenii str. b281
AJ232236.1 gg_id:10381 Yersinia pestis SS-Yp-114
FJ641890.1 gg_id:559301 Yersinia intermedia str. 5375
EF179132.1 gg_id:264397 Yersinia ruckeri str. CCUG 14190
NC_006155.1 gg_id:128947 Yersinia pseudotuberculosis IP 32953 str. IP32953
AJ627595.1 gg_id:107083 Yersinia kristensenii str. Y156
FJ641877.1 gg_id:543977 Yersinia intermedia str. Nr13/84
CP000720.1 gg_id:257703 Yersinia pseudotuberculosis str. IP 31758
AJ232239.1 gg_id:10384 Yersinia pestis SS-Yp-117
X75274.1 gg_id:10388 Yersinia pestis
FJ641882.1 gg_id:573766 Yersinia intermedia str. H9-36/83
DQ646383.1 gg_id:161584 Yersinia aldovae str. 04
EF515428.1 gg_id:224468 Electricigen Enrichment MFC upf microbial fuel cell anode clone 24c09
EF179120.1 gg_id:258690 Yersinia massiliensis str. CCUG 53444
NZ_AAYR01000015.1 gg_id:263525 Yersinia pestis biovar Antiqua str. UG05-0454
X75276.1 gg_id:10393 Yersinia rohdei
X75273.1 gg_id:10365 Yersinia frederiksenii

FN667
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NZ_ABAT01000008.1 gg_id:260769 Yersinia pestis biovar Orientalis str. F1991016 NZ_AB
AJ232237.1 gg_id:10382 Yersinia pestis SS-Yp-115 AJ2322
AJ627597.1 gg_id:107378 Yersinia aleksici str. Y159 AJ6275
NR_027543.1 gg_id:535819 Yersinia bercovieri str. CNY 7506; ATCC 43970 NR_02
U63135.1 gg_id:10347 Yersinia enterocolitica German U63135
AF282308.1 gg_id:41539 Yersinia enterocolitica str. 8081 AF2823
Z49830.1 gg_id:10349 Yersinia enterocolitica str. ER-31406-92 serotype O:5 Z49830
GU596500.1 gg_id:527323 Yersinia enterocolitica str. GP2 GU596
EF179130.1 gg_id:272269 Yersinia enterocolitica str. CCUG 8239A EF1791
X68674.1 gg_id:10341 Yersinia enterocolitica serotype 0:3; strain 11472 Princess Alexandra Hospital Brisbane A X68674
EU523225.1 gg_id:269635 Yersinia enterocolitica str. KM1 EU523
DQ486901.1 gg_id:158291 Yersinia frederiksenii 49 DQ486
AF366384.1 gg_id:34461 Yersinia rohdei str. ATCC 43380 AF3663
EF179123.1 gg_id:265704 Yersinia intermedia str. CCUG 11292 EF1791
DQ917929.1 gg_id:163194 Yersinia intermedia str. H-27 DQ917
NR_027546.1 gg_id:557655 Yersinia mollaretii str. CNY 7263; ATCC 43969 NR_02
NZ_ACCA01000078.1 gg_id:382211 Yersinia kristensenii str. ATCC 33638 NZ_AC
FM955884.1 gg_id:546539 Yersinia kristensenii str. Asd MY-1 FM955
EU401667.1 gg_id:263404 Yersinia ruckeri EU401
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FJ873802.1 gg_id:534783 Yersinia ruckeri str. LY0903 FJ8738
AY359283.1 gg_id:102805 Aquicella siphonis str. SGT-108 AY3592
EF688351.1 gg_id:245537 soil clone F4-96 EF6883
FJ542924.1 gg_id:526380 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone B FJ5429
EU801111.1 gg_id:320125 It's all ranking aquatic Delaware Bay NJ clone 2C229435 EU801
FM877663.1 gg_id:362619 Microbial several mining wastes Bulgaria vicinity uranium mine Sliven clone Sliv-27 FM877
EF019154.1 gg_id:212714 aspen rhizosphere clone Amb_16S_1801 EF0191
FJ382597.1 gg_id:542155 Potentially pathogenic and air stem cell transplant summer hospital shower water BN FJ3825
AY734242.1 gg_id:135830 dynamics aquifers indicates presence stable autochthonous microbial endokarst spri AY7342
AJ252651.1 gg_id:36918 agricultural soil clone SC-I-71 AJ2526
NR_025763.1 gg_id:552844 Aquicella lusitana str. SGT-39; CIP 107650 NR_02
GQ054582.1 gg_id:454783 Topographical and Temporal Human Skin Microbiome skin back clone nbw1092b02c GQ054
FJ793155.1 gg_id:529786 Archaea and Hot Spring Thailand Tao Dam hot spring clone TDB06 FJ7931
FJ542873.1 gg_id:529296 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone A FJ5428
DQ083104.1 gg_id:132329 Fnctnl and rspnss mcrbl cntr-old fld sl cln X174 DQ083
EF540406.1 gg_id:227017 oil-shale semi-coke solid waste clone 4_15MK EF5404
NC_011527.1 gg_id:356835 Coxiella burnetii str. CbuG_Q212 NC_01
EU881324.1 gg_id:314162 (maize-sweet cropping field) Karst region maize-sweet potato cropland soil clone KM EU8813
EU143669.1 gg_id:251151 Coxiella-like infection Psittacine birds liver clone 1358 EU1436

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

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DQ396109.1 gg_id:156557 deep-sea octacoral clone ctg_NISA135 DQ396
EU803079.1 gg_id:326446 It's all ranking aquatic Northeast Colon Panama clone 4C230497 EU803
AJ252619.1 gg_id:36221 agricultural soil clone SC-I-16 AJ2526
FJ444660.1 gg_id:578973 Cotton Rhizosphere cotton rhizosphere clone 2h-38 FJ4446
FJ444646.1 gg_id:587687 Cotton Rhizosphere cotton rhizosphere clone 2h-15 FJ4446
DQ431905.1 gg_id:207732 microorganisms catalyzing nitrogen removal and organic matter metabolism perme DQ431
GQ349429.1 gg_id:569326 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ349
EF515899.1 gg_id:225991 grassland soil clone FCPT587 EF5158
EU735661.1 gg_id:325840 archaeal structures oil contaminated and soils China pristine soil Jidong Oilfield clone EU735
CU466806.1 gg_id:317285 Evry wastewater treatment plant anoxic basin clone CU466
AB294332.1 gg_id:215917 Microbial structure deep coal seem groundwater stream clone SWB21 AB2943
EU202847.1 gg_id:347934 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo EU2028
FJ545549.1 gg_id:511371 Diveristy Seawater and Sediment Northern North Yel Sea sediment clone S2-5 FJ5455
GU305791.1 gg_id:534111 Research on changes structure during algae outbreak oligotrophic lakes (YangHe res GU305
FJ205343.1 gg_id:535383 Prokaryotic deep-sea hydrothermal region East Lau Spreading Centre deep marine se FJ2053
GQ350354.1 gg_id:587874 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ350
EU925916.1 gg_id:303457 sediments sediment station DBS1 northern Bering Sea clone 152H67 EU9259
AB015255.1 gg_id:8026 deepest cold-seep area Japan Trench clone JTB256 proteobacterium AB0152
EF574681.1 gg_id:229650 site S25 near Coco's Island marine clone S25_1025 EF5746
EU644214.1 gg_id:282458 and Samoylov Island Lena active layer -centred polygon near surface horizon; Rim_T EU6442
AF235121.1 gg_id:74504 North Sea clone KTc0924 AF2351
EU134760.1 gg_id:238980 tallgrass prarie soil clone FFCH7560 EU1347
EU249954.1 gg_id:246142 Polyphasic description Pocillopora seawater adjacent Pacillopora meandrina coral co EU2499
EF575249.1 gg_id:232669 site S25 near Coco's Island marine clone S25_1593 EF5752
EU134712.1 gg_id:245968 tallgrass prarie soil clone FFCH5316 EU1347
FJ468390.1 gg_id:555059 Bioaugmentation Pseudomonas sp. strain MHP41 promotes attenuation and changes FJ4683
FJ236047.1 gg_id:334364 three Parisian treatment plants approaches drinking water clone Orly7 FJ2360
FJ437972.1 gg_id:539237 Benthic okenone production Fayetteville New York Green Lake surface sediments 16. FJ4379
EF575079.1 gg_id:237689 site S25 near Coco's Island marine clone S25_1423 EF5750
FJ205338.1 gg_id:555799 Prokaryotic deep-sea hydrothermal region East Lau Spreading Centre deep marine se FJ2053
AF255642.1 gg_id:22253 EBPR sludge clone Ebpr12 AF2556
EU386125.1 gg_id:272458 Biogeographical and microbes sediments on subseafloor sediment South China Sea c EU3861
EU134733.1 gg_id:237253 tallgrass prarie soil clone FFCH11328 EU1347
EU134753.1 gg_id:248221 tallgrass prarie soil clone FFCH15155 EU1347
EF019986.1 gg_id:216743 aspen rhizosphere clone Elev_16S_1373 EF0199
EU805209.1 gg_id:326155 It's all ranking aquatic 250 miles Panama City clone 6C233205 EU8052
EU834797.1 gg_id:541438 Microbiology Aerobic Phosphorus Removal Process aerobic phosphorus-removing se EU8347
FJ712415.1 gg_id:523629 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) K FJ7124
EU193049.1 gg_id:357896 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo EU1930
Z32636.1 gg_id:8006 Legionella brunensis Z32636

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AF129524.1 gg_id:51847 Legionella pneumophila str. E5C1; ATCC700713 AF1295
X97361.1 gg_id:7908 Legionella sp str. LLAP8 X97361
NC_006368.1 gg_id:129226 Legionella pneumophila str. Paris NC_00
AB233212.1 gg_id:140544 Legionella landfill str. OA1-4 AB233
FJ542889.1 gg_id:522337 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone A FJ5428
FJ612289.1 gg_id:592165 and Biogeochemistry Dongping Lake Ecosystems lake water clone DP7.5.15 FJ6122
NR_026522.1 gg_id:565488 Legionella tucsonensis str. 087-AZ-H; ATCC 49180 NR_02
EU250236.1 gg_id:246283 acid mine drainage clone GXDC-22 EU250
FJ230896.1 gg_id:315994 under Level Antibiotic Selection Pressures river water clone F20 FJ2308
EU134790.1 gg_id:244967 tallgrass prarie soil clone FFCH3904 EU134
GQ002634.1 gg_id:507027 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbu GQ002
GQ264139.1 gg_id:564434 Structure Simulated Level Waste Site simulated level waste site clone WC3_79 GQ264
DQ814490.1 gg_id:168390 zebrafish digestive tract clone aaa29e09 DQ814
Z49722.1 gg_id:7972 Legionella fairfieldensis Z49722
DQ413099.1 gg_id:154202 Microbial -dependent and Approaches Anaerobic/Aerobic SBR Reactor EBPR sludge DQ413
Z49724.1 gg_id:7994 "Legionella donaldsonii" Z49724
DQ337039.1 gg_id:145455 subsurface water clone EV818EB5CPSAJJ36 DQ337
AY792279.1 gg_id:123281 Humic Lake clone CrystalBog1D4 AY792
FJ744881.1 gg_id:549676 Transporter genes expressed coastal response dissolved organic carbon surface wate FJ7448
AY662002.1 gg_id:137028 uranium-contaminated groundwater clone 300G-C11 AY662
DQ667196.1 gg_id:171418 Legionella taurinensis str. ATCC 700508 DQ667
X97363.1 gg_id:7946 Legionella sp str. LLAP10 X97363
FM877662.1 gg_id:359700 Microbial several mining wastes Bulgaria vicinity uranium mine Sliven clone Sliv-17 FM877
DQ327699.1 gg_id:166988 Biological filtration limits carbon availability affects downstream biofilm formation a DQ327
FJ542894.1 gg_id:518474 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone A FJ5428
X97356.1 gg_id:7948 Legionella sp str. LLAP2 X97356
AF467296.1 gg_id:64661 Xanthomonas sp. clone 88_5_2 AF467
AY598719.2 gg_id:99452 Amoeba proteus symbiotic AY598
AY957913.1 gg_id:114944 drinking water biofilm clone B3NR56D11 AY957
GU062706.1 gg_id:590087 Legionella sp. str. NML 93L054 GU062
Z49720.1 gg_id:7915 Legionella cherrii Z49720
Z49733.1 gg_id:7976 Legionella quinlivanii Z49733
AY050582.1 gg_id:21751 MCB-contaminated groundwater-treating reactor clone GOUTA10 AY0505
Z49739.1 gg_id:7955 Legionella worsliensis Z49739
EU937840.1 gg_id:331322 Biogeochemistry Iron Oxidation Circumneutral Freshwater Habitat riparian iron oxidi EU937
FJ543058.1 gg_id:528709 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone B FJ5430
EU800944.1 gg_id:306074 It's all ranking aquatic Delaware Bay NJ clone 2C229203 EU800
Z49719.1 gg_id:7922 Legionella bozemanii Z49719
AJ969023.1 gg_id:120376 Legionella anisa UCSC 25 AJ969
FJ479065.1 gg_id:590656 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4790

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GQ347573.1 gg_id:555343 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ347
DQ327700.1 gg_id:163406 Biological filtration limits carbon availability affects downstream biofilm formation a DQ327
EU835422.1 gg_id:318862 structure and quorum sensing reverse osmosis RO membrane biofilm clone 1B17 EU8354
Z49741.1 gg_id:7937 Legionella lytica str. LLAP-3 legionella like amoebal pathogen Z49741
Z32640.1 gg_id:7984 Legionella israelensis Z32640
EU236319.1 gg_id:298170 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg1bF3 EU2363
GQ054315.1 gg_id:463932 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw1108 GQ054
EU134769.1 gg_id:243485 tallgrass prarie soil clone FFCH9178 EU1347
Z49729.1 gg_id:7954 Legionella moravica Z49729
Z49728.3 gg_id:7971 Legionella londiniensis Z49728
AB255083.1 gg_id:173398 corroded concrete clone IC-85 AB2550
Z49736.1 gg_id:7956 Legionella shakespearei Z49736
Z49725.1 gg_id:7929 Legionella gratiana Z49725
Z49735.1 gg_id:7931 Legionella santicrucis Z49735
DQ413067.1 gg_id:153948 Microbial -dependent and Approaches Anaerobic/Aerobic SBR Reactor EBPR sludge DQ413
EU800974.1 gg_id:311942 It's all ranking aquatic Delaware Bay NJ clone 2C229243 EU8009
FJ382013.1 gg_id:543450 Potentially pathogenic and air stem cell transplant winter hospital shower water BMT FJ3820
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Z49734.1 gg_id:7927 Legionella sainthelensi Z49734
AM747393.1 gg_id:236913 Legionella dresdeniensis str. W03-356 AM747
EU835407.1 gg_id:318176 structure and quorum sensing reverse osmosis RO membrane biofilm clone 1T17 EU8354
EU835445.1 gg_id:340760 structure and quorum sensing reverse osmosis RO membrane biofilm clone 2B20 EU8354
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Z32642.1 gg_id:7981 Legionella oakridgenesis Z32642
AJ919271.1 gg_id:114678 Legionella nautarum AJ9192
GQ388900.1 gg_id:551369 quality deterioration drinking system during serious red water outbreak clone Z61 GQ388
FJ236838.1 gg_id:328884 Legionella sp. str. CDC-3041-AUS-E FJ2368
EU134750.1 gg_id:238279 tallgrass prarie soil clone FFCH14647 EU1347
Z49730.3 gg_id:7982 Legionella nautarum Z49730
NR_025196.1 gg_id:556395 Legionella busanensis str. K9951; KCTC 12084 NR_025
AF122884.2 gg_id:8008 Legionella beliardensis str. Montbeliard A1 AF1228
GQ009403.1 gg_id:500261 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw77 GQ009
EF612978.1 gg_id:233794 acid mine drainage clone YSK16S-15 EF6129
EF036512.1 gg_id:191570 Legionella jordanis NML 060502 EF0365
EF471571.1 gg_id:270320 Fast Screening and Estuarine Operon Libraries whole surface water Chesapeake Bay EF4715
EF520577.1 gg_id:229517 structure lakes: what controls ? acid-impacted lake clone ADK-RXe02-02 EF5205
DQ458002.1 gg_id:158776 acid mine drainage clone DX32 DQ458
EU491749.1 gg_id:263538 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU4917

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EU386109.1 gg_id:264331 Biogeographical and microbes sediments on subseafloor sediment South China Sea c EU386
GQ850579.1 gg_id:559606 bottom water northern Bering Sea clone d131 GQ850
AY050590.1 gg_id:52016 MCB-contaminated groundwater-treating reactor clone GOUTB2 AY0505
GQ261748.1 gg_id:550690 shifts taxa and response localized organic loading deep sea sediment whale falls clo GQ261
EU491526.1 gg_id:268607 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR4C EU491
EU491716.1 gg_id:267408 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU491
GQ472814.1 gg_id:574241 Biodiversity planktonic Northern surface water northern Bering Sea clone b45 GQ472
EU735642.1 gg_id:312981 archaeal structures and pristine soils China oil contaminated soil Jidong Oilfield clone EU735
EF520571.1 gg_id:230249 structure lakes: what controls ? acid-impacted lake clone ADK-HDe02-30 EF5205
EF516119.1 gg_id:221947 grassland soil clone FCPU740 EF5161
GU118075.1 gg_id:554366 Threatened Corals Provide Microbial Habitats clone Apal_M08 GU118
EU236332.1 gg_id:297516 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg5a2A5 EU236
FJ744812.1 gg_id:546723 Transporter genes expressed coastal response dissolved organic carbon surface wate FJ7448
EU236289.1 gg_id:292187 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone HgCo16 EU236
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AY536226.1 gg_id:101534 host gut clone LAgut--P14 AY536
DQ295893.1 gg_id:145412 Cohn's Crenothrix filamentous oxidizer unusual methane monooxygenase physical e DQ295
GQ390223.1 gg_id:548160 oxic-anoxic interface meromictic crater lake Lac Pavin clone eub62A8 GQ390
AB504955.1 gg_id:565012 structure microorganisms reddish-brown iron-rich snow clone oze05B47 AB504
DQ837251.1 gg_id:247086 Archaeal and pristine National Park Spain Donana coastal aquifer clone 49S1_2B_45 DQ837
FJ502272.1 gg_id:509929 Co-occurrence denitrification and nitrogen fixation meromictic lake (Switzerland) Lak FJ5022
AF152597.1 gg_id:8098 Methylobacter psychrophilus str. Z-0021 AF1525
AJ583183.1 gg_id:94840 radioactive site ground water clone S15B-MN136 AJ5831
AB240527.1 gg_id:141423 microbial structure rhizosphere biofilm Sapporo root-base (80 160 mm) Phragmites S AB2405
DQ984190.1 gg_id:205851 Clonothrix fusca str. AW-b DQ984
AF351235.1 gg_id:48494 coal tar waste-contaminated groundwater clone 8-4 proteobacterium AF3512
DQ367735.1 gg_id:150338 Fluorescence Situ Hybridization-F Cytometry-Cell Sorting-Based Method Enrichment DQ367
AB240465.1 gg_id:141872 microbial structure rhizosphere biofilm Sapporo root-tip (0 40 mm) Phragmites Sosei AB2404
EF125436.1 gg_id:175001 mangrove soil clone MSB-2D7 EF1254
AB240522.1 gg_id:140993 microbial structure rhizosphere biofilm Sapporo root-base (80 160 mm) Phragmites S AB2405
DQ066944.1 gg_id:135917 Lake Washington sediment clone pLW-18 DQ066
DQ066943.1 gg_id:131019 Lake Washington sediment clone pLW-17 DQ066
M95657.1 gg_id:8104 Methylobacter luteus str. 11914 M9565
AF304195.1 gg_id:40043 Methylobacter luteus str. NCIMB 11914 AF3041
AF304197.1 gg_id:37065 Methylobacter marinus str. A45 AF3041
DQ270621.1 gg_id:142869 hydrothermal carbonate chimney clone LC1133B-99 DQ270
AJ704662.1 gg_id:109268 marine sediment clone HMMVBeg-7 AJ7046
DQ521819.1 gg_id:160617 Anaerobic Methane Oxidizing ANME-1b Archaea Hypersaline Sediments Gulf Mexic DQ521

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

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AF307138.1 gg_id:39461 Methylomicrobium buryatense str. 5B AF307
U05570.1 gg_id:8080 Methylomicrobium pelagicum U0557
AF096091.1 gg_id:8060 Methylobacter alcaliphilus str. 5z AF096
EF495157.1 gg_id:222556 Methylobacter alcaliphilus str. 20Z EF4951
AF304194.1 gg_id:38046 Methylomonas rubra str. NCIMB 11913 AF304
AF150807.1 gg_id:8055 Methylomonas rubra AF150
AY995198.1 gg_id:119789 Methylomonas rubra str. UCM B-3075; NCIMB 11913; ACM3303; VKM-15m AY995
X72776.1 gg_id:8084 Methylomonas aurantiaca str. JB103 (phenon3) X72776
X72778.1 gg_id:8090 Methylomonas fodinarum str. ACM 3268 JB13 (phenon2) X72778
DQ837263.1 gg_id:245267 Archaeal and pristine National Park Spain Donana coastal aquifer clone 56S_1B_6 DQ837
GQ340208.1 gg_id:544467 Prokaryotic Marathonas Reservoir Greece water column clone VE07-15-BAC GQ340
NR_025040.1 gg_id:550440 Methylosarcina quisquiliarum str. AML-D4; ATCC 700908 NR_02
AF177296.1 gg_id:8051 Methylosarcina fibrata AML-C10 AF177
U67929.1 gg_id:8101 Methylosphaera hansonii str. AM6 U6792
DQ337085.1 gg_id:145089 subsurface water clone EV818SWSAP61 DQ337
DQ001669.1 gg_id:157473 Microbial seeps asphalt seep clone B91-30 DQ001
AM935153.1 gg_id:534315 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM935
AB486440.1 gg_id:585666 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC AB486
EU144025.1 gg_id:235630 Methylomicrobium album str. BG8 EU144
AM936189.1 gg_id:537819 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM936
X72775.1 gg_id:8059 Methylomicrobium pelagicum str. ACM 3505 NCIMB 2265 X72775
X72773.1 gg_id:8091 Methylobacter whittenburyi str. 3310 NCIMB 11128 ACM 3306 X72773
EU328101.1 gg_id:278818 dynamics during bioremediation crude oil contaminated moderate saline soil clone Y EU328
FM242408.1 gg_id:308594 sequences sediment clone 65 T12d-oil FM242
X72772.1 gg_id:8086 Methylobacter luteus str. ACM 3304 NCIMB 11914 X72772
AM936083.1 gg_id:539835 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM936
EF157165.1 gg_id:247809 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon EF1571
NR_029240.1 gg_id:594166 Methylomicrobium agile str. A30; ATCC 35068 NR_02
EU144026.1 gg_id:252662 Methylomicrobium agile str. ATCC 35068 EU144
AM936065.1 gg_id:564002 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM936
EF648094.1 gg_id:254304 dynamics during produced water treatment aerobic activated sludge clone HB102 EF648
EU735633.1 gg_id:353064 archaeal structures and pristine soils China oil contaminated soil Jidong Oilfield clone EU735
AY007295.1 gg_id:22040 Methylobacter sp. str. LW12 AY007
NR_025955.1 gg_id:555220 Cycloclasticus pugetii str. PS-1; ATCC 51542 NR_02
AF148215.1 gg_id:7712 Cycloclasticus oligotrophus AF148
AF126548.1 gg_id:7703 Thialkalimicrobium aerophilum str. AL3 AF126
AF126549.1 gg_id:7704 Thialkalimicrobium sibericum str. AL7 AF126
CP000109.2 gg_id:141093 Thiomicrospira crunogena str. XCL-2 CP000
AB166731.1 gg_id:99742 Thiomicrospira thermophila str. I78 AB166
FJ792079.1 gg_id:548362 Unexpectedly archaeal species shift between rare and dominant over thousand year FJ7920

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

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GQ153648.1 gg_id:581006 Alcanivorax dieselolei str. ANT-2400 S12 GQ153
EF647617.1 gg_id:270691 Alcanivorax dieselolei P40 EF6476
AB176073.1 gg_id:195877 Microbial Hydrothermal System Suiyo Seamount on Izu-Ogasawara Arc vent area wa AB1760
GU183681.1 gg_id:593585 Alcanivorax dieselolei str. H1673 GU183
DQ270698.1 gg_id:143401 Alcanivorax sp. B-3025 DQ270
DQ768648.1 gg_id:255548 Alcanivorax venustensis MARC4C DQ768
AJ244731.1 gg_id:73634 Smegmaraptor porcuscaenosi str. V4.BO.19 = MM_2368 AJ2447
GQ153640.1 gg_id:587714 Alcanivorax sp. str. ANT-2400 S4 GQ153
EU621895.1 gg_id:278807 Alcanivorax sp. str. LY2 EU6218
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GQ153643.1 gg_id:541649 Alcanivorax dieselolei str. ANT-2400 S7 GQ153
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EF648146.1 gg_id:244272 dynamics during produced water treatment aerobic activated sludge clone XJ93 EF6481
AY686709.1 gg_id:105070 Uruburuia balearica str. MACL04 AY6867
FM242351.1 gg_id:325493 sequences sediment clone 52 T9d+oil FM242
FM242291.1 gg_id:314738 sequences sediment clone 12 T9d-oil FM242
AB176167.1 gg_id:187343 Microbial Hydrothermal System Suiyo Seamount on Izu-Ogasawara Arc vent area wa AB1761
FM242201.1 gg_id:320352 sequences sediment clone 123 T0h-oil FM242
GQ009749.1 gg_id:499916 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw77 GQ009
EU440954.1 gg_id:345659 Alcanivorax sp. str. 2PR511-6 EU4409
AB053125.1 gg_id:32122 Alcanivorax sp. str. I4 AB0531
EU369139.1 gg_id:340580 libraries oyster shell clone MBIOS-23 EU3691
NR_027574.1 gg_id:560452 Kangiella koreensis str. SW-125; DSM 16069 NR_027
EU328013.1 gg_id:279401 dynamics during bioremediation crude oil contaminated moderate saline soil clone B EU3280
AY542567.1 gg_id:114206 Gulf Mexico seafloor sediment clone GoM GB425 02B-35 AY5425
AF382097.1 gg_id:79413 bacterioplankton clone ZA2202c AF3820
FJ905711.1 gg_id:551031 s Tonga-Kermadec iron oxide sediments Volcano 1 Tonga Arc clone V1F45b FJ9057
EF687362.1 gg_id:280438 Biogeochemistry iron- and sulfur-precipitating microbial mats (Nile Mediterranean) s EF6873
AY162089.1 gg_id:136096 Cultivating Sargasso Sea clone GMD38D11 AY1620
EU290714.1 gg_id:249481 microbial structure biogeochemical contrasting shelf sediments Namibian upwelling EU2907
FM242204.1 gg_id:313320 sequences sediment clone 317 T0h-oil FM242
EU652570.1 gg_id:278394 Seasonal variation microbial Yel Sea sediment clone B8S-19 EU6525
EU287139.1 gg_id:241890 Pacific arctic surface sediment clone P13-46 EU2871
EU050815.1 gg_id:240357 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_06_26 EU0508
FM242475.1 gg_id:321501 sequences sediment clone 29 T12d+oil FM242
EU037349.2 gg_id:259038 structure landfill sediments receiving long-term augmentations wastes chromium co EU0373
EU735618.1 gg_id:346955 archaeal structures and pristine soils China oil contaminated soil Jidong Oilfield clone EU7356

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FM242356.1 gg_id:353945 sequences sediment clone 5 T9d+oil FM242
GU061307.1 gg_id:582472 Evaluation culturing methods cultivate previously Yel Sea intertidal beach seawater GU061
AB015541.1 gg_id:8407 deep-sea sediment clone BD2-13 AB0155
FJ203036.1 gg_id:316869 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c FJ2030
FJ202771.1 gg_id:318714 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2027
EU491790.1 gg_id:275246 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU4917
DQ889922.1 gg_id:172811 natural product producing octocoral Erythropodium caribaeorum clone EC52 DQ889
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EU286987.1 gg_id:236857 Pacific arctic surface sediment clone B78-23 EU2869
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GQ263640.1 gg_id:576714 Structure Simulated Level Waste Site simulated level waste site clone FW3_27C GQ263
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AM935949.1 gg_id:537030 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM935
AB186843.1 gg_id:103183 polychlorinated dioxin dechlorinating microcosm clone TSBX24 AB1868
EF648042.1 gg_id:257504 dynamics during produced water treatment aerobic activated sludge clone HB32 EF6480
EF420207.1 gg_id:213653 Mature fine processing harbour methanogenic oil sands tailings pond clone MLSB_30 EF4202
EU735695.1 gg_id:316525 archaeal structures oil contaminated and soils China pristine soil Jidong Oilfield clone EU7356
FM242423.1 gg_id:331444 sequences sediment clone 66 T12d-oil FM242
AM935832.1 gg_id:535164 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM935
AM935433.1 gg_id:532686 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM935
AY033301.1 gg_id:68989 marine bacterioplankton clone MB11B11 AY0333
EU005741.1 gg_id:277139 Major activity inside and outside natural iron-fertilized phytoplankton bloom 3 micro EU0057
EU544831.1 gg_id:267517 free-living particle- aggregate- archaeal and Laptev Sea 1.0-60 um size fraction (susp EU5448
AY697919.1 gg_id:103045 Antarctica clone F4C67 AY6979
GU230303.1 gg_id:585217 Multilevel approach along Rio de la Plata-South Atlantic Ocean coastal water clone A GU230
EU328092.1 gg_id:278620 dynamics during bioremediation crude oil contaminated moderate saline soil clone Y EU3280
AY839870.2 gg_id:109919 Marinobacter sp. str. M18 AY8398
FJ152968.1 gg_id:331146 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX4C FJ1529
EU874388.1 gg_id:321327 Marinimicrobium sp. str. ISL-43 EU8743

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GQ200189.1 gg_id:548606 Marinobacter hydrocarbonoclasticus str. DQHS-3 GQ200
FJ984522.1 gg_id:382828 Marinobacter hydrocarbonoclasticus str. NBSL04 FJ9845
NR_028841.1 gg_id:565301 Marinobacter litoralis str. SW-45; JCM 11547 NR_02
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GQ214550.1 gg_id:556839 Marinobacter mobilis str. B17 GQ214
AB435646.1 gg_id:396810 Marinobacter sp. str. 2M46 AB435
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DQ530479.1 gg_id:168080 Marinobacter sp. str. gap-e-81 DQ530
DQ521387.1 gg_id:164240 Marinobacter sp. str. ice-oil-325 DQ521
EF368018.1 gg_id:208660 Marinobacter taiwanensis str. 1645 EF368
AB513677.1 gg_id:582394 Marinobacter sp. str. PAD-2 AB513
GU183677.1 gg_id:548886 Marinobacter alkaliphilus str. H1711 GU183
EU603452.1 gg_id:275327 Marinobacter bryozoorum str. PTG4-16 EU603
FJ675262.1 gg_id:517038 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6752
DQ325514.1 gg_id:149482 Marinobacter koreensis str. DD-M3 DQ325
NR_025116.1 gg_id:573563 Marinobacter lutaoensis str. T5054; CCRC 17087; JCM 11179 NR_02
FJ675204.1 gg_id:528351 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6752
FJ675118.1 gg_id:527584 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6751
AY592402.1 gg_id:103215 deep-sea mud volcano clone Amsterdam-2B-44; BC20-2B-44 AY592
GQ131626.2 gg_id:581833 Marinobacter sp. str. YCSA7 GQ131
FJ674834.1 gg_id:518091 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6748
FJ746583.1 gg_id:547174 Marinobacter sp. str. H184B35 FJ7465
EF660754.1 gg_id:240909 Marinobacter goseongensis str. En6 EF6607
AB305311.1 gg_id:234441 Marinobacter sp. str. IW11-2CT AB305
EF667989.1 gg_id:244324 and biogeochemical influences active heterotrophic prokaryotes off Palmer Peninsul EF6679
FJ425903.1 gg_id:590148 Marinobacter zhanjiangensis str. JSM 078120 FJ4259
U14584.1 gg_id:8799 gas vacuolate str. S36-W<gv>1 U1458
AF468259.1 gg_id:80533 Arctic pack ice; northern Fram Strait; 80 31.1 N; 01 deg 59.7 min E clone ARKDMS-57 AF468
EU287196.1 gg_id:246628 Pacific arctic surface sediment clone S11-13 EU287
EU328041.1 gg_id:277828 dynamics during bioremediation crude oil contaminated moderate saline soil clone B EU328
AY180101.1 gg_id:78569 Marinobacter excellens str. KMM 3809 AY180
FJ196021.1 gg_id:351303 Marinobacter sp. str. ZS3-32 FJ1960
DQ015835.1 gg_id:139700 Antarctic lake water clone ELB19-223 DQ015
AM503093.1 gg_id:311877 Marinobacter guineae str. LMG 24048 = M3B AM503
AJ292527.1 gg_id:37115 Marinobacter sp. Trimyema-1 1 AJ2925
AJ439500.1 gg_id:59259 Marinobacter squalenivorans str. 2Asq64 AJ4395
GU223379.1 gg_id:557645 Marinobacter sp. str. EM492 GU223

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AJ871937.1 gg_id:163334 hydrocarbonoclastic Guanabara Bay Brazil mangrove sediments AJ8719
AB252057.1 gg_id:170550 Brassica napus str. SKA S2 AB252
EU440995.1 gg_id:340108 Marinobacter flavimaris str. 2PR54-4 EU440
EU293413.1 gg_id:242328 Marinobacter sp. str. cn74 EU293
NR_025799.1 gg_id:549391 Marinobacter flavimaris str. SW-145; KCTC 12185 NR_02
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FJ675374.1 gg_id:528098 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6753
FJ675429.1 gg_id:526155 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6754
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EF428127.1 gg_id:277000 Marinobacter excellens str. LL406 EF4281
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DQ097521.1 gg_id:129808 Marinobacter giovannonii str. IS17 DQ097
DQ530455.1 gg_id:170366 Marinobacter sp. str. gap-d-2 DQ530
EU718223.1 gg_id:337093 Microbial farmed prawn preservation methods Marinobacter clone HL13 EU718
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DQ097526.1 gg_id:131161 Marinobacter koreensis str. KGB22 DQ097
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AY690675.1 gg_id:99388 Marinobacter sp. str. GC101 AY690
FJ973518.1 gg_id:454067 Marinobacter alkaliphilus str. NBSL07 FJ9735
FJ674980.1 gg_id:511539 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6749
AF173969.1 gg_id:21222 Marinobacter aquaeolei str. KT02ds19 AF173
EU440994.1 gg_id:353090 Marinobacter alkaliphilus str. 2PR56-13 EU440
GU223374.1 gg_id:554900 Marinobacter sp. str. EM491 GU223
EU196317.1 gg_id:255215 Marinobacter sp. NP38 EU196
EU907917.1 gg_id:326599 Marinobacter sp. str. SKUK MB1002 EU907
FJ897726.1 gg_id:547256 Marinobacter sp. str. Set74 FJ8977
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AB166970.1 gg_id:104848 Marinobacter sp. str. NT N14 AB166
AJ557854.1 gg_id:84236 Arctic deep sea Isolation common chemoorganotrophic oxygen-respiring polar current AJ5578
EU432582.1 gg_id:262300 Marinobacter sp. str. 10050 EU432
FJ497670.1 gg_id:509005 Marinobacter sp. str. VS-43 FJ4976
AM990796.1 gg_id:278977 Marinobacter sp. MOLA 20 AM990
EU164778.1 gg_id:250476 Marinobacter szutsaonensis str. Halo30-39 EU164
AY771710.1 gg_id:108686 Marinobacter lipolyticus str. S2-44 AY7717
AB304799.1 gg_id:255218 Microbulbifer agarolyticus str. JAMM 0654 AB304
GQ334398.1 gg_id:585495 Microbulbifer maritimus str. RV1 GQ334

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AB167354.2 gg_id:108039 Pelagiobacter variabilis str. Ni2088 AB1673
AJ510266.1 gg_id:69355 Microbulbifer arenaceous str. RSBr-1 AJ5102
GQ262812.1 gg_id:558634 Microbulbifer sp. str. Y215 GQ262
FJ169190.1 gg_id:338941 microbial and polyketide biosynthetic potential palmerolide-producing tunicate Synoi FJ1691
AB500893.1 gg_id:555088 Microbulbifer sp. str. ABABA 23 AB5008
EF486352.1 gg_id:222510 Microbulbifer celer str. ISL-39 EF4863
DQ340189.1 gg_id:147845 Dominance Mycoplasma guts Long-Jawed Mudsucker Gillichthys mirabilis five Califo DQ340
EF674853.1 gg_id:257184 Microbulbifer halotolerans str. YIM 91118 EF6748
AY224196.1 gg_id:81821 Microbulbifer sp. str. Th/B/38 AY2241
AF479688.1 gg_id:51065 Microbulbifer salipaludis str. SM-1 AF4796
AM180745.1 gg_id:145463 Pseudomonas sp. UC14a AM180
AB500894.1 gg_id:573761 Microbulbifer sp. str. ABABA 212 AB5008
AB052969.1 gg_id:24308 Pseudomonas sp. PE2 AB0529
AY862188.1 gg_id:111195 Microbulbifer sp. str. MY05 AY8621
AB456139.1 gg_id:551285 Microorganisms involved anaerobic phenol degradation treatment synthetic coke-o AB4561
EU491487.1 gg_id:263181 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X4 clone EU4914
DQ334644.1 gg_id:194566 Impact metals on sediments heavy metal polluted marine sediment clone HB2-9-21 DQ334
AB456140.1 gg_id:572166 Microorganisms involved anaerobic phenol degradation treatment synthetic coke-o AB4561
EU491452.1 gg_id:259455 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X4 clone EU4914
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GQ872422.1 gg_id:569907 Simiduia sp. str. M2-5 GQ872
EF617350.1 gg_id:234841 Simidua agarivorans str. SA1 EF6173
FJ202639.1 gg_id:341703 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2026
FJ356668.1 gg_id:541691 Intra- Microheterogeneity Multiple Displacement Single-cells Marine Cyanobacteria L FJ3566
EF092194.1 gg_id:269778 Persistent Axinella corrugata clone Ax29_A1 EF0921
FJ203003.1 gg_id:317569 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2030
GU391220.1 gg_id:530532 Spongiibacter sp. str. JYr4 GU391
NR_027564.1 gg_id:565759 Teredinibacter turnerae T7901 str. T7902; ATCC 39867 NR_02
DQ269073.1 gg_id:198202 marine macro-alga surface clone DPC012 DQ269
DQ272313.1 gg_id:141068 Lyrodus pedicellatus symbiont RT18 DQ272
EF061962.1 gg_id:194319 Xiamen China mangrove sediment clone XME54 EF0619
AB467280.1 gg_id:534461 Umboniibacter marinipuniceus str. KMM 3892 AB4672
EU236385.1 gg_id:298139 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg92A4 EU2363
GQ920839.1 gg_id:550044 Marinimicrobium sp. str. SX15 GQ920
AY845232.1 gg_id:110380 sponge clone 34P38 AY8452
EU050817.1 gg_id:237439 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_05_77 EU0508
AY375151.1 gg_id:96709 deep sea sediment clone D78 AY3751
EU799127.1 gg_id:348578 It's all ranking aquatic Newport Harbour RI clone 1C226690 EU7991
FJ628337.1 gg_id:555614 transition and zone within near-shore basin: brackish water anoxic fjord Nitinat Lake FJ6283
EU286983.1 gg_id:256729 Pacific arctic surface sediment clone B78-19 EU2869

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FJ347758.1 gg_id:370251 Endozoicomonas sp. str. CL-33 FJ3477
AM259915.1 gg_id:252743 Chondrilla nucula-specific sponge mesohyl clone CN34 AM259
AY700601.1 gg_id:109430 Australia: Great Barrier Reef clone PDA-OTU3 AY7006
AB205011.1 gg_id:113799 Spongiobacter nickelotolerans str. 00P-Ni033-1-1-2 AB2050
AM990755.1 gg_id:277802 Culturable along NW Mediterranean coast Petrosia ficiformis sponge AM990
FJ202634.1 gg_id:354436 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2026
EF516073.1 gg_id:223694 grassland soil clone FCPT525 EF5160
EU464803.1 gg_id:287677 Hartmann's mountain zebra feces clone AFZEB_aaj71b02 EU4648
EU104099.1 gg_id:351662 Evidence Comamonadaceae determinants settling performance activated sludge clo EU1040
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EU464904.1 gg_id:301529 Hartmann's mountain zebra feces clone AFZEB_aaj72h05 EU4649
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DQ824608.1 gg_id:180882 human fecal clone RL185_aaj70d02 DQ824
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EU104233.1 gg_id:352480 Evidence Comamonadaceae determinants settling performance activated sludge clo EU1042
EU464760.1 gg_id:291795 Hartmann's mountain zebra feces clone AFZEB_aaj70c11 EU4647
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EU104152.1 gg_id:319880 Evidence Comamonadaceae determinants settling performance activated sludge clo EU1041
DQ824679.1 gg_id:181704 human fecal clone RL185_aaj71e11 DQ824
CU466815.1 gg_id:307591 Evry wastewater treatment plant anoxic basin clone CU4668
AF195410.1 gg_id:24515 Hahella chejuensis str. KCTC 2396 AF1954
EF495227.1 gg_id:217600 Hahella antarctica str. IMCC3113 EF4952
AY676463.1 gg_id:107320 Hahella ganghwensis str. FR1050 AY6764
AY130995.1 gg_id:70229 Zooshikella ganghwensis str. JC2045 AY1309
AF400466.1 gg_id:36328 Primary endosymbiont Bemisia tabaci clone UG23 aleyrodidarum AF4004
Z11928.1 gg_id:8116 symbiont of Trialeurodes vaporariorum (greenhouse whitefly) Z11928
AF400467.1 gg_id:46892 Primary endosymbiont Bemisia tabaci clone UG26 aleyrodidarum AF4004
Z11927.1 gg_id:8122 symbiont of Siphoninus phillyreae (ash whitefly) Z11927
AY266108.1 gg_id:99204 Neomaskellia andropogonis symbiont AY2661
AF286123.1 gg_id:51913 symbiont AF2861
AY266098.1 gg_id:103124 Aleuroparadoxus arctostaphylli symbiont AY2660
AF400469.1 gg_id:54022 Primary endosymbiont Bemisia tabaci clone UG25 AF4004
AY268081.1 gg_id:88180 Bemisia tabaci symbiont AY2680
AY266100.1 gg_id:106952 Aleuroplatus sp. symbiont AY2661
AY266107.1 gg_id:99043 Dialeurodes hongkongensis symbiont AY2661
AY266096.1 gg_id:102829 Aleurodicus dispersus symbiont AY2660
AY266095.1 gg_id:102674 symbiont AY2660
AF400462.1 gg_id:19222 Primary endosymbiont Bemisia tabaci clone MEX4 aleyrodidarum AF4004
DQ396070.1 gg_id:154863 deep-sea octacoral clone ctg_NISA053 DQ396
EU799800.1 gg_id:326262 It's all ranking aquatic Newport Harbour RI clone 1C227454 EU7998

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AY458632.2 gg_id:101609 marine waters clone EBAC750-02H09 AY458
AY907736.1 gg_id:137300 identification picoplankton contrasting waters Arabian Sea water clone A313002 AY907
EU805263.1 gg_id:313140 It's all ranking aquatic 250 miles Panama City clone 6C233263 EU805
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EU800939.1 gg_id:313914 It's all ranking aquatic Delaware Bay NJ clone 2C229197 EU800
EU005838.1 gg_id:276035 Major activity inside and outside natural iron-fertilized phytoplankton bloom 3 micro EU005
AY033317.1 gg_id:55020 marine bacterioplankton clone MB12G11 AY033
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EF574293.1 gg_id:233685 site S25 near Coco's Island marine clone S25_637 EF574
GQ337298.1 gg_id:593315 Hydrography shapes biogeography deep Arctic Ocean water depth 252m clone NB2 GQ337
EU035854.2 gg_id:306650 Insight microbial structure Norwegian deep-water water deep-sea coral reef off Nor EU035
DQ071078.1 gg_id:129984 marine surface water clone PB1.39 DQ071
GU119483.1 gg_id:592804 Threatened Corals Provide Microbial Habitats reef water clone Reef_M13 GU119
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EU799709.1 gg_id:341723 It's all ranking aquatic Newport Harbour RI clone 1C227344 EU799
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GU061923.1 gg_id:532750 and function microbial mesoscale eddy perturbations South China Sea clone S-5m-8 GU061
EU804090.1 gg_id:330520 It's all ranking aquatic 250 miles Panama City clone 6C231982 EU804
GQ348088.1 gg_id:572910 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ348
AF406528.1 gg_id:60645 bacterioplankton clone AEGEAN_146 AF406
DQ009141.1 gg_id:119608 bacterioplankton clone SPOTSAUG01_5m95 DQ009
EU805314.1 gg_id:336262 It's all ranking aquatic 250 miles Panama City clone 6C233317 EU805

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AM941743.1 gg_id:273506 Halomonas elongata str. ATCC 33173 AM941
EU652046.1 gg_id:276670 Chromohalobacter salexigens str. aa-27 EU6520
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AJ277205.2 gg_id:27659 Chromohalobacter nigriandinum str. Taxon 4 4N AJ2772
AB021386.1 gg_id:8126 Pseudomonas beijerinckii str. ATCC 19372T AB0213
AF211862.1 gg_id:43545 Chromohalobacter israelensis str. DSM6768 AF2118
AJ295146.1 gg_id:48786 Halomonas elongata str. DSM 3043 AJ2951
AY373448.1 gg_id:94374 Chromohalobacter sarecensis str. LV4 AY3734
DQ375807.1 gg_id:153764 Chromohalobacter israelensis str. TVSP 101 DQ375
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DQ270679.1 gg_id:144129 Halomonas sp. B-1092 DQ270
EU937754.1 gg_id:324906 Haererehalobacter sp. str. JG 11 Iti 10 EU937
DQ235564.1 gg_id:141553 biofilm water pipeline biofilms steel pipelines Gulf Mexico clone 6 DQ235
EU175892.1 gg_id:261928 Drop-size lakes: transient microbial habitats soda lake on salt-secreting desert tree c EU1758
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EU135707.1 gg_id:242748 Halomonas sp. str. YIM C248 EU1357
EU308354.1 gg_id:360286 Halomonas sp. str. SB136_1 EU3083
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EU432570.1 gg_id:264242 Halomonas sp. str. 10112 EU4325
EU218533.1 gg_id:239013 Halomonas ilicicola str. SP8 EU2185
AJ564880.1 gg_id:100009 Halomonas alkantarctica str. CRSS AJ5648
EF554912.1 gg_id:219933 Halomonas sp. str. G-AMM1 EF5549
EU848479.1 gg_id:305095 Halomonas sp. str. SP1-3 EU8484
AF539764.1 gg_id:86698 Halomonas sp. str. R21 AF5397
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EF421176.1 gg_id:277105 Halomonas sp. ZB-2007 EF4211
DQ396289.1 gg_id:154439 deep-sea octacoral clone ctg_NISA091 DQ396
CU914816.1 gg_id:402482 and dynamics adapted microbiota during degradation Tunisian zarzatine enriched se CU914
EF533977.1 gg_id:267271 Halomonas sp. str. L24 EF5339
EU652039.1 gg_id:274013 Halomonas taeheungii str. aa-1 EU652
EU735634.1 gg_id:337872 archaeal structures and pristine soils China oil contaminated soil Jidong Oilfield clone EU735

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AY505526.1 gg_id:101462 Halomonas variabilis str. GSP28 AY5055
EU880513.1 gg_id:303578 Halomonas sp. str. P56 EU8805
X92151.1 gg_id:51042 Lake Bogoria isolate 24B1 X92151
DQ001682.1 gg_id:157952 Microbial seeps asphalt seep clone B101-20 DQ001
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U85873.1 gg_id:8145 Halomonas variabilis str. SW48 U85873
GU397430.1 gg_id:531203 Halomonas sp. str. AAD14 GU397
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AB305246.1 gg_id:229538 Halomonas sp. str. Sa6-3XX AB3052
DQ128258.1 gg_id:200527 Unique Microbial Fluids Chinese Continental Scientific Drilling drilling fluid clone CCS DQ128
GU001901.1 gg_id:593434 Halomonas halophila str. PLD GU001
EF143431.1 gg_id:188268 Halomonas aquamarina WP02-1-81 EF1434
FJ444974.1 gg_id:573554 Halomonas sp. str. whb28 FJ4449
EU722713.1 gg_id:352742 Halomonas salina str. SBC8 EU7227
AJ306893.1 gg_id:33823 Halomonas variabilis str. DSM 3051 AJ3068
EU432575.1 gg_id:259254 Halomonas sp. str. 10043 EU4325
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FJ607360.1 gg_id:542842 Halomonas sp. str. SeaH-As8w FJ6073
FJ152704.1 gg_id:321200 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX1A_ FJ1527
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GU397433.1 gg_id:523209 Halomonas sp. str. AAD2 GU397
GU166164.1 gg_id:579641 intestinal tract larvae (Musca domestica) direct cloning and sequencing genes whea GU166
FJ172099.1 gg_id:312851 Halomonas sp. str. SBC13 FJ1720
EU594554.1 gg_id:271380 Pseudomonas fluorescens str. 2-4 EU5945
FJ978736.1 gg_id:417685 feces clone CL_F_438 FJ9787
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GU397429.1 gg_id:516866 Halomonas sp. str. AAD12 GU397
AY647309.1 gg_id:104617 Halomonas desiderata str. MSU3810 AY6473
AF170753.1 gg_id:8146 Halomonas sp. str. QSSC9-11 AF1707
EU159469.4 gg_id:240141 Halomonas taiwanensis str. Halo30-01 EU1594
EF627999.1 gg_id:231117 Halomonas sp. str. P15 EF6279
FJ172096.1 gg_id:317854 Halomonas sp. str. SBC16 FJ1720

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FJ796247.1 gg_id:555230 Halomonas sp. str. JS46 FJ7962
EU822512.1 gg_id:317124 Halomonas xinjiangensis str. TRM 0175 EU8225
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EU308357.1 gg_id:363386 Halomonas sp. str. TB1612 EU3083
AF211860.1 gg_id:28015 Halomonas alimentaria str. YKJ-16 AF2118
U85871.1 gg_id:8143 Halomonas variabilis str. SW04 U85871
EF157249.1 gg_id:255098 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon EF1572
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FJ764764.1 gg_id:552836 Halomonas sp. str. E-090 FJ7647
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EF442769.1 gg_id:206143 Halomonas salaria str. 5-3 EF4427
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DQ087259.1 gg_id:132883 Salicola marensis 7Sa10 DQ087
GU397403.1 gg_id:515060 Salicola marasensis str. W4B GU397
DQ129689.1 gg_id:137579 Pseudomonas salina str. B2 DQ129
GU397402.1 gg_id:522270 Salicola salis str. W7B GU397
AF211871.1 gg_id:55625 Zymobacter palmae str. ATCC 51623 AF211
EU735693.1 gg_id:354231 archaeal structures oil contaminated and soils China pristine soil Jidong Oilfield clone EU735
DQ072719.1 gg_id:134569 Halospina denitrificans str. HGD 1-3 DQ072
D14555.1 gg_id:8114 Zymobacter palmae str. T109 D1455
AB021383.1 gg_id:8811 Pseudomonas halophila str. DSM 3050T AB021
EU305727.1 gg_id:340031 Pseudomonas sp. str. TBZ33 EU305
AY987840.1 gg_id:128215 Microbial Salterns Maras salterns clone 2B4 AY987
GQ375775.1 gg_id:564683 Chromohalobacter sp. str. B02 GQ375
EU308410.1 gg_id:368617 Halomonas sp. str. TB21_12 EU308
DQ641495.1 gg_id:215031 Chromohalobacter tunisiensis str. Lit 2 DQ641
GQ246216.1 gg_id:578822 Kushneria sp. str. YCWA18 GQ246
FJ463811.1 gg_id:580770 Chromohalobacter sp. str. ST307 FJ4638
FJ444986.1 gg_id:554249 Halomonas taeanensis str. whb40 FJ4449
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DQ421388.1 gg_id:156429 Halotalea alkalilenta str. AW-7 DQ421
EU487856.1 gg_id:568866 lucinid bivalve- symbiotic system: significance geochemical habitat on and gill symbi EU487
EU487858.1 gg_id:570303 lucinid bivalve- symbiotic system: significance geochemical habitat on and gill symbi EU487
EF508132.1 gg_id:241778 evidence unusual symbiont gills Acesta excavata bivalve gill specimen Ae1 320 m dep EF5081
AB054156.1 gg_id:48284 marine sponge clone HOC22 AB054
AB054159.1 gg_id:35099 marine sponge clone HOC25 AB054
FJ999614.1 gg_id:420931 sponge Haliclona simulans South China Sea clone B96 FJ9996
EF379881.1 gg_id:216695 sea water Victoria Harbor (Hong Kong) area clone PC-FL10-68 EF3798
EU799754.1 gg_id:306969 It's all ranking aquatic Newport Harbour RI clone 1C227399 EU799
AM259847.1 gg_id:210420 Spatial sponge- Mediterranean Tethya aurantium sponge cortex clone TAA-10-33 AM259
AY907757.1 gg_id:137084 identification picoplankton contrasting waters Arabian Sea water clone A314008 AY907
AY907755.1 gg_id:137083 identification picoplankton contrasting waters Arabian Sea water clone A314005 AY907
DQ513029.1 gg_id:161219 Microbial life fluids ridge flank crustal fluid clone FS142-29B-02 DQ513
EU287155.1 gg_id:243868 Pacific arctic surface sediment clone P13-62 EU287
EF572288.1 gg_id:228537 Coco's Island site 23 marine clone S23_387 EF5722
DQ289914.1 gg_id:167947 Microbial Carbon and Nitrogen Cycling Sediments South Atlantic Bight Permeable Sh DQ289
EU979089.1 gg_id:329740 Effects intercropping Rhizobium inoculation on microbial biomass and rhizosphere b EU979
EF574537.1 gg_id:239885 site S25 near Coco's Island marine clone S25_881 EF5745
AM259920.1 gg_id:237509 Chondrilla nucula-specific sponge mesohyl clone CN46 AM259
AY386332.1 gg_id:98593 marine str. HTCC2089 AY3863
EF061958.1 gg_id:181469 Xiamen China mangrove sediment clone XME25 EF0619

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EU887784.1 gg_id:317155 and RFLP anaerobes Nisargruna biogas plant anaerobic digester clone 21IISN EU887
AY212672.1 gg_id:104571 water 20 m downstream manure clone 224ds20 AY2126
DQ354722.1 gg_id:152853 subsurface water clone DR550SWSAEE23 DQ354
EU373830.1 gg_id:262549 southern Cretan margin (eastern Mediterranean Sea) canyon and slope sediment clc EU3738
DQ351750.1 gg_id:146687 Microbial Adherent Sediment Particles Heavy Metal Contaminated North Sea Surfac DQ351
EF157250.1 gg_id:235311 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon EF1572
AY344367.2 gg_id:91272 Lake Kauhako 30 m clone K2-30-25 AY3443
GU061024.1 gg_id:543804 Evaluation culturing methods cultivate previously Yel Sea intertidal beach clone SF2! GU061
GQ337269.1 gg_id:532913 Hydrography shapes biogeography deep Arctic Ocean water depth 428m clone CB18 GQ337
GQ349203.1 gg_id:544164 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ349
FM242421.1 gg_id:315848 sequences sediment clone 18 T12d-oil FM242
EU265950.1 gg_id:536666 transition and zone within near-shore anoxic basin: Nitinat Lake depth 20 m clone Ni EU2659
EU801454.1 gg_id:316013 It's all ranking aquatic Chesapeake Bay MD clone 3C002749 EU8014
AB262385.1 gg_id:160146 Microbial Ishigaki-jima Island Japan sea water Ishigaki Port clone IG-1-25 AB2623
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EU592358.1 gg_id:583231 Seasonal changes Salton Sea hypersaline water clone SSW83Ap EU5923
EU050827.1 gg_id:246352 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_06_91 EU0508
EU491768.1 gg_id:263897 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU4917
EU799676.1 gg_id:306629 It's all ranking aquatic Newport Harbour RI clone 1C227304 EU7996
GQ349449.1 gg_id:588121 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ349
AY907800.1 gg_id:137086 identification picoplankton contrasting waters Arabian Sea water clone A714013 AY9078
EU803061.1 gg_id:332281 It's all ranking aquatic Northeast Colon Panama clone 4C230470 EU8030
AY942761.1 gg_id:145162 but species richness marine sponge Cymbastela concentrica clone Cc044 AY9427
EU544859.1 gg_id:264271 free-living particle- aggregate- archaeal and Laptev Sea >60 um size fraction (aggreg EU5448
EU799735.1 gg_id:324875 It's all ranking aquatic Newport Harbour RI clone 1C227378 EU7997
AB526337.1 gg_id:546239 Spongiibacter sp. str. JAM-GA14 AB5263
AM990674.1 gg_id:278054 culturable oligotrophic ocean (South Pacific Gyre) sea water AM990
FJ889619.1 gg_id:559242 Melitea sp. str. ZS5-23 FJ8896
EF176580.1 gg_id:181920 Litincola lipolitica str. IMCC1097 EF1765
FJ745130.1 gg_id:565326 Transporter genes expressed coastal response dissolved organic carbon surface wate FJ7451
EU652550.1 gg_id:278194 Seasonal variation microbial Yel Sea sediment clone A8S-109 EU6525
AM930471.1 gg_id:275885 involved Tripneustes gratilla (Echinoidea) cloning and FISH host body wall lesions clc AM930
AB006765.1 gg_id:8206 Marinobacterium jannaschii str. IFO15466 AB0067
FN556570.1 gg_id:514502 Marinobacterium sp. str. JW3.2b FN5565
FJ202983.1 gg_id:326600 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2029
DQ219356.1 gg_id:142532 Marinobacterium sp. str. 2085(b) DQ219
EF190070.1 gg_id:193559 s Qinghai oilfield clone GSX3 EF1900
AY563030.1 gg_id:100162 Marinobacterium halophilum str. Mano11 AY5630
AJ843079.1 gg_id:114569 Marinomonas aquimarina str. 11OM3 = CECT 5078 AJ8430
EU188448.1 gg_id:366487 Marinomonas sp. str. IVIA-Po-101 EU1884

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g__Neptunomonas
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g__Oceanospirillum
g__Oceanospirillum
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s__Neptunomonas japonica	399
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s__unclassified	1437
s__unclassified	1875
s__Oceanospirillum maris	915
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s__unclassified	1340
s__unclassified	834

NR_028636.1 gg_id:582426 Marinomonas primoryensis str. KMM 3633 NR_02
DQ403809.1 gg_id:150764 Marinomonas blandensis str. MED 121 DQ403
EU195937.1 gg_id:248961 Marinomonas sp. str. P111 EU195
AJ238597.1 gg_id:8210 Marinomonas protea AJ2385
EU722311.1 gg_id:354249 Marinomonas sp. str. S3-34 EU722
EF382680.1 gg_id:209816 Marinomonas sp. BSi20579 str. Bsi20579 EF3826
DQ311094.1 gg_id:144989 Marinomonas sp. str. NJ548 DQ311
DQ517862.1 gg_id:160848 Marinomonas sp. str. BSi20385 DQ517
AB074194.1 gg_id:52278 Marinomonas primoryensis str. KMM 3634 AB074
DQ421580.2 gg_id:208776 Salt Marsh Prokaryotes salt marsh clone SIMO-4215 DQ421
AJ627909.1 gg_id:103719 Marinomonas ushuaiensis str. U1 AJ6279
AY539835.1 gg_id:101289 Marinomonas pontica str. 46-16 AY5398
DQ011528.1 gg_id:120729 Marinomonas communis str. LMG 2864 DQ011
DQ923437.1 gg_id:174575 Marinomonas sp. W-3 DQ923
AB242868.1 gg_id:142302 Marinomonas sanya str. F128 AB2428
AY730245.1 gg_id:101261 Marinomonas sp. M6-20A AY730
AF321017.2 gg_id:30213 Marinomonas sp. GOBB3-320 AF321
EU188447.1 gg_id:362695 Marinomonas sp. str. IVIA-Po-159 EU1884
AJ717294.1 gg_id:105555 Marinomonas sp. str. BJK13 AJ7172
NR_029228.1 gg_id:554750 Marinomonas vaga str. 40; ATCC 27119 NR_02
DQ676859.1 gg_id:172752 Marinomonas sp. str. ASs2032 DQ676
DQ007439.1 gg_id:124798 Marinomonas sp. str. BSi20101 DQ007
EU427306.1 gg_id:274342 Marinomonas sp. MSI03 EU427
EU188443.1 gg_id:359821 Marinomonas sp. str. IVIA-Po-145 EU1884
EU188441.1 gg_id:362238 Marinomonas sp. str. IVIA-Po-185 EU1884
DQ520888.1 gg_id:161293 Marinomonas sp. str. BSi20461 DQ520
DQ517876.1 gg_id:160773 Marinomonas sp. str. BSi20548 DQ517
DQ537501.1 gg_id:160057 Marinomonas sp. str. BSi20388 DQ537
AB098513.1 gg_id:75039 Marinospirillum insulare str. NB11 AB098
AB006769.1 gg_id:8111 Marinospirillum minutulum str. ATCC19193 AB006
AB006770.1 gg_id:8112 Marinospirillum megaterium AB006
AB291228.1 gg_id:246798 Neptunomonas japonica str. JAMM 1610 AB291
FJ889618.1 gg_id:544882 Neptunomonas sp. str. NF4-29 FJ8896
AB288092.1 gg_id:239047 Neptunomonas japonica str. JAMM 0745 AB288
AF053734.1 gg_id:8190 Neptunomonas naphthovorans str. NAG-2N-126 AF053
FJ764762.1 gg_id:570916 Nitrincola sp. str. E-048 FJ7647
FJ973520.1 gg_id:440184 Nitrincola lacisaponensis str. NBSL11 FJ9735
AB006763.1 gg_id:8178 Oceanospirillum maris subsp. williamsae str. IFO15468 AB006
AB006764.1 gg_id:8176 Oceanospirillum multiglobuliferum str. IFO13614 AB006
AB006761.1 gg_id:8184 Oceanospirillum beijerinckii subsp. pelagicum str. IFO13612 AB006
FJ403091.1 gg_id:367944 Disease- changes healthy and diseased colonies Caribbean coral Montastrea faveolat FJ4030

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s__proteobacterium symbiont of Osedax sp. MB4	2182
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AB435650.1 gg_id:461486 Oceanobacter sp. str. 1O14 AB435
AB006767.1 gg_id:8201 Oceanobacter kriegii str. IFO15467 AB006
AM930467.1 gg_id:272107 involved Tripneustes gratilla (Echinoidea) cloning and FISH host body wall lesions cl AM930
EF648125.1 gg_id:238098 dynamics during produced water treatment aerobic activated sludge clone XJ46 EF6481
DQ071156.1 gg_id:134464 marine surface water clone Surf1.32 DQ071
FJ403082.1 gg_id:364829 Disease- changes healthy and diseased colonies Caribbean coral Montastrea faveolat FJ4030
EF648167.1 gg_id:254655 dynamics during produced water treatment aerobic activated sludge clone XJ137 EF6481
GQ426888.1 gg_id:592739 Thalassolituus sp. IMCC1826 str. IMCC 1826 GQ426
AJ302699.1 gg_id:20487 Oceanospirillum sp. ME101 AJ3026
EU980447.1 gg_id:326525 Oleispira sp. str. DFH11 EU980
EU236351.1 gg_id:298239 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg91A7 EU2363
EU050832.1 gg_id:244721 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_09_46 EU0508
AJ426421.1 gg_id:47332 Oleispira antarctica str. RB-9 AJ4264
AY577900.1 gg_id:105462 roots new deep sea polychaete (Osedax frankpressi gen n. sp. novum) clone BoneC3 AY5779
DQ906761.1 gg_id:161773 and marine microorganisms Antarctic sea ice lower 10 cm clone AntCL3E3 DQ906
EU050834.1 gg_id:236381 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_02_57 EU0508
GQ349742.1 gg_id:587033 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ349
AY697896.1 gg_id:101312 Antarctica clone F3C18 AY6978
AY922202.1 gg_id:114064 whalefall clone 131636 AY9222
GU391221.1 gg_id:516971 Thalassolituus sp. str. JYr12 GU391
EF468717.1 gg_id:221209 Marinobacterium marisflavum str. IMCC4074 EF4687
DQ206422.1 gg_id:140325 microbial mediates arsenate reduction soda lake water clone ML-S-4 DQ206
DQ279852.1 gg_id:142469 Marinomonas sp. str. Y5 DQ279
AY967730.1 gg_id:115234 Influence starvation ozone and selected isolates on survival southern Jasus edwardsi AY9677
FN377729.1 gg_id:593776 Marinobacterium sp. RS-21 FN3777
AY549003.2 gg_id:101658 marine bone clone sacC13A1 AY5490
EF379568.1 gg_id:206232 sea water Victoria Harbor (Hong Kong) area clone VH-PA5-10 EF3795
EF422409.1 gg_id:213472 Marinospirillum sp. str. ANL-isoa EF4224
GU291323.1 gg_id:589506 Anaerobic sulfide-oxidizing couple acidification and nitrogen cycling heavy metal we GU291
EU544727.1 gg_id:262299 free-living particle- aggregate- archaeal and Laptev Sea 0.22-1.0 um size fraction (fre EU5447
NR_024654.1 gg_id:541001 Pseudospirillum japonicum str. ATCC 19191 NR_024
FJ628206.1 gg_id:555032 transition and zone within near-shore basin: brackish water anoxic fjord Nitinat Lake FJ6282
FJ403057.1 gg_id:364908 Disease- changes healthy and diseased colonies Caribbean coral Montastrea faveolat FJ4030
AM747817.1 gg_id:311032 Oceaniserpentilla haliotidis AM747
AY136131.2 gg_id:155199 Oceanobacter sp. str. RED65 AY1361
FJ202960.1 gg_id:353341 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2029
GQ131677.1 gg_id:376032 Neptuniibacter sp. str. antisso-13 GQ131
AY549004.2 gg_id:101822 marine bone clone Osedax_sym1 AY5490
AY549002.2 gg_id:101490 marine bone clone sacC13A2 AY5490
AF140000.1 gg_id:8195 Oceanospirillum sp. str. ML-158 AF1400
AF140002.1 gg_id:27457 Oceanospirillum sp. str. ML-165 AF1400

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EF067915.1 gg_id:245142 endolithic microbes marine basalts aerobic enrichment s innoculated basalt Brown B EF0679
AM930473.1 gg_id:274407 involved Tripneustes gratilla (Echinoidea) cloning and FISH host body wall lesions cl AM930
GQ349823.1 gg_id:569636 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ349
GQ349756.1 gg_id:561025 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ349
DQ123914.1 gg_id:154336 Oceanrickettsia ariakensis DQ123
DQ015830.1 gg_id:139543 Antarctic lake water clone ELB19-203 DQ015
GU061314.1 gg_id:578191 Evaluation culturing methods cultivate previously Yel Sea intertidal beach seawater GU061
FM242233.1 gg_id:333373 sequences sediment clone 26 T0h-oil FM242
FJ717225.1 gg_id:554141 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United King FJ7172
NR_025432.1 gg_id:537713 Oleiphilus messinensis str. ME102; DSM 13489 NR_02
EF067910.1 gg_id:251507 endolithic microbes marine basalts aerobic enrichment s innoculated basalt Brown B EF0679
AY007676.1 gg_id:26630 marine isolate NOR5 AY007
GU118892.1 gg_id:542707 Threatened Corals Provide Microbial Habitats clone Past_M04 GU118
EU707294.1 gg_id:336455 sulfur oxidizing Wadden Sea sediments Janssand intertidal sandy sediment 0 2 cm d EU707
DQ330945.1 gg_id:159205 Guerrero Negro hypersaline microbial mat clone 05D2Z66 DQ330
AM882556.1 gg_id:337698 Structure along hydrocarbon contamination coastal sediment oil polluted water pet AM882
DQ330798.1 gg_id:159069 Guerrero Negro hypersaline microbial mat clone 02D2Z51 DQ330
EU707308.1 gg_id:354827 sulfur oxidizing Wadden Sea sediments Janssand intertidal sandy sediment 0 3 cm d EU707
EF632657.1 gg_id:235343 Unique microbial contrasting aquatic altitude Andean Altiplano (northern Chile) sedi EF6326
EU707317.1 gg_id:350845 sulfur oxidizing Wadden Sea sediments Janssand intertidal sandy sediment middle f EU707
EU161717.1 gg_id:255918 Haliea rubra str. CM41_15a EU161
EF632658.1 gg_id:236929 Unique microbial contrasting aquatic altitude Andean Altiplano (northern Chile) sedi EF6326
AY386339.1 gg_id:96871 marine str. HTCC2080 AY3863
AAVV01000015.1 gg_id:190442 marine str. HTCC2080 AAVV0
NZ_AAVT01000006.1 gg_id:189314 marine str. HTCC2143 NZ_AA
GU230327.1 gg_id:589757 Multilevel approach along Rio de la Plata-South Atlantic Ocean coastal water clone GU230
EU544810.1 gg_id:275233 free-living particle- aggregate- archaeal and Laptev Sea 1.0-60 um size fraction (sus EU5448
DQ009134.1 gg_id:126508 bacterioplankton clone SPOTSAPR01_5m162 DQ009
EU700144.1 gg_id:295036 Study on Shantou Bay Marine Sediments Microorganisms sediment clone STU2 EU700
AB015519.1 gg_id:8181 deep-sea sediment clone BD1-7 AB015
EU394576.1 gg_id:335051 Coccolithophore bloom dynamics shape (NE-Atl) northern Bay Biscay pelagic particle EU394
EU491036.1 gg_id:262064 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount South Rift X EU491
EU491078.1 gg_id:273214 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount South Rift X EU491
EU491056.1 gg_id:262397 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount South Rift X EU491
EF379800.1 gg_id:206237 sea water Victoria Harbor (Hong Kong) area clone PC-PA11-51 EF3798
FN396694.1 gg_id:549550 constant flux thermophilic cold seabed Arctic marine surface sediment clone s5_0_V FN3966
AM882531.1 gg_id:338117 Structure along hydrocarbon contamination coastal sediment oil polluted water pet AM882
FJ203132.1 gg_id:351157 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c FJ2031
GU061619.1 gg_id:578346 and function microbial mesoscale eddy perturbations South China Sea clone CE2-DC GU061
FJ717243.1 gg_id:536934 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United King FJ7172

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EU491047.1 gg_id:265525 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount South Rift X EU491
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FN398053.1 gg_id:592957 Haliea sp. str. 7SM29 = CECT 7447 FN398
DQ513020.1 gg_id:159939 Microbial life fluids ridge flank crustal fluid clone FS142-64B-02 DQ513
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GU118865.1 gg_id:579784 Threatened Corals Provide Microbial Habitats clone Mfra_M11 GU118
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EU236417.1 gg_id:302021 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg92F9 EU236
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EU050825.1 gg_id:251646 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_07_55 EU050
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EU010139.1 gg_id:235473 Biogeography Singapore seawaters seawater clone B24 EU010
DQ070803.1 gg_id:149537 Prokaryotic Structures Seafloor Basalts Varying Age and Juan de Fuca Ridge basalt gl DQ070
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EU707310.1 gg_id:320148 sulfur oxidizing Wadden Sea sediments Janssand sediment -490cm clone JS9_43 EU707
AB476262.1 gg_id:561798 Compositional and functional transition epibiotic microbial hydrothermal vent galath AB476
GQ347899.1 gg_id:555942 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ347
AM259790.1 gg_id:216671 Spatial sponge- Mediterranean Tethya aurantium sponge endosome clone TAI-8-20 AM259
EU491031.1 gg_id:271029 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount South Rift X EU491
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AB479080.1 gg_id:454474 Calyptogena nautilei symbiont AB4790
EU403436.1 gg_id:275217 Calyptogena ponderosa endosymbiont 6 EU4034
AB112462.1 gg_id:90596 Suiyo Seamount hydrothermal plume clone SUP05-30 AB1124
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FJ825949.1 gg_id:568805 Succession during spring Sea filtered surface sea water period diatom bloom Yel Sea; FJ8259
GQ345617.1 gg_id:555029 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ345
GQ346688.1 gg_id:569285 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ346
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GQ346418.1 gg_id:578694 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ346
GQ346535.1 gg_id:585267 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ346
GQ337088.1 gg_id:580119 Hydrography shapes biogeography deep Arctic Ocean water depth 1000m clone BB(GQ337
DQ513047.1 gg_id:160840 Microbial life fluids ridge flank crustal fluid clone CTD005-15B-02 DQ513
GQ346389.1 gg_id:589239 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ346
EU638846.1 gg_id:322165 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU638
GQ345521.1 gg_id:582885 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ345
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GQ345830.1 gg_id:566044 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ345
AF382101.1 gg_id:79277 bacterioplankton clone ZA2329c AF382
FJ745105.1 gg_id:553872 Transporter genes expressed coastal response dissolved organic carbon surface wate FJ7451
GQ345572.1 gg_id:552427 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ345
EU638746.1 gg_id:306754 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU638
DQ351794.1 gg_id:147823 Microbial Adherent Sediment Particles Heavy Metal Contaminated North Sea Surfac DQ351
GU117979.1 gg_id:581250 Threatened Corals Provide Microbial Habitats clone Acer_F12 GU117
EU491869.1 gg_id:267568 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU491
AY386342.1 gg_id:97969 marine str. HTCC2151 AY386

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AF468261.1 gg_id:80175 Arctic pack ice; northern Fram Strait; 80 31.1 N; 01 deg 59.7 min E clone ARKDMS-58 AF4682
EU050830.1 gg_id:255358 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_08_75 EU0508
AJ581349.1 gg_id:92209 Mediterranean sponge clone E01-9C-12 AJ5813
GQ337223.1 gg_id:591094 Hydrography shapes biogeography deep Arctic Ocean water depth 900m clone CB1 GQ337
EU800017.1 gg_id:313341 It's all ranking aquatic Newport Harbour RI clone 1C227703 EU800
FJ403058.1 gg_id:361395 Disease- changes healthy and diseased colonies Caribbean coral Montastrea faveolat FJ4030
EU005712.1 gg_id:264274 Major activity inside and outside natural iron-fertilized phytoplankton bloom 3 micro EU005
GU061256.1 gg_id:540813 Evaluation culturing methods cultivate previously Yel Sea intertidal beach seawater GU061
GQ349050.1 gg_id:557301 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ349
DQ015809.1 gg_id:140174 Antarctic lake water clone ELB16-104 DQ015
FM242300.1 gg_id:337520 sequences sediment clone 3 T9d-oil FM242
EU050829.1 gg_id:255625 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_07_49 EU0508
AY701467.1 gg_id:108544 dinoflagellate symbiont clone GCDE08_AE AY7014
DQ666550.1 gg_id:167594 Actinobacillus capsulatus str. 266/7370 DQ666
DQ666548.1 gg_id:170688 Actinobacillus capsulatus str. 266/5603 DQ666
DQ229009.1 gg_id:160043 Haemophilus parasuis str. ME4 DQ229
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AF268965.1 gg_id:22523 Actinobacillus indolicus str. H1422 AF2689
AF268962.1 gg_id:31672 Actinobacillus indolicus str. H1269 AF2689
EF396307.1 gg_id:246454 Actinobacillus indolicus WB52/06-1 EF3963
DQ229002.1 gg_id:160636 Actinobacillus pleuropneumoniae 262/04 DQ229
FJ437063.1 gg_id:368836 Actinobacillus porcinus str. 35NTS FJ4370
EF173411.1 gg_id:207951 Actinobacillus porcitonsillarum str. WT6N EF1734
EF173406.1 gg_id:207735 Actinobacillus porcitonsillarum str. WT5A EF1734
EF173407.1 gg_id:212933 Actinobacillus porcitonsillarum str. WT1B EF1734
EF173404.1 gg_id:213833 Actinobacillus porcitonsillarum str. WT2A EF1734
AF025839.1 gg_id:9515 Actinobacillus rossii str. JF1390 AF0258
EU074771.1 gg_id:244021 Actinobacillus succinogenes str. S.JST EU0747
AY362898.1 gg_id:102230 Actinobacillus succinogenes str. CCUG 43843 AY3628
AF015299.1 gg_id:9589 Actinobacillus suis str. CCM5586 AF0152
AY362900.1 gg_id:106038 Actinobacillus ureae str. CCUG 2139 AY3629
AJ295746.3 gg_id:52835 Haemophilus parahaemolyticus str. NCTC 8479T AJ2957
AY029174.1 gg_id:69899 Actinobacillus arthritidis str. 13/225/95 AY0291
AF268949.1 gg_id:73428 Actinobacillus minor str. H1473 AF2689
FJ939592.1 gg_id:569406 Haemophilus parahaemolyticus str. PN129 FJ9395
AY465359.1 gg_id:109412 Actinobacillus equuli str. B96/12; JF2421 AY4653
GQ074659.1 gg_id:420587 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw164g GQ074
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EF396305.1 gg_id:244335 Haemophilus parasuis WB25/06-1 EF3963

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

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AY038591.1 gg_id:64296 Gallibacterium genomosp. 1 str. Gerl.3191 AY0385
EU339201.1 gg_id:571594 Gallibacterium genomosp. 3 str. F448 EU3392
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EU423995.1 gg_id:569567 Gallibacterium trehalosifermentans str. B7/99/1 EU4239
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GQ106447.1 gg_id:375695 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw! GQ106
GQ010997.1 gg_id:498669 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ010
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DQ228991.1 gg_id:160451 Haemophilus parasuis VS7-1 DQ228

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FJ463836.1 gg_id:363177 Haemophilus sp. str. HP 65-1 FJ4638
AB370297.1 gg_id:271851 Haemophilus parasuis str. 332 AB370
FJ667952.1 gg_id:540531 Haemophilus parasuis str. Nagasaki FJ6679
DQ229016.1 gg_id:161508 Haemophilus parasuis RW DQ229
FJ667979.1 gg_id:513849 Haemophilus parasuis str. NO145 FJ6679
EU909653.1 gg_id:354221 Haemophilus sp. str. CCUG 17210 EU909
FJ558112.1 gg_id:526872 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5581
FJ667959.1 gg_id:560868 Haemophilus parasuis str. HS1075 FJ6679
EU185432.1 gg_id:245942 Haemophilus haemolyticus str. 58122 EU185
GQ091882.1 gg_id:376235 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ091
GQ087742.1 gg_id:420505 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ087
AB078972.1 gg_id:30824 Haemophilus parasuis 312 AB078
EU185439.1 gg_id:239937 Haemophilus haemolyticus str. 654210 EU185
FJ558093.1 gg_id:517548 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5580
FJ983093.1 gg_id:414943 Aspects Oral Microbiome subgingival plaque clone FJ9830
GQ083506.1 gg_id:440265 Topographical and Temporal Human Skin Microbiome skin alar crease clone nbw24 GQ083
GQ114305.1 gg_id:423130 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw59 GQ114
GQ074383.1 gg_id:392625 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw162c GQ074
GQ116263.1 gg_id:457345 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw690c02 GQ116
GQ091843.1 gg_id:409269 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ091
EU341202.1 gg_id:255127 Evaluation Rapid Technologies Estimate Microbial Burden and Commercial Airline Ca EU341
GQ087761.1 gg_id:421332 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ087
EU185461.1 gg_id:235553 Haemophilus haemolyticus str. 93P10H4 EU185
X87978.1 gg_id:9509 Haemophilus influenzae str. 16N X87978
AY362910.1 gg_id:102232 Haemophilus parasuis str. Bakos B26 AY362
AY005033.1 gg_id:72532 subgingival dental plaque clone BJ095 AY005
GQ083015.1 gg_id:429541 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ083
DQ228998.1 gg_id:160846 Haemophilus parasuis P015/96 DQ228
EU909656.1 gg_id:340606 Haemophilus sp. str. CCUG 18082 EU909
AJ290754.2 gg_id:44396 Haemophilus parainfluenzae str. P1525 AJ2907
EU137565.1 gg_id:261499 Bartonella-positive fleas: and assembly patterns Oropsylla hirsuta (prairie dog flea) C EU137
GQ113941.1 gg_id:391680 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor GQ113
FJ558391.1 gg_id:531822 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5583
GQ116286.1 gg_id:429653 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw690g02 GQ116
EU909680.1 gg_id:307019 Haemophilus sp. str. PN24 EU909
AB176910.1 gg_id:114966 Histophilus somni str. 129Pt AB176
AF053901.1 gg_id:9609 Mannheimia granulomatis str. Ph13; CCUG 26828 AF053
DQ301924.2 gg_id:146654 Mannheimia granulomatis str. W4672/1 DQ301
AF053896.1 gg_id:9605 Mannheimia ruminalis str. HPA98; CCUG38466 AF053
AY425286.1 gg_id:107110 Mannheimia ruminalis str. HPA109 AY425
AY425283.1 gg_id:106648 Mannheimia ruminalis str. HPA113 AY425

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AY425290.1 gg_id:102351 Mannheimia ruminalis str. HPA114 AY4252
NR_024897.1 gg_id:575542 Mannheimia varigena str. 177; CCUG 38462 NR_02
DQ301926.2 gg_id:149765 Mannheimia varigena str. 3997/82 DQ301
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U57069.1 gg_id:9606 Mannheimia haemolytica str. PH192 U5706
AY362913.1 gg_id:102691 Mannheimia granulomatis str. ATCC 49244 AY3629
AF224287.1 gg_id:38515 Pasteurella haemolytica str. CCUG 28148 AF2242
AF053891.1 gg_id:9614 Mannheimia glucosida str. P737; CCUG 38459 AF0538
U57072.1 gg_id:9590 Mannheimia haemolytica str. PH704 U5707
DQ301923.1 gg_id:145499 Mannheimia glucosida str. P933 DQ301
AF224286.1 gg_id:72830 Mannheimia sp. MCCM 00145 AF2242
U57070.1 gg_id:9601 Mannheimia haemolytica str. PH40 U5707
AY425282.1 gg_id:106492 Mannheimia varigena str. V1835 AY4252
AY508828.1 gg_id:105688 Nicoletella semolina str. CCUG 43643 AY5088
U66492.1 gg_id:9498 Pasteurella aerogenes str. P U6649
EF579842.1 gg_id:278925 Pasteurella canis str. Group868/2 EF5798
DQ211736.1 gg_id:171809 Pasteurella mairii str. JF3176 DQ211
EU652767.1 gg_id:286210 Pasteurella subsp. multocida str. Pmww07824 EU6527
AY299318.1 gg_id:103885 Pasteurella multocida str. PM80 AY2993
AY507110.1 gg_id:104353 Pasteurella multocida str. X225 AY5071
AB279579.1 gg_id:187444 Pasteurella sp. str. V6 AB2795
AY299315.1 gg_id:103457 Pasteurella multocida str. PM64 AY2993
AY362925.1 gg_id:99002 Pasteurella stomatis str. CCUG 17979 AY3629
AY299319.1 gg_id:104032 Pasteurella multocida str. PM82 AY2993
AF224296.1 gg_id:69985 Pasteurella pneumotropica str. NCTC 10827 AF2242
AY362920.1 gg_id:107231 Pasteurella dagmatis str. CCUG 12397 AY3629
AY299316.1 gg_id:103590 Pasteurella multocida str. PM106 AY2993
FJ832327.1 gg_id:579924 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P1Q301_30F04 FJ8323
FJ976392.1 gg_id:552339 Interindividual healthy human oral microbiota mouth clone 24B192 FJ9763
AY362918.1 gg_id:103434 Pasteurella caballi str. ATCC 49197 AY3629
AJ251339.1 gg_id:32352 Bisgaardia hudsonenesis str. 98-D-690B AJ2513
AY362917.1 gg_id:103283 Pasteurella bettyae str. CCUG 2042 AY3629
EU681975.1 gg_id:289990 microflora imbalances intestine dogs inflammatory bowel disease duodenum dog IBI EU6819
EU681998.1 gg_id:293231 microflora imbalances intestine dogs inflammatory bowel disease duodenum health EU6819
GQ111280.1 gg_id:419174 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ111
AY172732.1 gg_id:91315 Bisgaard taxon 40 str. B301529/00/1 AY1727
AY465363.1 gg_id:109416 Actinobacillus rossii str. B96/45; JF2425 AY4653
AY362894.1 gg_id:101590 Actinobacillus muris str. NCTC 12432 AY3628
GQ111657.1 gg_id:453130 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ111
M75052.1 gg_id:9466 Pasteurella species M7505
AF224311.1 gg_id:36769 Haemophilus sp. str. MCCM 01557 AF2243

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

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DQ675067.1 gg_id:173204 microbial production water -temperature petroleum reservoir clone QHO-B17 DQ675
FJ193164.1 gg_id:343114 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior FJ1931
AY689035.1 gg_id:100228 Acinetobacter sp. str. 3C_8 AY689
GQ070596.1 gg_id:418636 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ070
DQ257427.1 gg_id:142775 Acinetobacter johnsonii str. CAI-14 DQ257
FJ191887.1 gg_id:343089 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior FJ1918
EU536549.1 gg_id:286873 profile human microbiota antecubital fossa (inner elbow) skin clone nbt215g07 EU5365
EU275352.1 gg_id:253188 Acinetobacter johnsonii str. CONC8 EU2753
FJ192142.1 gg_id:347156 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior FJ1921
DQ675069.1 gg_id:168062 microbial production water -temperature petroleum reservoir clone QHO-B26 DQ675
CU466803.1 gg_id:336593 Evry wastewater treatment plant anoxic basin clone CU466
FJ192398.1 gg_id:334639 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior FJ1923
EU705366.1 gg_id:309203 Microbial Burden and Analyses Phoenix Spacecraft Assembly Kennedy Space Centre EU7053
GU124494.1 gg_id:535160 endosymbiotic (Stal) (rice brown planthopper) Acinetobacter endosymbiont Nilapar GU124
FJ191727.1 gg_id:334971 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior FJ1917
AB196244.1 gg_id:115340 Acinetobacter johnsonii str. IC001 AB196
FJ900940.1 gg_id:563501 Polymorphism microbial reservoirs water cut stage oil field clone L-36 FJ9009
FJ192385.1 gg_id:316225 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior FJ1923
AY167841.1 gg_id:77294 Acinetobacter johnsonii str. SAFR-006 AY1678
FJ192696.1 gg_id:338444 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior FJ1926
DQ675057.1 gg_id:165070 microbial production water -temperature petroleum reservoir clone QHO-B9 DQ675
FJ192370.1 gg_id:310406 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior FJ1923
FJ192156.1 gg_id:320031 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior FJ1921
X86591.1 gg_id:8390 Acinetobacter sp str. 1F-19 X86591
AB369040.1 gg_id:537750 and microbial oils produced Asia petroleum crude oil (Qatar Land Light) clone PT-QTL AB369
AB369043.1 gg_id:573441 and microbial oils produced Asia petroleum crude oil (Qatar Land Light) clone PT-QTL AB369
GQ102953.1 gg_id:436668 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv GQ102
DQ675078.1 gg_id:165523 microbial production water -temperature petroleum reservoir clone QHO-B28 DQ675
FJ948288.1 gg_id:578231 Isolation and identification endophytic three medicinal plants leaf clone HQ FJ9482
FJ192211.1 gg_id:352732 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior FJ1922
FJ192879.1 gg_id:328708 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior FJ1928
GQ111297.1 gg_id:467170 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ111
EU169147.1 gg_id:241109 Acinetobacter johnsonii str. B33 EU169
GQ102212.1 gg_id:371878 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv GQ102
EU240429.1 gg_id:235992 Acinetobacter johnsonii str. B178 EU240
EU504845.1 gg_id:268774 cecal contents Mus musculus strain C57BL/6J; myd2 clone myd2_aaa03b10 EU5048
GQ102805.1 gg_id:450958 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv GQ102
GQ106991.1 gg_id:445417 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw543d0 GQ106
FJ192003.1 gg_id:322306 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior FJ1920
EU705479.1 gg_id:345817 Microbial Burden and Analyses Phoenix Spacecraft Assembly Kennedy Space Centre EU7054
FJ192503.1 gg_id:308433 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior FJ1925

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

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AY277552.1 gg_id:90549 Acinetobacter calcoaceticus str. AVP2-2 AY2775
AY364536.1 gg_id:94206 Acinetobacter rhizosphaerae str. IH9 AY3645
FJ976570.1 gg_id:578667 Acinetobacter calcoaceticus str. LCR61 FJ9765
DQ129724.2 gg_id:248172 Acinetobacter calcoaceticus str. HPC399 DQ129
FJ373024.1 gg_id:327004 Acinetobacter schindleri str. W1-2 FJ3730
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GU339299.1 gg_id:542053 Acinetobacter schindleri str. EH74 GU339
GU004025.1 gg_id:581771 heterotrophic nitrifying biofilm clone 16SN42 GU004
GQ082321.1 gg_id:426536 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw11 GQ082
GU004026.1 gg_id:554705 heterotrophic nitrifying biofilm clone 16SN43 GU004
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NR_028849.1 gg_id:537702 Acinetobacter towneri str. AB1110; DSM 14962 NR_02
AF509824.1 gg_id:60268 Acinetobacter towneri str. 2N01 AF5098
AJ275039.1 gg_id:54545 Acinetobacter ursingii str. LUH 4763 AJ2750
EU258609.1 gg_id:277749 Acinetobacter venetianus str. ACI574 EU258
GQ007238.1 gg_id:502426 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ007
AB286521.1 gg_id:210171 Reducing production and domination comamonadaceae reducing oxygen supply was AB2865
AF357182.1 gg_id:48029 Alvinella pompejana symbiont APG130A AF357
FJ674507.1 gg_id:518521 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6745
GQ451319.1 gg_id:569668 Fecal Yunnan snub-nosed monkey feces clone J341 GQ451
EF468657.1 gg_id:218490 Acinetobacter sp. str. TD5 EF4686
AY047216.1 gg_id:39106 Acinetobacter haemolyticus AY0472
EU467937.1 gg_id:293369 cheetah feces clone CE2_e09 EU4679
EU779466.1 gg_id:321405 Hartmann's Mountain Zebra feces clone AFZEB_aaj72f01 EU7794
EU467673.1 gg_id:302118 naked mole-rat feces clone molerat_2g12_1 EU4676
FJ976593.1 gg_id:550870 Acinetobacter sp. str. LCR84 FJ9765
FJ672033.1 gg_id:520896 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6720
EU779403.1 gg_id:311420 Hartmann's Mountain Zebra feces clone AFZEB_aaj70a08 EU7794
AY633608.1 gg_id:101304 Acinetobacter seohaensis str. SW-100 AY6336
EU463254.1 gg_id:294712 naked mole-rat feces clone molerat_aai72d06 EU4632
FJ672865.1 gg_id:517631 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6728
EU777000.1 gg_id:344560 Naked mole-rat feces clone molerat_2g01 EU7770
GQ077574.1 gg_id:415516 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1210e(GQ077
AM412161.1 gg_id:250903 Acinetobacter sp. str. P-134 AM412
FJ672928.1 gg_id:523993 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6729
AB207814.1 gg_id:167038 Acinetobacter psychrotolerans str. Ths AB2078
EU160535.1 gg_id:347520 diagnosis central-venous infections cultivation-dependent and techniques biofilm sc EU1605
EU604244.1 gg_id:274092 Acinetobacter baylyi str. 1477 EU6042
FJ193878.1 gg_id:338023 Genetic inventory 'KSC-Astrotek' spacecraft assembly clean room during DAWN missi FJ1938
EU463244.1 gg_id:290621 naked mole-rat feces clone molerat_aai72c02 EU4632

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

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EU360111.1 gg_id:582701 Acinetobacter calcoaceticus str. PB16 EU3601
EF432578.2 gg_id:206376 Acinetobacter calcoaceticus str. HB1-1 EF4325
Z93447.1 gg_id:8313 Acinetobacter sp. str. ATCC 17905 Group TU14 Z93447
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EU513394.1 gg_id:277540 Acinetobacter calcoaceticus str. TMPSB-D12 EU5133
EF205268.1 gg_id:199813 Arctic gold mine fracture water clone Lupin-1130m-1-MDA-aci1 EF2052
GQ069882.1 gg_id:445385 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw242h0 GQ069
FJ675523.1 gg_id:522826 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6755
EU467678.1 gg_id:301128 naked mole-rat feces clone molerat_2b06_1 EU4676
FJ009590.1 gg_id:546906 Acinetobacter baumannii str. IP026 FJ0095
FJ193144.1 gg_id:352821 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior FJ1931
AJ296556.1 gg_id:30013 uranium mining depository deponie B1 clone GR-B1-2-35 GR-B1-2-35 AJ2965
EF429004.1 gg_id:204497 Acinetobacter sp. str. GIST-Out1 EF4290
EU918130.1 gg_id:332182 Acinetobacter junii str. PM-8 EU9181
FJ527818.1 gg_id:540395 Acinetobacter sp. str. KSL5401-037 FJ5278
GQ284482.1 gg_id:590067 Acinetobacter sp. str. TDWCW1 GQ284
AY823621.1 gg_id:115347 Acinetobacter calcoaceticus str. SW1 AY8236
EU594561.1 gg_id:277462 Acinetobacter sp. str. 4-2 EU5945
FJ151628.1 gg_id:342972 Acinetobacter calcoaceticus str. HNR FJ1516
EU774032.1 gg_id:314572 Cheetah feces clone CE2_e07 EU7740
AB167206.1 gg_id:107919 Acinetobacter sp. str. c33 AB1672
FJ675182.1 gg_id:524252 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6751
EU240404.1 gg_id:256200 Acinetobacter calcoaceticus str. B120 EU2404
X80285.1 gg_id:8331 Acinetobacter calcoaceticus X80285
EU705523.1 gg_id:354028 Microbial Burden and Analyses Phoenix Spacecraft Assembly Kennedy Space Centre EU7055
FJ820996.1 gg_id:511035 Acinetobacter sp. str. PT22 FJ8209
DQ856498.1 gg_id:250517 intestinal microflora Chinese mitten crab (Eriocheir sinensis) clone C1A DQ856
Z93434.1 gg_id:8311 Acinetobacter calcoaceticus str. ATCC 23055T group one Z93434
EU272861.1 gg_id:358174 Acinetobacter sp. str. MK28 EU2728
GQ174293.1 gg_id:414197 Acinetobacter sp. str. PP-2 GQ174
FJ263921.1 gg_id:318166 Acinetobacter septicus str. BA9 FJ2639
GQ092219.1 gg_id:403040 Topographical and Temporal Human Skin Microbiome skin palm clone nbw411b09c1 GQ092
AM412160.1 gg_id:247994 Acinetobacter sp. str. P-133 AM412
DQ464150.1 gg_id:158313 acid mine drainage clone D1-48 DQ464
EU073105.1 gg_id:350209 Acinetobacter sp. str. TS39 EU0731
FJ193900.1 gg_id:317914 Genetic inventory 'KSC-Astrotek' spacecraft assembly clean room during DAWN missi FJ1939
EF203410.1 gg_id:264736 Acinetobacter sp. str. URAM1 EF2034
FJ671719.1 gg_id:525292 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6717

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

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

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

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AY212663.1 gg_id:99626 water 20 m downstream manure clone 216ds20 AY2126
AY622230.1 gg_id:101684 subsurface soil clone C-CL42 AY6222
DQ660872.1 gg_id:237806 DongChuan copper pyrites PRC determined acid mine drainage (AMD) clone DC-II-2 DQ660
DQ458033.1 gg_id:158925 acid mine drainage clone DX63 DQ458
DQ354716.1 gg_id:153505 subsurface water clone DR550SWSAEE15b DQ354
DQ824588.1 gg_id:176013 human fecal clone RL185_aaj70b01 DQ824
AJ830006.1 gg_id:104541 Psychrobacter aquaticus str. CMS 58 AJ8300
AY842259.1 gg_id:110467 Psychrobacter celer str. SW-238 AY8422
AY771717.1 gg_id:108691 Psychrobacter fozii str. S2-83 AY7717
NC_007969.1 gg_id:157086 Psychrobacter cryohalolentis str. K5 NC_007
DQ270712.1 gg_id:141337 Psychrobacter sp. B-3151 DQ270
EU652044.1 gg_id:275703 Psychrobacter marincola str. aa-20 EU6520
AF441202.1 gg_id:44896 Psychrobacter jeotgali str. YKJ-105 AF4412
NR_025458.1 gg_id:562316 Psychrobacter marincola str. KMM 277 NR_025
AJ539104.1 gg_id:79510 Psychrobacter salsus str. DD48 AJ5391
AJ313425.1 gg_id:101537 Psychrobacter nivimaris str. 88/2-7 AJ3134
AB016054.1 gg_id:24089 Psychrobacter pacificensis str. NIBH P2J2 AB0160
AY057116.1 gg_id:27938 Psychrobacter meningitidis str. SGHMS AY0571
AB016056.1 gg_id:18681 Psychrobacter pacificensis str. NIBH P2J13 AB0160
AY167308.1 gg_id:82364 Psychrobacter glacincola str. ANT9253 AY1673
AY372913.1 gg_id:144095 marine sponge Rhabdastrella globostellata symbiont AY3729
EU434452.1 gg_id:269448 Psychrobacter pulmonis str. a40 EU4344
EU434447.1 gg_id:263373 Psychrobacter pulmonis str. a72 EU4344
EU434352.1 gg_id:276381 Psychrobacter pulmonis str. a161 EU4343
EU434446.1 gg_id:263158 Psychrobacter pulmonis str. a60 EU4344
AJ437696.1 gg_id:85442 Psychrobacter pulmonis str. CECT 5989T AJ4376
EU434362.1 gg_id:269048 Psychrobacter pulmonis str. a131 EU4343
NC_009524.1 gg_id:229173 Psychrobacter sp. str. PRwf-1 NC_009
FJ613297.1 gg_id:533763 Psychrobacter faecalis str. hyss7 FJ6132
EU000245.1 gg_id:324143 Psychrobacter maritimus str. KOPRI_22337 EU0002
EU845548.1 gg_id:313200 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8455
EU880519.1 gg_id:311744 Psychrobacter nivimaris str. P24a EU8805
EF101551.1 gg_id:182841 Psychrobacter pulmonis str. KOPRI24933 EF1015
AY167281.1 gg_id:82289 Psychrobacter glacincola str. ANT9104 AY1672
EU433332.1 gg_id:271451 Psychrobacter sp. str. BSs20154 EU4333
AJ312213.1 gg_id:32985 Psychrobacter glacincola str. DSM 12194T AJ3122
DQ860047.1 gg_id:251317 anchovy intestinal microflora clone F2N DQ860
AM110989.1 gg_id:140965 Psychrobacter sp. str. 3035 AM110
EU434353.1 gg_id:264946 Psychrobacter pulmonis str. a163 EU4343
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AM111050.1 gg_id:140908 Psychrobacter sp. str. 7195 AM111
NR_027204.1 gg_id:566452 Psychrobacter arenosus str. R7; KMM 3659 NR_02
EU434405.1 gg_id:263288 Psychrobacter maritimus str. a336 EU434
GQ093417.1 gg_id:420929 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ093
EF101546.1 gg_id:181752 Psychrobacter aquimaris str. KOPRI24928 EF1015
AM111057.1 gg_id:140806 Psychrobacter sp. str. 7319 AM111
AY722804.1 gg_id:103680 Psychrobacter aquimaris str. SW-210 AY7228
AY864643.1 gg_id:110044 Psychrobacter sp. str. DVS7b AY8646
AY198113.1 gg_id:80503 Psychrobacter sp. HLA AY198
AY513645.1 gg_id:103196 Psychrobacter alimentarius str. JG-100 AY5136
NR_027225.1 gg_id:543076 Psychrobacter maritimus str. Pi2-20; KMM 3646 NR_02
AY167286.1 gg_id:81385 Psychrobacter sp. str. ANT9153 AY167
AJ272303.1 gg_id:71508 Psychrobacter proteolyticus str. 116 AJ2723
AY771724.1 gg_id:143446 Psychrobacter glacincola S3-14 AY771
EU845549.1 gg_id:332859 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU845
AJ309942.1 gg_id:51114 Psychrobacter immobilis str. DSM 7229T AJ3099
EU075123.1 gg_id:242630 Psychrobacter sp. str. En40 EU075
AM269904.1 gg_id:160677 Psychrobacter sp. str. ES-10 AM269
EU434395.1 gg_id:273089 Psychrobacter maritimus str. a325 EU4343
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EU370412.1 gg_id:266113 Psychrobacter faecalis str. 88Z1 EU370
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EU434433.1 gg_id:275103 Psychrobacter pulmonis str. a195 EU4344
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EU845208.1 gg_id:323141 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU845
AM237354.1 gg_id:154195 Psychrobacter faecalis OS-38 AM237
EU434386.1 gg_id:271742 Psychrobacter maritimus str. a281 EU4343
AJ609556.1 gg_id:100627 Psychrobacter frigidicola str. DSM 12411 AJ6095
EU834258.1 gg_id:312816 Psychrobacter frigidicola str. DS35 EU834
DQ337513.1 gg_id:147051 Psychrobacter psychrophilus BBDP29 DQ337
U85878.1 gg_id:8302 Psychrobacter glacincola str. IC018 U85878
U39399.1 gg_id:8253 Psychrobacter immobilis str. ATCC 43116 U39399
U85876.1 gg_id:8300 Psychrobacter glacincola str. IC084 U85876
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EF154276.1 gg_id:176716 Psychrobacter alimentarius str. 36 EF1542
AM111006.1 gg_id:140871 Psychrobacter sp. str. 3055 AM111
AF170743.1 gg_id:8257 Psychrobacter sp. str. QSSC5-4 AF1707
EU915471.1 gg_id:326012 Psychrobacter phenylpyruvicus str. 123 EU915

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EU434577.1 gg_id:265418 Psychrobacter pulmonis str. b105 EU4345
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AJ609555.1 gg_id:100472 Psychrobacter urativorans str. DSM 14009 AJ6095
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AY771725.1 gg_id:142863 Psychrobacter alimentarius S3-15 AY7717
DQ156147.1 gg_id:220416 Moraxella boevrei str. ATCC 700022 DQ156
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GQ008884.1 gg_id:500783 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ008
AM231087.1 gg_id:155496 Moraxella sp. Vas1N8 AM231
GQ093299.1 gg_id:437819 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw42 GQ093
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AY753196.2 gg_id:124309 Xenorhabdus nematophila str. PDBC SCX3 Indian AY7531
AB175658.1 gg_id:162524 Azomonas insignis str. ATCC 29361 AB1756
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AB175654.1 gg_id:173614 Azomonas macrocytogenes str. IAM 15003 AB1756
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AB175655.1 gg_id:168352 Azotobacter armeniacus str. DSM 2284 AB1756
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AB041885.1 gg_id:41050 Pseudomonas psychrophila str. E-3 AB0418
AY195842.1 gg_id:81514 Pseudomonas fragi str. SAPA2 AY1958
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GU213303.1 gg_id:535039 Pseudomonas sp. str. 4-13 GU213
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AJ006109.1 gg_id:8516 Pseudomonas mendocina str. ATCC 25413 AJ0061
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AB361588.1 gg_id:267059 Pseudomonas putida str. 152 AB3615

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FJ217181.1 gg_id:575069 Pseudomonas oryzihabitans str. BBAL-03d
EU047553.1 gg_id:236258 Pseudomonas oleovorans str. TMPSB5
EF028693.1 gg_id:189438 Pseudomonas sp. str. BCL-53
AY623816.1 gg_id:159881 Pseudomonas oleovorans
EU977740.1 gg_id:544679 Pseudomonas oryzihabitans str. 1P03PC
EU977588.1 gg_id:569674 Pseudomonas plecoglossicida str. 1P03MC
AB248284.1 gg_id:150864 Pseudomonas fulva str. 10 (= KMM 3881)
EU977738.1 gg_id:569323 Pseudomonas oryzihabitans str. 1P03PA
EU977587.1 gg_id:553834 Pseudomonas oryzihabitans str. 1P03MB
AB125366.1 gg_id:100555 Pseudomonas pachastrellae str. KMM 330
AY152673.1 gg_id:78571 Pseudomonas rhizosphaerae str. IH5
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AM265390.1 gg_id:178656 Pseudomonas savastanoi pv. fraxini str. PVFiF1
NR_024707.1 gg_id:546957 Pseudomonas savastanoi str. ATCC 13522

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EF382724.1 gg_id:214723 Pseudomonas str. BSi20450 EF3827
AJ288148.1 gg_id:53166 Pseudomonas stutzeri Makran AJ2881
FJ671729.1 gg_id:526385 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6717
AY647159.1 gg_id:100165 Pseudomonas stutzeri str. ZWLR2-1; CCTCC (China Center Type Collection) M203096 AY6471
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AB176955.1 gg_id:104939 Pseudomonas stutzeri str. KMM 235 AB1769
GQ280051.1 gg_id:585761 Pseudomonas stutzeri str. BJ-41 GQ280
AM236234.1 gg_id:151046 Methylobacterium extorquens AM1 AM236
EU327995.1 gg_id:243015 Pseudomonas stutzeri str. DA-1 EU3279
EU771075.1 gg_id:338443 Pseudomonas stutzeri str. F22 EU7710
AM236235.1 gg_id:154066 Pseudomonas sp. AM2 AM236
AF237677.1 gg_id:38888 Pseudomonas stutzeri str. M14C AF2376
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AJ270452.1 gg_id:18824 Pseudomonas stutzeri str. 11C2 marine sediment Schillig AJ2704
AB001445.1 gg_id:50962 Pseudomonas syringae pv. morsprunorum str. MAFF 302280 pv. AB0014
AY574913.1 gg_id:106878 Pseudomonas syringae str. PNA29.1a AY5749
AB001441.1 gg_id:20629 Pseudomonas syringae pv. broussonetiae str. KOZ 8101 pv. AB0014
AB001449.1 gg_id:52123 Pseudomonas syringae pv. tagetis str. MAFF 302271 pv. AB0014
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AM399035.1 gg_id:171964 Pseudomonas syringae pv. coryli str. ISPaVe 598 AM399
AM399036.1 gg_id:163475 Pseudomonas pv. syringae str. NCPPB 3869 AM399
AF506040.1 gg_id:66299 Pseudomonas fluorescens LCSAOTU1 AF5060
AF068259.1 gg_id:8625 Pseudomonas jessenii str. CIP 105274 AF0682

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AB038136.1 gg_id:47594 Pseudomonas putida str. P-2 AB038
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DQ178231.1 gg_id:140491 Pseudomonas fluorescens str. PC33 DQ178
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DQ392980.1 gg_id:153042 Pseudomonas veronii DQ392
AY081814.1 gg_id:68487 Pseudomonas veronii str. CA-4 AY081
AF268029.1 gg_id:22349 Pseudomonas grimontii str. CFML 97-514T AF268
DQ178235.1 gg_id:139966 Pseudomonas fluorescens str. PC38 DQ178
AY512620.1 gg_id:102881 Pseudomonas veronii str. A1YC2-5 AY512
AY512621.1 gg_id:103030 Pseudomonas veronii str. A1YdBTEX2-5 AY512
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FM213379.2 gg_id:306680 Pseudomonas meridiana str. KJPB15 FM213
DQ178232.1 gg_id:139953 Pseudomonas fluorescens str. PC34 DQ178
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AF364098.1 gg_id:59382 Pseudomonas marginalis str. NZCX27 AF364
AB506066.1 gg_id:576116 Pseudomonas sp. str. StFRB209 AB506
Z76671.1 gg_id:8633 Pseudomonas viridiflava str. LMG 2352T () Z76671
AB021398.1 gg_id:8638 Pseudomonas cichorii str. ATCC 10857T AB021

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EU538392.1 gg_id:284751 profile human microbiota antecubital fossa (inner elbow) skin clone nbt88e05 EU5383
AB088844.1 gg_id:79576 Pseudomonas sp. str. K23 AB0888
EF672050.1 gg_id:253349 Burkholderia cepacia str. M45 EF6720
EU536489.1 gg_id:280173 profile human microbiota antecubital fossa (inner elbow) skin clone nbt214f09 EU5364
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EU535774.1 gg_id:286476 profile human microbiota antecubital fossa (inner elbow) skin clone nbt10f05 EU5357
EU539846.1 gg_id:280184 profile human microbiota antecubital fossa (inner elbow) skin clone nbt106c10 EU5398
EU538445.1 gg_id:282737 profile human microbiota antecubital fossa (inner elbow) skin clone nbt229g12 EU5384
EF154273.1 gg_id:178880 Pseudomonas syringae str. 33 EF1542
EU535280.1 gg_id:280196 profile human microbiota antecubital fossa (inner elbow) skin clone nbt01b07 EU5352
AB547166.1 gg_id:515561 Pseudomonas sp. str. DSP-S3 AB5471
FJ892984.1 gg_id:548837 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota HM2; ear p FJ8929
EU877075.1 gg_id:341197 Pseudomonas putida str. EC3_2001 EU8770
EU540274.1 gg_id:281449 profile human microbiota antecubital fossa (inner elbow) skin clone nbt113e10 EU5402
AJ846274.1 gg_id:106541 Pseudomonas sp. HHS8 AJ8462
EF471903.1 gg_id:217410 Pseudomonas sp. str. GW28-5 EF4719
AF320994.1 gg_id:33806 Pseudomonas tolaasii str. NZ027 AF3209
Z76669.1 gg_id:8639 Pseudomonas syringae str. LMG 1247t1T (; pathovar reference strain) Z76669
EU540055.1 gg_id:281519 profile human microbiota antecubital fossa (inner elbow) skin clone nbt112e11 EU5400
AY538263.1 gg_id:100141 Pseudomonas fluorescens str. PC17 AY5382
AB108691.1 gg_id:83881 Pseudomonas putida str. AN2 AB1086
EU538374.1 gg_id:280440 profile human microbiota antecubital fossa (inner elbow) skin clone nbt88b03 EU5383
FJ893864.1 gg_id:554161 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B1E; ear pu FJ8938
EF565945.1 gg_id:227761 Pseudomonas sp. str. 1043 EF5659
AF094726.1 gg_id:71021 Pseudomonas fluorescens str. ATCC 17386 AF0947
EU540294.1 gg_id:282548 profile human microbiota antecubital fossa (inner elbow) skin clone nbt114c12 EU5402
FJ893943.1 gg_id:549107 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B1E; ear pu FJ8939
AJ936933.1 gg_id:175024 Pseudomonas simiae AJ9369
FJ894257.1 gg_id:543206 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B2E; ear pu FJ8942
AY303316.1 gg_id:129966 Pseudomonas sp. str. ps6-35 AY3033
EU930815.1 gg_id:307397 Pseudomonas putida str. PC EU9308
EU111704.2 gg_id:509199 Pseudomonas poae str. T23 EU1117
AF313466.1 gg_id:35880 Pseudomonas veronii AF3134
EU538996.1 gg_id:284817 profile human microbiota antecubital fossa (inner elbow) skin clone nbt98h04 EU5389
AJ295374.1 gg_id:19794 rape rhizosphere cse074 AJ2953
FJ788425.1 gg_id:537584 Pseudomonas putida str. Rs-198 FJ7884

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AF411855.1 gg_id:27138 Pseudomonas sp. str. 5B AF411
FJ895023.1 gg_id:535208 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota BME; ear p FJ8950
AM111013.1 gg_id:140933 Pseudomonas sp. str. 7001 AM111
FJ894165.1 gg_id:567845 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B1E; ear pı FJ8941
FJ893919.1 gg_id:535538 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B1E; ear pı FJ8939
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FJ893323.1 gg_id:548944 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota WT1; ear p FJ8933
EU537276.1 gg_id:280469 profile human microbiota antecubital fossa (inner elbow) skin clone nbt72c07 EU537
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EU540622.1 gg_id:281237 profile human microbiota antecubital fossa (inner elbow) skin clone nbt120h05 EU540
DQ256083.1 gg_id:143611 Pseudomonas fluorescens str. sp-f DQ256
AB294558.1 gg_id:204838 Pseudomonas putida str. NCB0308-456 AB294
FJ892909.1 gg_id:538158 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota HM1; ear p FJ8929
DQ289076.1 gg_id:144195 Bacillus subtilis FM21 DQ289
FJ893397.1 gg_id:563933 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota WT1; ear p FJ8933
EU535682.1 gg_id:281049 profile human microbiota antecubital fossa (inner elbow) skin clone nbt09e10 EU535
EU539232.1 gg_id:286562 profile human microbiota antecubital fossa (inner elbow) skin clone nbt101f11 EU539
AJ271219.1 gg_id:72969 Pseudomonas putida str. P1 AJ2712
AY303321.1 gg_id:131310 Pseudomonas sp. str. ps6-49 AY3033
EF016112.1 gg_id:195370 Pseudomonas sp. str. BSLY EF0161
AF374472.1 gg_id:67535 Pseudomonas costantinii str. CFBP 5705; HAMBI 2444 AF3744
EU538183.1 gg_id:283248 profile human microbiota antecubital fossa (inner elbow) skin clone nbt81g06 EU538
Z76655.1 gg_id:8568 Pseudomonas asplenii str. LMG 2137T () Z76655
FJ894960.1 gg_id:535843 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota BME; ear p FJ8949
EU169189.1 gg_id:237380 Pseudomonas tolaasii str. B34 EU169
DQ318867.1 gg_id:152043 Pseudomonas syringae str. 6 DQ318
FJ405884.1 gg_id:363503 Pseudomonas putida str. YJF1-21 FJ4058
EU538954.1 gg_id:283838 profile human microbiota antecubital fossa (inner elbow) skin clone nbt95h09 EU538
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EU537169.1 gg_id:285856 profile human microbiota antecubital fossa (inner elbow) skin clone nbt67g03 EU537
EU539367.1 gg_id:286796 profile human microbiota antecubital fossa (inner elbow) skin clone nbt237f01 EU539

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AJ249825.2 gg_id:74089 Pseudomonas putida str. GPo1 (TF4-1L) AJ2498
DQ402053.1 gg_id:155811 Pseudomonas fluorescens TC222 DQ402
FJ894348.1 gg_id:548110 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B2E; ear pu FJ8943
GU372931.1 gg_id:514461 Pseudomonas sp. str. CS3 GU372
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EU534747.1 gg_id:280344 profile human skin microbiota ear punch biopsy female C57BL/6J mouse clone nbt21 EU534
AF502594.1 gg_id:66559 Pseudomonas monteilii str. C11 AF502
AY900171.1 gg_id:142050 Pseudomonas fluorescens str. PCL1751 AY900
AF130950.1 gg_id:8581 Pseudomonas syringae str. A90 AF130
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EU539948.1 gg_id:283585 profile human microbiota antecubital fossa (inner elbow) skin clone nbt108c07 EU539
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FM955873.1 gg_id:540744 Pseudomonas sp. str. Asd M6-4 FM955
DQ257632.1 gg_id:147233 Pseudomonas putida str. MTCC 5110 DQ257
EF062802.1 gg_id:183293 Pseudomonas sp. str. MY1402 EF0628
AY690673.1 gg_id:99074 Sulfitobacter sp. str. GC07 AY690
AF100323.1 gg_id:8681 Pseudomonas thivervalensis str. SBK26; CFBP 11261T AF100
DQ536518.1 gg_id:161371 Pseudomonas poae str. BIHB 752 DQ536
EU434546.1 gg_id:258577 Pseudomonas fluorescens str. b59 EU434
EU539834.1 gg_id:287212 profile human microbiota antecubital fossa (inner elbow) skin clone nbt105h10 EU539
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GU186124.1 gg_id:548053 Pseudomonas fluorescens str. IHB B 1427 GU186
GQ174492.1 gg_id:446815 Pseudomonas sp. str. 32A GQ174
EU827496.1 gg_id:320652 Pseudomonas putida str. TFD49 EU827
FJ911604.1 gg_id:535159 Rhizobium sp. str. SPC RN2 FJ9116
GQ451221.1 gg_id:552947 Fecal Yunnan snub-nosed monkey feces clone J87 GQ451
FJ894687.1 gg_id:574364 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota BME; ear p FJ8946
EU538372.1 gg_id:286077 profile human microbiota antecubital fossa (inner elbow) skin clone nbt88a05 EU538
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FJ950670.1 gg_id:426126 Pseudomonas fluorescens str. d112 FJ9506
EF154274.1 gg_id:190873 Pseudomonas tolaasii str. 34 EF1542
EU537208.1 gg_id:286436 profile human microbiota antecubital fossa (inner elbow) skin clone nbt68e07 EU537
GQ900609.1 gg_id:583278 Pseudomonas synxantha str. A1 GQ900
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Z29622.1 gg_id:8723 Pseudomonas species Z29622

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AJ889838.1 gg_id:113026 Pseudomonas avellanae str. BPIC 714 AJ8898
FJ894440.1 gg_id:542748 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B2E; ear pu FJ8944
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EU539417.1 gg_id:281214 profile human microbiota antecubital fossa (inner elbow) skin clone nbt238e04 EU5394
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FJ981653.1 gg_id:535517 Flea Vectors Plague clone XC7 FJ9816
AY574282.1 gg_id:140321 Pseudomonas putida str. S16 AY5742
AF134705.1 gg_id:46201 Pseudomonas fluorescens str. F113 AF1347
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FJ894122.1 gg_id:558498 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B1E; ear pu FJ8941
EU434349.1 gg_id:260230 Pseudomonas fluorescens str. a258 EU4343
FJ894378.1 gg_id:556184 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B2E; ear pu FJ8943
EU601175.1 gg_id:279245 Pseudomonas putida str. PBRs5 EU601
FJ892805.1 gg_id:572626 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota HM1; ear p FJ8928
EF102852.1 gg_id:252507 Pseudomonas sp. str. G-229-23 EF1028
FJ605372.1 gg_id:451091 Pseudomonas plecoglossicida str. Fn-2 FJ6053
EU373377.1 gg_id:276371 Pseudomonas fluorescens str. HNR16 EU3733
EU652104.1 gg_id:274750 Pseudomonas sp. str. ybd-1 EU6521
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EU536830.1 gg_id:286409 profile human microbiota antecubital fossa (inner elbow) skin clone nbt222d01 EU5368
EU539844.1 gg_id:283892 profile human microbiota antecubital fossa (inner elbow) skin clone nbt106c05 EU5398
FJ422406.1 gg_id:360669 Pseudomonas fluorescens str. CB32 FJ4224
EU537106.1 gg_id:279854 profile human microbiota antecubital fossa (inner elbow) skin clone nbt220g07 EU5371
FJ894060.1 gg_id:561617 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B1E; ear pu FJ8940
GU186116.1 gg_id:589957 Pseudomonas putida str. IHB B 1369 GU186
FN675869.1 gg_id:518676 Pseudomonas trivialis RE*1-1-14 FN6758
EU538939.1 gg_id:285340 profile human microbiota antecubital fossa (inner elbow) skin clone nbt95f03 EU5389
EU360314.1 gg_id:261260 Pseudomonas fluorescens str. 2313 EU3603
FJ894338.1 gg_id:564449 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B2E; ear pu FJ8943
GQ499333.1 gg_id:539966 Pseudomonas putida str. M1 GQ499
DQ087528.1 gg_id:128047 Pseudomonas putida str. PBM11 DQ087
FJ894369.1 gg_id:536140 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B2E; ear pu FJ8943
AF320990.1 gg_id:37361 Pseudomonas tolaasii str. NCPPB 2325 AF3209
FJ893610.1 gg_id:549815 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota WT3; ear p FJ8936
NR_024909.1 gg_id:560291 Pseudomonas orientalis str. CFML 96-170; CIP 105540 NR_024
EU539533.1 gg_id:285381 profile human microbiota antecubital fossa (inner elbow) skin clone nbt241d02 EU5395
EU439425.1 gg_id:594417 Pseudomonas putida str. OK-St EU4394
FJ950631.1 gg_id:401370 Pseudomonas putida str. c255 FJ9506
EU434416.1 gg_id:264637 Pseudomonas fluorescens str. a1 EU4344
EU535748.1 gg_id:286344 profile human microbiota antecubital fossa (inner elbow) skin clone nbt10c12 EU5357
FM211694.1 gg_id:325970 Pseudomonas putida str. P9 FM211
FJ894346.1 gg_id:538400 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B2E; ear pu FJ8943
EF102849.1 gg_id:241842 Pseudomonas putida str. G-4-14-1 EF1028
AF482685.1 gg_id:66956 Pseudomonas sp. str. NMX AF4826
AY785748.1 gg_id:108233 Pseudomonas fluorescens OUCZ118 AY7857
AB302402.1 gg_id:221292 Pseudomonas multiaromavorans str. C-18 AB3024
AY738626.1 gg_id:102117 Pseudomonas putida AY7386
FJ893958.1 gg_id:571781 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B1E; ear pu FJ8939
EU540301.1 gg_id:283128 profile human microbiota antecubital fossa (inner elbow) skin clone nbt114f12 EU5403

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EU540286.1 gg_id:279871 profile human microbiota antecubital fossa (inner elbow) skin clone nbt113h09 EU540
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AY303300.1 gg_id:129613 Pseudomonas sp. str. ps4-28 AY3033
EU537958.1 gg_id:282775 profile human microbiota antecubital fossa (inner elbow) skin clone nbt228a05 EU537
FJ894406.1 gg_id:573458 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B2E; ear pu FJ8944
AF100322.1 gg_id:8680 Pseudomonas brassicacearum str. NFM421; CFBP 11874 AF1003
EU536400.1 gg_id:285545 profile human microbiota antecubital fossa (inner elbow) skin clone nbt213c12 EU536
DQ071557.1 gg_id:128217 Pseudomonas monteilii str. R1 DQ071
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EU169164.1 gg_id:243916 Pseudomonas fluorescens str. B67 EU169
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EF645247.1 gg_id:238269 Pseudomonas plecoglossicida str. CGMCC 2093 EF6452
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FJ894690.1 gg_id:551928 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota BME; ear p FJ8946
EU536050.1 gg_id:285952 profile human microbiota antecubital fossa (inner elbow) skin clone nbt07g11 EU536
DQ318865.1 gg_id:156534 Pseudomonas syringae str. 8535 DQ318
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FJ894423.1 gg_id:538102 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B2E; ear pu FJ8944
EU434397.1 gg_id:276367 Pseudomonas fluorescens str. a311 EU4343
GU177878.1 gg_id:591085 Pseudomonas fluorescens str. FE1326 GU177
AF131104.1 gg_id:8590 Pseudomonas putida str. MTB5 AF131
EU539817.1 gg_id:285462 profile human microbiota antecubital fossa (inner elbow) skin clone nbt105d10 EU5398
DQ377742.1 gg_id:151735 Pseudomonas migulae PD 1 DQ377
EU538358.1 gg_id:280546 profile human microbiota antecubital fossa (inner elbow) skin clone nbt87a03 EU5383
FJ895027.1 gg_id:573710 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota BME; ear p FJ8950
FJ893564.1 gg_id:549060 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota WT2; ear p FJ8935
EU535249.1 gg_id:280188 profile human microbiota antecubital fossa (inner elbow) skin clone nbt172g06 EU535
EU539660.1 gg_id:283327 profile human microbiota antecubital fossa (inner elbow) skin clone nbt243f12 EU539
EU434368.1 gg_id:276148 Pseudomonas lundensis str. a301 EU4343
DQ453709.1 gg_id:156806 Pseudomonas pv. savastanoi str. ITM-317 DQ453
EU539126.1 gg_id:279910 profile human microbiota antecubital fossa (inner elbow) skin clone nbt98f01 EU539
EF528261.1 gg_id:227324 Pseudomonas migulae AE2 EF5282
EU647701.1 gg_id:276918 Pseudomonas mandelii str. REG46 EU647
GQ502786.1 gg_id:582124 Pseudomonas putida str. xyz-zjut GQ502
DQ465009.2 gg_id:227277 Pseudomonas sp. str. VTT E-052906 DQ465
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EU169190.1 gg_id:245659 Pseudomonas tolaasii str. B35 EU169

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FJ894079.1 gg_id:536394 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B1E; ear pu FJ8940
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FJ418774.1 gg_id:366431 Pseudomonas syringae pv. tomato str. 2 FJ4187
EU539823.1 gg_id:286118 profile human microbiota antecubital fossa (inner elbow) skin clone nbt105f04 EU5398
FM955865.1 gg_id:554111 Pseudomonas sp. str. Asd M4-6 FM955
EU434384.1 gg_id:269895 Pseudomonas fluorescens str. a95 EU4343
EU439421.1 gg_id:538528 Pseudomonas putida str. LH-S1 EU4394
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EU537178.1 gg_id:285666 profile human microbiota antecubital fossa (inner elbow) skin clone nbt67h12 EU5371
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DQ112333.1 gg_id:136213 Pseudomonas putida str. RW-28 DQ112
AB334768.1 gg_id:238610 Pseudomonas veronii str. MPU43 AB3347
FJ893939.1 gg_id:554355 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B1E; ear pu FJ8939
AM495258.1 gg_id:252526 Pseudomonas putida str. INBP1 AM495
DQ177468.1 gg_id:140357 Pseudomonas sp. str. Tibet-IIA21 DQ177
EU538277.1 gg_id:282428 profile human microbiota antecubital fossa (inner elbow) skin clone nbt84c03 EU5382
EU855189.1 gg_id:307393 Pseudomonas fulva str. CTSP6 EU8551
EU540081.1 gg_id:283910 profile human microbiota antecubital fossa (inner elbow) skin clone nbt245b09 EU5400
AJ132993.1 gg_id:46263 Pseudomonas putida #HR9 AJ1329
EU538386.1 gg_id:279796 profile human microbiota antecubital fossa (inner elbow) skin clone nbt87h04 EU5383
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FJ893421.1 gg_id:543846 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota WT1; ear p FJ8934
DQ095909.1 gg_id:128213 Pseudomonas plecoglossicida str. S20 DQ095
EU162042.1 gg_id:243921 Pseudomonas sp. str. B2 EU1620
EU784140.1 gg_id:354316 Azotobacter sp. str. HY1141 EU7841
DQ314545.1 gg_id:149377 Pseudomonas sp. str. BWDY-41 DQ314
AY303255.1 gg_id:134368 Pseudomonas sp. str. ps10-14 AY3032
EU373390.1 gg_id:275232 Pseudomonas synxantha str. HNR22 EU3733
EU539911.1 gg_id:284759 profile human microbiota antecubital fossa (inner elbow) skin clone nbt107f10 EU5399
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FJ893186.1 gg_id:533616 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota HM3; ear p FJ8931

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AF094730.1 gg_id:73624 Pseudomonas fluorescens str. ATCC 17573 AF0947
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EU540288.1 gg_id:281800 profile human microbiota antecubital fossa (inner elbow) skin clone nbt114a07 EU5402
DQ455072.1 gg_id:156940 Pseudomonas monteilii str. VK58 DQ455
EU538335.1 gg_id:280356 profile human microbiota antecubital fossa (inner elbow) skin clone nbt84a04 EU5383
GU244412.1 gg_id:529178 Pseudomonas fulva str. 132 GU244
FJ787327.1 gg_id:567597 Pseudomonas fluorescens str. NPRs4 FJ7873
DQ536520.1 gg_id:160291 Pseudomonas trivialis str. BIHB 759 DQ536
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FM210032.1 gg_id:347743 Pseudomonas lini str. T1P26 FM210
EU540133.1 gg_id:285657 profile human microbiota antecubital fossa (inner elbow) skin clone nbt245h09 EU5401
EU586044.1 gg_id:271160 Pseudomonas mandelii str. REG45 EU5860
EU534917.1 gg_id:286166 profile human skin microbiota ear punch biopsy female C57BL/6J mouse clone nbt21 EU5349
GQ368179.1 gg_id:577495 Pseudomonas koreensis str. JDM-2 GQ368
DQ313382.1 gg_id:180841 Pseudomonas putida str. PCL1759 DQ313
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GU372963.1 gg_id:564991 Pseudomonas putida str. BA-2 D-2 GU372
EU537224.1 gg_id:282390 profile human microbiota antecubital fossa (inner elbow) skin clone nbt68h09 EU5372
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GQ073242.1 gg_id:402914 Topographical and Temporal Human Skin Microbiome skin palm clone nbw206g04c1 GQ073
DQ095914.1 gg_id:136320 Pseudomonas mosselii DQ095
EU537429.1 gg_id:282749 profile human microbiota antecubital fossa (inner elbow) skin clone nbt78c06 EU5374
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AB189452.1 gg_id:112760 Pseudomonas azotifigens str. 6H33b AB1894
FJ892875.1 gg_id:564952 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota HM1; ear p FJ8928
GU198123.1 gg_id:579684 Pseudomonas fluorescens str. LMG 14673 GU198
EU111689.2 gg_id:511952 Pseudomonas migulae str. T8 EU1116
EU535172.1 gg_id:281864 profile human microbiota antecubital fossa (inner elbow) skin clone nbt171h04 EU5351
EU862561.1 gg_id:328338 Pseudomonas putida str. AB35 EU8625
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EU434358.1 gg_id:271891 Pseudomonas libanensis str. a110 EU4343
FJ894768.1 gg_id:546879 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota BME; ear p FJ8947
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DQ482656.1 gg_id:158174 Pseudomonas putida str. Dsp-1 DQ482
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DQ482655.1 gg_id:158425 Pseudomonas putida str. Dsp-3 DQ482
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AY242068.1 gg_id:102312 Pseudomonas pv. syringae str. FG11 AY242
EF526503.1 gg_id:218860 Pseudomonas putida str. NAPC3 EF5265
AY730552.1 gg_id:105687 Pseudomonas fluorescens str. VH060479 AY7305
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GU136489.1 gg_id:559336 Pseudomonas sp. str. DY1 GU136
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FJ950635.1 gg_id:419521 Pseudomonas putida str. c315 FJ9506
FJ894174.1 gg_id:568497 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B1E; ear pı FJ8941
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EU534713.1 gg_id:285416 profile human skin microbiota ear punch biopsy female C57BL/6J mouse clone nbt18 EU5347
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FJ893927.1 gg_id:540978 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B1E; ear pı FJ8939
EU539515.1 gg_id:283300 profile human microbiota antecubital fossa (inner elbow) skin clone nbt104e09 EU5395
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FJ894815.1 gg_id:540259 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota BME; ear p FJ8948
EU540308.1 gg_id:284991 profile human microbiota antecubital fossa (inner elbow) skin clone nbt114h10 EU5403
EU539830.1 gg_id:287180 profile human microbiota antecubital fossa (inner elbow) skin clone nbt105g10 EU5398
GU186122.1 gg_id:558279 Pseudomonas mandelii str. IHB B 1384 GU186
AY267197.1 gg_id:107228 Pseudomonas fluorescens str. SK1 AY2671
EU538366.1 gg_id:282513 profile human microbiota antecubital fossa (inner elbow) skin clone nbt87f02 EU5383
EU169162.1 gg_id:254921 Pseudomonas fluorescens str. B59 EU1691
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EU538477.1 gg_id:283326 profile human microbiota antecubital fossa (inner elbow) skin clone nbt230d10 EU5384
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EU414476.1 gg_id:270637 Pseudomonas gingeri str. SDLi-1 EU4144
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AB021397.1 gg_id:8571 Pseudomonas asplenii str. ATCC 23835T AB0213
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