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AY701560.1 gg_id:107303 Anabaena ellipsoides str. AnaHB AY7015
AY701548.1 gg_id:107359 Anabaena planktonica str. 1403/27 AY7015
DQ023199.1 gg_id:128225 Anabaena lemmermannii 'BC 0005' BC Ana 0005 DQ023
AY196086.1 gg_id:88724 Aphanizomenon gracile 'Aph NH-5' str. Aph NH-5 AY1960
AJ630419.1 gg_id:107969 Anabaena flos-aquae str. 1tu31s11 AJ6304
AJ630443.1 gg_id:107992 Aphanizomenon flos-aquae str. 1tu26s2 AJ6304
EU157987.1 gg_id:348194 Aphanizomenon flos-aquae str. A8 EU1579
FJ830571.1 gg_id:575863 Anabaena circinalis str. CENA191 FJ8305
AF317632.1 gg_id:28360 Aphanizomenon flos-aquae str. NIES81 AF3176
EU157997.1 gg_id:355112 Aphanizomenon flos-aquae str. AFA-6 EU1579
AJ293105.1 gg_id:20833 Anabaena solitaria str. 82 AJ2931
GU434227.1 gg_id:525004 Anabaena sedovii str. ACCS 058 GU434
AJ630425.1 gg_id:107974 Anabaena mucosa str. 1tu35s5 AJ6304
AJ630440.1 gg_id:107991 Anabaena spiroides str. 1tu39s17 AJ6304
AJ293112.1 gg_id:40671 Anabaena crassa str. 215 AJ2931
AB093488.1 gg_id:82666 Anabaena planctonica NIES-810 str. NIES 810 NIES-810 AB0934
AF247590.1 gg_id:38208 Anabaena flos-aquae str. AWQC112D AF2475
AF247573.1 gg_id:23978 Anabaena circinalis str. AWQC150A AF2475
AY354194.1 gg_id:101150 Aphanizomenon gracile str. LMECYA40 AY3541
AJ293118.1 gg_id:43523 Anabaena spiroides str. PMC9702 AJ2931
EU340226.1 gg_id:256707 on Aquatic Macrophytes Geothermally Active Area Sedge Bay Yellowstone Lake WY EU3402
FJ592868.1 gg_id:511684 Fumarole-supported islands biodiversity within hyperarid -elevation landscape on Pu FJ5928
AJ781148.1 gg_id:110881 Nodularia sphaerocarpa str. UTEX B 2093 AJ7811
AJ781144.1 gg_id:110114 Nodularia sphaerocarpa str. Fae19 AJ7811
AF268023.1 gg_id:51799 Nodularia spumigena str. PCC73104 AF2680
AF268006.2 gg_id:37800 Nodularia spumigena str. L575 AF2680
AY038034.1 gg_id:20340 Nodularia spumigena str. PCC 9350 AY0380
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DQ185257.1 gg_id:148513 Nostoc punctiforme str. SAG 69.79 DQ185
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AB325714.1 gg_id:310463 Nostoc cf. commune str. KG-54 AB3257
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DQ234824.1 gg_id:143784 Anabaena flos-aquae str. UTEX LB2391 DQ234
DQ185223.1 gg_id:148113 Nostoc commune '0'Brien 02011101' DQ185
EU178144.1 gg_id:256672 Nostoc sphaeroides str. HBHF0604 EU178
DQ234825.1 gg_id:142304 Anabaena flos-aquae str. UTEX LB2557 DQ234
FJ592873.1 gg_id:554414 Fumarole-supported islands biodiversity within hyperarid -elevation landscape on Pu FJ5928
DQ185226.1 gg_id:148337 Nostoc sp. 'Peltigera membranacea 1 cyanobiont' DQ185
DQ185256.1 gg_id:149796 Nostoc punctiforme str. SAG 68.79 DQ185
AY218833.1 gg_id:81294 Nostoc commune str. UTEX 584 AY218
AB251860.1 gg_id:327757 Nostoc commune AB251
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AY742447.1 gg_id:101785 Nostoc sp. str. 8916 AY7424
AF506239.1 gg_id:58861 Nostoc sp. 'Peltigera pruinosa cyanobiont 14' 'Peltigera AF5062
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AB113666.1 gg_id:110233 Nostoc commune AB113
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GU396093.1 gg_id:522456 Nostoc piscinale str. BF3 GU396
AF506243.1 gg_id:58858 Nostoc sp. 'Peltigera pruinosa cyanobiont 18' 'Peltigera AF5062
AB428654.1 gg_id:331170 Nostoc commune AB428
AF506247.1 gg_id:58854 Nostoc sp. 'Peltigera praetextata cyanobiont 22' 'Peltigera AF5062
FJ815321.1 gg_id:542307 Microcystin Production Tripartite Cyanolichen Peltigera leucophlebia Finland clone U FJ8153
AB275349.1 gg_id:205766 Nostoc sp. str. Ni4-C1 AB2753
EU282431.1 gg_id:253266 Nostoc sp. str. 195-A21 EU2824
FJ592874.1 gg_id:532880 Fumarole-supported islands biodiversity within hyperarid -elevation landscape on Pu FJ5928
FJ592872.1 gg_id:546107 Fumarole-supported islands biodiversity within hyperarid -elevation landscape on Pu FJ5928
AF506251.1 gg_id:58852 Nostoc sp. 'Nephroma parile cyanobiont 26' 'Nephroma AF5062
AJ344563.1 gg_id:35715 Nostoc sp. DM103 str. SAG 2028 AJ3445
AB098071.1 gg_id:110216 Nostoc commune str. SO-42 AB098
AY328897.1 gg_id:99213 Nostoc sp. str. 113.5 AY328
AB088405.2 gg_id:63340 Nostoc commune str. M-13 AB088
AF506240.1 gg_id:56511 Nostoc sp. 'Peltigera venosa cyanobiont 15' 'Peltigera AF5062
AB251862.1 gg_id:311353 Nostoc commune AB2518
AJ630450.1 gg_id:108003 Nostoc ellipsosporum str. V AJ6304
AY701573.1 gg_id:103881 Anabaena flos-aquae str. NIES73 AY7015
DQ234831.1 gg_id:141547 Trichormus variabilis str. KCTC AG10178 DQ234
EF088341.1 gg_id:199561 Nostoc sp. str. CENA 107 EF0883
AY218828.1 gg_id:82104 Nostoc muscorum str. CENA61 AY218
AF160256.1 gg_id:36477 Anabaena bergii str. 283A AF1602
AF247597.1 gg_id:48640 Anabaena flos-aquae str. NRC525-17 AF2475
AF268018.1 gg_id:50096 Nodularia sphaerocarpa str. CDAC1966/93-1 AF2680

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AB325906.1 gg_id:333578 Nostoc carneum str. IAM M-35 AB3259
AF247595.1 gg_id:28828 Anabaenopsis circularis str. NIES21 AF2475
DQ897365.1 gg_id:170580 Cylindrospermum sp. A1345 DQ897
AF317629.1 gg_id:44470 Anabaena sp. str. PCC 7108 AF3176
DQ364237.1 gg_id:157669 Anabaena sp. str. SSM-00 DQ364
AY493624.1 gg_id:178988 Petalonema sp. ANT.GENTNER2.8 AY4936
AM230668.1 gg_id:198952 Tolypothrix sp. str. PCC 7415 AM230
AJ630428.1 gg_id:107978 Anabaena oscillarioides 'BO 1984/43' str. BO HINDAK 1984/43 AJ6304
AF132789.1 gg_id:136153 Cylindrospermum stagnale PCC 7417 str. ATCC 29204 AF1327
EU340175.1 gg_id:237315 on Aquatic Macrophytes Geothermally Active Area Sedge Bay Yellowstone Lake WY EU3401
AM711529.1 gg_id:268782 Nostoc calcicola str. TH2S22 AM711
GU396091.1 gg_id:515321 Anabaena torulosa str. BF1 GU396
AM711522.1 gg_id:266459 Nostoc sp. str. Al1 AM711
AJ133161.1 gg_id:24012 Nostoc sp. str. 152 AJ1331
DQ185207.1 gg_id:148662 Nostoc sp. 'Mollenhauer 1:1-067' str. Mollenhauer 1:1-067 DQ185
EF568905.1 gg_id:278305 Anabaena sp. str. XPORK15F EF5689
AY785313.1 gg_id:108357 Stigonematales cyanobacterium str. AEL04-Oct-6-03 AY7853
AB074504.1 gg_id:80820 Calothrix brevissima str. IAM M-249 AB0745
AY642569.1 gg_id:150707 and carbonate precipitation giant microbialites ly alkaline Lake Van Turkey microbiali AY6425
AB093486.1 gg_id:83776 Tolypothrix sp. str. IAM M-259 AB0934
EU022706.1 gg_id:245919 Nostoc sp. SKS8 EU0227
AF425995.1 gg_id:56651 Aphanizomenon sp. str. NH-5 AF4259
AJ781143.1 gg_id:110879 Nodularia harveyana str. Bo53 AJ7811
AB187507.1 gg_id:111394 Nostoc sp. str. YK-01 AB1875
EF516817.1 gg_id:221130 grassland soil clone FCPT534 EF5168
AY218831.1 gg_id:81241 Cylindrospermum sp. str. CENA33 AY2188
AJ544082.1 gg_id:105653 Stigonema ocellatum str. SAG 48.90 AJ5440
AM711544.1 gg_id:258214 Nostoc sp. str. Mau15 AM711
GU434226.1 gg_id:527300 Wollea saccata str. ACCS 045 GU434
AJ293110.1 gg_id:73220 Anabaena cf. cylindrica str. 133 AJ2931
AM711543.1 gg_id:267299 Nostoc sp. str. Cam2S01 AM711
FJ592869.1 gg_id:548891 Fumarole-supported islands biodiversity within hyperarid -elevation landscape on Pu FJ5928
DQ185231.1 gg_id:145091 Nodularia harveyana 'Huebel 1983/300' str. Huebel 1983/300 DQ185
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EU340174.1 gg_id:249819 on Aquatic Macrophytes Geothermally Active Area Sedge Bay Yellowstone Lake WY EU3401
AB325536.1 gg_id:318589 Rivularia sp. str. IAM M-261 AB3255
DQ532230.1 gg_id:166201 Geographical Variation Microbial Burden and Spacecraft Assembly Johnson Space C DQ532
EU009149.1 gg_id:261638 Rivularia sp. UAM 305 str. MU24 UAM-305 EU0091
FJ192908.1 gg_id:312572 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior FJ1929

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AM230684.1 gg_id:184879 Calothrix sp. str. CAL3363 AM230
AM230681.1 gg_id:179952 Calothrix sp. str. UKK3412 AM230
GU230463.1 gg_id:551391 Multilevel approach along Rio de la Plata-South Atlantic Ocean coastal water clone A GU230
EF150855.2 gg_id:185766 Brasilonema octagenarum str. UFV-OR1 EF1508
AY069954.1 gg_id:44224 Scytonema sp. str. U-3-3 AY0699
DQ486055.1 gg_id:158785 Brasilonema bromeliae str. SPC 951 DQ486
EF490447.1 gg_id:222253 Brasilonema terrestre str. CENA 116 EF4904
AJ544085.1 gg_id:106108 Symphyonemopsis sp. str. VAPOR1 AJ5440
AJ544084.1 gg_id:105960 Symphyonema sp. str. 1517 AJ5440
DQ786171.1 gg_id:253968 Fischerella sp. str. MV11 DQ786
AJ544078.1 gg_id:101565 Hapalosiphon sp. str. 804-1 AJ5440
DQ430999.1 gg_id:198758 Chlorogloeopsis sp. Greenland_4 4 DQ430
AB093489.1 gg_id:83035 Chlorogloeopsis fritschii str. PCC 6912 AB0934
AJ544080.1 gg_id:105355 Nostochopsis lobatus str. 92.1 AJ5440
AJ544081.1 gg_id:105509 Nostochopsis sp. str. 89-45 AJ5440
AY039703.1 gg_id:70960 Fischerella sp. str. CENA19 AY0397
GQ375044.1 gg_id:565214 Chroococcus sp. str. CCALA 702 GQ375
EU188123.1 gg_id:340419 Uncultivated oceanic unicellular N2-fixing cyanobacteria are picoplankton unusual 7(EU1881
AB119259.1 gg_id:93641 Aphanothece sacrum AB1192
AM258981.1 gg_id:226595 Cyanobacterium stanieri PCC 7202 str. SAG 88.79 AM258
FJ358912.1 gg_id:576348 and redox-stratified sediments marine reef sandy sediment clone AO26 FJ3589
AB039001.1 gg_id:29085 Synechocystis sp. str. PCC 6308 AB0390
GU118753.1 gg_id:563811 Threatened Corals Provide Microbial Habitats clone Mfra_B24 GU118
AJ000710.1 gg_id:3246 Euhalothece sp. 'MPI 95AH13' str. MPI 95AH13 'MPI AJ0007
AJ000709.1 gg_id:3245 Euhalothece sp. 'MPI 95AH10' str. MPI 95AH10 'MPI AJ0007
AJ000708.1 gg_id:3244 Cyanothece sp. str. PCC 7418 AJ0007
AB067577.1 gg_id:67719 Gloeothece sp. str. KO11DG AB0675
DQ357946.1 gg_id:200320 Host specificity and phylogeography Prochlorophyte Prochloron sp. obligate symbio DQ357
EF126149.1 gg_id:175235 Polyphasic unicellular cyanobacteria Graneticolobacter lagoonensis gen. sp. nov. Mic EF1261
DQ058891.1 gg_id:160743 Halothece sp. str. PCyano42 DQ058
DQ289927.1 gg_id:165105 Microbial Carbon and Nitrogen Cycling Sediments South Atlantic Bight Permeable Sh DQ289
EU249123.1 gg_id:247531 Aphanocapsa sp. str. HBC6 EU2491
AJ582391.1 gg_id:106754 Rhopalodia gibba AJ5823
AB039008.1 gg_id:28876 Stanieria cyanosphaera str. PCC 7437 AB0390
AJ781040.1 gg_id:149911 Snowella litoralis str. 0TU37s04 AJ7810
BA000022.2 gg_id:137040 Synechocystis sp. str. PCC 6803 BA0000
GQ375043.1 gg_id:566848 Synechocystis sp. str. CCALA 700 GQ375
D89033.1 gg_id:3135 Microcystis viridis str. NIES102 D89033
DQ648029.1 gg_id:163938 Microcystis viridis str. NIES-1058 DQ648
U03403.1 gg_id:3136 Microcystis aeruginosa NIES-89 str. NIES89 U03403

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AB012336.1 gg_id:3134 Microcystis novacekii TAC20 AB0123
AB012338.1 gg_id:3170 Microcystis ichthyoblabe TAC48 AB0123
FJ595698.1 gg_id:575918 Microcystis sp. str. CHAB727 FJ5956
EU541974.1 gg_id:569350 Microcystis panniformis str. MCYS-OB06 EU5419
EU541970.1 gg_id:576831 Microcystis aeruginosa str. MCYS-LB01 EU5419
AJ133171.1 gg_id:71454 Microcystis aeruginosa str. PCC 7941 AJ1331
AJ635434.1 gg_id:142200 Microcystis ichthyoblabe str. 0BB35S01 AJ6354
U40340.2 gg_id:3119 Microcystis aeruginosa PCC 7941 str. PCC7941 U40340
U03402.1 gg_id:3191 Microcystis aeruginosa PCC 7806 str. PCC7806 U03402
U40333.2 gg_id:3121 Microcystis wesenbergii NIES-107 str. NIES107 U40333
EU815063.1 gg_id:311839 Microcystis aeruginosa str. NPCD-1 EU8150
AB012340.1 gg_id:3171 Microcystis aeruginosa TAC170 AB0123
D89032.1 gg_id:3236 Microcystis aeruginosa str. NIES98 D89032
U40338.1 gg_id:3113 Microcystis aeruginosa PCC 7005 str. PCC7005 U40338
U40332.2 gg_id:3122 Microcystis viridis NIES-102 str. NIES102 U40332
D89031.1 gg_id:3114 Microcystis aeruginosa str. NIES87 D89031
D89034.1 gg_id:3237 Microcystis wesenbergii str. NIES111 D89034
EU541973.1 gg_id:553922 Microcystis novacekii str. MCYS-CH01 EU5419
AM710389.1 gg_id:236754 Radiocystis sp. str. JJ30-3 30-3 AM710
AM710384.1 gg_id:236194 Chroococcus sp. str. JJCM Chroo-M AM710
AB039007.1 gg_id:49254 Pleurocapsa sp. str. PCC 7327 AB0390
CP001291.1 gg_id:531797 Cyanothece sp. str. PCC 7424 CP0012
X78680.1 gg_id:3240 Gloeothece membranacea PCC 6501 str. PCC6501 X78680
ABVE01000002.1 gg_id:356043 Cyanothece sp. str. PCC 7822 ABVE01
X63141.1 gg_id:3253 Prochloron species X63141
DQ357947.1 gg_id:202308 Host specificity and phylogeography Prochlorophyte Prochloron sp. obligate symbio DQ357
AY845229.1 gg_id:110862 Synechocystis sp. clone 36P1 AY8452
AB003166.1 gg_id:3232 Spirulina subsalsa str. M-223 AB0031
AF329394.1 gg_id:56680 Spirulina subsalsa str. FACHB351 AF3293
AF445678.1 gg_id:74772 travertine hot spring clone SM1D12 AF4456
GQ441342.1 gg_id:565917 and dynamic mat present vs. active nitrogen-fixing microorganisms marine microbia GQ441
GQ441247.1 gg_id:556204 and dynamic mat present vs. active nitrogen-fixing microorganisms marine microbia GQ441
AF091109.1 gg_id:3233 Spirulina sp. str. P7 AF0911
AJ639890.1 gg_id:141039 Spirulina major str. 0BB36S18 AJ6398
Y18789.1 gg_id:39534 Halospirulina sp. 'MPI S3' str. MPI S3 Y18789
AF448074.1 gg_id:62924 Synechococcus sp. str. UH7 AF4480
DQ455751.1 gg_id:156826 Synechococcus sp. 'Salton Sea' str. Salton Sea DQ455
AB003164.1 gg_id:3125 Oscillatoria rosea str. M-220 AB0031
FJ203524.1 gg_id:305855 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h FJ2035

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AF132784.1 gg_id:136187 Gloeocapsa sp. str. PCC 73106 AF1327
GQ340127.1 gg_id:587573 Prokaryotic Marathonas Reservoir Greece water column clone B07-41-BAC GQ340
EF429517.2 gg_id:210875 Thermophilic microbial mats tropical geothermal location display pronounced season EF4295
AY493599.1 gg_id:190488 Chondrocystis sp. ANT.LH59B.1 AY4935
EU409845.1 gg_id:554144 microbial fouling painted and unpainted structures outdoor concrete surfaces clone EU4098
EF522288.1 gg_id:227059 Endolithic Microbial Ecosystems Rocky Mountain endolithic sandstone clone FQSS06 EF5222
GQ129887.1 gg_id:427017 Genetic inventory 'JPL-SAF' during MSL mission spacecraft assembly clean room floc GQ129
FJ595625.1 gg_id:536201 rock Black Canyon New Mexico: and Geochemistry varnish covered rocks clone V22_ FJ5956
DQ471449.1 gg_id:159374 unicellular thermophilic cyanobacterium tBTRCCn 23 DQ471
EU134272.1 gg_id:250650 tallgrass prarie soil clone FFCH11821 EU134
AJ344553.1 gg_id:34564 Chroococcidiopsis sp. BB82.3 str. SAG 2024 BB82.3 AJ3445
DQ471448.1 gg_id:159142 unicellular thermophilic cyanobacterium tBTRCCn 28 DQ471
DQ914865.2 gg_id:172573 Chroococcidiopsis sp. str. CC3 DQ914
DQ532182.1 gg_id:167334 Geographical Variation Microbial Burden and Spacecraft Assembly Johnson Space C DQ532
EF032781.1 gg_id:182352 cyanobacterial mat in lava cave clone HAVOmat11 EF0327
AJ344555.1 gg_id:35765 Chroococcidiopsis sp. BB96.1 str. SAG 2026 BB96.1 AJ3445
FJ595626.1 gg_id:560231 rock Black Canyon New Mexico: and Geochemistry varnish covered rocks clone V23_ FJ5956
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FJ890996.1 gg_id:540977 Hypolithic structure hyperaird core Atacama Desert quartz clone AY1_7 FJ8909
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GQ214113.1 gg_id:583323 China loess clone P913 GQ214
DQ914863.2 gg_id:166256 Chroococcidiopsis sp. str. CC1 DQ914
GQ092934.1 gg_id:429375 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw407a02 GQ092
GQ087815.1 gg_id:386885 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw359a0 GQ087
AB177177.1 gg_id:129771 seafloor methane hydrate clone ODP1230B22.23 AB177
GQ002512.1 gg_id:507150 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbu GQ002
DQ451473.1 gg_id:156813 forest soil clone FAC34 DQ451
X78681.1 gg_id:3207 Pleurocapsa sp. PCC 7516 str. PCC7516 X78681
AB039009.1 gg_id:46080 Stanieria sp. str. PCC 7301 AB039
AJ344556.1 gg_id:24838 Chroococcidiopsis sp. str. CCMP1489 AJ3445
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AJ344562.1 gg_id:45178 Myxosarcina sp. str. SAG 30.84; PCC 7325 AJ3445
FJ358911.1 gg_id:534175 and redox-stratified sediments marine reef sandy sediment clone SO78 FJ3589
EF208682.1 gg_id:200249 Vertical and horizontal structure microbial sandy carbonate sediment clone CI5cm.B1 EF2086
AB115964.1 gg_id:244883 Crinalium epipsammum str. SAG 22.89 AB115
FJ356670.1 gg_id:535815 Lyngbya majuscula str. PNG6-221 FJ3566
GQ231522.1 gg_id:587135 Lyngbya majuscula str. PAL-8-17-08-2 GQ231
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FJ147304.1 gg_id:343887 Lyngbya polychroa str. PNG6-45 FJ1473

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EU315909.1 gg_id:248466 Lyngbya majuscula str. 3L	EU315
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FJ151527.1 gg_id:344676 Lyngbya majuscula str. 3L B	FJ1515
FJ147302.1 gg_id:343319 Lyngbya bouillonii str. PNG6-41	FJ1473
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EF432315.1 gg_id:271081 Arthrospira platensis str. Sp-12	EF4323
DQ393279.1 gg_id:153397 Arthrospira platensis str. NIES 39	DQ393
EF564663.1 gg_id:224023 Arthrospira maxima str. FACHB438	EF5646
EF222475.1 gg_id:207971 Arthrospira platensis str. CG590	EF2224
DQ279773.1 gg_id:144559 Spirulina platensis str. Sp-4	DQ279
EF432311.1 gg_id:258261 Arthrospira platensis str. Sp-4	EF4323
AY575933.1 gg_id:106421 Phormidium cf. terebriformis str. AB2002/07	AY575
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EF432317.1 gg_id:262022 Arthrospira platensis str. Sp-15	EF4323
DQ279769.1 gg_id:141269 Spirulina platensis str. Sp-9	DQ279
EF432319.1 gg_id:265464 Arthrospira platensis str. Sp-17	EF4323
EF154084.1 gg_id:241791 Geitlerinema sp. str. W-1	EF1540
AF132780.1 gg_id:136142 Geitlerinema sp. str. PCC 7105	AF1327
EU244875.1 gg_id:247111 Oscillatoria nigroviridis str. 3LOSC	EU2448
EU249124.1 gg_id:252166 Hydrocoleum lyngbya subsp. str. HBC7	EU2491
AF132933.1 gg_id:74791 Oscillatoria sancta str. PCC 7515	AF1329
GQ441298.1 gg_id:560803 and dynamic mat present vs. active nitrogen-fixing microorganisms marine microbia	GQ441
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EF654034.1 gg_id:278990 Microcoleus chthonoplastes GNP5	EF6540
EF654062.1 gg_id:278966 Microcoleus vaginatus CJI-U2-KK1	EF6540
EF580970.1 gg_id:279122 Survey Microbial Freshwater Calcareous Mats freshwater calcareous mat clone CM1	EF5809
DQ493874.1 gg_id:159802 Phormidium autumnale str. Ant-Ph68	DQ493
FJ866615.1 gg_id:567709 submerged sinkhole ecosystems sediment clone AM-20-10	FJ8666
AF218373.1 gg_id:51024 Phormidium subfuscum str. UTCC474	AF2183
DQ181701.1 gg_id:163111 Biogeographical and ecological ranges benthic cyanobacteria East Antarctic lakes mi	DQ181
DQ493873.2 gg_id:160601 Phormidium autumnale str. Arct-Ph5	DQ493
FJ866616.1 gg_id:587732 submerged sinkhole ecosystems sediment clone TS-36-39	FJ8666
FJ866617.1 gg_id:509463 submerged sinkhole ecosystems sediment clone AM-20-36	FJ8666
GQ131852.1 gg_id:373820 Oscillatoria sp. str. Ck2	GQ131
FJ516843.1 gg_id:533121 semiarid 'Tablas de Daimiel National Park' wetland (Central Spain) unravelled lower s	FJ5168
DQ917838.1 gg_id:224272 Microbial profiles bleached and wild-type Muricea elongata Oscillatoria clone BME1	DQ917

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DQ129355.1 gg_id:137925 microarray level air two cities Texas urban aerosol clone AKIW1097 DQ129
EF654090.1 gg_id:278136 Microcoleus paludosus str. SAG 1449-1a EF6540
AJ630647.1 gg_id:99755 Oscillatoriales cyanobacterium str. UVFP3 AJ6306
AB003167.1 gg_id:3094 Phormidium ambiguum str. M-71 AB0031
EF516628.1 gg_id:225760 grassland soil clone FCPP724 EF5166
GQ055321.1 gg_id:443892 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1113g(GQ055
AY493600.1 gg_id:194616 Phormidium pseudopristleyi ANT.ACEV5.3 AY4936
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EF654061.1 gg_id:278544 Pseudanabaenaceae cyanobacterium ANP1-KK1 EF6540
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FJ230826.1 gg_id:323974 Microclimate and limits photosynthesis cyanobacteria Northern Australia hypolithic s FJ2308
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AB074507.1 gg_id:80934 Planktothrix agardhii str. IAM M-244 AB0745
FJ184392.1 gg_id:509807 Planktothrix mougeotii str. HAB002 FJ1843
AB045966.1 gg_id:55562 Planktothrix pseudagardhii str. T19-6'-8 AB0459
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AB039021.1 gg_id:36962 Symploca atlantica str. PCC 8002 AB0390
AY032932.1 gg_id:45181 Symploca sp. str. VP642a AY0329
GU118223.1 gg_id:577015 Threatened Corals Provide Microbial Habitats clone Dstr_K13 GU118
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AABK04000002.1 gg_id:137926 Trichodesmium erythraeum str. IMS101 AABK0
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AF013028.1 gg_id:3054 Trichodesmium contortum AF0130
AF013029.1 gg_id:3053 Trichodesmium tenue AF0130

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AB039013.1 gg_id:40937 Lyngbya aestuarii str. PCC 7419 AB039(
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FJ230829.1 gg_id:355265 Microclimate and limits photosynthesis cyanobacteria Northern Australia hypolithic s FJ2308
FJ595531.1 gg_id:558201 rock Black Canyon New Mexico: and Geochemistry rocks no varnish clone NV43_2f1 FJ5955
DQ847441.1 gg_id:167052 human forearm skin clone GL2-53 DQ847
GQ094019.1 gg_id:442222 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ094
AJ583205.1 gg_id:94666 radioactive site ground water clone S15D-MN45 AJ5832
AB487357.1 gg_id:592973 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNIR0(AB487
AY921818.1 gg_id:112746 farm soil clone AKYG461 AY9218
EU276547.1 gg_id:368210 -DGGE and Approaches Analyze Effect Agricultural Practices on Soil agricultural soil c EU2765
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EU196364.1 gg_id:369012 filamentous cyanobacterium str. FLK9 EU1963
DQ786167.1 gg_id:257398 filamentous cyanobacterium str. LLi71 DQ786
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AY493612.1 gg_id:199630 Leptolyngbya frigida ANT.LH52B.3 AY4936
AY493590.1 gg_id:188868 Leptolyngbya antarctica ANT.FIRELIGHT.1 AY4935
AJ133106.1 gg_id:38561 Oscillatoria sp AJ1331
DQ181680.1 gg_id:172516 Biogeographical and ecological ranges benthic cyanobacteria East Antarctic lakes mi DQ181
EU022730.1 gg_id:240402 Calothrix sp. KVSF5 EU022
EU255703.1 gg_id:568166 serpentinized spring water freshwater mesophilic microbial mat clone Mat-CYANO-S EU255
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DQ471447.1 gg_id:159383 filamentous thermophilic cyanobacterium tBTRCCn 407 DQ471
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EF522259.1 gg_id:223924 Endolithic Microbial Ecosystems Rocky Mountain endolithic sandstone clone FQSS03 EF5222
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EU753636.1 gg_id:348181 modern freshwater stromatolites Ruidera Pools Natural Park Spain dry stromatolite EU753
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DQ181740.1 gg_id:170530 Biogeographical and ecological ranges benthic cyanobacteria East Antarctic lakes mi DQ181
EU196365.1 gg_id:359531 filamentous cyanobacterium str. 72-1 EU1963
EF126240.1 gg_id:274997 Phototrophic microbial build laminated Fe-formations on Sulawesi Indonesia mesoph EF1262
AF445691.1 gg_id:28685 travertine hot spring clone SM1F09 AF4456

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AB039016.1 gg_id:16700 Pseudanabaena sp. str. PCC 6802 AB039
GU117964.1 gg_id:563947 Threatened Corals Provide Microbial Habitats clone Acer_M19 GU117
EF032779.1 gg_id:189054 cyanobacterial mat in lava cave clone HAVOmat08 EF0327
AJ630648.1 gg_id:99912 Oscillatoriales cyanobacterium str. UVFP2 AJ6306
FJ444635.1 gg_id:567570 Cotton Rhizosphere cotton rhizosphere clone 2h-1 FJ4446
EU255708.1 gg_id:559534 serpentinized spring water freshwater mesophilic microbial mat clone Mat-CYANO-S EU255
AY493984.1 gg_id:136196 Fingerprinting aggregates soil clone 349 AY4939
GU118152.1 gg_id:577676 Threatened Corals Provide Microbial Habitats clone Dstr_B02 GU118
AY151728.1 gg_id:99678 microbial mat clone Fr121 AY1517
GQ487938.1 gg_id:554238 Microbial metal soil polluted heavy metals clone T7-132 GQ487
EF654073.1 gg_id:278028 Pseudanabaenaceae cyanobacterium PBP-U-KK1 EF6540
AB488091.1 gg_id:535035 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSSUR0 AB488
DQ431005.1 gg_id:190474 phototrophic microbial mats Arctic springs (Greenland) hot spring DQ431
FJ933259.1 gg_id:539884 Leptolyngbya sp. FYG FJ9332
AF448079.1 gg_id:62919 Synechococcus sp. str. IR11 AF448
FJ202607.1 gg_id:344914 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2026
NC_009925.1 gg_id:238741 Acaryochloris marina str. MBIC11017 NC_00
AB486797.1 gg_id:554203 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCOR0 AB486
FJ902633.1 gg_id:570149 phreatic limestone sinkholes northeastern Mexico biofilm 1m deep hydrothermal ver FJ9026
AM710386.1 gg_id:249359 Acaryochloris sp. str. JJ7-5 7-5 AM710
EU340178.1 gg_id:237480 on Aquatic Macrophytes Geothermally Active Area Sedge Bay Yellowstone Lake WY EU340
AF076162.1 gg_id:3261 Antarctic LB3-80 clone AF076
EU805341.1 gg_id:334597 It's all ranking aquatic 250 miles Panama City clone 6C233345 EU805
EU703363.1 gg_id:455236 lakes on Eastern Tin Plateau freshwater lake altitude 4298 masl clone XZTSH29 EU703
FJ999597.1 gg_id:426115 sponge Haliclona simulans South China Sea clone B16 FJ9995
FJ381976.1 gg_id:582549 Potentially pathogenic and air stem cell transplant winter hospital shower water BMT FJ3819
AF448063.1 gg_id:62935 Synechococcus sp. str. UBR AF448
EU703182.1 gg_id:558485 taxon richness -altitude lakes eastern tin plateau predominance Bacteroidetes and S EU703
EF574289.1 gg_id:232723 site S25 near Coco's Island marine clone S25_633 EF5742
GU061586.1 gg_id:557211 and function microbial mesoscale eddy perturbations South China Sea clone CE2-5m GU061
EF575274.1 gg_id:227868 site S25 near Coco's Island marine clone S25_1618 EF5752
EU237304.1 gg_id:236472 Genes transcripts Eastern and Western Equatorial North Atlantic Ocean microbial as EU237
FJ382039.1 gg_id:512103 Potentially pathogenic and air stem cell transplant winter hospital shower water BMT FJ3820
GU305759.1 gg_id:550168 Research on changes structure during algae outbreak oligotrophic lakes (YangHe res GU305
EF574827.1 gg_id:235076 site S25 near Coco's Island marine clone S25_1171 EF5748
EU237266.1 gg_id:250183 Genes transcripts Eastern and Western Equatorial North Atlantic Ocean microbial as EU237
FJ382047.1 gg_id:583334 Potentially pathogenic and air stem cell transplant winter hospital shower water BMT FJ3820
GU119261.1 gg_id:578434 Threatened Corals Provide Microbial Habitats reef water clone Reef_B17 GU119
FJ497746.1 gg_id:581946 Synechococcus sp. str. KORDI-36 FJ4977

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EU802974.1 gg_id:355538 It's all ranking aquatic Northeast Colon Panama clone 4C230373 EU802
AF448070.1 gg_id:62928 Synechococcus sp. str. PS845 AF448
EU237323.1 gg_id:257932 Genes transcripts Eastern and Western Equatorial North Atlantic Ocean microbial as: EU237
EU703496.1 gg_id:375870 lakes on Eastern Tin Plateau freshwater lake altitude 4279 masl clone XZZLH78 EU703
EU802573.1 gg_id:342607 It's all ranking aquatic Northeast Colon Panama clone 4C229920 EU802
EF574201.1 gg_id:233862 site S25 near Coco's Island marine clone S25_545 EF574
EF574424.1 gg_id:229355 site S25 near Coco's Island marine clone S25_768 EF574
GU118310.1 gg_id:581829 Threatened Corals Provide Microbial Habitats clone Dstr_D01 GU118
AF330250.1 gg_id:53206 Synechococcus sp. str. LBB3 AF330
EU703334.1 gg_id:409409 lakes on Eastern Tin Plateau freshwater lake altitude 4298 masl clone XZTSH6 EU703
EF573792.1 gg_id:234682 site S25 near Coco's Island marine clone S25_136 EF573
AJ347056.1 gg_id:60158 sponge clone TK09 AJ347
EU237326.1 gg_id:242635 Genes transcripts Eastern and Western Equatorial North Atlantic Ocean microbial as: EU237
EF572237.1 gg_id:232120 Coco's Island site 23 marine clone S23_336 EF572
AM710354.1 gg_id:227959 Cyanobium sp. str. JJ19B5 19-B5 AM710
EF574923.1 gg_id:232787 site S25 near Coco's Island marine clone S25_1267 EF574
NC_008319.1 gg_id:161964 Synechococcus sp. str. CC9311 NC_00
EU703246.1 gg_id:398037 lakes on Eastern Tin Plateau oligosaline lake altitude 4718 masl clone XZNMC20 EU703
FJ382144.1 gg_id:558480 Potentially pathogenic and air stem cell transplant summer hospital shower water BM FJ382
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EU802507.1 gg_id:339262 It's all ranking aquatic Northeast Colon Panama clone 4C229843 EU802
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EU237285.1 gg_id:251143 Genes transcripts Eastern and Western Equatorial North Atlantic Ocean microbial as: EU237
FJ437825.1 gg_id:566422 Benthic okenone production Fayetteville New York Green Lake chemocline 20.5 m wa FJ437
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AY884059.1 gg_id:140190 Synechococcus sp. str. TS-104 AY884
AY884052.1 gg_id:139842 Synechococcus sp. str. JA-3-3Ab AY884
AF132773.1 gg_id:3159 Synechococcus sp. str. C9 AF132
EF205469.1 gg_id:216560 among geographically regions central Tibet geothermal spring mat clone YCB43 EF205
DQ471441.1 gg_id:159447 filamentous thermophilic cyanobacterium tBTRCCn 301 DQ471
EU000446.1 gg_id:238052 unculutured clones (IW) Western Ghats region IRDE water clone IWENVB17 EU000
EU091541.1 gg_id:246617 clones IRDE (IW) Western Ghats region India water clone IWENVC5 EU091

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NC_004113.1 gg_id:55947 Thermosynechococcus elongatus BP-1 NC_00
AF448081.1 gg_id:62920 Synechococcus sp. str. PCC 6312 AF448
AF448078.1 gg_id:62921 Synechococcus sp. str. PCC 7336 AF448
FJ425596.1 gg_id:361402 communnities healthy and diseased colonies Caribbean coral Montastrea faveolata c FJ4255
AF216946.1 gg_id:40082 Synechococcus sp. PCC 7902 str. PCC7902 AF216
EF438248.1 gg_id:215715 Temporal spatial variability epilithic Bacteroidetes and Cyanobacteria forested river c EF4382
FJ999729.1 gg_id:378810 Caldithrix sp. str. MC FJ9997
AF323775.1 gg_id:53652 benzoate-degrading consortium clone BA059 AF323
FJ484504.1 gg_id:550182 microbial autonomous rover world's deepest phreatic sinkhole wall biomat El Zacator FJ4845
EU487910.1 gg_id:565473 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU487
AB177153.1 gg_id:130950 seafloor methane hydrate clone ODP1230B14.21 AB177
DQ811935.1 gg_id:164927 mangrove soil clone MSB-4E9 DQ811
AF286031.1 gg_id:31738 saltmarsh clone LCP-26 AF286
EU592472.1 gg_id:543260 Seasonal changes Salton Sea hypersaline sediment clone SSS10A EU592
DQ811933.1 gg_id:171914 mangrove soil clone MSB-4A2 DQ811
AJ515882.1 gg_id:57548 Deferribacter abyssi str. JR AJ5158
AP011529.1 gg_id:521936 Deferribacter desulfuricans str. SSM1 AP011
FN356326.1 gg_id:544906 Prokaryotic structure sulfate reducer activity -temperature reservoirs and without ni FN356
U75602.1 gg_id:1863 Deferribacter thermophilus str. BMA1 U7560
FN356319.1 gg_id:568730 Prokaryotic structure sulfate reducer activity -temperature reservoirs and without ni FN356
EU407777.1 gg_id:263407 Deferribacter sp. str. SL50 EU407
AB364234.1 gg_id:350097 Calditerrivibrio nitroreducens str. Yu37-1 (= NBRC 101217) AB364
AF220344.1 gg_id:74231 Flexistipes sp. vp180 AF2203
FJ901100.1 gg_id:563173 Polymorphism microbial reservoirs water cut stage oil field clone Z-47 FJ9011
FJ900968.1 gg_id:509886 Polymorphism microbial reservoirs water cut stage oil field clone G-6 FJ9009
AJ299402.1 gg_id:25709 Geovibrio agilis AJ2994
AY387671.1 gg_id:95739 Mucispirillum schaedleri str. UNSW I23 AY387
EF097086.1 gg_id:186413 mouse cecum clone SWPT18_aaa01c01 EF097
AF146526.1 gg_id:43329 Denitrovibrio acetiphilus AF146
NR_029235.1 gg_id:549883 Dictyoglomus thermophilum str. H-6-12; DSM 3960 NR_02
CP001251.1 gg_id:526493 Dictyoglomus turgidum str. DSM 6724 CP001
CP001055.1 gg_id:278168 Elusimicrobium minutum str. Pei191 CP001
AB198564.1 gg_id:135579 termite gut wall fraction clone RsW02-112 AB198
FJ879997.1 gg_id:447372 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8799
FJ879844.1 gg_id:406473 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8798
FJ825512.1 gg_id:552696 Microbial during start-up mesophilic biogas plant clone 2B_BS5_13 FJ8255
AJ583207.1 gg_id:94589 radioactive site ground water clone S15B-MN11 AJ5832
AB426236.1 gg_id:260316 -situ identification study benzene-degrading s under methanogenic condition anaerc AB426
DQ837258.1 gg_id:241732 Archaeal and pristine National Park Spain Donana coastal aquifer clone 49S1_2B_60 DQ837
AF407708.1 gg_id:60591 Great Artesian Basin clone G58 AF407

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s__Fibrobacter succinogenes	53005

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

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s__Alicyclobacillus disulfidooxidans	49536
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AB275500.1 gg_id:163075 Fibrobacter succinogenes str. OS118 AB2755
AB275485.1 gg_id:170693 Fibrobacter succinogenes str. AS211 AB2754
EU473538.1 gg_id:290276 Somali wild ass feces clone WA_aaa04b07 EU4735
AJ496186.1 gg_id:63459 Fibrobacter succinogenes str. HM2 AJ4961
EU459511.1 gg_id:288501 capybara feces clone CAP_aah98h04 EU4595
EU381839.1 gg_id:260857 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU3818
EU463562.1 gg_id:293363 domesticated horse feces clone horsem_aai96b08 EU4635
EU473558.1 gg_id:301021 Somali wild ass feces clone WA_aaa01h11 EU4735
AB275496.1 gg_id:165381 Fibrobacter succinogenes str. OS102 AB2754
AB275498.1 gg_id:164826 Fibrobacter succinogenes str. OS112 AB2754
AB275501.1 gg_id:173599 Fibrobacter succinogenes str. OS119 AB2755
EU473606.1 gg_id:289079 Somali wild ass feces clone WA_aaa01d09 EU4736
EU779396.1 gg_id:329327 Somali Wild Ass feces clone WA_aaa03d04 EU7793
GU303627.1 gg_id:576830 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU303
EF190824.1 gg_id:245678 Evidence occurrence members genus Fibrobacter sites landfill clone Brom F11 EF1908
AM982635.2 gg_id:278133 microbial and slurry pig saw dust spent bedding clone PISD-AJG03 AM982
EF190823.1 gg_id:242362 Evidence occurrence members genus Fibrobacter sites landfill clone Brom F10 EF1908
EF190825.1 gg_id:251106 Evidence occurrence members genus Fibrobacter sites landfill clone Brom F7 EF1908
AB192084.1 gg_id:141091 termite gut homogenate clone M1PT4-02 AB1920
EF454459.2 gg_id:219116 termite hindgut clone 290cost002-P3L-2166 EF4544
AB255935.1 gg_id:170934 Localization Cell Morphologies Members Candidate TG3 and Subphylum Phylum Fibr AB2559
AB255932.1 gg_id:172833 Localization Cell Morphologies Members Candidate TG3 and Subphylum Phylum Fibr AB2559
AB243279.1 gg_id:147943 acetone-preserved termite gut clone M2PB4a-059 AB2432
AB192090.1 gg_id:142085 termite gut homogenate clone M2PT2-85 AB1920
AB042056.1 gg_id:38100 Alicyclobacillus acidocaldarius str. ATCC 27009T AB0420
EU740980.1 gg_id:352119 Alicyclobacillus acidocaldarius str. DT-M7 EU7409
AY573797.1 gg_id:115084 Alicyclobacillus acidoterrestris str. ATCC 49025 AY5737
AB042058.1 gg_id:18608 Alicyclobacillus acidoterrestris str. DSM 3923 AB0420
X51928.1 gg_id:14346 Alicyclobacillus cycloheptanicus X51928
AB233323.1 gg_id:151272 Alicyclobacillus disulfidooxidans AB2333
AJ133633.1 gg_id:46515 Alicyclobacillus hesperidum str. FR-11 AJ1336
AJ564766.1 gg_id:102873 New record moss thermophilic species and physico-chemic al properties geothermal AJ5647
AB084128.1 gg_id:67142 Alicyclobacillus sendaiensis str. NTAP-1 AB0841
AJ133634.1 gg_id:30162 Alicyclobacillus sp. str. FR-3 AJ1336
AB059665.1 gg_id:38406 Alicyclobacillus acidocaldarius subsp. genomic species 1 str. DSM 455 AB0596
EU680819.1 gg_id:283968 Alicyclobacillus sp. str. AYTae-7 EU6808
AM749794.1 gg_id:235845 Alicyclobacillus sp. K1 AM749
EU680818.1 gg_id:284287 Alicyclobacillus sp. str. ATSae-10 EU6808
AB004581.1 gg_id:14337 Alicyclobacillus sp. str. KHA-31 AB0045
DQ838045.1 gg_id:170052 Alicyclobacillus acidocaldarius Tc-12-31 DQ838
AB004580.1 gg_id:14336 Alicyclobacillus sp. str. MIH-2 AB0045

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Y07608.2 gg_id:14393 Drentse grassland soil clone DA113 Y07608
DQ464146.1 gg_id:158365 acid mine drainage clone D1-23 DQ464
EU571186.1 gg_id:258187 eubacterium sp. str. 23-2 EU571
EU282873.1 gg_id:236165 Alicyclobacillus sp. str. Talven1 EU282
AB264021.1 gg_id:219729 Alicyclobacillus sp. str. S-TAB AB264
AY911435.1 gg_id:122869 rock interior clone NEC02064 AY911
AM749773.1 gg_id:255809 Isolation ing candidate division soils New Zealand steam-affected geothermal soil AM749
AB264024.1 gg_id:218349 Alicyclobacillus sp. str. 4-A336 AB264
AB264025.1 gg_id:225783 Alicyclobacillus sp. str. 5A239-2O AB264
AJ617864.1 gg_id:110806 oxic-anoxic interphase flooded paddy soil clone D282111 AJ6178
DQ444975.2 gg_id:157680 Tumebacillus permanentifrigoris str. Eur1 9.5 DQ444
NR_028637.1 gg_id:571645 Alicyclobacillus acidiphilus str. TA-67; DSM 14558 NR_02
NR_024753.1 gg_id:534871 Alicyclobacillus herbarius str. CP-1; DSM 13609 NR_02
EU638395.1 gg_id:324634 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU638
Z21979.1 gg_id:14348 Alicyclobacillus tolerans str. K1 Z21979
AM749772.1 gg_id:249259 Isolation ing candidate division soils New Zealand steam-affected geothermal soil AM749
EU137838.1 gg_id:247268 Alicyclobacillus ferrooxidans str. TC-34 EU137
AB369003.1 gg_id:559429 and microbial oils produced Asia petroleum crude oil (Arabian Extra light) clone PT-A AB369
DQ129298.1 gg_id:138337 microarray level air two cities Texas urban aerosol clone AKIW802 DQ129
AF137502.2 gg_id:71417 Alicyclobacillus tolerans str. K1 AF137
EU137837.1 gg_id:253241 Alicyclobacillus ferripilum str. TC-71 EU137
NR_024801.1 gg_id:558567 Alicyclobacillus pomorum str. 3A; DSM 14955 NR_02
DQ999995.1 gg_id:207114 Isolation microorganisms undisturbed argillaceous formation under evaluation repo DQ999
EU360507.1 gg_id:263805 pilot biological ferrous iron oxidation mine water treatment plant clone W-Z-135 EU360
AB487996.1 gg_id:579786 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSSUR0 AB487
FM179383.1 gg_id:306748 Alicyclobacillus sp. str. ZJ-6 FM179
AB052970.1 gg_id:29823 this relatively close relationship to Alicyclobacillus and Sulfobacillus. However there is AB052
AJ617865.1 gg_id:110321 oxic-anoxic interphase flooded paddy soil clone D02302 AJ6178
EU419142.1 gg_id:264263 Microbial and ecology selected andesitic hydrothermal acidic hydrothermally modifi EU419
EU282871.1 gg_id:252896 Alicyclobacillus sp. str. CLA EU282
GU001882.1 gg_id:564204 Alkalibacillus sp. str. PL203 GU001
AJ238041.1 gg_id:26016 Bacillus haloalkaliphilus str. DSM 5271T AJ238
EU874387.1 gg_id:350384 Alkalibacillus sp. str. ISL-17 EU874
X72876.1 gg_id:14602 Bacillus sp str. DSM5271 X72876
AB264528.1 gg_id:164233 Alkalibacillus silvaisolus str. BM2 AB264
GU083678.1 gg_id:579049 Microorganism Xiarinur soda lake sediment clone x95 GU083
AJ865469.1 gg_id:109033 Bacillus arseniciselenatis str. DSM 15340 AJ8654
EU143680.1 gg_id:239928 Bacillus alkalidiazotrophicus str. MS 6 EU143
FJ430064.1 gg_id:368030 Anoxybacillus sp. E243 FJ4300
AY770577.1 gg_id:108674 Anoxybacillus flavithermus str. KWF-1 AY770
FJ430004.1 gg_id:359437 Anoxybacillus sp. A402b FJ4300

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FJ430018.1 gg_id:368045 Anoxybacillus sp. D36
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AY248707.1 gg_id:84072 Anoxybacillus gonensis str. A4
AY248708.1 gg_id:83767 Anoxybacillus gonensis str. A7
AY248706.1 gg_id:85315 Anoxybacillus gonensis str. A2
AY122325.1 gg_id:64346 Anoxybacillus gonensis str. G2T
AF004589.1 gg_id:14519 Anoxybacillus flavithermus str. DSM2641
AB234213.1 gg_id:154371 Anoxybacillus pushchinoensis str. -1
AY248709.1 gg_id:84979 Anoxybacillus kestanbolensis str. K1
FJ808726.1 gg_id:529278 Anoxybacillus gonensis str. P89
GQ342689.1 gg_id:583473 Anoxybacillus flavithermus str. HBB-134
Z26932.1 gg_id:14518 Anoxybacillus flavithermus str. DSM 2641
AF001962.1 gg_id:14523 Anoxybacillus flavithermus AB03
FJ430043.1 gg_id:359099 Anoxybacillus sp. D486
FJ430012.1 gg_id:362918 Geobacillus sp. C161ab
DQ452021.1 gg_id:223469 Anoxybacillus sp. FB7
FJ808725.1 gg_id:523983 Anoxybacillus gonensis str. P39
FJ430059.1 gg_id:363871 Anoxybacillus sp. E184aa
NR_024690.1 gg_id:567725 Bacillus carboniphilus str. JCM9731
GQ389780.1 gg_id:573608 Bacillus acidicola str. TSAS-1
AF547209.1 gg_id:71698 Bacillus acidogenesis str. 105-2
GU263833.1 gg_id:549331 Bacillus sp. str. HB09009
AF140005.1 gg_id:14502 Bacillus sp. str. ML-172
AY669375.1 gg_id:101461 Bacillus sp. str. SFB
EU432565.1 gg_id:269646 Bacillus sp. str. 10089
EU818841.1 gg_id:307283 Bacillus sp. str. FR
NR_029077.1 gg_id:580042 Bacillus algicola str. F12; KMM 3737
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AY462196.1 gg_id:110378 Bacillus subtilis str. DF3
EF473134.1 gg_id:227033 Bacillus subtilis qd382
AB301017.1 gg_id:244529 Bacillus amyloliquefaciens str. GH14
EF666489.1 gg_id:253477 Bacillus subtilis str. 0G
AY867792.1 gg_id:110184 Bacillus subtilis str. C2

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DQ177319.1 gg_id:154463 Bacillus amyloliquefaciens str. ES-2
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EU586781.1 gg_id:275467 Bacillus amyloliquefaciens str. MZ-15
AF058766.1 gg_id:14746 Bacillus subtilis str. TB11
EU826022.1 gg_id:330407 Bacillus subtilis str. CDB10
FJ435222.1 gg_id:358462 Bacillus licheniformis str. 11
EU056571.1 gg_id:251864 Bacillus subtilis SK1
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EF523474.1 gg_id:225817 Bacillus subtilis str. BSD-2
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EU884650.1 gg_id:317915 Bacillus subtilis str. Ht01
AY296804.1 gg_id:105773 Bacillus subtilis str. IBT012
AY279207.1 gg_id:87398 Bacillus subtilis str. HA401
FJ889051.1 gg_id:521011 Bacillus amyloliquefaciens str. Bac7M3
AB115959.1 gg_id:91208 Bacillus subtilis str. KT1003
GQ395245.1 gg_id:584805 Bacillus subtilis str. Czk1(BRZ1)
EF101720.1 gg_id:194233 Bacillus subtilis str. HU83
EU056572.1 gg_id:244688 Bacillus subtilis K1
EU373438.1 gg_id:273306 Bacillus subtilis str. YRR10

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AB301010.1 gg_id:241568 Bacillus amyloliquefaciens str. GH40
EU326481.1 gg_id:256348 Bacillus subtilis str. K22-13
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AB300817.1 gg_id:243193 Bacillus amyloliquefaciens str. Y13
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AB301004.1 gg_id:237064 Bacillus amyloliquefaciens str. GH3
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EU257444.1 gg_id:252115 Bacillus subtilis C4-1
EU871706.1 gg_id:316462 Bacillus subtilis str. Kb003
EF101716.1 gg_id:188219 Bacillus subtilis str. HU63
DQ659145.1 gg_id:169741 Bacillus polyfermenticus str. GR010
EU736102.1 gg_id:356656 Bacillus subtilis str. CD-10
EU360724.1 gg_id:268146 Bacillus subtilis str. BF11
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AY808064.1 gg_id:113038 Bacillus subtilis str. B53
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DQ779885.1 gg_id:169394 Bacillus subtilis str. PCL1612
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AY603963.1 gg_id:102408 Bacillus subtilis str. RAZ01
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EU862566.1 gg_id:308253 Bacillus subtilis str. ABc0
FJ157236.1 gg_id:345338 Bacillus subtilis str. FM-R3
AB211023.1 gg_id:115299 Bacillus subtilis str. SSCS21-1
EU586780.1 gg_id:277086 Bacillus amyloliquefaciens str. MZ-40
GQ302520.1 gg_id:576407 Bacillus subtilis str. BP-5
EF488170.1 gg_id:301350 Bacillus subtilis str. SC2-4
DQ415893.3 gg_id:150939 Bacillus subtilis str. MA139

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EU753871.1 gg_id:309228 Bacillus subtilis str. Bs9-1
EU257439.1 gg_id:241982 Bacillus subtilis C9-2
EU257441.1 gg_id:245083 Bacillus subtilis C11-3
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EU373330.1 gg_id:265541 Bacillus subtilis str. HNL01
EU722405.1 gg_id:354353 Bacillus subtilis str. E20
EU373397.1 gg_id:270586 Bacillus subtilis str. TPR02
EU266581.1 gg_id:255824 Bacillus subtilis str. K 3; SLU 3
EU884651.1 gg_id:319039 Bacillus subtilis str. HUSS-4AG
EF517121.1 gg_id:224820 Bacillus subtilis str. JKC-13
EU882847.1 gg_id:344584 Bacillus subtilis str. M6-7
FJ867945.1 gg_id:552423 Bacillus subtilis str. HUB-004
AM778999.1 gg_id:559860 Bacillus thuringiensis str. SBS-BT3
ABDA02000001.1 gg_id:319697 Bacillus cereus str. AH1134
AE016877.1 gg_id:148198 Bacillus cereus str. ATCC 14579
AE016877.1 gg_id:148282 Bacillus cereus str. ATCC 14579
AY224383.1 gg_id:107220 Bacillus cereus str. BGSC 6A5
NC_012472.1 gg_id:471271 Bacillus cereus str. 03BB102
AY138270.1 gg_id:70008 Bacillus cereus str. H1439
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CP001177.1 gg_id:523696 Bacillus cereus str. AH187
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AJ605773.3 gg_id:191440 Bacillus sp. K1-5	AJ6057
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GQ497939.1 gg_id:545039 Bacillus badius str. KO_CM52	GQ497
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AB425362.1 gg_id:526725 Bacillus sp. str. S207	AB4253
EU169170.1 gg_id:246151 Bacillus badius str. B22	EU1691
AY505500.1 gg_id:99298 Bacillus baekryungensis str. GSP36	AY5055
FJ907965.1 gg_id:556964 Bacillus baekryungensis str. LY096	FJ9079
FJ999563.1 gg_id:400929 Bacillus arsenicus str. HLSB44	FJ9995
AJ422145.1 gg_id:103946 Bacillus barbaricus str. V2-BIII-A2	AJ4221
GQ200827.1 gg_id:545867 Bacillus barbaricus str. P2	GQ200
EU867386.1 gg_id:548056 Bacillus barbaricus str. CCGE2121	EU8673
EU373318.1 gg_id:272802 Bacillus clausii str. SSR06	EU3733
AY066000.1 gg_id:17073 Bacillus clausii str. za-w-3	AY0660
EU571192.1 gg_id:262229 Bacillus sp. str. 25-4	EU5711
AF329474.1 gg_id:71598 Bacillus clausii str. LMG 19610	AF3294
GU296472.1 gg_id:565057 Engineered heat treated methanogenic granules (EHTG): promising biotechnological	GU296
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EF428124.1 gg_id:260802 Bacillus sp. str. LL2	EF4281
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AM747232.1 gg_id:242373 Bacillus cereus str. INRA AF2	AM747

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EU434382.1 gg_id:267998 Bacillus endophyticus str. a107 EU4343
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AY443036.1 gg_id:101066 Bacillus farraginis str. R-6540 AY4430
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EU867351.1 gg_id:591316 Bacillus firmus str. CCGE2067 EU8673
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DQ870697.1 gg_id:223236 Bacillus megaterium str. KSC_SF2j DQ870
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AY422986.1 gg_id:97150 Bacillus flexus str. R-6558 AY4229
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FJ527662.1 gg_id:546932 Bacillus subtilis str. rif200882 FJ5276
FJ527637.1 gg_id:535676 Bacillus megaterium str. rif200893 FJ5276
FJ393316.1 gg_id:358958 Bacillus megaterium str. TCCC11368 FJ3933
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EU867366.1 gg_id:574708 Bacillus megaterium str. CCGE2048 EU8673
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DQ416793.1 gg_id:274123 Bacillus sp. G2DM-33 DQ416
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AB112727.1 gg_id:99488 Bacillus methanolicus str. NCIMB 13113T
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EF634026.1 gg_id:254351 Paenibacillus polymyxa str. ISSDS-853
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EU071558.1 gg_id:247017 Bacillus muralis str. EHFS2_S05Ha
EU249563.1 gg_id:235309 Bacillus simplex str. TPBF2
EU647708.1 gg_id:273793 Bacillus muralis str. REG23
FJ544333.1 gg_id:418436 Bacillus simplex str. 816
FJ390478.1 gg_id:365017 Bacillus simplex str. HY1-2
DQ659140.1 gg_id:165620 Bacillus simplex str. L1
EU647709.1 gg_id:276019 Bacillus muralis str. REG52
EF154253.1 gg_id:189650 Bacillus simplex str. 13
GU339279.1 gg_id:548055 Bacillus nealsonii str. EH51

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AB271138.1 gg_id:163533 Bacillus niabensis str. S2-1
AJ542512.1 gg_id:81403 Bacillus novalis str. LMG 21837
X82492.1 gg_id:14591 Bacillus oleronius str. DSM 9356
AF393508.1 gg_id:48382 Bacillus oleronius str. LMG 17886; MB397
AF519460.1 gg_id:70683 Bacillus pichinotyi str. RS1; CIP 106 662
GQ980242.1 gg_id:580245 Bacillus pocheonensis str. NBK29
FJ009384.1 gg_id:340114 Bacillus pocheonensis str. F5
FJ009411.1 gg_id:348661 Bacillus drentensis str. G18
FJ009379.1 gg_id:356165 Bacillus soli str. G8
EU533950.1 gg_id:405006 Bacillus pseudofirmus str. SVB1
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FJ577677.1 gg_id:563057 Bacillus safensis str. B1-1
FJ549008.1 gg_id:550529 Bacillus pumilus str. SH-B3
FJ607352.1 gg_id:572654 Pseudomonas monteilii str. SeaH-As4w
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AF302120.1 gg_id:30814 Bacillus sonorensis str. NRRL B-23156
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AF302122.1 gg_id:41964 Bacillus sonorensis str. NRRL B-23158
AF302125.1 gg_id:22715 Bacillus sonorensis str. NRRL B-23161
AB540647.1 gg_id:580155 Bacillus sp. str. NCCP-62

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AJ586361.1 gg_id:103073 Bacillus thermoamylovorans str. R-19047 AJ5863
NR_026145.1 gg_id:574109 Bacillus pseudalcaliphilus str. DSM 8725 NR_02
AB434284.2 gg_id:274005 Bacillus trypoxylicola str. SU1 AB4342
FJ944648.1 gg_id:570600 Bacillus anthracis str. KUDC1024 FJ9446
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CP000903.1 gg_id:244782 Bacillus weihenstephanensis str. KBAB4 CP000
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AF144645.1 gg_id:14949 Bacillus mycoides str. DRC1 AF1446
Z84580.1 gg_id:14934 Bacillus cereus str. WSBC10210 Z84580
EF210282.1 gg_id:222605 Bacillus weihenstephanensis str. CCM 4965 EF2102
EU169143.1 gg_id:256275 Bacillus weihenstephanensis str. B28 EU169
Z84577.1 gg_id:14931 Bacillus cereus str. WSBC10201 Z84577
Z84578.1 gg_id:14932 Bacillus cereus str. WSBC10204 Z84578
AY277557.1 gg_id:90026 Bacillus weihenstephanensis str. P2-14 AY2775
Z84579.1 gg_id:14933 Bacillus cereus str. WSBC10206 Z84579
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AJ277907.1 gg_id:111676 Bacillus cereus str. Biosubtyl-Dalat AJ2779
AB363736.1 gg_id:243254 Bacillus mycoides str. NBRC 100169 AB3637
FJ435224.1 gg_id:364671 Bacillus megaterium str. 13 FJ4352
DQ078742.1 gg_id:131320 Bacillus thuringiensis str. LDC-9 DQ078
GU171377.1 gg_id:586881 Bacillus mycoides str. JS03-04 GU171
EF582416.1 gg_id:232949 Bacillus cereus str. HDYM-14 EF5824
GQ263498.1 gg_id:593429 Structure Simulated Level Waste Site simulated level waste site clone FW2_192B GQ263
EU661712.1 gg_id:282658 Bacillus cereus str. NBRAJATH9 EU6617
AY221057.1 gg_id:106573 sediments collected at Charon's Cascade near Echo River October 2000 clone CCM22 AY2210
FJ859684.2 gg_id:574826 Bacillus pseudomycoides str. BIHB 337 FJ8596
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AY803744.1 gg_id:108980 Bacillus cereus str. PGS2 AY8037
AY373361.1 gg_id:95158 Bacillus cereus str. T1 AY3733
EF210302.1 gg_id:225543 Bacillus thuringiensis serovar graciosensis str. IEBC-T66 001 EF2103

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EU240372.1 gg_id:256396 Bacillus thuringiensis str. B106 EU240
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DQ855661.1 gg_id:167765 Bacillus sp. str. KA-10 DQ855
DQ232746.1 gg_id:143250 Bacillus anthracis str. JH18 DQ232
EU240420.1 gg_id:235911 Bacillus cereus str. B170 EU240
AJ577281.1 gg_id:88623 Bacillus cereus str. B 412 AJ5772
AF206326.1 gg_id:25668 Bacillus cereus AF2063
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AJ277908.1 gg_id:111533 Bacillus cereus str. Bactisubtil AJ2779
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AM062679.1 gg_id:137266 Bacillus cereus AB1A1 AM062
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GU451184.1 gg_id:529958 Bacillus cereus str. HLB-5 GU451
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DQ148952.1 gg_id:139137 Bacillus alkalitolerans str. N39138 DQ148
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AY148429.1 gg_id:71520 Bacillus hackensackii AY148
AB364962.1 gg_id:242335 Bacillus lentus str. S3 AB364
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EU647707.1 gg_id:277002 Bacillus mycoides str. REG65 EU647
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EU019990.1 gg_id:252281 Bacillus cereus str. LAM 30 EU019
AF390086.1 gg_id:28561 Bacillus cereus str. S-5 AF390
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EU169186.1 gg_id:239266 Bacillus weihenstephanensis str. B31 EU169
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EU366380.1 gg_id:273324 Bacillus thuringiensis str. IV18 EU366
DQ286344.1 gg_id:143435 Bacillus thuringiensis DQ286

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EU834245.1 gg_id:336418 Bacillus cereus str. DS16
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FM179769.1 gg_id:307651 Acetobacter pasteurianus str. AUC29
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FJ601906.1 gg_id:517014 Bacillus thuringiensis str. INRS10
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DQ286355.1 gg_id:143331 Bacillus thuringiensis
NC_007530.2 gg_id:128590 Bacillus anthracis 'Ames Ancestor' str. Ames Ancestor; A2084
EU168402.1 gg_id:262529 Bacillus cereus str. IBL10048
EU240439.1 gg_id:251847 Bacillus weihenstephanensis str. B158
AE017194.1 gg_id:148272 Bacillus cereus str. ATCC 10987
DQ983194.1 gg_id:189670 Bacillus cereus str. ABPL 107
AY176771.2 gg_id:78603 Bacillus cereus str. HJ9
FJ641037.1 gg_id:547878 Bacillus cereus str. IMAUB1020; BM6-2
FJ859688.1 gg_id:534972 Bacillus cereus str. BIHB 342
L27478.1 gg_id:14594 Bacillus thermoamylovorans str. CNCM I-1378
AM293342.1 gg_id:543726 Bacillus thuringiensis str. DNB-Bt4
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AY279195.1 gg_id:86963 Bacillus cereus str. KNUC53
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EU862564.1 gg_id:345324 Bacillus cereus str. AB31
EU047593.1 gg_id:236591 Bacillus cereus str. JZ
EU429663.1 gg_id:552736 Bacillus thuringiensis serovar kurstaki str. B6066
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EU384285.1 gg_id:268205 Bacillus sp. B31(2008) str. B31
GQ495095.1 gg_id:539375 Bacillus cereus str. BC002
AJ288157.1 gg_id:30826 Bacillus cereus Ki 2l
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EF694696.1 gg_id:253079 Bacillus cereus B11-11
AE017194.1 gg_id:147956 Bacillus cereus str. ATCC 10987
EU915686.1 gg_id:306944 Bacillus cereus str. HY-1
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EF063149.1 gg_id:178210 Bacillus thuringiensis str. SRDD
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NC_008600.1 gg_id:191302 Bacillus thuringiensis str. Al Hakam
AJ577282.1 gg_id:88453 Bacillus cereus str. RIVM BC00067
EU874878.1 gg_id:338180 Bacillus cereus W77
FJ393296.1 gg_id:364850 Bacillus cereus str. TCCC11197
GQ199759.1 gg_id:593828 Bacillus sp. str. 210_57
NZ_ABDI01000027.1 gg_id:263069 Bacillus cereus str. B4264
EU240374.1 gg_id:238262 Bacillus cereus str. B79
EU240370.1 gg_id:248317 Bacillus thuringiensis str. B75
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DQ870690.1 gg_id:223264 Bacillus cereus str. KSC_SF6e
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EU915688.1 gg_id:337668 Bacillus cereus str. HY-4
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EF173327.1 gg_id:189594 Bacillus cereus MKI13
FJ393301.1 gg_id:368881 Bacillus cereus str. TCCC11289
EU794727.1 gg_id:345174 Bacillus cereus str. FM-4
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EU169144.1 gg_id:249918 Bacillus weihenstephanensis str. B27
FM178868.1 gg_id:331746 Acetobacter pasteurianus str. CCM 3614
EU435384.1 gg_id:262184 Bacillus thuringiensis str. AAJ17
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FJ263046.1 gg_id:369371 Bacillus cereus str. ZD19
EU118117.1 gg_id:238591 Bacillus cereus
EF126181.1 gg_id:186107 Bacillus cereus str. HCY02

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FJ373030.1 gg_id:350988 Bacillus selenatarsenatis str. S3-3 FJ3730
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GQ918255.1 gg_id:563322 Bacillus aestuarii str. JP1 GQ918
EU660355.1 gg_id:295089 Bacillus horikoshii str. CT1 EU6603
GQ980238.1 gg_id:559130 Bacillus humi str. NBK2 GQ980
AF221061.1 gg_id:28181 Bacillus jeotgali str. YKJ-10 AF2210
DQ448759.1 gg_id:157767 Bacillus sp. str. CNJ748 PL04 DQ448
EU221357.1 gg_id:248557 Bacillus simplex str. J2S3 EU2213
AB245380.1 gg_id:145947 Bacillus panaciterrae str. Gsoil 1517 AB2453
EU623596.1 gg_id:292837 Bacillus pumilus str. B-15 EU6235
AM084896.1 gg_id:139148 airborne fungal spores boreal forests contrasting human disturbance soil uranium n AM084
EU723827.1 gg_id:343771 Bacillus megaterium str. HDDMM05 EU7238
GQ855295.1 gg_id:557777 Bacillus shandongensis str. YH221 GQ855
AB190040.2 gg_id:156768 Bacillus megaterium str. N-18-25-9 AB1900
GQ889251.1 gg_id:551677 Bacillus megaterium str. S13 GQ889
AJ550460.1 gg_id:83070 Bacillus horikoshii AJ5504
AB486733.1 gg_id:550115 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCORC AB4867
FJ527649.1 gg_id:554625 Bacillus megaterium str. rif200888 FJ5276
DQ298329.1 gg_id:152305 studies on and nifH Lasiurus sindicus Sewan grass Thar Desert Rajasthan India rhizos DQ298
AJ491841.1 gg_id:78046 Bacillus megaterium str. C1 AJ4918
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AY030336.1 gg_id:33074 Bacillus megaterium str. KL-181 AY0303

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FM180507.1 gg_id:346953 Bacillus megaterium str. A3 FM180
GQ284398.1 gg_id:586246 Bacillus megaterium str. TSWCS6 GQ284
GQ355276.1 gg_id:576569 Bacillus sp. str. DL006 GQ355
AJ000981.2 gg_id:14641 soil clone DA036 AJ0009
FJ544338.1 gg_id:457472 Bacillus boroniphilus str. 822 FJ5443
EF113321.1 gg_id:187551 Bacillus halmapalus LB 16 EF1133
AY493966.1 gg_id:136840 Fingerprinting aggregates soil clone 1469 AY4939
FJ009399.1 gg_id:303812 Bacillus megaterium str. F6 FJ0093
FJ435229.1 gg_id:368409 Bacillus pumilus str. 18 FJ4352
AJ853532.1 gg_id:111121 landfill leachate clone GZKB38 AJ8535
AB488269.1 gg_id:541821 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSSUR0 AB488
FJ713099.1 gg_id:566717 Bacillus sp. str. EBL3-7 FJ7130
FJ527635.1 gg_id:553940 Bacillus megaterium str. rif200805 FJ5276
AF423304.1 gg_id:136610 oligonucleotide fingerprinting genes soil clone 48-1 AF4233
AM292611.1 gg_id:165187 Influence uranyl and sodium nitrate on natural soil uranium mining waste pile clone AM292
X64465.1 gg_id:14575 Bacillus methanolicus str. C1 X64465
EU182894.1 gg_id:248222 Bacillus sp. str. MH66 EU1828
AY642542.1 gg_id:151003 and carbonate precipitation giant microbialites ly alkaline Lake Van Turkey microbiali AY6425
FJ435233.1 gg_id:368404 Bacillus subtilis str. 24 FJ4352
EF612335.1 gg_id:248729 Bacillus sp. str. OS-03 EF6123
AY167803.1 gg_id:77353 Bacillus megaterium str. SAFN-040 AY1678
GQ866974.1 gg_id:542801 Bacillus megaterium str. Bm-10 sludge GQ866
AY167809.1 gg_id:77431 Bacillus niacini str. SAFN-021 AY1678
EU621912.1 gg_id:279144 Bacillus sp. str. CCBAU 10711 EU6219
EU240385.1 gg_id:257603 Bacillus mycoides str. B96 EU2403
EU221410.1 gg_id:257133 Bacillus megaterium str. A2P4 EU2214
EF513609.1 gg_id:224098 Bacillus megaterium str. E38 EF5136
EU817577.1 gg_id:326762 Colonization overlaying water dry sediments river sediment clone MUL-09 EU8175
AY373358.1 gg_id:95154 Bacillus megaterium str. c5 AY3733
EU194337.1 gg_id:248142 Bacillus megaterium str. XJUHX-40 EU1943
EU257442.1 gg_id:242832 Bacillus subtilis C6-3 EU2574
DQ129455.1 gg_id:138279 microarray level air two cities Texas urban aerosol clone AKIW1087 DQ129
AJ315063.1 gg_id:73206 Bacillus sp. LMG 19495 AJ3150
AJ132749.1 gg_id:14644 Bacillus sp. IDA629 AJ1327
AY422985.1 gg_id:98079 Bacillus sp. str. R-7413 AY4229
AJ236893.1 gg_id:14638 Bacillus sp. IDA624 AJ2368
EU249555.1 gg_id:243238 Bacillus asahii str. TSC12 EU2495
GQ980243.1 gg_id:540654 Bacillus aestuarii str. NBK30 GQ980

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DQ084539.1 gg_id:130986 Bacillus sp. GD0705	DQ084
EU427313.1 gg_id:265143 Bacillus drentensis str. MD	EU4273
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GU125638.1 gg_id:550049 Bacillus megaterium str. IMAU80222	GU125
EU977669.1 gg_id:575144 Bacillus sp. str. 2P03AE	EU977
DQ079002.1 gg_id:157632 Bacillus sp. str. GB02-29	DQ079
DQ870699.1 gg_id:221727 Bacillus drentensis str. KSC_SF1a	DQ870
EU244583.1 gg_id:246332 Bacillus megaterium str. 39	EU2445
AB043862.1 gg_id:31425 Bacillus sp. str. KX6	AB0438
FJ897776.1 gg_id:554312 Bacillus sp. str. BH85161	FJ8977
FJ006895.1 gg_id:344390 Bacillus sp. str. WPCB111	FJ0068
AY559426.1 gg_id:100562 hot spring water clone LS8	AY5594
EU373355.1 gg_id:271561 Bacillus megaterium str. HNL16	EU3733
DQ448750.1 gg_id:158948 Bacillus sp. str. CNJ816 PL04	DQ448
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FJ393314.1 gg_id:356703 Bacillus megaterium str. TCCC11353	FJ3933
EF451042.1 gg_id:211366 Bacillus aeris str. HIO-9	EF4510
EU652093.1 gg_id:276320 Bacillus megaterium str. ra-10	EU6520
GQ903460.1 gg_id:533975 Halobacillus sp. str. XJSL9-1	GQ903
EF428245.2 gg_id:227217 Bacillus megaterium str. HDYM-21	EF4282
GU395997.1 gg_id:523931 Bacillus flexus str. NT	GU395
EF688339.1 gg_id:236657 soil clone F1-249	EF6883
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EU867376.1 gg_id:578786 Bacillus herbersteinensis str. CCGE2319	EU8673
EU660347.1 gg_id:295408 Bacillus boroniphilus str. CM25	EU6603
AF218239.1 gg_id:111679 Bacillus sp	AF2182
AF227833.1 gg_id:49305 str. 31284	AF2278
AB331453.1 gg_id:241651 dynamics changes physicochemical parameters during aerobic treatment aerated pi	AB3314
AF423288.1 gg_id:52810 soil clone 720-1	AF4232
AF423299.1 gg_id:24269 soil clone 911-1	AF4232
FJ897758.1 gg_id:574270 Bacillus firmus str. RKS161	FJ8977

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EU660327.1 gg_id:299384 Bacillus horikoshii str. CM13	EU6603
FJ973529.1 gg_id:376634 Bacillus djibelorensis str. NBPP23 B23	FJ9735
GQ980245.1 gg_id:540946 Bacillus niacini str. NBK36	GQ980
EU221362.1 gg_id:253472 Bacillus licheniformis str. B2S1	EU2213
EU880507.1 gg_id:342033 Bacillus megaterium str. PRE6	EU8805
D16282.1 gg_id:14924 Sporolactobacillus dextrus str. IAM 12380	D16282
FJ644597.1 gg_id:562015 toxic marine dinoflagellates and Ostreopsis ovata malaysian waters benthic dinoflage	FJ6445
AY167861.1 gg_id:77319 Bacillus megaterium str. SAFR-040	AY1678
DQ523498.1 gg_id:161560 Bacillus megaterium str. B69	DQ523
X77791.1 gg_id:14626 Bacillus pseudomegaterium str. ATCC 49866	X77791
FJ227525.1 gg_id:353069 Identification unculturable species growing sludge methane reactor after methanoge	FJ2275
EU709019.1 gg_id:299152 Bacillus sp. str. CN40	EU709
DQ129522.1 gg_id:137910 microarray level air two cities Texas urban aerosol clone AKIW925	DQ129
AJ229207.1 gg_id:26443 anoxic bulk soil flooded rice microcosm clone BSV55 clone	AJ2292
FJ976616.1 gg_id:582339 Bacillus megaterium str. LCR107	FJ9766
FJ973528.1 gg_id:425655 Bacillus niacini str. NBPP53 B53	FJ9735
GQ386842.1 gg_id:553886 Bacillus sp. str. GS2	GQ386
EU257450.1 gg_id:239919 Bacillus subtilis CS-1-3	EU2574
DQ079004.1 gg_id:158163 Bacillus sp. str. GB02-14C	DQ079
DQ298337.1 gg_id:153253 studies on and nifH Lasiurus sindicus Sewan grass Thar Desert Rajasthan India rhizos	DQ298
FJ227532.1 gg_id:313454 Identification unculturable species growing sludge methane reactor after methanoge	FJ2275
DQ013307.1 gg_id:132308 Bacillus chandigarhensis str. SK 47	DQ013
AY606801.1 gg_id:105668 Bacillus sp. str. TM 5	AY6068
DQ346519.1 gg_id:155997 during composting libraries compost clone 3B05	DQ346
DQ298356.1 gg_id:154482 studies on and nifH Lasiurus sindicus Sewan grass Thar Desert Rajasthan India rhizos	DQ298
AF252320.1 gg_id:17518 hot synthetic compost clone pPD7	AF2523
AJ971870.1 gg_id:133358 Bacillus sp. Bt 18	AJ9718
DQ129501.1 gg_id:138249 microarray level air two cities Texas urban aerosol clone AKIW897	DQ129
DQ365583.1 gg_id:149726 Bacillus megaterium str. GS07	DQ365
EU620409.1 gg_id:277655 Bacillus boroniphilus str. S8-01	EU6204
GQ980244.1 gg_id:561398 Bacillus arbutinivorans str. NBK31	GQ980
EU465848.1 gg_id:287776 argali sheep feces clone AS2_aao36h03	EU4658
GQ129958.1 gg_id:441209 Genetic inventory 'JPL-SAF' during MSL mission spacecraft assembly clean room floc	GQ129
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FJ527639.1 gg_id:537851 Bacillus megaterium str. rif200886	FJ5276
GU397392.1 gg_id:520247 Bacillus megaterium str. C13	GU397
GU434676.1 gg_id:520638 Bacillus sp. str. CCBAU 05776	GU434
EU169572.1 gg_id:248760 Bacillus sp. str. CRRI 5	EU1695

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

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AB034715.1 gg_id:28732 compost clone 4-57 AB0347
AB198720.1 gg_id:131715 Bacillus borophilicus str. T-17s AB1987
GQ479946.1 gg_id:549663 Bacillus megaterium str. L4 GQ479
FJ393317.1 gg_id:356944 Bacillus megaterium str. TCCC11370 FJ3933
AM411966.1 gg_id:244199 Bacillus sp. str. P-43 AM411
EU221360.1 gg_id:256079 Bacillus niacini str. J2S7 EU2213
DQ906820.1 gg_id:253527 Oman subsurface soil clone 5C-13 DQ906
EU834241.1 gg_id:342723 Bacillus vireti str. DS11 EU8342
EU571116.1 gg_id:264293 Paenibacillus sp. str. 1-2 EU5711
AM411965.1 gg_id:253372 Bacillus sp. str. P-30 AM411
EU004564.1 gg_id:235358 Bacillus sp. str. HM06-02 EU0045
AY509228.1 gg_id:104385 Bacillus niacini str. S154 AY5092
AY167813.1 gg_id:77415 Bacillus megaterium str. SAFN-017 AY1678
DQ079008.1 gg_id:157487 Bacillus sp. str. GB02-2A DQ079
DQ298264.1 gg_id:154068 studies on and nifH Lasiurus sindicus Sewan grass Thar Desert Rajasthan India rhizos DQ298
FJ435230.1 gg_id:367954 Bacillus pumilus str. 19 FJ4352
EU620419.1 gg_id:278318 Bacillus megaterium str. S8-12 EU6204
AY920317.1 gg_id:140024 Bacillus sp. str. KT-1 AY9203
FJ851432.1 gg_id:532099 Bacillus sp. str. 1NLA3E FJ8514
AF423214.1 gg_id:34585 soil clone 1200-1 AF4232
FJ416490.1 gg_id:370385 Bacillus sp. str. BL4-6 FJ4164
AB245377.1 gg_id:146955 Bacillus pocheonensis str. Gsoil 420 AB2453
FJ535471.1 gg_id:510800 Bacillus sp. B7(2008) str. B7 FJ5354
AB486217.1 gg_id:591208 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC AB4862
GQ304778.1 gg_id:592464 Bacillus horikoshii str. A2 GQ304
GQ083176.1 gg_id:392856 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ083
AY603978.1 gg_id:99208 Bacillus sp. str. BH030017 AY6039
EU465102.1 gg_id:300373 African elephant feces clone AFYEL_aaj68b02 EU4651
FJ222553.1 gg_id:314498 Bacillus subtilis str. WR-W2 FJ2225
EU870509.1 gg_id:312403 Bacillus pumilus str. Sua-BAC014 EU8705
EF101699.1 gg_id:182801 Bacillus subtilis str. HU75 EF1016
EU216752.1 gg_id:244321 Bacillus pumilus str. JH1-1 EU2167
EU221348.1 gg_id:248169 Bacillus subtilis str. AM1C4 EU2213
AY296812.1 gg_id:101635 Bacillus licheniformis str. IBT017 AY2968
AY905693.1 gg_id:112084 Bacillus subtilis str. CICC10265 AY9056
AB547219.1 gg_id:527595 Bacillus axarquiensis str. NCCP-51 AB5472
AB044748.1 gg_id:29235 Bacillus sp. KSM-K38 AB0447
EF646827.1 gg_id:241931 Bacillus licheniformis str. YS01 EF6468
AJ532701.1 gg_id:76003 uranium mill tailings clone Gitt-KF-76 AJ5327

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DQ298263.1 gg_id:151865 studies on and nifH Lasiurus sindicus Sewan grass Thar Desert Rajasthan India rhizos DQ298
AY907698.1 gg_id:112579 Bacillus subtilis str. CICC10080 AY907
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DQ129423.1 gg_id:138175 microarray level air two cities Texas urban aerosol clone AKIW703 DQ129
GQ865645.1 gg_id:543387 Bacillus subtilis str. DSVP25 GQ865
EU071555.1 gg_id:249702 Bacillus licheniformis str. EHFS2_S05Hd EU071
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EF173323.1 gg_id:175072 Bacillus licheniformis MKI9 EF1733
AY739691.1 gg_id:114611 lubricant-contaminated soil clone KUD46A AY739
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EU719191.1 gg_id:337655 Bacillus pumilus str. A1 EU719
EU240965.1 gg_id:274648 Bacillus subtilis str. YC-12B EU240
FJ687490.1 gg_id:545577 Bacillus aquimaris str. VITP4 FJ6874
GQ199593.1 gg_id:543593 Bacillus subtilis str. DL-3-4-3 GQ199
GQ983544.1 gg_id:593069 Bacillus amyloliquefaciens str. HYD-B17 GQ983
FJ937899.1 gg_id:567864 Bacillus sp. str. LS48 FJ9378
EU162839.1 gg_id:251156 Bacillus licheniformis str. 8-37-0-1 EU162
EF633685.1 gg_id:242176 Bacillus sp. 'TS 33' str. TS IW 33 EF6336
EF101727.1 gg_id:191042 Bacillus subtilis str. GB12 EF1017
EU571103.1 gg_id:272881 Bacillus subtilis str. EM 11 EU571
AY842874.1 gg_id:109651 Bacillus licheniformis str. CICC10093 AY8428
GQ375214.1 gg_id:571371 Bacillus amyloliquefaciens str. CICC 20164 GQ375
EU117278.1 gg_id:257156 Bacillus licheniformis str. B8 EU117
FN395277.1 gg_id:428974 Bacillus sp. str. FR-W2C1 FN395
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AY805232.1 gg_id:109012 Bacillus subtilis str. BSK AY805
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EU921229.1 gg_id:326750 Bacillus pumilus str. BM-F13 EU921
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DQ785743.1 gg_id:161720 Bacillus subtilis str. WSH-062 DQ785
NR_028709.1 gg_id:577421 Bacillus siralis str. 171544; DSM 13140 NR_02
EU826027.1 gg_id:317297 Bacillus subtilis str. CDB86 EU826

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FJ607434.1 gg_id:544209 Bacillus cibi str. 102 FJ6074
FJ263034.1 gg_id:368912 Bacillus subtilis str. RC22 FJ2630
FJ951435.1 gg_id:444096 Streptomyces indiaensis str. IF 5 FJ9514
FJ999559.1 gg_id:385478 Bacillus sp. str. HLSB39 FJ9995
AY296813.1 gg_id:101803 Bacillus licheniformis str. IBT018 AY2968
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EU874880.1 gg_id:322338 Bacillus pumilus W93 EU8748
EU379270.1 gg_id:271984 Bacillus pumilus str. 3L-10c EU3792
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AY995569.2 gg_id:122232 Bacillus subtilis str. IDCC1102 AY9955
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AY920496.1 gg_id:112943 Bacillus subtilis str. Fds-1 AY9204
FJ907196.1 gg_id:574051 Bacillus licheniformis 13 FJ9071
AY462210.1 gg_id:110364 Bacillus pumilus str. DF39 AY4622
EU982438.1 gg_id:321882 Enrichment and detection moderate thermophilic microorganisms vents Lau Basin h EU9824
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X60611.1 gg_id:14659 Bacillus benzoevorans str. NCIMB 12555 X60611
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EF064205.1 gg_id:184943 Bacillus subtilis str. NA
EU407552.1 gg_id:270598 Bacillus pumilus str. UFV-E34

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EU815066.1 gg_id:309278 Bacillus subtilis str. W-9
EF473131.1 gg_id:221106 Bacillus amyloliquefaciens qd128
X92168.1 gg_id:23919 Lake Nakuru isolate 17N1
EF465458.1 gg_id:204167 Bacillus pumilus SF4
AY289504.1 gg_id:100575 Bacillus sp. IDA4917
AY167806.1 gg_id:77320 Bacillus licheniformis str. SAFN-031
AY310301.1 gg_id:88830 Bacillus subtilis str. BGSC 3A23
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AY279209.2 gg_id:84256 Bacillus subtilis str. IBT015
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GQ375242.1 gg_id:510128 Bacillus licheniformis str. CICC 10332
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GQ161967.1 gg_id:593815 Bacillus subtilis str. CRB115
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FJ897775.1 gg_id:574392 Bacillus sp. str. BH85065-2
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AM888178.1 gg_id:239470 Bacillus sp. str. TSWCSN2
GU397397.1 gg_id:523649 Bacillus pumilus str. H4
AJ494732.1 gg_id:63740 Bacillus pumilus EI-31-12
AB300800.1 gg_id:255945 Bacillus subtilis str. ND1
AJ494729.1 gg_id:63744 Bacillus pumilus EI-26-5
AY647307.1 gg_id:104302 Bacillus aquimaris str. MSU1110
EU231620.1 gg_id:257555 Bacillus subtilis str. TCCC11002
AB301016.1 gg_id:254047 Bacillus subtilis str. GHGH1
AB536966.1 gg_id:536973 Bacillus sp. str. MB142
AB547220.1 gg_id:517018 Bacillus nealsonii str. NCCP-28
GQ199594.1 gg_id:584451 Bacillus subtilis str. DMJS-2-1
AY740598.1 gg_id:100517 Bacillus pumilus str. 115b
EU620418.1 gg_id:279135 Bacillus pumilus str. S8-11
DQ005494.1 gg_id:122715 Bacillus subtilis str. CICC10156
GQ470396.1 gg_id:590065 Bacillus pumilus str. DQgbc1
EU071546.1 gg_id:236711 Bacillus atrophaeus str. EHFS1_S11Hb
FJ393319.1 gg_id:366264 Bacillus subtilis str. TCCC11377
AY030332.1 gg_id:40827 Bacillus subtilis str. KL-120
AB301012.1 gg_id:236191 Bacillus subtilis str. GH41
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EU366372.1 gg_id:262423 Bacillus subtilis str. IV2
FJ999558.1 gg_id:416262 Bacillus pumilus str. HLSB33
FJ966221.1 gg_id:576226 Bacillus subtilis str. Bio AA3
EF101735.1 gg_id:187170 Bacillus licheniformis str. HU53
DQ351930.2 gg_id:147897 Bacillus licheniformis str. K10
AY219900.1 gg_id:83777 Bacillus subtilis
EF101707.1 gg_id:177700 Bacillus subtilis str. HU48
EU293872.1 gg_id:253939 Bacillus licheniformis str. ER-15
AY162126.1 gg_id:76500 Bacillus subtilis str. GA1-5
DQ187380.1 gg_id:140126 Brevibacterium halotolerans

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EF672040.1 gg_id:242290 Bacillus atrophaeus str. XJU
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EU927408.1 gg_id:303436 Bacillus aquimaris str. 8-N60
EU430991.1 gg_id:262130 Bacillus sporothermodurans 19
AB305270.1 gg_id:234885 Bacillus subtilis str. YS1-4
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AB196350.1 gg_id:140905 Bacillus licheniformis str. PS2
EU656111.1 gg_id:281486 Bacillus nealsonii str. DSM 15077
EU466040.1 gg_id:289634 African elephant feces clone AFEL3_aao16e01
GQ214132.1 gg_id:580418 Bacillus subtilis str. C8K1
DQ837547.1 gg_id:165976 Bacillus pumilus str. XJU-4
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EU379297.1 gg_id:266973 Bacillus pumilus str. 6J-4c
FJ686821.1 gg_id:559334 Bacillus pumilus str. LB4
AY897211.1 gg_id:111931 Bacillus subtilis str. ZJY-116
AJ628743.1 gg_id:100629 Bacillus simplex str. LMG 11160
EU231625.1 gg_id:251346 Bacillus pumilus str. TCCC11012

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EU784137.1 gg_id:323453 Bacillus pumilus str. UFPEDA 831
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AF008220.1 gg_id:14713 Bacillus subtilis
EU294410.1 gg_id:237176 Bacillus subtilis str. JT1 sullage
DQ118016.1 gg_id:201755 Bacillus pumilus str. RGR7
EU231630.1 gg_id:243969 Bacillus subtilis str. TCCC11021
EU257430.1 gg_id:248624 Bacillus subtilis SCS-4
EU231624.1 gg_id:243661 Bacillus pumilus str. TCCC11010
CP000560.1 gg_id:254749 Bacillus amyloliquefaciens str. FZB42
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EU624321.1 gg_id:278645 Bacillus subtilis str. 81-4
EF101728.1 gg_id:177609 Bacillus subtilis str. GB13
DQ129260.1 gg_id:138122 microarray level air two cities Texas urban aerosol clone AKIW777
EF113957.1 gg_id:239695 Bacillus pumilus str. CBS
AB301013.1 gg_id:236388 Bacillus subtilis str. GH44
EU071564.1 gg_id:238526 Bacillus subtilis str. EHFS1_S02Hb
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ABRX01000004.1 gg_id:319639 Bacillus pumilus str. ATCC 7061
EU231614.1 gg_id:254702 Bacillus subtilis str. TCCC17017

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EU780103.1 gg_id:330308 Bacillus pumilus str. DT83 EU780
EU869264.1 gg_id:339196 Bacillus subtilis str. BG-B81 EU869
EU873181.1 gg_id:342551 Bacillus pumilus str. BM-Y10 EU873
AY030324.1 gg_id:71264 Bacillus macroides str. KL-009 AY030
GQ903332.1 gg_id:574670 Bacillus licheniformis str. dhs-40 GQ903
AY603656.2 gg_id:106861 Bacillus malacitensis str. CR-95 AY603
EF528262.1 gg_id:221178 Bacillus subtilis str. CICCHLJ Q34 EF5282
EU624429.1 gg_id:281207 Bacillus pumilus str. S6-05 EU624
EU124559.1 gg_id:257350 Bacillus simplex str. OSS 24 EU124
FJ268976.1 gg_id:357376 unculturable unpolluted rhizospheric loamy soil Phragmites cummunis growing fresh FJ2689
X92161.1 gg_id:40983 Lake Elmenteita isolate WE4 X92161
EF187430.2 gg_id:190564 Bacillus sp. str. CP1 EF1874
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EU302589.1 gg_id:250531 Bacillus subtilis str. HA Cheonggukjang EU302
EU240379.1 gg_id:244299 Bacillus simplex str. B76 EU240
EF427892.1 gg_id:203939 Bacillus subtilis str. JKC-16 EF4278
EU882846.1 gg_id:308994 Bacillus subtilis str. H10-5-5 EU8828
GU132507.1 gg_id:576641 Bacillus sp. str. JJM-1 GU132
DQ112221.1 gg_id:137047 Bacillus licheniformis str. CICC10266 DQ112
AJ250318.1 gg_id:69789 Bacillus shackletonii str. LMG 18435 AJ2503
EU620445.1 gg_id:275997 Aerobic Facultative Alkalitolerant and Halotolerant Endospore Formers Soil Alvord B EU620
AY373018.1 gg_id:94983 Bacillus sp. str. DIT030428 AY3730
EF528273.1 gg_id:227083 Bacillus pumilus str. CICCHLJ Q47 EF5282
EU870503.1 gg_id:345937 Bacillus licheniformis str. Sua-BAC006 EU870
AJ550463.1 gg_id:82717 Bacillus pumilus AJ5504
FJ380930.1 gg_id:360936 Bacillus sp. str. K-05 FJ3809
AY162136.1 gg_id:77146 Bacillus licheniformis str. GA8 AY162
AF142575.1 gg_id:14706 Bacillus sp. str. Biosubtyl AF1425
DQ906100.1 gg_id:171545 Bacillus subtilis str. N391 DQ906
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DQ295037.1 gg_id:142381 Bacillus licheniformis str. ZCS1 DQ295

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AY189750.1 gg_id:79819 Bacillus mojavensis str. M-1 AY1897
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EU366367.1 gg_id:260710 Bacillus velezensis str. I14 EU3663
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EU571158.1 gg_id:271497 eubacterium sp. str. 11-10
DQ659146.1 gg_id:171063 Bacillus subtilis str. GR011
AJ494731.1 gg_id:63741 Bacillus pumilus EI-26-8
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AB364963.1 gg_id:253331 Bacillus subtilis str. S4
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EF101714.1 gg_id:194456 Bacillus subtilis str. HU24
FJ999577.1 gg_id:395703 Bacillus sp. str. HLSB174

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EU870502.1 gg_id:318100 Bacillus amyloliquefaciens str. Sua-BAC005 EU870
EU624418.1 gg_id:283388 Bacillus arsenicus str. S8-14 EU624
GQ284374.1 gg_id:553701 Bacillus sp. str. PCWCS1 GQ284
GQ853552.1 gg_id:567428 Bacillus subtilis str. BRZ5 GQ853
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EF379274.1 gg_id:276657 Bacillus sp. str. SL213 EF3792
EU231638.1 gg_id:243631 Bacillus subtilis str. TCCC11024 EU231
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AY995570.2 gg_id:125804 Bacillus subtilis str. IDCC1103 AY9955
EU586322.1 gg_id:265692 Bacillus licheniformis str. H*1 EU5863
GQ280082.1 gg_id:513749 Bacillus subtilis str. JS-12 GQ280
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GQ280017.1 gg_id:580384 Bacillus licheniformis str. BJ-7 GQ280
GQ302521.1 gg_id:537803 Bacillus subtilis str. BP-13 GQ302
EU379284.1 gg_id:261753 Bacillus pumilus str. 4RS-5f EU379
EU557029.1 gg_id:269982 Bacillus subtilis str. KU3 EU557
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EF439667.1 gg_id:215811 Bacillus pumilus str. S2 EF4396
AY913756.1 gg_id:112580 Bacillus subtilis str. CICC10081 AY9137
EU008574.1 gg_id:236385 Bacillus licheniformis str. PS7 EU008
EU753616.1 gg_id:354902 modern freshwater stromatolites Ruidera Pools Natural Park Spain dry stromatolite EU753
AY913755.1 gg_id:112686 Bacillus subtilis str. CICC10078 AY9137
FJ514932.1 gg_id:557292 Bacillus sp. str. CAU 348 FJ5149
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DQ071560.1 gg_id:132973 Bacillus licheniformis str. MKU 1 DQ071
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DQ118379.1 gg_id:130032 Bacillus licheniformis str. CICC 10183 DQ118

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EF101717.1 gg_id:189913 Bacillus subtilis str. HU67
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AM910588.1 gg_id:272861 Bacillus licheniformis str. 68.5 AM910
AB508839.1 gg_id:588430 Bacillus licheniformis str. CMBL-Hg2 AB5088
GQ280023.1 gg_id:564208 Bacillus licheniformis str. BJ-13 GQ280
EU722711.1 gg_id:341178 Bacillus sp. str. SBC4 EU7227
EU918561.1 gg_id:320060 Bacillus marisflavi str. NY-4 EU9185
EU366369.1 gg_id:276519 Bacillus subtilis str. I1 EU3663
FM180523.1 gg_id:325682 Bacillus pumilus str. B9 FM180
AY929251.1 gg_id:113947 Bacillus subtilis str. CG-312 AY9292
FJ538256.1 gg_id:566024 Bacillus sp. str. DHVB1 FJ5382
FJ686818.1 gg_id:563067 Bacillus amyloliquefaciens str. LB1 FJ6868
DQ911348.1 gg_id:235458 Bacillus subtilis str. BMT4i DQ911
DQ870689.1 gg_id:225483 Bacillus pumilus str. KSC_SF6h DQ870
EU182884.1 gg_id:238431 Bacillus sp. str. MH56 EU1828
EU867370.1 gg_id:577641 Bacillus asahii str. CCGE2069 EU8673
FJ392725.1 gg_id:369758 Bacillus subtilis str. F1-5 FJ3927
AF157696.1 gg_id:14668 Bacillus macroides str. dhr2 AF1576
EU341173.1 gg_id:247284 Evaluation Rapid Technologies Estimate Microbial Burden and Commercial Airline Ca EU3411
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EU689157.1 gg_id:367096 Bacillus amyloliquefaciens str. ATCC 23842 EU6891
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AY971363.1 gg_id:115327 Bacillus subtilis str. CICC10150 AY9713
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FJ808724.1 gg_id:529616 Geobacillus pallidus str. P161 FJ8087
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AY608948.1 gg_id:102908 Geobacillus stearothermophilus str. BGSC 9A5 AY6089
GQ255948.1 gg_id:533915 Geobacillus toebii str. HBB-218 GQ255
EU381187.1 gg_id:352606 Geobacillus stearothermophilus str. GBPI-13 EU3811
AY466700.1 gg_id:104680 Anoxybacillus toebii str. NS1-1 AY4667
AY608945.1 gg_id:102443 Geobacillus lituanicus str. BGSC W9A89 AY6089
NR_025143.1 gg_id:563677 Geobacillus toebii str. SK-1; KCTC 0306BP NR_025
Z26930.1 gg_id:14542 Geobacillus pallidus str. DSM 3670* Z26930
AJ489330.1 gg_id:70432 Geobacillus thermoleovorans I80 AJ4893
AY312404.1 gg_id:88427 Geobacillus jurassicus str. DS1 AY3124
AJ489328.1 gg_id:70679 Geobacillus thermoleovorans T70 AJ4893
GQ112279.1 gg_id:374316 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ112
EU484350.1 gg_id:275411 Geobacillus lituanicus str. BCRC 17562 EU4843
NR_028708.1 gg_id:588849 Geobacillus caldoxylosilyticus str. S1812; DSM 12041; ATCC 700356 NR_028
EU214631.1 gg_id:334523 Geobacillus stearothermophilus mb-5 EU2146
DQ298736.1 gg_id:183369 Geobacillus thermoglucosidasius str. NP-1 DQ298
AY450926.1 gg_id:100906 Geobacillus thermoleovorans str. GE-7 AY4509
GQ097137.1 gg_id:382259 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw GQ097
AB543491.1 gg_id:573601 Geobacillus pallidus str. NCCP-131 AB5434
GQ180113.1 gg_id:547508 Bacillus clausii str. DF4 GQ180
FJ808714.1 gg_id:515344 Geobacillus toebii str. G7 FJ8087
GQ112234.1 gg_id:416050 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ112
EF490600.2 gg_id:245586 Geobacillus pallidus str. C5 EF4906
GQ111503.1 gg_id:421722 Topographical and Temporal Human Skin Microbiome skin alar crease clone nbw581 GQ111
FJ808712.1 gg_id:524476 Geobacillus stearothermophilus str. Ah22 FJ8087
Z26929.1 gg_id:14566 Bacillus sp str. DSM 2349 Z26929
AB210953.1 gg_id:115284 Geobacillus toebii str. SSCT84-3 AB2109
AY682097.1 gg_id:106402 Geobacillus stearothermophilus str. 49 AY6820
Z26922.1 gg_id:14568 Bacillus caldotenax str. DSM 406 Z26922
DQ355387.1 gg_id:147769 Solubilization and biodegradation polycyclic aromatic hydrocarbons under condition DQ355
AJ005759.1 gg_id:14531 Geobacillus stearothermophilus str. NUB3621 AJ0057
AY550104.1 gg_id:104797 Geobacillus thermocatenulatus hs6 AY5501
AF411064.1 gg_id:45180 Geobacillus anatolicus str. SB AF4110
EU214619.1 gg_id:309162 Geobacillus stearothermophilus ir-25 EU2146
AF411065.1 gg_id:34112 Geobacillus kaue str. HU AF4110
FJ808717.1 gg_id:515154 Geobacillus toebii str. M66A FJ8087
AJ564619.1 gg_id:87954 Geobacillus caldoxylosilyticus Tk AJ5646
AB210959.1 gg_id:115180 Geobacillus toebii str. SSCT82-1 AB2109
AB089238.1 gg_id:58657 Bacillus sp. str. VA2 AB0892
AB210957.1 gg_id:115310 Geobacillus toebii str. SSCT82-3 AB2109

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GQ487459.1 gg_id:590908 Geobacillus toebii str. HBB-247 GQ487
EU381193.1 gg_id:352145 Geobacillus stearothermophilus str. GBPI-12 EU381
AY608936.1 gg_id:106419 Geobacillus thermoleovorans str. BGSC 96A1 AY608
GQ096866.1 gg_id:406506 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw GQ096
FJ417401.1 gg_id:362377 Geobacillus pallidus str. P4 FJ4174
EU214620.1 gg_id:336321 Geobacillus stearothermophilus it-8 EU214
EU652071.1 gg_id:273513 Geobacillus stearothermophilus str. mm-19 EU652
EU381183.1 gg_id:325891 Geobacillus stearothermophilus str. GBPI-5 EU381
NC_006510.1 gg_id:128657 Geobacillus kaustophilus str. HTA426 NC_00
FN428682.1 gg_id:571762 Geobacillus pallidus str. R-35634 FN428
EU214627.1 gg_id:335894 Geobacillus toebii mc-12 EU214
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EF469734.1 gg_id:222519 Geobacillus vulgivagus str. CDZ 1 EF4697
EF025325.1 gg_id:186620 Geobacillus stearothermophilus str. ARM 1 EF0253
EU621361.1 gg_id:279618 Geobacillus pallidus str. DR03 EU6213
EU484353.1 gg_id:272744 Bacillus caldovelox str. BCRC 11957 EU4843
L09227.1 gg_id:14553 Saccharococcus thermophilus L09227
EF535794.1 gg_id:218748 Geobacillus toebii str. T85 EF5357
AY248718.1 gg_id:86077 Geobacillus caldoxylosilyticus str. TK4 AY2487
AY491497.1 gg_id:107338 Geobacillus stearothermophilus AY4914
M77488.1 gg_id:14564 Bacillus thermoleovorans M7748
EU484357.1 gg_id:268222 Geobacillus kaustophilus str. BCRC 11223 EU4843
AY248717.1 gg_id:85270 Geobacillus thermoleovorans str. G1 AY2487
EU884294.1 gg_id:338217 Geobacillus stearothermophilus str. BMSCE-1 EU8842
AM947545.1 gg_id:260757 Minor changes detected microbial structure and after three week thermophilic dige AM947
X57309.1 gg_id:14552 Geobacillus stearothermophilus str. T10 X57309
EU652094.1 gg_id:276376 Geobacillus subterraneus str. ra-11 EU652
EU214626.1 gg_id:318116 Geobacillus toebii mc-9 EU214
AY952967.1 gg_id:114690 Bacillus caldotenax str. CCSD 3900 AY9529
AY297092.2 gg_id:88437 Geobacillus stearothermophilus str. BGSC 9A21; DSM 13240 AY2970
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DQ923400.1 gg_id:197471 Geobacillus stearothermophilus str. 5 DQ923
AF276305.1 gg_id:23251 Geobacillus uzenensis str. X AF2763
DQ452018.1 gg_id:219154 Bacillus sp. HT4 DQ452
FN428688.1 gg_id:541063 Geobacillus uzenensis str. R-35640 FN428
AY608938.1 gg_id:106733 Bacillus caldovelox str. BGSC 96A5 AY608
EU428777.1 gg_id:274145 Geobacillus toebii str. DPE7 EU428

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EU710557.1 gg_id:349122 Bacillus sp. str. TSSC-3 EU7105
GQ903452.1 gg_id:580022 Halobacillus dabanensis str. XJSL8-3 GQ903
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GQ903455.1 gg_id:552668 Halobacillus dabanensis str. XJSL8-6 GQ903
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AY190534.1 gg_id:80237 Halobacillus locisalis str. MSS-155 AY1905
NR_025244.1 gg_id:543606 Halobacillus salinus str. HSL-3; KCCM 41590 NR_025
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AM160651.1 gg_id:249267 Halobacillus sp. str. Hallo B AM160
FJ444988.1 gg_id:567005 Halobacillus trueperi str. whb42 FJ4449
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EF533970.1 gg_id:265846 Halobacillus sp. str. Y13 EF5339
DQ458839.1 gg_id:156629 Halobacillus sp. str. YT242 DQ458
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AB198758.1 gg_id:110746 Halobacillus sp. str. IS-Hb9 AB1987
EU624420.1 gg_id:282283 Halobacillus trueperi str. S8-16 EU6244
FJ444952.1 gg_id:584666 Halobacillus trueperi str. whb6 FJ4449
AM161501.1 gg_id:144741 Halobacillus virgiliensis str. S21 AM161
AB305176.1 gg_id:229439 Halobacillus sp. str. S19-3 AB3051
EU170130.1 gg_id:242105 Halobacillus sp. str. T15 EU1701
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EU308337.1 gg_id:366337 Halobacillus sp. str. FIB248 EU308
EU602318.2 gg_id:587130 Halobacillus halophilus str. MMD047 EU602
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AB362694.1 gg_id:249393 Halolactibacillus halophilus str. NRIC 0628 AB362
AB196783.1 gg_id:132611 Halolactibacillus halophilus str. M2-2 AB196
AB231905.1 gg_id:137844 Lentibacillus kapialis str. PN7-6 AB231
AY762976.1 gg_id:102689 Salibacillus sp. str. BH113 AY762
AB191345.1 gg_id:100303 Lentibacillus halophilus str. PS11-2 AB191
AB365482.1 gg_id:235720 Virgibacillus siamensis str. MS3-4 AB365
AY667497.1 gg_id:103142 Virgibacillus sp. str. BH260 AY667
EU442366.1 gg_id:274948 Marinococcus sp. str. 05 EU442
X90835.1 gg_id:14475 Marinococcus halophilus str. DSM 20408 X90835
EU281853.2 gg_id:242528 Alkalilactibacillus ikkense str. GCM68 EU281
EU143688.1 gg_id:247337 Natronobacillus azotifixans str. ES 3 EU143
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AB010863.2 gg_id:14611 Oceanobacillus iheyensis str. HTE831 AB0108
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AB366005.1 gg_id:263096 Oceanobacillus kapialis str. SSK2-2 AB3660
AJ309561.1 gg_id:47685 Bacillus litoralis str. IB-B4 AJ3095
AY647302.1 gg_id:103563 Oceanobacillus iheyensis str. MSU3110 AY6473
DQ089680.1 gg_id:128071 Virgibacillus picturae str. IV9 DQ089
EU680961.1 gg_id:299980 Oceanobacillus iheyensis str. OMA1 8 EU6809
EU624422.1 gg_id:283122 Oceanobacillus iheyensis str. S8-19 EU6244
AB034713.1 gg_id:40994 compost clone 4-49 AB0347
EF201774.1 gg_id:211259 Virgibacillus sp. LCKS000-Isolate10 EF2017
GQ903467.1 gg_id:594077 Oceanobacillus picturae str. XJSL9-8 GQ903
EU330342.1 gg_id:247179 Oceanobacillus sp. str. BSi20641 EU3303
DQ115985.1 gg_id:132563 rbl flr whch inhbt cnls hlth lcttng bvns bvn tt cnl cln B-7 DQ115
DQ129339.1 gg_id:152700 microarray level air two cities Texas urban aerosol clone AKIW466 DQ129
DQ190427.1 gg_id:139007 Oceanobacillus sp. 5 DQ190
DQ468656.1 gg_id:157247 Oceanobacillus chironomi str. T3944D DQ468
AB275883.1 gg_id:193390 Oceanobacillus sp. str. S-11 AB2758
EF660762.1 gg_id:244150 Oceanobacillus cibarius str. A34 EF6607
DQ129338.1 gg_id:138206 microarray level air two cities Texas urban aerosol clone AKIW1021 DQ129
AY762978.1 gg_id:102984 Halobacillus sp. str. BH178 AY7629
AY553296.1 gg_id:106986 Pontibacillus chungwhensis str. BH030062 AY5532
AY603362.1 gg_id:102560 Pontibacillus chungwhensis str. BH030080 AY6033
EU308474.1 gg_id:358650 Pontibacillus sp. str. TB138 EU3084
EF533969.2 gg_id:273625 Pontibacillus sp. str. Y32 EF5339
DQ448765.1 gg_id:157160 Pontibacillus sp. str. CNJ912 PL04 DQ448
EU308475.1 gg_id:370058 Pontibacillus sp. str. TB238 EU3084
EU583724.1 gg_id:263804 Pontibacillus sp. str. JSM 072002 EU5837
FJ937904.1 gg_id:510492 Pontibacillus chungwhensis str. LS59 FJ9379
FJ232474.1 gg_id:363725 Pontibacillus sp. str. NH11EB76 FJ2324
AY603977.1 gg_id:99045 Bacillus sp. str. BH030004 AY6039
GU001908.1 gg_id:575458 Salimicrobium halophilum str. PLF GU001
EU868872.1 gg_id:344756 Salimicrobium luteum str. M1-1 EU8688
DQ093355.1 gg_id:134586 Marinococcus albus str. 63 DQ093
AY321437.1 gg_id:89985 salt lake water isolate str. W11-1 AY3214
AM905297.1 gg_id:235359 Sediminibacillus halophilus str. EN8d AM905
FJ999948.1 gg_id:577242 Terribacillus saccharophilus str. EQH19 FJ9999
DQ519571.1 gg_id:161113 Goribacillus litoralis str. CL-GR16 DQ519
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GQ304893.1 gg_id:588713 Terribacillus sp. str. DB2 GQ304

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

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EU430986.1 gg_id:260081 Paucisalibacillus globulus 5 EU430
FJ357159.1 gg_id:358728 Virgibacillus sp. str. ISL-24 FJ3571
EU369133.1 gg_id:325308 libraries oyster shell clone MBIOS-17 EU369
DQ842544.1 gg_id:173209 Application Glucose Glutamate Temperature Biotrickling Filtration Hydrogen Sulphic DQ842
AB197126.1 gg_id:129671 Gracilibacillus borotolerans str. T16X AB197
DQ346527.1 gg_id:156308 during composting libraries compost clone 3B13 DQ346
NR_028649.1 gg_id:587710 Cerasibacillus quisquiliarum str. BLx; DSM 15825 NR_02
AB189333.1 gg_id:99420 Filobacillus sp. str. SA-Fb1 AB189
FJ348416.1 gg_id:552637 Investigation microbial soil method saltern 15 cm be surface clone DGGE gel band ntu FJ3484
AM292417.2 gg_id:192309 Salirhabdus caputitis str. CVS14 AM292
FN428698.1 gg_id:574818 Geobacillus caldoproteolyticus str. R-35652 FN428
NR_028642.1 gg_id:569518 Paraliobacillus ryukyuensis str. O15-7; DSM 15140 NR_02
EU143689.1 gg_id:236513 Amphibacillus diazotrophicus str. 22KS-2 EU143
EU135676.1 gg_id:248158 Virgibacillus sp. str. YIM C834 EU135
AM400872.1 gg_id:244314 Bacillus sp. str. Jsl1 AM400
AB176374.1 gg_id:187575 Microbial Hydrothermal System Suiyo Seamount on Izu-Ogasawara Arc vent area wa AB1763
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EF422411.1 gg_id:203680 Bacillus sp. str. ANL-iso4 EF4224
AY762977.1 gg_id:102843 Bacillus sp. str. BH164 AY762
GQ009179.1 gg_id:500487 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw GQ009
EU620444.1 gg_id:276370 Aerobic Facultative Alkalitolerant and Halotolerant Endospore Formers Soil Alvord B EU620
FM244839.1 gg_id:359288 Bacillus sp. str. HS-136 FM244
AM492160.1 gg_id:206482 Salsuginibacillus kocurii str. CH9d AM492
DQ115802.2 gg_id:133117 Bacillus sp. CM1 DQ115
FJ437873.1 gg_id:548924 Benthic okenone production Fayetteville New York Green Lake 25 m water depth clo FJ4378
GU217709.1 gg_id:590271 Bacillus sp. str. ljh-13 GU217
FJ380159.1 gg_id:363860 ornithogenic Ross Sea region Antarctica AB1 soil clone 9/4/2D FJ3801
AY376312.1 gg_id:105770 Bacillus bogoriensis str. LBB3 AY3763
EU620448.1 gg_id:276903 Aerobic Facultative Alkalitolerant and Halotolerant Endospore Formers Soil Alvord B EU620
AJ717379.1 gg_id:110222 Bacillus sp. AC6t AJ7173
FJ764775.1 gg_id:541211 Bacillus sp. str. E-172 FJ7647
EU491818.1 gg_id:267423 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU491
AY553128.1 gg_id:101804 Bacillus sp. str. GSP69 AY553
DQ344635.1 gg_id:147585 Sinococcus beijingensis str. IMBZ007 DQ344
AB002644.1 gg_id:14473 G+C gram-positive HTA454 AB002
EU091310.1 gg_id:255095 Bacillus halodurans str. C7 EU091
EF422410.1 gg_id:206803 Bacillus sp. str. ANL-isoa2 EF4224
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AM050346.1 gg_id:134015 Bacillus sp. str. BR AM050

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DQ516994.1 gg_id:160836 Cultivation-intensive study ephemeral hypereutrophic aquatic microbial Mojave Des DQ516
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DQ227672.1 gg_id:146657 Bacillus sp. M115 DQ227
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EU090232.1 gg_id:244156 Bacillus pseudofirmus str. SJ2 EU090
FJ429990.1 gg_id:362192 Geobacillus sp. A142 FJ4299
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GQ280018.1 gg_id:514033 Bacillus sp. str. BJ-8 GQ280
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FJ430003.1 gg_id:366859 Geobacillus sp. A394 FJ4300
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AY543020.1 gg_id:103099 Brochothrix thermosphacta MF 154 AY5430

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CP001604.1 gg_id:528087 Listeria monocytogenes str. 08-5923 CP0016
CP001604.1 gg_id:528088 Listeria monocytogenes str. 08-5923 CP0016
NC_002973.6 gg_id:108681 Listeria monocytogenes str. 4b F2365 NC_00
CP001175.1 gg_id:522930 Listeria monocytogenes str. HCC23 CP0011
DQ065845.1 gg_id:133743 Listeria seeligeri str. ATCC 35967 DQ065
DQ065844.1 gg_id:133797 Listeria seeligeri str. 2436KA DQ065
DQ065846.1 gg_id:130677 Listeria welshimeri str. ATCC 35897 DQ065
NC_003212.1 gg_id:128465 Listeria innocua str. Clip11262 NC_00
FJ774219.1 gg_id:566482 Listeria monocytogenes str. N9 FJ7742
CP001604.1 gg_id:528090 Listeria monocytogenes str. 08-5923 CP0016
Y12757.1 gg_id:16370 Listeria-like organism clone Y12757
AJ535698.1 gg_id:100269 Listeria seeligeri 50 AJ5356
NC_008555.1 gg_id:196027 Listeria welshimeri serovar 6b str. SLCC5334 NC_00
X98532.1 gg_id:15046 Listeria welshimeri str. ATCC35897 X98532
FJ557241.1 gg_id:376496 Listeria sp. str. CIP 109804 FJ5572
Y14580.1 gg_id:14467 Ammoniphilus oxalivorans str. RAOx-FS Y14580
Y14579.1 gg_id:14469 Ammoniphilus oxalaticus str. RAOx-FF Y14579
Y14578.1 gg_id:14468 Ammoniphilus oxalaticus str. RAOx1 Y14578
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DQ129329.1 gg_id:154541 microarray level air two cities Texas urban aerosol clone AKIW1124 DQ129
DQ378179.1 gg_id:155936 oil-polluted soil clone F14_Pitesti DQ378
GQ062548.1 gg_id:410410 Topographical and Temporal Human Skin Microbiome skin nare clone nbw12b03c1 GQ062
DQ129330.1 gg_id:138087 microarray level air two cities Texas urban aerosol clone AKIW1134 DQ129
AM930509.1 gg_id:252328 Mobilizing agents enhance fungal degradation polycyclic aromatic hydrocarbons an AM930
Y14581.1 gg_id:14466 Oxalophagus oxalicus str. DSM 5503T Y14581
AB271755.1 gg_id:166364 Aneurinibacillus aneurinilyticus str. NBRC 15521 AB2717
X77789.1 gg_id:14455 Bacillus acidovorans str. ATCC 51159 X77789
GU397386.1 gg_id:521475 Aneurinibacillus migulanus str. A72 GU397
D78462.1 gg_id:14454 Aneurinibacillus migulanus str. ATCC9999 D78462
AJ715385.1 gg_id:100842 Aneurinibacillus terranovensis str. LMG 22483 AJ7153
EF032876.1 gg_id:174619 Aneurinibacillus thermoaerophilus str. AFNA 1 EF0328
X94196.1 gg_id:14460 Aneurinibacillus thermoaerophilus str. DSM 10154 X94196
DQ890194.1 gg_id:162600 Aneurinibacillus thermoaerophilus str. HZ DQ890
X94197.1 gg_id:14461 Aneurinibacillus thermoaerophilus str. DSM 10155 X94197
AB112725.1 gg_id:99186 Aneurinibacillus danicus str. NCIMB 13288T AB1127
DQ350838.1 gg_id:146417 Aneurinibacillus migulanus str. U603 DQ350
AJ586382.1 gg_id:104351 Brevibacillus borstelensis str. R-16402 AJ5863
DQ350837.1 gg_id:146165 Brevibacillus borstelensis str. U404 DQ350
EU714903.1 gg_id:323091 Brevibacillus borstelensis str. SRDTh2 EU7149

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AY372925.1 gg_id:141313 Brevibacillus sp. str. PC6 AY3729
AF378231.1 gg_id:72419 Brevibacillus invocatus str. LMG 18167 AF3782
AY745239.1 gg_id:107154 Brevibacillus laterosporus AY7452
AJ715383.1 gg_id:100531 Brevibacillus levickii str. R-22010 AJ7153
D78464.1 gg_id:14444 Brevibacillus reuszeri str. NRRL NRS-1206 D78464
AY196006.1 gg_id:82008 Brevibacillus thermoruber str. WR-249 AY1960
DQ452016.1 gg_id:220136 Brevibacillus sp. FB2 DQ452
AB048253.1 gg_id:27343 Brevibacillus agri str. MC-C1 AB0482
EF690427.1 gg_id:242098 Brevibacillus formosus M13-7 EF6904
EU497965.1 gg_id:266742 Brevibacillus sp. str. P-6 EU4979
EU730932.1 gg_id:318433 Brevibacillus invocatus str. 176 EU7309
FJ009377.1 gg_id:349508 Brevibacillus brevis str. G14 FJ0093
GQ495662.1 gg_id:560159 Brevibacillus brevis str. L-25 GQ495
EF055990.1 gg_id:181337 Brevibacillus parabrevis str. LH1-1 EF0559
AJ457160.1 gg_id:67396 Brevibacillus sp. str. AV-Pb AJ4571
AY493971.1 gg_id:136682 Fingerprinting aggregates soil clone 1047 AY4939
EU605978.1 gg_id:271212 Brevibacillus brevis str. B12 EU6059
EU621907.1 gg_id:277682 Brevibacillus sp. str. CCBAU 10720 EU6219
EU730938.1 gg_id:335118 Brevibacillus centrosporus str. 218 EU7309
D78460.1 gg_id:14443 Brevibacillus formosus str. NRRL NRS-863 D78460
EU221377.1 gg_id:253356 Brevibacillus laterosporus str. Y2S9 EU2213
AB362271.1 gg_id:268437 Brevibacillus sp. str. JAM-FM0601 AB3622
FJ430060.1 gg_id:362530 Brevibacillus sp. E187 FJ4300
AP008955.1 gg_id:560716 Brevibacillus brevis str. NBRC 100599 (= 47) AP0089
AB112717.1 gg_id:103446 Brevibacillus limnophilus str. DSM 6472 AB1127
AY072721.1 gg_id:77296 Brevibacillus sp. str. SE004 AY0727
FJ592179.1 gg_id:556989 Brevibacillus agri str. Q6-2 FJ5921
EU638360.1 gg_id:307934 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU6383
FJ430048.1 gg_id:361257 Brevibacillus sp. D505a FJ4300
AJ971483.1 gg_id:130970 Cohnia thermotolerans str. CCUG 47242 AJ9714
AB362828.1 gg_id:251819 Paenibacillus sp. str. YT1101 AB3628
AF227835.1 gg_id:16553 str. 31295 AF2278
EF203083.2 gg_id:206849 Paenibacillus sp. str. HIO-4 EF2030
EU134631.1 gg_id:253479 tallgrass prarie soil clone FFCH11327 EU1346
DQ129381.1 gg_id:137918 microarray level air two cities Texas urban aerosol clone AKIW1107 DQ129
AM900791.1 gg_id:244571 Cohnella sp. PA228 AM900
EU284591.1 gg_id:253236 Microbacterium sp. str. sq5 EU2845
EF368009.1 gg_id:214536 Cohnella soli str. 5GH36-9 EF3680
NR_028674.1 gg_id:565706 Bacillus edaphicus str. T7; CIP 105814 NR_028
DQ898308.1 gg_id:173293 Bacillus mucilaginosus str. AS1.231 DQ898
AF182807.2 gg_id:17949 Paenibacillus velasolus str. P1 AF1828

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EF103205.1 gg_id:182312 Paenibacillus sp. str. MSCB-8 EF1032
EF690415.1 gg_id:252209 Paenibacillus amylolyticus M18-5 EF6904
AJ884854.1 gg_id:186123 Paenibacillus sp. DF4MM5 AJ8848
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AJ884852.1 gg_id:199597 Paenibacillus sp. DF4MM1 AJ8848
FJ944661.1 gg_id:545044 Paenibacillus amylolyticus str. KUDC1039 FJ9446
AJ495806.1 gg_id:55541 Paenibacillus sp. p22D AJ4958
AJ884856.1 gg_id:174753 Paenibacillus sp. DF4SC1 AJ8848
AB073201.1 gg_id:77745 Paenibacillus apiarius str. DSM 5581 AB0732
GQ284360.1 gg_id:549779 Paenibacillus barengoltzii str. THWCSN11 GQ284
GQ284370.1 gg_id:559070 Paenibacillus barengoltzii str. THWCSN47 GQ284
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GQ284353.1 gg_id:577062 Paenibacillus barengoltzii str. THWCS6 GQ284
GQ284361.1 gg_id:547686 Paenibacillus barengoltzii str. THWCSN13 GQ284
GQ284355.1 gg_id:548873 Paenibacillus barengoltzii str. THWCS8 GQ284
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GQ284369.1 gg_id:583230 Paenibacillus barengoltzii str. THWCSN46 GQ284
GQ284371.1 gg_id:567491 Paenibacillus barengoltzii str. THWCSN50 GQ284
AB073364.1 gg_id:78279 Paenibacillus borealis str. DSM 13118 AB0733
FJ266315.1 gg_id:513350 Paenibacillus borealis str. RFNB4 FJ2663
AJ011322.1 gg_id:14376 Paenibacillus borealis KK19 AJ0113
NR_024857.1 gg_id:555585 Paenibacillus campinasensis str. 324; KCTC 364BP NR_024
AF181573.1 gg_id:73805 Paenibacillus cf. polymyxa 6 AF1815
EF516124.1 gg_id:225551 grassland soil clone FCPP694 EF5161
EF492898.1 gg_id:243136 Iron-manganese Nodule and Its Surrounding Soil soil around iron-manganese nodule EF4928
DQ906781.1 gg_id:250537 Oman subsurface soil clone 2A-10 DQ906
EU240430.1 gg_id:245111 Paenibacillus chondroitinus str. B179 EU2404
AB245386.1 gg_id:150342 Paenibacillus pocheonensis str. Gsoil 1138 AB2453
AJ438302.1 gg_id:67648 Paenibacillus cookii str. R-11600 AJ4383
D78466.1 gg_id:14415 Paenibacillus curdlanolyticus str. IFO15724T D78466
FJ944652.1 gg_id:539755 Paenibacillus elgii str. KUDC1030 FJ9446
AY090110.1 gg_id:89996 Paenibacillus elgii str. SD17 AY0901
FJ189797.1 gg_id:571764 Paenibacillus illinoisensis str. CSB12 FJ1897
D85397.1 gg_id:14360 Paenibacillus illinoisensis str. NRRL NRS-1356T D85397
FJ973530.1 gg_id:465403 Paenibacillus lactis str. NBPP29 B29 FJ9735
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EU236729.1 gg_id:247052 Paenibacillus lautus str. X6 EU2367
EU249589.1 gg_id:251174 Paenibacillus sp. str. TPSB9 EU2495
AJ491842.1 gg_id:78091 Paenibacillus lautus str. C2 AJ4918
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FJ974058.1 gg_id:382810 Paenibacillus lautus str. SK21 FJ9740
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EF190503.1 gg_id:238399 Paenibacillus lentimorbus str. DNG 16 EF1905
EU071599.1 gg_id:237117 Paenibacillus macerans str. EHFS1_S05Ta EU0715
EF459546.1 gg_id:205051 Paenibacillus macquariensis KFC-81 EF4595
AY230766.1 gg_id:84901 Paenibacillus massiliensis str. Smarlab BioMol-2301065 AY2307
AF353681.1 gg_id:51767 Paenibacillus naphthalenovorans str. PR-N1; ATCC BAA-206; DSM14203 AF3536
AF480935.1 gg_id:84099 Paenibacillus nematophilus str. NEM1a AF4809
EF190490.1 gg_id:239823 Paenibacillus popilliae str. Dutky 1S EF1904
EF190489.1 gg_id:250407 Paenibacillus popilliae str. NRRL B-2524 EF1904
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DQ338446.1 gg_id:147466 Paenibacillus sabina str. T49 DQ338
FJ973543.1 gg_id:418246 Paenibacillus sp. str. NBPP40 B40 FJ9735
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AJ316013.1 gg_id:48149 Paenibacillus stellifer str. IS1 AJ3160
EF690404.1 gg_id:255964 Paenibacillus terrae M1-4 EF6904
AJ318910.2 gg_id:77277 Paenibacillus terrae str. MH72 AJ3189
AJ297714.1 gg_id:42642 Paenibacillus sp. P15-9 AJ2977
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EU867345.1 gg_id:553260 Paenibacillus sp. str. CCGE3112 EU8673
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AB092351.1 gg_id:71025 Paenibacillus fujiensis str. Br1 AB0923
DQ338448.1 gg_id:146263 Paenibacillus sabina str. G18-7 DQ338
EU257517.1 gg_id:268656 Paenibacillus ourofinensis str. AC13MSD EU2575
NR_028886.1 gg_id:579344 Paenibacillus graminis str. RSA19; ATCC BAA-95 NR_028
AM162329.1 gg_id:141176 Paenibacillus sp. L47 AM162
FN563205.1 gg_id:564674 Impact changing HRT OLR on prokaryotes involved biomethanizitaion and fuzzy logic FN5632
EU391155.1 gg_id:410549 Paenibacillus pueri str. b13i-1 EU3911
EF194764.2 gg_id:187176 Paenibacillus sp. str. FH2071 EF1947
AB162693.1 gg_id:122657 Paenibacillus sp. str. SH-55 AB1626
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AY328609.1 gg_id:88221 drinking water system simulator clone HOClCi60 AY3286
AM930274.1 gg_id:571641 gradual cooling stage mass and its spatial composting clone SMG8 AM930
DQ346513.1 gg_id:154742 during composting libraries compost clone 2B29 DQ346
DQ129556.1 gg_id:138658 microarray level air two cities Texas urban aerosol clone AKIW1130 DQ129
AJ251193.1 gg_id:21436 Paenibacillus sp. str. TRO4 (=LMG 19081) AJ2511
GQ249618.1 gg_id:589407 Microbial anaerobic sediments Bay Cadiz (Spain) marine sediment: 18-20 cm layer cl GQ249
AM492794.1 gg_id:555079 Paenibacillus darangshiensis str. DSL-01 = JBRI 2110 AM492
EU257201.2 gg_id:278281 Paenibacillus riograndensis str. SBR5 EU2572
EF452662.1 gg_id:214602 Paenibacillus sp. str. DCY16 EF4526
AM900790.1 gg_id:235287 Paenibacillus sp. PA227 AM900
DQ816106.1 gg_id:166366 mouse cecum clone aaa87h04 DQ816
FN395280.1 gg_id:421089 Paenibacillus sp. str. FR-W5cb FN3952
GU272267.1 gg_id:535255 library dichlorvos treatment rape phyllosphere clone TF178 GU272
EU730934.1 gg_id:312510 Paenibacillus validus str. 197 EU7309
X77792.1 gg_id:14409 Bacillus viscosus str. ATCC 51155 X77792
AB045094.1 gg_id:99679 Paenibacillus pabuli str. HSCC 492T (NRRL NRS-924T) AB0450
DQ338444.1 gg_id:146742 Paenibacillus sabina str. T27 DQ338
EU571156.1 gg_id:276668 Paenibacillus sp. str. 11-5 EU5711
EU798300.1 gg_id:350178 Paenibacillus favisporus str. GXN153 EU7983
AY728023.1 gg_id:163477 Paenibacillus sp. str. H3029 AY7280
EU464732.1 gg_id:302066 Hartmann's mountain zebra feces clone AFZEB_aaj69h02 EU4647
FJ544322.1 gg_id:461651 Paenibacillus graminis str. 801 FJ5443
AY279193.1 gg_id:86920 Paenibacillus favisporus str. KNUC56 AY2791
EU464951.1 gg_id:300927 African elephant feces clone AFYEL_aaj65f10 EU4649
EU570250.1 gg_id:275303 Paenibacillus sp. str. CJ25 EU5702
EU003588.1 gg_id:235578 Paenibacillus sp. str. NCCB 100172 EU0035
EF690429.1 gg_id:243542 Paenibacillus sp. M9-2 EF6904
EU571197.1 gg_id:269962 Paenibacillus sp. str. 25-14 EU5711
AJ318909.2 gg_id:77280 MH21 earthworm gut AJ3189
AY559427.1 gg_id:202319 Hot Springs Taiwan hot spring water clone LS35 AY5594
EU240395.1 gg_id:245141 Paenibacillus amylolyticus str. B87 EU2403
AY326632.1 gg_id:136867 Amazon soil clone 43-1 AY3266
EU240394.1 gg_id:239112 Paenibacillus sp. str. B113 EU2403
AM745263.1 gg_id:243849 Paenibacillus caespitis str. LMG 23879 AM745
AJ131119.1 gg_id:14368 Paenibacillus sp. vortex AJ1311
AY772704.1 gg_id:110061 Paenibacillus polymyxa str. CP7 AY7727
EF025575.1 gg_id:185569 Paenibacillus ehimensis str. IB5 EF0255
DQ129332.1 gg_id:137603 urban aerosol clone AKIW967 DQ129
DQ407277.1 gg_id:156397 Paenibacillus sp. str. PALXIL02 DQ407
AM906087.1 gg_id:252504 Paenibacillus sp. str. P117 AM906

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AB257600.1 gg_id:262550 Paenibacillus sp. str. KSM-318 AB257
AB073189.1 gg_id:78298 Paenibacillus glucanolyticus str. DSM 5162 AB073
EU249588.1 gg_id:237405 Paenibacillus sp. str. DFVB13 EU249
GQ244430.1 gg_id:579358 Paenibacillus sp. str. R2 GQ244
GQ007872.1 gg_id:501793 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ007
DQ272469.1 gg_id:141630 Paenibacillus sp. str. ADC2 DQ272
EU134647.1 gg_id:252877 tallgrass prarie soil clone FFCH14175 EU134
DQ291142.1 gg_id:142876 Paenibacillus sepulcri str. CCM 7311; LMG 19508 DQ291
FJ432004.1 gg_id:366723 Paenibacillus chibensis str. ZYb3 FJ4320
EF690424.1 gg_id:240189 Paenibacillus sp. M10-6 EF6904
GQ476810.2 gg_id:578500 Paenibacillus sp. str. R172 GQ476
AF071860.1 gg_id:14395 Paenibacillus popilliae str. NRRL B-4081 AF071
AY592793.1 gg_id:103973 deep-sea mud volcano clone Napoli-4B-79; BC07-4B-79 AY592
AF130254.1 gg_id:42610 Paenibacillus koreensis str. YC300 AF130
AY302187.1 gg_id:90699 Paenibacillus polymyxa str. BS04 AY302
DQ816367.1 gg_id:168948 mouse cecum clone aab17b06 DQ816
EF620476.1 gg_id:247159 Paenibacillus polymyxa str. ISSDS-307 EF6204
AB042938.1 gg_id:43825 Paenibacillus glycanilyticus str. DS-1 AB042
AB294155.1 gg_id:210271 Paenibacillus sp. str. BS2 AB294
GU187433.1 gg_id:569728 Paenibacillus sp. str. CAU 9324 GU187
AY289501.2 gg_id:100104 Paenibacillus sp. IDA4508 AY289
AY556414.1 gg_id:100022 Paenibacillus sp. str. SSL4 AY5564
AJ576374.1 gg_id:99041 midgut homogenate Pachnoda ephippiata larva clone PeM01 AJ5763
GQ497919.1 gg_id:586156 Paenibacillus sp. str. KO_CM21 GQ497
AJ863291.1 gg_id:120989 poplar tree microcosm rhizosphere unflooded clone 4RHU38 AJ8632
AB073192.1 gg_id:78185 Paenibacillus illinoisensis str. JCM 9907 AB073
GQ202679.1 gg_id:577284 Paenibacillus sp. str. U4 STR GQ202
AM162295.1 gg_id:143576 Paenibacillus sp. 6M20 AM162
AF480934.1 gg_id:84499 Paenibacillus sp. str. NEM3 AF480
EU722403.1 gg_id:342726 Paenibacillus sp. str. 13-4-17 EU722
AB119649.2 gg_id:94822 Paenibacillus abekawaensis str. MG1 AB119
FJ542823.1 gg_id:520512 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone A FJ5428
AY382189.1 gg_id:98371 Paenibacillus sp. str. R-7652 AY382
EF212892.1 gg_id:272047 Paenibacillus urinalis str. 5402403 EF2128
AM745265.1 gg_id:258150 Paenibacillus telluris str. LMG 23881T AM745
AM162324.1 gg_id:143178 Paenibacillus sp. HO2-R17 AM162
GU080334.1 gg_id:539906 Paenibacillus sp. str. XP13 GU080
AY266990.1 gg_id:86275 Paenibacillus sp. str. 448-L5 AY266
AB179866.1 gg_id:99385 Paenibacillus sp. str. SG AB179
AF515611.1 gg_id:64883 Paenibacillus polymyxa str. GBR-1 AF515

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FJ006910.1 gg_id:347359 Paenibacillus sp. str. WPCB158 FJ0069
DQ816059.1 gg_id:169712 mouse cecum clone aaa86h05 DQ816
EU134623.1 gg_id:241881 tallgrass prarie soil clone FFCH7271 EU134
GQ263672.1 gg_id:573776 Structure Simulated Level Waste Site simulated level waste site clone FW3_62C GQ263
EU464927.1 gg_id:296158 African elephant feces clone AFYEL_aaj65c09 EU464
DQ407283.1 gg_id:151967 Paenibacillus sp. str. PALXIL11 DQ407
EU571198.1 gg_id:275621 Paenibacillus sp. str. 27-7 EU571
EU982512.1 gg_id:513039 Paenibacillus polymyxa str. 1207 EU982
EU134664.1 gg_id:257557 tallgrass prarie soil clone FFCH7932 EU134
AF355463.1 gg_id:42808 Paenibacillus polymyxa AF355
DQ836314.1 gg_id:166697 Paenibacillus validus str. S3 DQ836
DQ890521.1 gg_id:163114 Paenibacillus taiwanensis str. BCRC 17411 DQ890
AF164345.1 gg_id:46987 Paenibacillus chinjuensis str. WN9 AF164
AB045096.1 gg_id:99994 Bacillus sp. str. HSCC 1471 (NCIMB 9651) AB045
AB111937.2 gg_id:100108 Paenibacillus sp. str. A63 AB111
AY439226.1 gg_id:106608 Paenibacillus sp. GIC16 AY439
EF079062.1 gg_id:179040 Paenibacillus donghaensis str. JH 8 EF079
AF395028.1 gg_id:38098 Paenibacillus sp. str. C15 AF395
AJ229199.1 gg_id:50002 anoxic bulk soil flooded rice microcosm clone BSV44 clone AJ2291
AF006077.1 gg_id:14405 Bacillus mucilaginosus str. 1480D AF006
AM162334.1 gg_id:141122 Paenibacillus sp. YN08-04 AM162
GQ058441.1 gg_id:430478 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1 GQ058
EU464831.1 gg_id:289481 Hartmann's mountain zebra feces clone AFZEB_aaj71f03 EU464
GQ476811.2 gg_id:546073 Paenibacillus sp. str. R12-2 GQ476
EF127602.1 gg_id:207635 Fossil Genes and Microbes Entombed Oldest Ice on Earth ice clone EME078 EF1276
EU571139.1 gg_id:263497 Paenibacillus sp. str. 3-1 EU571
EU888525.1 gg_id:334762 Paenibacillus sp. str. FR1_23 EU888
GQ263441.1 gg_id:579869 Structure Simulated Level Waste Site simulated level waste site clone FW2_127B GQ263
GQ284352.1 gg_id:568865 Paenibacillus barengoltzii str. THWCS4 GQ284
AF468220.1 gg_id:110511 Paenibacillus sp. 1 AF468
NR_025754.1 gg_id:574476 Paenibacillus sanguinis str. 2301083; CCUG 48214 NR_02
DQ816668.1 gg_id:165977 mouse cecum clone aaa97a09 DQ816
AY167820.1 gg_id:77386 Paenibacillus sp. str. SAFN-007 AY167
NR_029109.1 gg_id:563078 Paenibacillus xylanilyticus str. XIL14; LMG 21957 NR_02
DQ085279.1 gg_id:137505 Paenibacillus ruminocola str. G22 DQ085
DQ125886.1 gg_id:134126 uranium contaminated soil clone AKAU4139 DQ125
FJ040809.1 gg_id:572351 Paenibacillus macerans str. HR13 FJ0408
AM162300.1 gg_id:143828 Paenibacillus sp. F11 AM162
X77846.1 gg_id:14423 Paenibacillus durus str. DSM 1735 X77846
AB362821.1 gg_id:241963 Paenibacillus sp. str. YT0003 AB362

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AJ011321.1 gg_id:14375 Paenibacillus borealis KM8 AJ0113
AY397766.1 gg_id:96549 Paenibacillus sp. str. R-6466 AY3977
EU464438.1 gg_id:288992 African elephant feces clone AFEL_aai29b10 EU4644
AB045097.1 gg_id:100154 Bacillus sp. str. HSCC 1649T (IK-5) AB0450
EF620469.1 gg_id:245314 Paenibacillus polymyxa str. ISSDS-795 EF6204
EU379277.1 gg_id:270084 Paenibacillus pabuli str. 4RS-1a EU3792
EU249590.1 gg_id:257331 Paenibacillus xylanilyticus str. DPBS5 EU2495
DQ338443.1 gg_id:145299 Paenibacillus forsythia str. T98 DQ338
GU328687.1 gg_id:566956 Paenibacillus sp. str. Nz32 GU328
GQ423056.1 gg_id:557058 Paenibacillus sp. str. S22 GQ423
AB073363.1 gg_id:77737 Paenibacillus kobensis str. DSM 10249 AB0733
GQ355278.1 gg_id:590264 Paenibacillus sp. str. GT-L27 GQ355
DQ298737.1 gg_id:144677 soybean rhizosphere DQ298
AB482199.1 gg_id:553697 Paenibacillus abekawaensis str. MG1 (= DSM 16939 = NBRC 100733) AB4821
AY725249.1 gg_id:102292 decayed velvetleaf seed clone S1-1-CL12 AY7252
EU134644.1 gg_id:257088 tallgrass prarie soil clone FFCH13623 EU1346
EF626690.1 gg_id:240072 Paenibacillus sp. str. CKOBP-6 EF6266
AJ000984.2 gg_id:14396 soil clone DA116 AJ0009
AB073197.1 gg_id:77646 Paenibacillus thiaminolyticus str. IFO 15656 AB0731
AB366401.1 gg_id:277860 Paenibacillus pabuli str. SW12 AB3664
AM162321.1 gg_id:141438 Paenibacillus sp. HS16-12 AM162
NR_025106.1 gg_id:548770 Paenibacillus brasilensis str. PB1 72; ATCC BAA-413 NR_025
GU213302.1 gg_id:588836 Paenibacillus sp. str. 4-10 GU213
AB362822.1 gg_id:248417 Paenibacillus sp. str. YT0011 AB3628
GQ284368.1 gg_id:573503 Paenibacillus barengoltzii str. THWCSN26 GQ284
FN673694.1 gg_id:517700 Paenibacillus anaericanus str. DSM 15890 FN6736
EU331367.1 gg_id:242588 Influence Nitrate on Microbial Reduction Pertechnetate nitrate microcosm sediment EU3313
FN293173.1 gg_id:543248 Paenibacillus sp. str. MC-246 FN2931
EU373421.1 gg_id:273400 Paenibacillus polymyxa str. YRL13 EU3734
DQ023221.2 gg_id:132196 Paenibacillus sp. str. GPTSA 19T DQ023
DQ309072.1 gg_id:150196 Paenibacillus soli str. DCY03 DQ309
EU497637.1 gg_id:259802 Paenibacillus sp. str. Dg-1009 EU4976
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AB045102.1 gg_id:104520 Paenibacillus ehimensis str. HSCC 594 (IFO 15658) AB0451
AF537343.3 gg_id:104054 Bacillus sp. str. MZLU AF5373
GU457786.1 gg_id:520530 Paenibacillus sp. str. R1-12-4 GU457
AM162305.1 gg_id:142343 Paenibacillus sp. A26 AM162
EU661711.1 gg_id:285693 Paenibacillus ehimensis str. NBRAJATH7 EU6617
EF125184.1 gg_id:188416 Paenibacillus sp. str. SA-7-6 EF1251

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AJ716019.1 gg_id:100354 Paenibacillus barcinonensis str. BP-23 AJ7160
AB245383.1 gg_id:146833 Paenibacillus ginsengagri str. Gsoil 3125 AB2453
DQ243815.1 gg_id:151279 Paenibacillus sp. str. 2S6 DQ243
EU391157.1 gg_id:419476 Paenibacillus pectinilyticus str. RCB-08 EU3911
DQ112247.1 gg_id:131383 Paenibacillus sp. str. CWBI-B1070 DQ112
AY154489.1 gg_id:107622 earthworm intestine clone wi32 AY1544
EU647520.1 gg_id:545572 Paenibacillus sp. str. TeW EU6475
FN563170.1 gg_id:582506 Impact changing HRT OLR on prokaryotes involved biomethanizitaion and fuzzy logic FN5631
AM162341.1 gg_id:141288 Paenibacillus sp. GR13-04 AM162
Y13062.1 gg_id:80385 Bacillus circulans str. WSBC20030 Y13062
EU571189.1 gg_id:260618 Paenibacillus sp. str. 23-13 EU5711
EF199999.1 gg_id:189311 Paenibacillus odorifer str. PNF4 EF1999
AJ863305.1 gg_id:119660 poplar tree microcosm rhizosphere unflooded clone 16RHU11 AJ8633
AJ223990.1 gg_id:14384 Paenibacillus odorifer str. TOD45 AJ2239
AM162322.1 gg_id:141541 Paenibacillus sp. YO4-02 AM162
AF290916.1 gg_id:28736 Paenibacillus daejeonensis str. AP-20 AF2909
EU638756.1 gg_id:353899 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU6387
DQ444985.1 gg_id:158562 Paenibacillus sp. Eur1 9.25 DQ444
EF682937.1 gg_id:245965 Eastern Mediterranean atmosphere clone F12_5F_FL EF6829
FJ479476.1 gg_id:573137 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4794
AB369185.1 gg_id:240501 Microbiological Assessment Circulation Mud Fluids During First Operation Drilling De AB3691
GU214173.1 gg_id:534180 and biota slimes Canadian paper mills slime mill taken wet section around papermal GU214
EF208754.1 gg_id:200803 Paenibacillus sp. str. Ao3 EF2087
FJ859876.1 gg_id:574741 Paenibacillus sp. str. MSL-9 FJ8598
AF492843.1 gg_id:67227 Bacillus sp. str. NK395 AF4928
AB271758.1 gg_id:170195 Paenibacillus polymyxa str. NBRC 15309 AB2717
FJ999582.1 gg_id:410196 Paenibacillus sp. str. HLSBA1 FJ9995
AB362823.1 gg_id:246316 Paenibacillus sp. str. YT0039 AB3628
AF465647.1 gg_id:34110 Bacillus sp. str. YNPRH6P-1 AF4656
DQ816052.1 gg_id:163426 mouse cecum clone aaa86f09 DQ816
EF694702.1 gg_id:235485 Paenibacillus terrae EH23-5 EF6947
FN433032.1 gg_id:533274 Paenibacillus alvei CCM2B FN4330
GQ074220.1 gg_id:392310 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ074
AM991254.1 gg_id:277951 Microbial groundwater and their potential use biomonitoring karst spring water clo AM991
EU867347.1 gg_id:545107 Paenibacillus sp. str. CCGE3115 EU8673
GU214160.1 gg_id:587713 and biota slimes Canadian paper mills slime mill taken wet section around papermal GU214
AJ011327.1 gg_id:14381 Paenibacillus borealis HM31 AJ0113
AY493972.1 gg_id:136753 Fingerprinting aggregates soil clone 449 AY4939
EU465045.1 gg_id:296852 African elephant feces clone AFYEL_aaj67b11 EU4650

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EU046270.1 gg_id:236825 Paenibacillus xinjiangensis str. HR1 EU0462
AY839866.1 gg_id:110036 Paenibacillus sp. str. B518 AY8398
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EU134635.1 gg_id:237941 tallgrass prarie soil clone FFCH12118 EU1346
AB041721.1 gg_id:50544 Paenibacillus koleovorans str. TK AB0417
GQ015112.1 gg_id:494553 Topographical and Temporal Human Skin Microbiome skin back clone nbw816b06c1 GQ015
DQ787687.1 gg_id:172955 holocene lake sediment clone SLB315 DQ787
DQ129261.1 gg_id:137642 urban aerosol clone AKIW887 DQ129
AJ005795.1 gg_id:14413 Thermobacillus xylanilyticus str. XE AJ0057
GQ471930.1 gg_id:551611 Toward Plant Cell Wall Degradation Under Thermophilic Condition: Unique Microbia GQ471
AB234269.1 gg_id:148244 Biotransformation Polychlorinated Dioxins Microbial Dynamics Sediment Microcosm AB2342
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AF375881.1 gg_id:38647 Pasteuria penetrans AF3758
AF516396.1 gg_id:86730 Pasteuria nishizawae str. Tohoku AF5163
AJ878853.1 gg_id:111838 Pasteuria hartismerei AJ8788
AF254387.1 gg_id:44324 Candidatus Pasteuria usgae S-1 AF2543
AF515699.1 gg_id:87218 Pasteuria goettingianae AF5156
U34688.1 gg_id:14343 Daphnia endosymbiotic bacterium U34688
GQ448221.1 gg_id:589624 Microbiome neonatal calves: shedding microorganisms fecal clone calf32_10wks_gr GQ448
GU385871.1 gg_id:522968 Bacillus psychrodurans str. QT25 GU385
AM980508.1 gg_id:269916 Bacillus insolitus str. DSM 5T AM980
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EU778690.1 gg_id:345702 Springbok feces clone SBK_e12_1 EU7786
EF377312.1 gg_id:203909 Bacillus sp. str. CCBAU 10775 EF3773
EU458350.1 gg_id:292185 spotted hyena feces clone HY1_b04 EU4583
AB017538.1 gg_id:15018 Renibacterium salmoninarum AB0175
EU249570.1 gg_id:243498 Bacillus sp. str. TSG11 EU2495
EF377302.1 gg_id:204730 Bacillus sp. str. CCBAU 13244 EF3773
EU249572.1 gg_id:237395 Bacillus sp. str. DFVB3 EU2495
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AB199593.2 gg_id:119659 Bacillus borotolerans str. T-12B AB1995
AF169518.1 gg_id:74854 Bacillus sp. str. BD-83 AF1695
FM178866.1 gg_id:330655 Acetobacter pasteurianus str. CCM 3612 FM178
GQ280058.1 gg_id:592898 Bacillus sp. str. BJ-48 GQ280
EU867354.1 gg_id:543461 Lysinibacillus fusiformis str. CCGE2086 EU8673
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EU187497.1 gg_id:257140 Lysinibacillus sphaericus str. X-17 EU187
EU252508.1 gg_id:238118 Bacillus sp. str. AM20 EU252
GU129144.1 gg_id:588459 Lysinibacillus sphaericus str. TMB5 GU129
AF169523.1 gg_id:42176 Bacillus sp. str. BD-94 AF169
GU385849.1 gg_id:522769 Acetobacter pasteurianus str. QT3 GU385
GQ501071.1 gg_id:549791 Lysinibacillus fusiformis str. Ma-Su CECRI 2 GQ501
GQ284348.1 gg_id:580342 Lysinibacillus fusiformis str. PCWCS3 GQ284
DQ289063.1 gg_id:144100 Bacillus macroides WST 1 DQ289
L38654.1 gg_id:14988 Bacillus sphaericus L38654
GU084135.1 gg_id:540739 Lysinibacillus fusiformis str. DB-1 GU084
GQ280094.1 gg_id:585121 Bacillus sp. str. JS-24 GQ280
FJ266320.1 gg_id:509099 Lysinibacillus sphaericus str. RFNB10 FJ2663
EU240383.1 gg_id:248547 Lysinibacillus sphaericus str. B85 EU240
EU647711.1 gg_id:273725 Lysinibacillus fusiformis str. REG60 EU647
EU855791.1 gg_id:346402 Lysinibacillus sphaericus Drngp EU855
GQ889259.1 gg_id:569561 Lysinibacillus sphaericus str. S8 GQ889
DQ990064.1 gg_id:195474 Microbial Profiling Some Heterotrophic isolates Waters and Shal Groundwater Wells DQ990
AB199591.2 gg_id:123207 Bacillus borotolerans str. T-10a AB199
GQ284508.1 gg_id:540272 Lysinibacillus sp. str. TSSAS2-47 GQ284
GU201856.1 gg_id:529798 Lysinibacillus fusiformis str. Zw-13-3 GU201
AJ237708.1 gg_id:14648 Marinibacillus marinus str. DSM 1297 AJ2377
EU812465.1 gg_id:326668 Bacillus sp. str. B-9987 EU812
AY190535.1 gg_id:79732 Marinibacillus campisalis str. SF-57 AY190
AF281158.1 gg_id:28627 Jeotgalibacillus alimentarius str. YKJ-13 AF281
FJ263020.1 gg_id:367827 Sporosarcina sp. str. ZD30 FJ2630
DQ444983.1 gg_id:157780 Sporosarcina sp. Eur1 9.21 DQ444
FJ999934.1 gg_id:562449 Paenisporosarcina macmurdoensis str. EQH5 FJ9999
AF237975.1 gg_id:73281 Planococcus citreus str. MS20 AF237
FJ373028.1 gg_id:354487 Planococcus citreus str. W2-3 FJ3730
NR_026090.1 gg_id:544445 Planococcus citreus str. NCIMB 1493 NR_02
AJ966515.2 gg_id:119206 Planococcus columbaii str. PgEx11 AJ9665
EF467308.1 gg_id:215171 Planococcus maitriensis str. Anita I EF4673
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AM411996.1 gg_id:191228 Planococcus rifietoensis Z19-2zhy AM411
AJ314745.1 gg_id:29551 Planococcus antarcticus str. CMS 26or AJ3147
AJ314747.1 gg_id:37775 Planococcus antarcticus str. CMS 84or AJ3147

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AM111009.1 gg_id:140923 Planococcus sp. str. 3059 AM111
DQ435614.1 gg_id:154002 Planococcus sp. str. L4 DQ435
EU362181.1 gg_id:324748 Paenibacillus sp. str. C8 EU362
FJ717184.1 gg_id:534668 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United Kingc FJ7171
AY771711.1 gg_id:108687 Planococcus psychrotoleratus str. S2-46 AY7717
AF324659.1 gg_id:74784 Planococcus psychrotoleratus str. JCM 11080 AF3246
AY538695.1 gg_id:103548 Planococcus sp. str. Smarlab 3302355 AY5386
EU845048.1 gg_id:321091 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8450
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AY771727.1 gg_id:143378 Planococcus psychrotoleratus S3-21 AY7717
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AY260168.1 gg_id:87474 Planococcus kazaiensis str. K01-30 AY2601
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FJ265708.1 gg_id:328050 Planomicrobium sp. str. ISL-41 FJ2657
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EU468086.1 gg_id:289850 cheetah feces clone CE2_e08_3 EU4680
FJ675233.1 gg_id:517131 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6752
EU773781.1 gg_id:324889 Cheetah feces clone CE2_f11_1 EU7737
EU467969.1 gg_id:289010 cheetah feces clone CE2_c09_1 EU4679
FJ671794.1 gg_id:515670 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6717
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EU881980.1 gg_id:334555 Kurthia gibsonii str. HDDMN09 EU8819
EU266058.1 gg_id:279405 Bacillus sp. str. SL170 EU2660
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EU776120.1 gg_id:316126 Spotted hyena feces clone HY1_h08_1 EU7761
EU794212.1 gg_id:330402 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_R41 EU7942
EU867363.1 gg_id:574930 Solibacillus silvestris str. CCGE2032 EU8673
EU464938.1 gg_id:302898 African elephant feces clone AFYEL_aaj65e03 EU4649
EU366378.1 gg_id:273023 Bacillus silvestris str. IV13 EU3663
FJ379320.1 gg_id:555419 Bacillus sp. str. KHg2 FJ3793

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EU466752.1 gg_id:298191 African elephant feces clone AFEL2_aao29a02 EU466
EU467027.1 gg_id:298756 African elephant feces clone AFEL2_aao32h06 EU467
EU464619.1 gg_id:288715 African elephant feces clone AFEL_aai31h12 EU464
EU458355.1 gg_id:298357 spotted hyena feces clone HY1_c04_1 EU458
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EU466911.1 gg_id:295611 African elephant feces clone AFEL2_aao31c04 EU466
EU464646.1 gg_id:297510 African elephant feces clone AFEL_aai32e01 EU464
EU466769.1 gg_id:291375 African elephant feces clone AFEL2_aao29c04 EU466
X70319.1 gg_id:14991 Caryophanon latum str. NCDO 2034 X70319
EU466938.1 gg_id:296817 African elephant feces clone AFEL2_aao31f02 EU466
GQ448631.1 gg_id:562030 Microbiome neonatal calves: shedding microorganisms fecal clone calf784_6wks_gr GQ448
FJ676958.1 gg_id:514467 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6769
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EU464508.1 gg_id:289686 African elephant feces clone AFEL_aai30d01 EU464
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EU466996.1 gg_id:300307 African elephant feces clone AFEL2_aao32e02 EU466
EU467023.1 gg_id:296178 African elephant feces clone AFEL2_aao32h01 EU467
EU458363.1 gg_id:303075 spotted hyena feces clone HY1_d11_1 EU458
FJ683349.1 gg_id:524261 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6833
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FJ683448.1 gg_id:526268 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6834
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AJ491302.1 gg_id:64192 Caryophanon latum str. DSM 14151 AJ4913
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EU466995.1 gg_id:294075 African elephant feces clone AFEL2_aao32d11 EU466
FJ227504.1 gg_id:304321 Identification unculturable species growing sugarcane molasses based distillery spent FJ2275
EU466017.1 gg_id:297626 African elephant feces clone AFEL3_aao15h09 EU466
AM934693.1 gg_id:274290 Bacillus sp. str. CL1.8 AM934

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AY167819.1 gg_id:77326 Sporosarcina aquimarina str. SAFN-008 AY1678
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EU468034.1 gg_id:292404 cheetah feces clone CE2_f04_1 EU468
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X54968.1 gg_id:15012 Sporosarcina psychrophila str. W16A X54968
X54969.1 gg_id:15013 Sporosarcina psychrophila str. W5 X54969
EU939438.1 gg_id:356519 Fecal wild pygmy loris feces clone WF16S_292 EU939
DQ337594.1 gg_id:149329 Bacillus sp. CHNTR52 DQ337
D16277.1 gg_id:15015 Sporosarcina psychrophila str. IAM 12468 D16277
EU308121.1 gg_id:237733 Sporosarcina ginsengisoli str. FT7 EU308
AF548880.1 gg_id:55578 Bacillus sp. str. CPB 9 AF5488
AM237400.1 gg_id:153553 Sporosarcina globispora OS-253 AM237
EU308120.1 gg_id:252542 Sporosarcina aquimarina str. FT1 EU308
AY167816.1 gg_id:77347 Filibacter limicola str. SAFN-012 AY1678
AF548874.1 gg_id:57755 Bacillus sp. str. CPB 2 AF5488
AJ831845.1 gg_id:107690 Bacillus sp. str. 41KF1 AJ8318
FJ894720.1 gg_id:574272 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota BME; ear p FJ8947
X68415.1 gg_id:15008 Sporosarcina globispora str. DSM 4 X68415
AJ292316.1 gg_id:51589 Filibacter limicola str. DSM 13886T AJ2923
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AB547124.1 gg_id:523827 Bacillus sp. str. NCCP-36 AB5471
EU464503.1 gg_id:299250 African elephant feces clone AFEL_aai30c05 EU4645
EU465114.1 gg_id:291402 African elephant feces clone AFYEL_aaj68c06 EU4651
AM888194.1 gg_id:256287 Bacillus sp. str. TSWCSN5 AM888
EU464435.1 gg_id:289502 African elephant feces clone AFEL_aai29b05 EU4644
EU464428.1 gg_id:303291 African elephant feces clone AFEL_aai29a09 EU4644
EU464595.1 gg_id:294723 African elephant feces clone AFEL_aai31e08 EU4645
EU223959.1 gg_id:247009 -RFLP microbes Qinghai-Tin rail soil clone 142 EU2239
EU469326.1 gg_id:294062 springbok feces clone SBK_e10 EU4693
EU464637.1 gg_id:290772 African elephant feces clone AFEL_aai32d01 EU4646
AB245381.1 gg_id:147870 Sporosarcina ginsengisoli str. Gsoil 1433 AB2453
EU464521.1 gg_id:293562 African elephant feces clone AFEL_aai30e07 EU4645
EU465008.1 gg_id:290826 African elephant feces clone AFYEL_aaj66f03 EU4650
AB243859.1 gg_id:252210 Sporosarcina saromensis str. HG645 AB2438
AY372918.1 gg_id:141968 Bacillus sp. str. PC2 AY3729
EU464628.1 gg_id:294015 African elephant feces clone AFEL_aai32b05 EU4646
EU464656.1 gg_id:298694 African elephant feces clone AFEL_aai32f04 EU4646
FJ681965.1 gg_id:530313 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6819
EU128488.1 gg_id:248552 Bacillus sp. str. CWBI B1434 EU1284
EU771617.1 gg_id:344433 African elephant feces clone AFEL2_aao31a11 EU7716
DQ125520.1 gg_id:134154 uranium contaminated soil clone AKAU3481 DQ125
EU464620.1 gg_id:290547 African elephant feces clone AFEL_aai32a04 EU4646
EU464601.1 gg_id:297706 African elephant feces clone AFEL_aai31f03 EU4646
AM180748.1 gg_id:147511 Planococcus citreus UC15 AM180
EU465860.1 gg_id:299202 African elephant feces clone AFEL3_aao13b02 EU4658
EU464657.1 gg_id:301998 African elephant feces clone AFEL_aai32f06 EU4646
AF500007.1 gg_id:66683 Planococcus maritimus str. TF-9 AF5000
DQ345467.1 gg_id:151317 during composting libraries compost clone 0B14 DQ345
EU458324.1 gg_id:300849 spotted hyena feces clone HY1_d11 EU4583
AY677116.1 gg_id:138589 Bacillus massiliensis str. 4400831 AY6771
EU464967.1 gg_id:302579 African elephant feces clone AFYEL_aaj65h11 EU4649
EU778726.1 gg_id:306956 Springbok feces clone SBK_g04_1 EU7787
EU771809.1 gg_id:313253 African elephant feces clone AFEL3_aao14a04 EU7718
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EU465862.1 gg_id:299731 African elephant feces clone AFEL3_aao13b04 EU4658
EU771667.1 gg_id:318825 African elephant feces clone AFEL_aai30b08 EU7716
EU466815.1 gg_id:301287 African elephant feces clone AFEL2_aao29g12 EU4668
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EU464648.1 gg_id:287337 African elephant feces clone AFEL_aai32e03 EU4646

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EU465924.1 gg_id:294077 African elephant feces clone AFEL3_aao14b11 EU4659
EU467924.1 gg_id:300689 cheetah feces clone CE2_c04 EU4679
DQ350822.1 gg_id:147600 Bacillus massiliensis str. 625 DQ350
DQ350820.1 gg_id:149022 Bacillus sphaericus str. 601 DQ350
FJ373039.2 gg_id:328019 Bacillus sp. str. S7-3 FJ3730
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FJ681317.1 gg_id:520320 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6813
FJ682537.1 gg_id:515638 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6825
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DQ351921.1 gg_id:168183 manganese oxidation soil clone JH-GY13 DQ351
AM295339.1 gg_id:323201 Crocinobacterium jejui str. SW2G-14 AM295
EU464457.1 gg_id:293528 African elephant feces clone AFEL_aai29d11 EU4644
EF061442.1 gg_id:193195 Bacillus sp. NJSN49 EF0614
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AB170018.1 gg_id:104224 Ureibacillus sp. MM122 AB1700
AM932266.1 gg_id:272689 Ureibacillus sp. str. S22-30 AM932
AB375754.1 gg_id:340308 Bacillus sp. str. 50LAy-1 AB3757
NR_025394.1 gg_id:533566 Ureibacillus terrenus str. DSM 12654 TH9A NR_025
DQ348072.1 gg_id:149858 Ureibacillus koreensis str. HC 148 DQ348
DQ348071.1 gg_id:148390 Ureibacillus rudaensis str. HC 145 DQ348
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AY850380.1 gg_id:112588 Ureibacillus sp. 6T29 AY8503

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s__Salinicoccus roseus	42956

AB210992.1 gg_id:115344 Ureibacillus thermosphaericus str. SSCS46-2 AB210
AB211000.1 gg_id:115243 Ureibacillus thermosphaericus str. SSCS41-1 AB211
AB211003.1 gg_id:115348 Ureibacillus thermosphaericus str. SSCS39-2 AB211
AB211004.1 gg_id:115248 Ureibacillus thermosphaericus str. SSCS39-1 AB211
EF690414.1 gg_id:245684 Bacillus arenosi M18-3 EF690
EU741070.1 gg_id:548314 Viridibacillus arenosi str. 13630P EU741
NR_025628.1 gg_id:542641 Viridibacillus arenosi str. LMG 22166 NR_02
AJ627211.1 gg_id:101984 Bacillus arvi str. LMG 22165 AJ627
AF169520.1 gg_id:48079 Bacillus neidei str. BD-87 AF169
AJ535733.1 gg_id:91416 Bacillus sp. str. US149 AJ535
AB021193.1 gg_id:26043 Bacillus naganoensis str. ATCC53909 AB021
D16288.1 gg_id:14489 Sporolactobacillus inulinus str. IAM 12384 D1628
D16287.1 gg_id:14484 Sporolactobacillus kofuensis str. M18 D1628
D16285.1 gg_id:14478 Sporolactobacillus laevis str. IAM 12387 D1628
AB374522.1 gg_id:269392 Sporolactobacillus sp. str. QC81-06 AB374
D16270.1 gg_id:14486 Bacillus laevolacticus str. IAM12321 D1627
EF581819.1 gg_id:279322 Sporolactobacillus sp. str. SL153 EF581
D16290.1 gg_id:14491 Sporolactobacillus terrae str. IAM 12395 D1629
GQ344411.1 gg_id:540404 Sporolactobacillaceae str. b09s-2 GQ344
AB231785.1 gg_id:154718 Tuberibacillus calidus str. 606b AB231
GQ016497.1 gg_id:493171 Topographical and Temporal Human Skin Microbiome skin interdigital web space cl GQ016
EF463102.1 gg_id:265870 Jeotgalicoccus psychrophilus str. S190 EF463
FJ674640.1 gg_id:526461 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface FJ6746
GQ085599.1 gg_id:401412 Topographical and Temporal Human Skin Microbiome skin palm clone nbw278a08c GQ085
AY038633.1 gg_id:36078 lacustrine subsurface sediment clone GL178.18 AY038
EU194336.1 gg_id:243071 Jeotgalicoccus psychrophilus str. XJUHX-36 EU194
EU583727.1 gg_id:266449 Jeotgalicoccus sp. str. JSM 076033 EU583
AY028925.1 gg_id:44574 Jeotgalicoccus halotolerans str. YKJ-101 AY028
FJ675373.1 gg_id:525451 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface FJ6753
FJ674485.1 gg_id:528297 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface FJ6744
GQ086237.1 gg_id:425277 Topographical and Temporal Human Skin Microbiome skin interdigital web space cl GQ086
Y15711.1 gg_id:14905 Macrococcus caseolyticus str. ATCC 13548 Y15711
NR_029057.1 gg_id:589163 Macrococcus lamae str. R 16089; CCM 4815 NR_02
Y15714.1 gg_id:14908 Macrococcus bovicus str. L2F4 Y15714
AM237362.1 gg_id:154444 Macrococcus equipercicus OS-58.a2 AM237
AB079788.1 gg_id:61797 Micrococcus luteus B-P 26 AB079
AY119685.1 gg_id:64394 Macrococcus hajekii str. CCM 4809 AY1196
Y15713.1 gg_id:14912 Macrococcus carouselicus str. H8b16 Y15713
EU432572.1 gg_id:265732 Salinicoccus sp. str. 10093 EU432
DQ989633.1 gg_id:192272 Salinicoccus sp. str. W24 DQ989
DQ093353.1 gg_id:134112 Salinicoccus roseus str. Iii10 DQ093

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DQ352839.2 gg_id:145617 Salinicoccus aurantium str. YIM 70202 DQ352
EF177689.1 gg_id:198961 Salinicoccus sp. str. Y22 EF1776
AF275710.1 gg_id:37750 Salinicoccus alkaliphilus str. T8 AF2757
EU534791.1 gg_id:282310 profile human skin microbiota ear punch biopsy female C57BL/6J mouse clone nbt21 EU534
EF397606.1 gg_id:215022 Salinicoccus siamensis str. PN7-1 EF3976
AY028927.1 gg_id:26423 Salinicoccus hispanicus str. DSM 5352 AY0289
DQ767692.2 gg_id:164495 Salinicoccus sp. str. QW6 DQ767
FJ182049.2 gg_id:332643 Salinicoccus sp. str. Crm FJ1820
GQ280080.1 gg_id:549014 Staphylococcus gallinarum str. JS-10 GQ280
DQ355389.1 gg_id:158047 Staphylococcus saprophyticus DQ355
EU660331.1 gg_id:301632 Staphylococcus arlettae str. CM18 EU6603
AF015929.1 gg_id:14788 Staphylococcus aureus str. ATCC 29740 AF0159
AF146368.1 gg_id:14885 Staphylococcus aureus str. 71382 AF1463
EF510513.1 gg_id:220229 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aerug EF5105
DQ226212.1 gg_id:144797 Staphylococcus aureus DR.Y11 DQ226
DQ630753.1 gg_id:160169 Staphylococcus aureus DQ630
L36472.1 gg_id:138458 Staphylococcus aureus L36472
EF463060.1 gg_id:223814 Staphylococcus aureus str. RKA6 EF4630
X70648.1 gg_id:14825 Staphylococcus aureus str. NCDO 949 X70648
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AJ938182.1 gg_id:144650 Staphylococcus aureus str. RF122 AJ9381
DQ997836.1 gg_id:196205 Staphylococcus aureus str. F155 DQ997
EF463058.1 gg_id:224473 Staphylococcus aureus str. RKA4 EF4630
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FJ609418.1 gg_id:534669 Staphylococcus aureus str. PRSR-4 FJ6094
EU604543.1 gg_id:278032 Staphylococcus aureus str. 185060 (VRSA) EU6045
GQ919290.1 gg_id:567156 Staphylococcus aureus str. SGC801 GQ919
EU604544.1 gg_id:279269 Staphylococcus aureus str. 185100 EU6045
AY727530.2 gg_id:122846 Staphylococcus simiae str. CCM 7213 AY7275
GU213356.1 gg_id:561986 Staphylococcus aureus str. 44 GU213
EU807758.1 gg_id:305525 Staphylococcus aureus str. X13 EU807
EU730931.1 gg_id:338529 Staphylococcus cohnii str. 175 EU7309
NR_028996.1 gg_id:581219 Staphylococcus nepalensis str. CW1; DSM 15150 NR_02
EF173930.1 gg_id:177509 Staphylococcus cohnii str. COL4 EF1739
GQ052971.1 gg_id:380781 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbu GQ052
GQ073909.1 gg_id:466553 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor GQ073
GQ053940.1 gg_id:412476 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1 GQ053
GQ103291.1 gg_id:413254 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw698f01 GQ103
GU354324.1 gg_id:528574 Staphylococcus epidermidis str. DGC-1 GU354
GQ069570.1 gg_id:421820 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1 GQ069

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GQ003596.1 gg_id:506066 Topographical and Temporal Human Skin Microbiome skin alar crease clone nbu54h GQ003
GQ058573.1 gg_id:370643 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ058
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AE015929.1 gg_id:146872 Staphylococcus epidermidis str. ATCC 12228 AE015
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GQ054387.1 gg_id:461609 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv GQ054

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GQ078562.1 gg_id:450683 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ078
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GQ002107.1 gg_id:507555 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbu16 GQ002
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GQ021844.1 gg_id:487826 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ021
GQ003694.1 gg_id:505968 Topographical and Temporal Human Skin Microbiome skin alar crease clone nbu56b GQ003
GQ001372.1 gg_id:508290 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbu17 GQ001
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GQ026318.1 gg_id:433852 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl GQ026
GQ002163.1 gg_id:507499 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbu16 GQ002
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GQ056304.1 gg_id:378894 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor GQ056
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GQ057522.1 gg_id:373817 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ057
GQ058381.1 gg_id:460846 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1 GQ058
FJ380952.1 gg_id:574348 Staphylococcus epidermidis str. BQEL1-01b FJ3809
GQ042058.1 gg_id:456762 Topographical and Temporal Human Skin Microbiome skin alar crease clone nbw935 GQ042
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GQ073443.1 gg_id:391568 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor GQ073
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GQ114233.1 gg_id:453143 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw59 GQ114
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GQ058773.1 gg_id:421285 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ058
GQ107890.1 gg_id:442266 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw555g0 GQ107
X68417.1 gg_id:14794 Staphylococcus aureus str. ATCC 12600 X68417
AY308046.1 gg_id:89118 Staphylococcus epidermidis str. AZ22L3 AY308
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GQ081939.1 gg_id:376646 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor GQ081
X75944.1 gg_id:14817 Staphylococcus epidermidis str. GH 654 X75944
EU855190.1 gg_id:346511 Staphylococcus equorum str. CTSP8 EU855
EF061907.1 gg_id:181589 Staphylococcus sp. str. M210 EF0619
GQ304781.1 gg_id:592590 Staphylococcus haemolyticus str. A5 GQ304
GQ045534.1 gg_id:459324 Topographical and Temporal Human Skin Microbiome skin interdigital web space cl GQ045
L37600.1 gg_id:14857 Staphylococcus haemolyticus L37600
X86640.1 gg_id:14867 Staphylococcus sp str. 1F-23 X86640
FN393802.1 gg_id:575037 Staphylococcus haemolyticus str. ES-263-1 FN3938
EU071616.1 gg_id:256023 Staphylococcus haemolyticus str. EHFS1_AU1Ha EU071
EU379304.1 gg_id:262934 Staphylococcus haemolyticus str. 6R-J-5 EU3793
EF522132.1 gg_id:225987 Staphylococcus haemolyticus str. CU37-21 EF5221
GQ037885.1 gg_id:385469 Topographical and Temporal Human Skin Microbiome skin interdigital web space cl GQ037
X86636.1 gg_id:14837 Staphylococcus sp str. 1F-09 X86636
X86650.1 gg_id:14838 Staphylococcus sp str. S5-96 X86650
AY903256.1 gg_id:111564 Staphylococcus lugdunensis str. Inje L2 AY9032
AF322002.2 gg_id:26685 Staphylococcus pettenkoferi str. B3117 AF3220
GQ104965.1 gg_id:448537 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ104
GQ038197.1 gg_id:427149 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbu GQ038
GQ038333.1 gg_id:432252 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbu GQ038
AJ780978.1 gg_id:137754 Staphylococcus pseudintermedius str. LMG 22221 AJ7809
GQ261178.1 gg_id:573127 Staphylococcus sciuri str. YL081101 GQ261
AY820254.1 gg_id:141666 Staphylococcus sciuri str. SCBM1 AY8202
AB523707.1 gg_id:471521 Staphylococcus sciuri str. -S05-2 AB5237
AB212276.1 gg_id:148758 Staphylococcus sciuri AB2122
FJ573173.1 gg_id:550011 Staphylococcus sciuri str. E9-3 FJ5731
GU140036.1 gg_id:549509 Staphylococcus sciuri str. HBSD GU140
AJ320272.1 gg_id:21472 Staphylococcus succinus str. SB72 AJ3202
GU143799.1 gg_id:539557 Staphylococcus succinus str. SV17 GU143
AB009942.1 gg_id:14879 Staphylococcus pulvereri str. ATCC 51698T AB0099
EU428955.1 gg_id:549555 Staphylococcus epidermidis str. BP/SU1 EU4289
GQ068053.1 gg_id:393219 Topographical and Temporal Human Skin Microbiome skin alar crease clone nbw14 GQ068

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GQ022501.1 gg_id:487167 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbu31 GQ022
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GQ100456.1 gg_id:414429 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl GQ100
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NC_007168.1 gg_id:130949 Staphylococcus haemolyticus str. JCSC1435 NC_00
GQ085695.1 gg_id:455731 Topographical and Temporal Human Skin Microbiome skin palm clone nbw279c03c1 GQ085
GQ046433.1 gg_id:380303 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ046
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FJ189773.1 gg_id:553926 Staphylococcus pasteuri str. NSB07 FJ1897
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GQ022322.1 gg_id:487348 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbu31 GQ022
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GQ072395.1 gg_id:465742 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw195f12 GQ072
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EU861984.1 gg_id:330679 Staphylococcus epidermidis str. ICIRC142 EU861
GQ056314.1 gg_id:455165 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor GQ056
GQ110998.1 gg_id:446128 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw GQ110
GQ022451.1 gg_id:487218 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbu31 GQ022
EU660348.1 gg_id:296554 Staphylococcus sciuri str. CM26 EU660
GQ091168.1 gg_id:439595 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw343a0 GQ091
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GQ086785.1 gg_id:448762 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw3 GQ086
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NR_024667.1 gg_id:555928 Staphylococcus kloosii str. ATCC 43959 NR_02
GQ022602.1 gg_id:487068 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbu31 GQ022
GQ058790.1 gg_id:408516 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ058
GQ020516.1 gg_id:489150 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl GQ020
EU867337.1 gg_id:586661 Staphylococcus epidermidis str. CCGE2317 EU867
GQ113721.1 gg_id:468501 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw(GQ113
S83569.1 gg_id:14880 Staphylococcus sciuri S83569
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EU434592.1 gg_id:269729 Staphylococcus saprophyticus str. e35 EU434

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FN646068.1 gg_id:521848 Staphylococcus saprophyticus 108 FN646
AB009938.1 gg_id:14872 Staphylococcus delphini str. ATCC 49171T AB009
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GU369804.1 gg_id:519827 Staphylococcus simulans str. YH-13-3 GU369
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FN393800.1 gg_id:537866 Staphylococcus haemolyticus str. ES-230-1b FN3938
GU197539.1 gg_id:572188 Staphylococcus saprophyticus str. YSY1-8 GU197
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GQ058751.1 gg_id:391994 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ058
GQ080676.1 gg_id:395347 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1 GQ080
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GQ100667.1 gg_id:439095 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl GQ100
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L37598.1 gg_id:14763 Staphylococcus aureus L37598
GQ111528.1 gg_id:377601 Topographical and Temporal Human Skin Microbiome skin alar crease clone nbw581 GQ111
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EU834242.1 gg_id:331162 Staphylococcus epidermidis str. DS12 EU834

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DQ991032.1 gg_id:195138 Staphylococcus intermedius Gent30Groot DQ991
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DQ350835.1 gg_id:147170 Staphylococcus gallinarum str. S1004 DQ350
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GQ110764.1 gg_id:378177 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ110

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GQ056225.1 gg_id:374799 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl GQ056
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AB009943.1 gg_id:14779 Staphylococcus piscifermentans str. ATCC51136T AB009
EU652069.1 gg_id:275202 Staphylococcus epidermidis str. mm-17 EU652
GQ110094.1 gg_id:446609 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw61 GQ110
GQ022492.1 gg_id:487174 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbu31 GQ022
GQ022384.1 gg_id:487285 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbu31 GQ022
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S83566.1 gg_id:14834 Staphylococcus muscae str. MB4 = CCM 4175 S83566
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GQ041896.1 gg_id:466216 Topographical and Temporal Human Skin Microbiome skin alar crease clone nbw934 GQ041
X86641.1 gg_id:14824 Staphylococcus sp str. AG-30 X86641
GQ065874.1 gg_id:381321 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw94a04c GQ065
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GQ020542.1 gg_id:489127 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl GQ020
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GQ099584.1 gg_id:439243 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw51 GQ099
GU084442.1 gg_id:550096 Staphylococcus succinus str. AT4 GU084
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GQ074269.1 gg_id:428713 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor GQ074
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EU379296.1 gg_id:258529 Staphylococcus hominis str. 6J-4b EU379
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GQ042504.1 gg_id:449327 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl GQ042
GQ039994.1 gg_id:452485 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor GQ039

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EU554432.1 gg_id:273710 Staphylococcus haemolyticus str. Ag06 EU554
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GQ075294.1 gg_id:454723 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ075
GQ051586.1 gg_id:466741 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbu5(GQ051
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GQ112684.1 gg_id:373346 Topographical and Temporal Human Skin Microbiome skin nare clone nbw586e07c1 GQ112
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FJ389203.1 gg_id:553809 Staphylococcus devriesei str. KS-SP_27 FJ3892
GQ058627.1 gg_id:371105 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ058
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GQ030425.1 gg_id:390991 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw878a06c GQ030
GQ109937.1 gg_id:420186 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw6 GQ109
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FJ380980.1 gg_id:576172 Staphylococcus haemolyticus str. BQN2T-01d FJ3809
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DQ069223.1 gg_id:128398 sbsrfc mcrrgnsms mfc sll: implctns SLME's SA A mn cln SRB36 DQ069
DQ115992.1 gg_id:132839 bovine teat canal clone B-63 DQ115
DQ069205.1 gg_id:128067 gold mine clone MAB24 DQ069
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EU240887.1 gg_id:252685 Nosocomiicoccus ampullae str. TC-9 EU2408
AY167812.1 gg_id:77365 Bacillus sp. str. SAFN-018 AY1678
GQ153851.1 gg_id:396595 Laceyella sacchari str. T11-7 GQ153
NR_025007.1 gg_id:559489 Laceyella putida str. KCTC 3666 NR_025
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AJ251778.1 gg_id:41281 Thermoactinomyces sanguinis str. CCUG 38657T AJ2517
GQ163470.1 gg_id:593230 Trigonala elaeagnus str. HBUM2132 GQ163
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AB088364.1 gg_id:78806 Thermoactinomyces sp. str. H0165 AB0883
GU002061.1 gg_id:565318 Shimazuella sp. str. FXJ7.246 GU002
AF138732.1 gg_id:111744 Thermoactinomyces vulgaris str. KCTC 9557 () AF1387
AF138734.1 gg_id:112113 Thermoactinomyces intermedius str. KCTC 9646 () AF1387
AB362275.1 gg_id:272839 Thermoactinomyces sp. str. JAM-FM1001 AB3622
AB002650.1 gg_id:14561 G+C gram-positive HTA1420 AB0026
GQ015481.1 gg_id:494185 Topographical and Temporal Human Skin Microbiome skin back clone nbw817b04c1 GQ015
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EF371926.1 gg_id:212584 Planococcus pelagicus str. /HsP6(II) EF3719
EU465810.1 gg_id:289883 argali sheep feces clone AS2_aao35h09 EU4658
EU466486.1 gg_id:297742 bighorn sheep feces clone BH2_aao24e06 EU4664
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EU778808.1 gg_id:328205 Springbok feces clone SBK_h08_1_1 EU7788
EU773972.1 gg_id:327895 Cheetah feces clone CE2_e08_1 EU7739
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EU467930.1 gg_id:293972 cheetah feces clone CE2_d10 EU4679
EU469351.1 gg_id:290034 springbok feces clone SBK_f02_1 EU4693
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EF636829.1 gg_id:277855 Metagenomic and Namib desert sand clone 1 EF6368

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AM711118.1 gg_id:265604 Scopulibacillus darangshiensis str. DLS-06 AM711
DQ083102.1 gg_id:131214 soil clone X17 DQ083
EF515940.1 gg_id:224822 grassland soil clone FCPN728 EF5159
DQ448756.1 gg_id:157711 Bacillus sp. str. CNJ775 PL04 DQ448
FJ478789.1 gg_id:591482 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4787
EU134633.1 gg_id:246398 tallgrass prarie soil clone FFCH11580 EU1346
EU571191.1 gg_id:268803 Bacillus sp. str. 25-3 EU5711
FJ671330.1 gg_id:523662 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6713
AB002648.1 gg_id:14559 G+C gram-positive HTA1422 AB0026
NR_025005.1 gg_id:562523 Thermoflavimicrobium dichotomicum str. KCTC 3667 NR_025
AF332545.1 gg_id:40011 Bacillus thuringiensis B73 AF3325
AY597525.2 gg_id:150661 Photorhabdus luminescens PDBC EPN6.71 AY5975
AF332544.1 gg_id:41058 Bacillus megaterium B70 AF3325
EU365680.1 gg_id:269842 Bacillus cereus str. M-7 EU3656
DQ351341.1 gg_id:155340 Exiguobacterium homiense str. H1-R8 DQ351
AF227839.1 gg_id:40417 str. 61610 AF2278
DQ235551.1 gg_id:143456 biofilm water pipeline biofilms steel pipelines Gulf Mexico DQ235
X70316.1 gg_id:14691 Exiguobacterium aurantiacum str. NCDO 2321 X70316
X70313.1 gg_id:14688 Exiguobacterium acetylicum str. NCIMB 9889 X70313
GQ284484.1 gg_id:570858 Exiguobacterium indicum str. TDWCW4 GQ284
GQ284470.1 gg_id:590797 Exiguobacterium indicum str. PCWCW1 GQ284
CP001022.1 gg_id:267150 Exiguobacterium sibiricum str. 255-15 CP0010
DQ019165.1 gg_id:153908 Exiguobacterium undae str. DSM 14481 DQ019
D55730.1 gg_id:14687 Exiguobacterium acetylicum str. IFO12146 D55730
FJ970034.1 gg_id:374212 Exiguobacterium acetylicum str. QD-3 FJ9700
DQ019164.1 gg_id:154203 Exiguobacterium antarcticum str. DSM 14480 DQ019
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AB334767.1 gg_id:253456 Exiguobacterium undae str. 5 AB3347
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AB105164.1 gg_id:93416 Exiguobacterium oxidotolerans str. T-2-2 AB1051
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Y13364.1 gg_id:14922 Gemella sanguinis str. 2045-94 Y13364

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

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FJ671853.1 gg_id:520766 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6718
FJ674961.1 gg_id:517319 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6749
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GQ060659.1 gg_id:463917 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw03g08 GQ060
FM873468.1 gg_id:369668 occupant source house floor dust clone FD04B03 FM873
EU341289.1 gg_id:240694 Evaluation Rapid Technologies Estimate Microbial Burden and Commercial Airline Ca EU341
FJ672272.1 gg_id:515704 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6722
Y17780.1 gg_id:74511 Eremococcus coleocola str. M1832/95/2 Y17780
GQ068237.1 gg_id:399188 Topographical and Temporal Human Skin Microbiome skin alar crease clone nbw148 GQ068
AJ279038.1 gg_id:16600 Aerosphaera taetra str. CCUG 43036T AJ2790
AY959019.1 gg_id:132717 Microbes on human vaginal epithelium clone rRNA246 AY9590
GQ020706.1 gg_id:488962 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ020
FJ672416.1 gg_id:527548 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6724
GQ024094.1 gg_id:485575 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw GQ024
FJ672485.1 gg_id:531811 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6724
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AB188091.1 gg_id:104418 Alkalibacterium iburiensis str. M3 AB1880
AB268550.1 gg_id:186973 Alkalibacterium polygonumreducens str. F11 AB2685
AB294173.1 gg_id:368743 Alkalibacterium kapii str. T82-5-1 AB2941
EU845714.1 gg_id:349078 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8457
GQ351352.1 gg_id:542881 Alkalibacterium sp. str. G4 GQ351
AF143512.2 gg_id:15252 Alkalibacterium olivapovliticus str. WW2-SN4c AF1435
AB294176.1 gg_id:361292 Alkalibacterium psychrotolerans str. JCM 12281 AB2941
AB294169.1 gg_id:364463 Alkalibacterium putridalgicola str. O26-12-2 AB2941
X92169.1 gg_id:27088 Lake Nakuru isolate WN16 X92169
GQ848212.1 gg_id:556700 and Archaeal Xiarinur Soda Lake Water-sediment Interface water-sediment interfac GQ848
X59765.1 gg_id:15237 Alloiococcus otitis str. NCFB 2890 X59765
AY543021.1 gg_id:103243 Carnobacterium divergens MF 156 AY5430
AY543036.1 gg_id:100049 Carnobacterium divergens MF 66 AY5430
AY543031.1 gg_id:99269 Carnobacterium maltaromaticum MF 204 AY5430
GQ304934.1 gg_id:568366 Carnobacterium maltaromaticum str. MMF-26 GQ304
GQ304938.1 gg_id:581552 Carnobacterium maltaromaticum str. MMF-30 GQ304
GQ304920.1 gg_id:559437 Carnobacterium maltaromaticum str. MMF-12 GQ304
AM179873.1 gg_id:150460 Carnobacterium maltaromaticum B26 AM179
DQ027061.1 gg_id:134675 Carnobacterium sp. str. AT7 DQ027
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EU845247.1 gg_id:313812 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8457
L08623.1 gg_id:15257 Carnobacterium alterfunditum L08623
EU845677.1 gg_id:309286 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8456

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EU817500.1 gg_id:332765 Carnobacterium sp. str. MS3 EU817
EU845027.1 gg_id:353898 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU845
AF184247.1 gg_id:36062 Carnobacterium maltaromaticum str. BA AF184
S86170.1 gg_id:15243 Carnobacterium funditum str. pf3 (DSM 5970) S86170
AJ387905.1 gg_id:16452 Carnobacterium gallinarum str. DSM 4847(T) NCFB 2766(T) AJ3879
AM179875.1 gg_id:146934 Carnobacterium divergens B33 AM179
GQ008057.1 gg_id:501608 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ008
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GQ008163.1 gg_id:501503 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ008
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Y17300.1 gg_id:15259 Desemzia incerta str. DSM 20581 Y17300
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FJ674427.1 gg_id:515642 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface FJ6744
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FJ671977.1 gg_id:516168 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface FJ6719
FJ674634.1 gg_id:527071 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface FJ6746
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AF016390.1 gg_id:15054 Granulicatella elegans str. DSM 11693; B1333 AF016
AB022026.1 gg_id:15057 Granulicatella elegans str. HHC5 AB022
AB252689.1 gg_id:216513 Granulicatella elegans str. PAGU 792 AB252
AJ312375.1 gg_id:70105 Granulicatella adiacens str. 10/833 AJ3123
AY879298.1 gg_id:143622 Granulicatella paradiacens str. 04401102 AY879
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FJ558447.1 gg_id:521851 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5584
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AB247277.1 gg_id:147894 Marinilactibacillus piezotolerans str. JCM 12337 AB247
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AY485792.1 gg_id:99434 Marinilactibacillus piezotolerans str. LT20 AY485

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EU434534.1 gg_id:266599 Trichococcus collinsii str. b258 EU4345
EU434512.1 gg_id:264683 Trichococcus collinsii str. b239 EU4345
EU434551.1 gg_id:268210 Trichococcus collinsii str. b140 EU4345
EU434537.1 gg_id:275949 Trichococcus collinsii str. b253 EU4345
EU434536.1 gg_id:274539 Trichococcus collinsii str. b255 EU4345
EU434554.1 gg_id:259750 Trichococcus collinsii str. b205 EU4345
EU434507.1 gg_id:275512 Trichococcus collinsii str. b354 EU4345
EU434495.1 gg_id:277597 Trichococcus collinsii str. b362 EU4344
EU434510.1 gg_id:266846 Trichococcus collinsii str. b237 EU4345
NR_025435.1 gg_id:572224 Trichococcus palustris str. DSM 9172 NR_025
EU434478.1 gg_id:265112 Trichococcus collinsii str. b279 EU4344
FJ672147.1 gg_id:529854 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6721
AJ306612.1 gg_id:47658 Trichococcus collinsii str. 37AN3 AJ3066
AB186878.1 gg_id:101202 polychlorinated dioxin dechlorinating microcosm clone TSBX03 AB1868
L76599.1 gg_id:15246 Trichococcus pasteurii str. ATCC 35945 L76599
EU844884.1 gg_id:327706 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8448
EU434522.1 gg_id:263346 Trichococcus flocculiformis str. b328 EU4345
FJ675543.1 gg_id:509026 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6755
Y17301.1 gg_id:15254 Trichococcus flocculiformis str. DSM 2094 Y17301
FJ672105.1 gg_id:527794 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6721
DQ337518.1 gg_id:145184 tetracycline and tylosin resistance genes impacted swine effluent holding pit DQ337
EU434437.1 gg_id:272157 Trichococcus flocculiformis str. a209 EU4344
FJ674344.1 gg_id:527737 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6743
FJ672700.1 gg_id:527399 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6727
EU434501.1 gg_id:265834 Trichococcus flocculiformis str. b319 EU4345
FJ671856.1 gg_id:511164 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6718
FJ671301.1 gg_id:526709 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6713
GQ080732.1 gg_id:409174 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1 GQ080
NR_026454.1 gg_id:552567 Granulicatella balaenopterae str. M1975/96/1; CCUG 37380 NR_026
FJ764779.1 gg_id:565642 Marinilactibacillus sp. str. E-109 FJ7647
FJ671733.1 gg_id:514230 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6717
FJ671721.1 gg_id:518863 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6717
FJ672820.1 gg_id:513562 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6728
FJ671872.1 gg_id:532281 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6718
X70907.1 gg_id:15241 Dolosigranulum pigrum str. NCFB 2975 X70907
GU395995.1 gg_id:526359 Dolosigranulum pigrum str. 33929-06 GU395
FJ670957.1 gg_id:516363 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6709
FJ672814.1 gg_id:520671 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6728
FJ675030.1 gg_id:515465 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6750
FJ674957.1 gg_id:519350 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6749

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FJ825559.1 gg_id:559774 Microbial during start-up mesophilic biogas plant clone 46_BS5_10 FJ8255
FJ672294.1 gg_id:517005 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6722
FJ672544.1 gg_id:525845 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6725
FJ671690.1 gg_id:530430 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6716
FJ672168.1 gg_id:514023 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6721
GQ080691.1 gg_id:466222 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1 GQ080
GQ085654.1 gg_id:407470 Topographical and Temporal Human Skin Microbiome skin palm clone nbw278f11c1 GQ085
FJ674468.1 gg_id:520088 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6744
FJ672461.1 gg_id:509077 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6724
FJ675572.1 gg_id:516872 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6755
FJ672927.1 gg_id:514848 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6729
FJ893130.1 gg_id:545089 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota HM3; ear p FJ8931
GQ079378.1 gg_id:445962 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw1129f(GQ079
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FJ671894.1 gg_id:523062 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6718
FJ671904.1 gg_id:530966 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6719
FJ674889.1 gg_id:511294 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6748
DQ376550.1 gg_id:154459 Microbial ecology removing phosphate wastewater EBPR process aerobic sequencin DQ376
AY581816.1 gg_id:106773 feces clone 1D3 AY5818
AJ302648.1 gg_id:20210 Isobaculum melis CCUG 37660T AJ3026
FM875568.1 gg_id:365920 occupant source house dust skin surface swab clone SD01E05 FM875
FJ672609.1 gg_id:513204 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6726
AJ576362.1 gg_id:102730 hindgut homogenate Pachnoda ephippiata larva clone PeH49 AJ5763
GU166170.1 gg_id:561594 intestinal tract larvae (Musca domestica) direct cloning and sequencing genes whea GU166
Y11621.1 gg_id:15298 Enterococcus asini str. AS2 Y11621
GQ155330.1 gg_id:581895 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ155347.1 gg_id:592273 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
NR_028748.1 gg_id:586815 Enterococcus avium str. E6844; CIP 103019 NR_02
AJ301825.1 gg_id:45325 Enterococcus avium str. LMG 10744 AJ3018
EF199997.1 gg_id:183702 Enterococcus casseliflavus str. ELS3 EF1999
X76177.1 gg_id:15285 Enterococcus sp str. LMG12316 X76177
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FJ538215.1 gg_id:536036 Enterococcus casseliflavus str. BPSr32 FJ5382
GQ337020.1 gg_id:544389 Enterococcus casseliflavus str. SS1229 GQ337
AJ420804.1 gg_id:42419 Enterococcus casseliflavus str. CECT969T AJ4208
AB547326.1 gg_id:515778 Enterococcus casseliflavus str. NCCP-53 AB5473
DQ395285.1 gg_id:156436 Enterococcus casseliflavus F00186 DQ395
FJ915804.1 gg_id:561364 Enterococcus casseliflavus str. IMAU10148; WH15-3-3 FJ9158

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U30931.1 gg_id:15301 Enterococcus saccharolyticus U3093
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EU075043.1 gg_id:239422 Enterococcus casseliflavus str. thirtyfourmpalpha EU075
EU459407.1 gg_id:294670 cheetah feces clone CE3_aai07e07 EU459
Y18355.1 gg_id:15280 Enterococcus cecorum str. NCDO 2674T Y18355
DQ057437.1 gg_id:132661 str. ii1209 DQ057
AJ301828.1 gg_id:17976 Enterococcus columbae str. LMG 11740 AJ3018
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FJ749767.1 gg_id:539955 Enterococcus durans str. IMAU60041; XZ12301 FJ7497
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GU177630.1 gg_id:556032 Enterococcus durans str. 6-2 GU177
FJ607264.1 gg_id:548980 Enterococcus durans str. KLDS6.0618 FJ6072
FJ917730.1 gg_id:573141 Enterococcus durans str. IMAU60177; ZLG3-3 FJ9177
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GU299085.1 gg_id:534960 Enterococcus faecalis str. 3-12 GU299
DQ295035.1 gg_id:144018 Lactobacillus plantarum str. PFK2 DQ295
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AB092693.1 gg_id:58583 Enterococcus faecalis str. K-4 AB092
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FN377815.1 gg_id:574542 Enterococcus faecalis str. S5 FN3778
DQ340074.1 gg_id:145783 Enterococcus faecalis str. KLDS 6.0319 DQ340
DQ340071.1 gg_id:145866 Enterococcus faecalis str. KLDS 6.0317 DQ340
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AB362599.1 gg_id:250917 Enterococcus faecalis str. NRIC 0110 AB3625

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FJ378667.1 gg_id:365418 Enterococcus faecalis str. HN-N12 FJ3786
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AB244434.1 gg_id:257698 Enterococcus faecalis str. A19-2 AB244
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EF025905.1 gg_id:253248 Enterococcus gallinarum str. B2 EF0259
AJ420805.1 gg_id:19924 Enterococcus gallinarum str. CECT970T AJ4208
EU477410.1 gg_id:563672 Enterococcus saccharolyticus str. SD1 EU477
AF286831.1 gg_id:70378 Enterococcus moraviensis str. CCM 4856T AF2868
GQ337032.1 gg_id:586775 Enterococcus moraviensis str. SS1689 GQ337
AF286832.1 gg_id:28186 Enterococcus haemoperoxidus str. CCM 4851T AF2868
GQ337028.1 gg_id:549794 Enterococcus hermanniensis str. SS1760 GQ337
FJ851687.1 gg_id:592320 Enterococcus faecium str. HS3 FJ8516
AB186307.1 gg_id:136967 Enterococcus hirae str. DST 2010 AB186

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EF591816.1 gg_id:232955 Enterococcus mundtii str. CWBI-B1431\(A2-17) EF5918
GU213907.1 gg_id:564647 Enterococcus hirae str. -12 GU213
GU255468.1 gg_id:583493 Enterococcus hirae str. ST3 GU255
AJ301834.1 gg_id:37447 Enterococcus hirae str. LMG 6399 AJ3018
AM050562.1 gg_id:138572 Enterococcus inusitatus str. E2ET29 AM050
AB507170.1 gg_id:393887 Enterococcus faecalis str. JCM 20313 AB507
EU717955.1 gg_id:340166 Enterococcus faecium str. wh05 EU7179
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AB018210.1 gg_id:25976 Enterococcus faecium str. E 26 AB0182
EU857635.1 gg_id:367979 Enterococcus faecium EU8576
EF533988.1 gg_id:222834 Enterococcus faecium str. IDCC 2102 EF5339
AY692451.1 gg_id:100464 Enterococcus faecium str. SL2 AY6924
EU857636.1 gg_id:366313 Enterococcus lactis EU8576
EU717965.1 gg_id:327400 Enterococcus faecalis str. Zy05 EU7179
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EU887827.1 gg_id:341145 Enterococcus faecalis str. H13 EU8878
GQ337034.1 gg_id:533020 Enterococcus phoeniculicola str. SS1721 GQ337
AJ301839.1 gg_id:43998 Enterococcus saccharolyticus str. LMG 11427 AJ3018
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FJ378684.1 gg_id:359101 Enterococcus faecium str. HN-N29 FJ3786
AF070223.1 gg_id:15287 Enterococcus faecium str. GUCR AF0702
Y18294.1 gg_id:15290 Enterococcus faecium str. NCFB 942T Y18294
AJ459875.1 gg_id:62639 larval intestine clone E AJ4598
AJ301838.1 gg_id:20443 Enterococcus raffinosus str. LMG 12999 AJ3018
GQ155811.1 gg_id:566795 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EU560859.1 gg_id:557059 Assessment genetic Apriona germari (Hope) larvae normalization techniques intestir EU5608
AJ301827.1 gg_id:37798 Enterococcus cecorum str. LMG 12902 AJ3018
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FJ378672.1 gg_id:359990 Enterococcus faecium str. HN-N17
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EU074827.1 gg_id:256245 Enterococcus mundtii str. MC6
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FJ378682.1 gg_id:367316 Enterococcus faecium str. HN-N27
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EF428252.2 gg_id:221584 Enterococcus mundtii str. HDYM-33
EU878169.1 gg_id:346951 Enterococcus faecium str. SH 528
GQ337037.1 gg_id:592016 Enterococcus termitis str. SS1793
DQ223885.1 gg_id:169662 Enterococcus raffinosus str. P6
GU384204.1 gg_id:516700 Enterococcus sp. str. CJ-1
EU428012.1 gg_id:263573 Enterococcus faecium str. SM21
FJ378676.1 gg_id:361678 Enterococcus faecium str. HN-N21

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

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GQ131184.1 gg_id:424771 Enterococcus italicus str. IMAU70068; HS2301 GQ131
AF349930.1 gg_id:67810 Enterococcus sp. str. CR-303S AF3499
EU717957.1 gg_id:355438 Enterococcus faecium str. Yl05 EU7179
GU255467.1 gg_id:555823 Enterococcus faecium str. ST2 GU255
EU789396.1 gg_id:325104 Enterococcus faecium str. M0138 EU7893
FJ378697.1 gg_id:357775 Enterococcus faecium str. HN-N42 FJ3786
DQ411812.1 gg_id:155933 Enterococcus pallens str. ATCC BAA-351 DQ411
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EF428246.2 gg_id:226289 Enterococcus mundtii str. HDYM-22 EF4282
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FJ378694.1 gg_id:368401 Enterococcus faecium str. HN-N39 FJ3786
EU459175.1 gg_id:288293 hedgehog feces clone HH_aai33c04 EU4591
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EU807757.1 gg_id:322616 Enterococcus faecalis str. NR1 EU8077
EU878170.1 gg_id:315043 Enterococcus faecium str. SH 632 EU8781
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EU689058.1 gg_id:352407 Tetragenococcus halophilus str. JCM 2015; T19 EU6890
EU522084.1 gg_id:305691 Tetragenococcus halophilus str. T2 EU5220
EU522090.1 gg_id:315186 Tetragenococcus halophilus str. T9 EU5220
D88824.1 gg_id:15292 Tetragenococcus muriaticus D88824
AJ301840.1 gg_id:20568 Enterococcus solitarius str. DSM 5634 AJ3018
Y18338.1 gg_id:15294 Enterococcus solitarius str. NCIMB 12902T Y18338
AY690334.1 gg_id:106000 Tetragenococcus koreensis str. Wan-Taek Im AY6903
GQ502552.1 gg_id:553330 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf4- GQ502
FJ675076.1 gg_id:519677 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6750
AJ576414.1 gg_id:101516 midgut homogenate Pachnoda ephippiata larva clone PeM56 AJ5764
AJ854484.1 gg_id:145696 Catellicoccus marimammalium str. M34/04/3 AJ8544
GQ156063.1 gg_id:565384 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
AJ576356.1 gg_id:107176 hindgut homogenate Pachnoda ephippiata larva clone PeH40 AJ5763
FJ672320.1 gg_id:512239 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6723
FJ675223.1 gg_id:524674 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6752
FJ192638.1 gg_id:330592 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior FJ1926
AJ576341.1 gg_id:101355 hindgut homogenate Pachnoda ephippiata larva clone PeH24 AJ5763
AY571409.1 gg_id:114659 termite gut clone RsaHf388 AY5714
Y16546.1 gg_id:43965 Atopobacter phocae str. m1590/94/2 Y16546
EU560817.1 gg_id:571665 Assessment genetic Apriona germari (Hope) larvae normalization techniques intestir EU5608

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NR_025689.1 gg_id:566186 Vagococcus carniphilus str. 1843-02; ATCC BAA-640 NR_02
AY669387.1 gg_id:110054 Vagococcus carniphilus 12J AY6693
GU166171.1 gg_id:570199 wheat bran (Musca domestica) direct cloning and sequencing genes intestinal tract GU166
NR_025360.1 gg_id:533589 Vagococcus fessus str. m2661/98/1; CCUG 41755 NR_02
DQ860043.1 gg_id:240763 anchovy intestinal microflora clone F2G DQ860
FJ211190.1 gg_id:334656 Vagococcus sp. str. AC-1 FJ2111
FJ360897.1 gg_id:590532 Vagococcus penaei str. CD 276 FJ3608
AM490371.1 gg_id:200615 Vagococcus carniphilus str. JIP 14-01 AM490
EU660371.1 gg_id:301246 Vagococcus fluvialis str. CT21 EU6603
Y17152.2 gg_id:15276 Vagococcus lutrae str. m1134/97/1; CCUG 39187 Y17152
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NC_006814.3 gg_id:128961 Lactobacillus acidophilus str. NCFM NC_00
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DQ057474.1 gg_id:137026 str. ii1369 DQ057
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AB175732.1 gg_id:221299 Lactobacillus aviarius str. LAV7 AB1757
EU177639.1 gg_id:334767 Lactobacillus brevis str. NS125 EU1776
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GU116478.1 gg_id:542716 Lactobacillus brevis str. TCCC13007 GU116
GQ289387.1 gg_id:572012 Lactobacillus plantarum str. TJ2 GQ289
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DQ974207.1 gg_id:184047 Lactobacillus brevis str. BH2 DQ974
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EU194344.1 gg_id:335435 Lactobacillus brevis str. LMG 11992 EU1943

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AB425925.1 gg_id:580392 Lactobacillus coleohominis str. TB-C19 AB4259
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AF243141.1 gg_id:41700 Lactobacillus crispatus str. BLB2 AF2431
GQ074725.1 gg_id:452720 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv GQ074
GQ070874.1 gg_id:455412 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw GQ070
GQ074133.1 gg_id:371731 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ074
GQ074601.1 gg_id:402842 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ074
GQ074192.1 gg_id:391592 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ074
GQ074160.1 gg_id:427907 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ074
GQ011573.1 gg_id:498091 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw793f10 GQ011
AJ242969.1 gg_id:15129 Lactobacillus crispatus str. NCTC 4 AJ2429
DQ317604.1 gg_id:149002 Lactobacillus crispatus str. 15L08 DQ317
GQ070816.1 gg_id:441240 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw GQ070
DQ057450.1 gg_id:133039 str. ii1269 DQ057
DQ057440.1 gg_id:131154 str. ii1225 DQ057
AF243171.1 gg_id:33386 Lactobacillus crispatus str. TL23a AF2431
GQ010914.1 gg_id:498752 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ010
GQ078614.1 gg_id:422527 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ078
AM285451.1 gg_id:199536 Lactobacillus crustorum str. LMG 23702 R-19087 AM285
AY204891.1 gg_id:81329 Lactobacillus curvatus str. YMRS3a AY2048
AY204890.1 gg_id:82190 Lactobacillus curvatus str. PSTJA3a AY2048
AF349922.1 gg_id:67818 derived cheese sample clone 51CR AF3499
EU722745.1 gg_id:326330 Lactobacillus delbrueckii str. L4 EU7227
FJ749581.1 gg_id:548624 Lactobacillus diolivorans str. IMAU10018; SY5-2 FJ7495
AB262731.1 gg_id:180597 Lactobacillus farraginis str. NRIC 0676 AB2627
AM266587.1 gg_id:161232 Lactobacillus faeni str. TMW 1.1303 = DSM 180 AM266
EU419594.1 gg_id:260994 Lactobacillus fermentum str. KLDS 1.0617 EU4195
EF535257.1 gg_id:220122 Lactobacillus fermentum str. KLB 261 EF5352
AF302116.1 gg_id:52471 Lactobacillus fermentum str. KLD AF3021
EU547297.1 gg_id:557918 Lactobacillus fermentum str. BCS25 EU5472
EU469860.1 gg_id:302890 western lowland gorilla feces clone GOR_aag72g08 EU4698
U62624.1 gg_id:15140 Lactobacillus fermentum str. KRM U62624
EF460496.1 gg_id:214156 Lactobacillus fermentum str. SR2 EF4604

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

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s__Lactobacillus oligofermentans	72421
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AF243145.1 gg_id:18857 Lactobacillus mucosae str. BLB1c AF243
EU821350.1 gg_id:538942 Lactobacillus oeni str. 103 EU8213
AY733083.1 gg_id:104517 Lactobacillus oligofermentans str. MARL13 AY733
X94230.1 gg_id:15148 Lactobacillus panis str. DSM 6035T X94230
AB257867.1 gg_id:158349 Lactobacillus pantheris FP37-1 AB2578
NR_025189.1 gg_id:573944 Lactobacillus pantheris str. LMG 21017 NR_02
AB512779.1 gg_id:580959 Lactobacillus parabrevis str. YIT 12113 AB512
AB297927.1 gg_id:253940 Lactobacillus senmaizukensis str. L13 AB297
AB473626.1 gg_id:528967 Lactobacillus paracollinoides str. JCM 15729 AB473
NR_029039.1 gg_id:566740 Lactobacillus parakefiri str. GCL 1731; LMG 15133 NR_02
NR_025045.1 gg_id:550403 Lactobacillus kimchii str. MT-1077; AP1077; JCM 10707 NR_02
AB191250.1 gg_id:107631 Lactobacillus paraplantarum str. II 32 AB191
AY383631.1 gg_id:95489 Lactobacillus plantarum str. MiLAB14 AY383
DQ486145.1 gg_id:158659 Lactobacillus plantarum str. SFCB2-7c DQ486
GU138564.1 gg_id:557831 Lactobacillus plantarum str. LSBM6-5 GU138
AB362711.1 gg_id:249730 Lactobacillus pentosus str. NRIC 1554 AB362
AB362739.1 gg_id:238712 Lactobacillus plantarum str. NRIC 1739 AB362
EU559599.1 gg_id:264917 Lactobacillus plantarum str. ZDY128 EU559
AB326363.1 gg_id:588823 Lactobacillus pobuzihi str. NBRC 103224 E100326 AB326
X76329.1 gg_id:15142 Lactobacillus pontis str. LTH 2587 X76329
AJ422032.1 gg_id:76876 Lactobacillus pontis str. LMG 14187T = R-1465 AJ4220
GQ155597.1 gg_id:511199 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
CP000705.1 gg_id:231242 Lactobacillus reuteri F275 str. DSM 20016 CP000
CP000705.1 gg_id:231245 Lactobacillus reuteri F275 str. DSM 20016 CP000
EF412975.1 gg_id:214229 Lactobacillus reuteri str. C1 EF4129
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GQ156435.1 gg_id:591239 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
GQ155466.1 gg_id:556287 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
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GQ155469.1 gg_id:585860 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ155455.1 gg_id:575693 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ155615.1 gg_id:579207 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ155669.1 gg_id:558815 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
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GQ155573.1 gg_id:538440 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
AY735406.1 gg_id:108135 Lactobacillus reuteri str. LU3 AY7354
GQ448922.1 gg_id:585264 Microbiome neonatal calves: shedding microorganisms fecal clone calf783_2wks_gr GQ448
GQ155509.1 gg_id:540888 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155

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AB425927.1 gg_id:555024 Lactobacillus reuteri str. TB-D21 AB425
AB370880.1 gg_id:268385 Lactobacillus rossiae str. DSM 15814 AB370
EU180606.1 gg_id:307389 Lactobacillus reuteri str. NS98 EU180
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GU138561.1 gg_id:544158 Lactobacillus rossiae str. LSAM1-2 GU138
AB034088.1 gg_id:26075 rumen clone 3C3d-2 AB034
AB425942.1 gg_id:551940 Lactobacillus saerimneri str. TB-I37 AB425
AB186340.1 gg_id:137150 Lactobacillus salivarius str. DLS 0811 AB186
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NR_028658.1 gg_id:585770 Lactobacillus satsumensis str. NRIC 0604 NR_02
AB370882.1 gg_id:276238 Lactobacillus siligionis str. NBRC 101315 AB370
AB458681.1 gg_id:591269 Lactobacillus sucicola str. NRIC 0735 AB458
AJ621556.2 gg_id:132461 Lactobacillus vaccinostercus str. LMG 9215 AJ6215
AB218799.1 gg_id:159914 Lactobacillus vaccinostercus str. YIT 10316 AB218
AJ315640.1 gg_id:74107 Lactobacillus durianis str. LMG 19193 AJ3156
AB218797.1 gg_id:160167 Lactobacillus vaccinostercus str. YIT 10300 AB218
EF460497.1 gg_id:215674 Lactobacillus vaginalis str. SR8 EF4604
NR_025371.1 gg_id:536754 Lactobacillus frumenti str. TMW 1.666; DSM 13145 NR_02
AB242320.1 gg_id:142448 Lactobacillus mobilis str. SIID2227-1-3b AB242
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AF243146.1 gg_id:48136 Lactobacillus rhamnosus str. F11 AF243
AY735405.2 gg_id:108112 Lactobacillus paracasei str. LPC4 AY7354
EU825659.1 gg_id:445624 Lactobacillus rhamnosus EU825
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AJ558112.1 gg_id:83495 Lactobacillus casei str. CWBI-B623 AJ5581
EF495247.1 gg_id:218969 Lactobacillus rhamnosus str. L60 EF4952
AY773957.1 gg_id:107860 Lactobacillus rhamnosus 5D AY773
AB362692.1 gg_id:249164 Lactobacillus paracasei str. NRIC 0625 AB362
AY773945.1 gg_id:108736 Lactobacillus casei str. BCRC10697 AY773
AY773958.1 gg_id:107861 Lactobacillus rhamnosus 11D AY773
AY675253.1 gg_id:100985 Lactobacillus rhamnosus str. LR3 AY675
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EU454546.1 gg_id:325815 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU454
EU453007.1 gg_id:331646 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75 EU453
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EF096822.1 gg_id:181275 mouse cecum clone SWPT13_aaa01c03 EF0968
EU621849.1 gg_id:278869 Lactobacillus plantarum str. K2 EU621
GU125607.1 gg_id:563127 Lactobacillus alimentarius str. IMAU80187 GU125

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EU453133.1 gg_id:323257 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H80N EU453
EF614861.1 gg_id:232078 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o EF6148
EU456847.1 gg_id:316572 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU4568
EU453072.1 gg_id:330003 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H78S EU453
EF097553.1 gg_id:182410 mouse cecum clone SWPT19_aaa04c08 EF0975
EU450981.1 gg_id:310929 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU450
AB362726.1 gg_id:250627 Lactobacillus plantarum str. NRIC 1592 AB3627
EU455101.1 gg_id:304585 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU455
AY445127.1 gg_id:107784 Lactobacillus sp. str. RA2113 AY445
AY204896.1 gg_id:82312 Lactobacillus sakei str. HNSL5a AY2048
EU526815.1 gg_id:263646 Lactobacillus paracasei str. L7 EU5268
EU509472.1 gg_id:261492 cecal contents Mus musculus strain C57BL/6J; MD9 clone MD9_aap58h09 EU5094
GQ155657.1 gg_id:583427 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
AB186322.1 gg_id:136262 Lactobacillus johnsonii str. DLM 1701 AB1863
AM113780.1 gg_id:140659 Lactobacillus homohiochii str. DSM 20571 AM113
AY667698.1 gg_id:112026 Lactobacillus alvei str. 1G2 AY6676
AB262735.1 gg_id:190397 Lactobacillus parafarraginis str. NRIC 0680 AB2627
AB008209.1 gg_id:257632 Lactobacillus gasseri DSM 20243 AB0082
AY590777.1 gg_id:106640 Lactobacillus plantarum str. lp-onlly AY5907
AM113785.1 gg_id:139929 Lactobacillus suebicus str. DSM 5007 AM113
EU451093.1 gg_id:337269 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H78S EU451
EU456268.1 gg_id:336900 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K79S EU4562
EU455863.1 gg_id:318335 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83N EU4558
EU457595.1 gg_id:352447 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83N EU4575
AJ417737.1 gg_id:61751 Lactobacillus gallinarum str. ATCC 33199 AJ4177
EU451738.1 gg_id:332402 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU4517
EU455031.1 gg_id:311151 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU4550
EU455929.1 gg_id:333597 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H79S EU4559
EU722746.1 gg_id:322818 Lactobacillus reuteri str. L7 EU7227
EU451068.1 gg_id:324226 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU451
EU773885.1 gg_id:320037 Cheetah feces clone CE2_b07 EU7738
EU455600.1 gg_id:353888 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N EU4556
EU463871.1 gg_id:293298 Seba's short-tailed bat feces clone bat_aaj06b09 EU4638
EU468211.1 gg_id:300202 lion feces clone LI1_f05_1 EU4682
DQ399354.1 gg_id:153558 Lactobacillus paracasei str. SFCB2-5 DQ399
AB366389.1 gg_id:553644 Lactobacillus rapi str. YIT 11204 (= NRIC 0743 = JCM 15 AB3663
EU457577.1 gg_id:320463 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU4575
FJ749595.1 gg_id:561759 Lactobacillus reuteri str. IMAU10037; ZL12-1-1 FJ7495
AB257866.1 gg_id:157489 Lactobacillus suebicus MCH2-2 AB2578

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

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AY253657.1 gg_id:84126 Lactobacillus kalixensis str. Kx127A2; LMG 22115T; DSM 16043T; CCUG 48459T AY253
GQ156506.1 gg_id:536680 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
EU453934.1 gg_id:312564 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU453
EU460844.1 gg_id:300935 short-beaked echidna feces clone ECH_aai39b05 EU460
NC_009513.1 gg_id:232292 Lactobacillus reuteri F275 str. DSM 20016 NC_00
FM177140.1 gg_id:338587 Lactobacillus casei str. BL23 FM177
AM113783.1 gg_id:140595 Lactobacillus malefermentans str. DSM 5705 AM113
AB425933.1 gg_id:576004 Lactobacillus equigenerosi str. TB-F27 AB425
AB330933.1 gg_id:240133 Lactobacillus paracasei str. 1532 AB330
FJ532361.1 gg_id:585123 Lactobacillus plantarum str. 14W FJ5323
AJ272031.1 gg_id:73879 Lactobacillus plantarum str. HSW36 AJ2720
GQ900597.1 gg_id:590725 Lactobacillus plantarum str. A15 GQ900
AJ417499.1 gg_id:70957 Lactobacillus farciminis str. DSM 20185 AJ4174
AB018528.1 gg_id:18684 Lactobacillus paralimentarius str. TB 1 AB018
EU457235.1 gg_id:336661 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H78S EU457
EU453395.1 gg_id:326168 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU453
GU177629.1 gg_id:582937 Lactobacillus casei str. 3-2 GU177
EU776515.1 gg_id:314385 Lion feces clone LI1_d02 EU776
EU460828.1 gg_id:288584 short-beaked echidna feces clone ECH_aai38h04 EU460
EF187245.1 gg_id:348593 Lactobacillus sp. str. Bin4 EF1872
EU504694.1 gg_id:259726 cecal contents Mus musculus strain C57BL/6J; myd1 clone myd1_aaa04f04 EU504
AF243163.1 gg_id:43142 Lactobacillus sp. str. KC45a AF243
GQ030443.1 gg_id:446566 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw878c09c GQ030
GQ155448.1 gg_id:591100 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
AB268119.1 gg_id:192776 Lactobacillus composti str. NRIC 0690 AB268
EU454159.1 gg_id:323205 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU454
EU510722.1 gg_id:265346 cecal contents Mus musculus strain C57BL/6J; WD5 clone WD5_aak40a07 EU510
EU454340.1 gg_id:323666 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H79S EU454
EU505289.1 gg_id:263903 cecal contents Mus musculus strain C57BL/6J; myd4 clone myd4_aaa01h10 EU505
EU460768.1 gg_id:301085 short-beaked echidna feces clone ECH_aai37g02 EU460
DQ815603.1 gg_id:171781 mouse cecum clone aab43d12 DQ815
EF097628.1 gg_id:177863 mouse cecum clone SWPT20_aaa01e05 EF0976
FN185731.1 gg_id:578837 Lactobacillus sp. 1.1424 FN185
EU453153.1 gg_id:324998 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N EU453
EU454019.1 gg_id:313356 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75N EU454
AM500777.1 gg_id:534519 proof spatial heterogeneity hot composting clone E12 AM500
FJ751792.1 gg_id:568482 Lactobacillus farciminis str. DSPV 353T FJ7517
AB512778.1 gg_id:559510 Lactobacillus lindneri str. YIT 10387 AB512
EU505411.1 gg_id:271014 cecal contents Mus musculus strain C57BL/6J; myd4 clone myd4_aaa04a08 EU505
GQ131124.1 gg_id:436188 Lactobacillus casei str. IMAU70007; BM2302 GQ131

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AY212750.1 gg_id:100041 equine manure clone wet199 AY212
AB048833.1 gg_id:74053 Lactobacillus equi str. YIT 0455 AB048
DQ014569.1 gg_id:133995 mouse cecum clone M1_b08 DQ014
EU776667.1 gg_id:351922 Lion feces clone LI2_aae47g12 EU776
EU728754.1 gg_id:340933 Lactobacillus reuteri str. DJF_RP45 EU728
FJ192637.1 gg_id:356529 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior FJ1926
EF098373.1 gg_id:192635 mouse cecum clone SWPT15_aaa01g09 EF0983
EF096254.1 gg_id:189201 mouse cecum clone obob1_aaa03e05 EF0962
AM279150.1 gg_id:185189 Lactobacillus secaliphilus str. TMW 1.1309 AM279
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Y11374.1 gg_id:15179 Lactobacillus kunkeei str. YH-15 Y11374
EU454221.1 gg_id:326198 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H80N EU454
AF197125.1 gg_id:15202 Lactobacillus sp. str. C33LV5 AF197
EU419599.1 gg_id:275265 Lactobacillus plantarum str. KLDS 1.0623 EU419
EU463024.1 gg_id:297096 southern three-banded armadillo feces clone arma_aaj56f06 EU463
AB284944.1 gg_id:177366 Lactobacillus sp. str. TS1 AB284
DQ015596.1 gg_id:130744 mouse cecum clone M3_a03_3 DQ015
GQ202837.1 gg_id:551236 Lactobacillus plantarum str. C06 GQ202
EF096361.1 gg_id:174939 mouse cecum clone obob2_aaa01f01 EF0963
EU504983.1 gg_id:260003 cecal contents Mus musculus strain C57BL/6J; myd3 clone myd3_aaa01b10 EU504
AY281292.1 gg_id:105149 Lactobacillus curvatus str. KNUC04 AY281
X76330.1 gg_id:15190 Lactobacillus fructivorans str. DSM 20203 T X7633
AAPZ02000002.1 gg_id:325109 Lactobacillus reuteri str. 100-23 AAPZ0
AY735409.1 gg_id:108246 Lactobacillus plantarum str. LP2 AY735
EU507666.1 gg_id:270372 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_aaa02g07 EU507
EU451014.1 gg_id:316980 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU451
DQ239699.1 gg_id:144704 Lactobacillus plantarum str. L6 DQ239
EU460890.1 gg_id:302821 short-beaked echidna feces clone ECH_aai40a07 EU460
EU455582.1 gg_id:335842 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU455
GQ155531.1 gg_id:594070 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EU453262.1 gg_id:311179 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU453
AB498046.1 gg_id:590362 Lactobacillus sp. str. F9-2 AB498
EF096134.1 gg_id:191524 mouse cecum clone obob1_aaa01b04 EF0961
AJ417738.1 gg_id:56512 Lactobacillus letivazi str. JCL3994 AJ4177
EU453171.1 gg_id:337918 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K77S EU453
NC_009513.1 gg_id:232290 Lactobacillus reuteri F275 str. DSM 20016 NC_00
NR_028617.1 gg_id:577716 Lactobacillus algidus str. M 6 A9; JCM 10491 NR_02
DQ015578.1 gg_id:133239 mouse cecum clone M3_g04_2 DQ015
EU451147.1 gg_id:340145 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75N EU451

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NR_024885.1 gg_id:538781 Paralactobacillus selangorensis str. LMG 17710 NR_02
GQ131183.1 gg_id:426143 Lactobacillus reuteri str. IMAU70067; HS1302 GQ131
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GU125459.1 gg_id:569558 Lactobacillus alimentarius str. IMAU80037 GU125
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EU461951.1 gg_id:292302 white-faced saki feces clone Saki_aaj64c05 EU461
AY773954.1 gg_id:107854 Lactobacillus paracasei 4C AY773
EU454930.1 gg_id:338011 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU454
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EU456468.1 gg_id:322647 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75N EU456
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L23507.1 gg_id:15143 Lactobacillus reuteri L23507
AB362735.1 gg_id:247913 Lactobacillus pentosus str. NRIC 1732 AB362
AY690834.1 gg_id:123663 Lactobacillus nantesii str. Lp33 AY690
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EU456289.1 gg_id:316723 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU456
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AF049743.1 gg_id:15206 Lactobacillus sp. str. LMG 17676 AF049
EU457691.1 gg_id:318641 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU457
AM905388.1 gg_id:268188 Lactobacillus fabifermentans str. LMG 24284 AM905
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EU508681.1 gg_id:270597 cecal contents Mus musculus strain C57BL/6J; MD4 clone MD4_aap49d02 EU508
EU509957.1 gg_id:261239 cecal contents Mus musculus strain C57BL/6J; WD11 clone WD11_aak24c10 EU509
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EU450898.1 gg_id:344695 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75N EU450

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EU456918.1 gg_id:340234 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU456
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EU453721.1 gg_id:316608 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83N EU453
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AB290830.1 gg_id:514694 Lactobacillus equicursoris str. DI70 AB290
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FM177140.1 gg_id:338585 Lactobacillus casei str. BL23 FM177
EF098024.1 gg_id:182758 mouse cecum clone SWPT12_aaa04c03 EF0980
EU507563.1 gg_id:267604 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_aaa01b05 EU5075
EU455156.1 gg_id:339840 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU4551
DQ239695.1 gg_id:141655 Lactobacillus plantarum str. L2 DQ239
AB470237.1 gg_id:363520 Lactobacillus sakei str. S2 AB4702
EU460915.1 gg_id:296432 short-beaked echidna feces clone ECH_aai40d09 EU4609
EF097172.1 gg_id:182972 mouse cecum clone SWPT18_aaa02d10 EF0971
EF097176.1 gg_id:190167 mouse cecum clone SWPT18_aaa02e05 EF0971
EU454503.1 gg_id:326900 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU4545
EU510255.1 gg_id:266771 cecal contents Mus musculus strain C57BL/6J; WD3 clone WD3_aak03f06 EU5102
AY204897.1 gg_id:81036 Lactobacillus sakei str. HNSL5c AY2048
EU455625.1 gg_id:315788 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N EU4556
EU451160.1 gg_id:335029 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N EU4511
EF412985.1 gg_id:208876 Lactobacillus gallinarum str. I26 EF4129
EU507280.1 gg_id:272684 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_2aaa01a06 EU5072
FJ405227.1 gg_id:359669 Lactobacillus casei str. ZJ3 FJ4052
AB368904.1 gg_id:282265 Lactobacillus plantarum str. T8-7 AB3689
AF308146.1 gg_id:72717 Lactobacillus thermotolerans str. G 12 AF3081
EU474952.1 gg_id:299475 red river hog feces clone RRH_aaa04g03 EU4749
EU508709.1 gg_id:264123 cecal contents Mus musculus strain C57BL/6J; MD4 clone MD4_aap49g05 EU5087
AB362741.1 gg_id:249746 Lactobacillus pentosus str. NRIC 1753 AB3627
AY735404.1 gg_id:108108 Lactobacillus plantarum str. LP1 AY7354
GQ131182.1 gg_id:376168 Lactobacillus reuteri str. IMAU70066; HS1301 GQ131
DQ015426.1 gg_id:130724 mouse cecum clone M3_h10 DQ015
AB368903.1 gg_id:282170 Lactobacillus plantarum str. T4-5 AB3689
EU074828.1 gg_id:243630 Lactobacillus plantarum str. TC41 EU0748
AB162131.1 gg_id:106519 Lactobacillus nagelii str. NRIC 0559 AB1621
EU457936.1 gg_id:323012 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N EU4579
DQ399353.1 gg_id:154984 Lactobacillus paracasei str. SFCB2-4 DQ399
EU453809.1 gg_id:318211 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU4538
GQ461596.1 gg_id:593464 Lactobacillus plantarum str. K25 GQ461
EU457051.1 gg_id:317830 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU4570
EU451427.1 gg_id:354114 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU4514
GQ156407.1 gg_id:537937 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
EU456062.1 gg_id:308210 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N EU4560
AB362731.1 gg_id:255682 Lactobacillus sakei str. NRIC 1609 AB3627
GU177634.1 gg_id:578809 Lactobacillus casei str. C-1 GU177
EU474892.1 gg_id:287698 red river hog feces clone RRH_aaa04e08 EU4748

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EU453867.1 gg_id:313722 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU453
EU457601.1 gg_id:337406 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H74N EU457
EU455334.1 gg_id:317894 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU455
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AB362607.1 gg_id:244469 Lactobacillus sakei str. NRIC 0126 AB362
EU510005.1 gg_id:274605 cecal contents Mus musculus strain C57BL/6J; WD1 clone WD1_aaf15e11 EU510
GU369759.1 gg_id:524305 Lactobacillus plantarum str. YM-4-5 GU369
EU452893.1 gg_id:303591 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU452
GQ155548.1 gg_id:512953 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
AB362667.1 gg_id:258139 Lactobacillus pentosus str. NRIC 0403 AB362
GQ231436.1 gg_id:588182 Lactobacillus reuteri str. DSPV 002C GQ231
GU299083.1 gg_id:534440 Lactobacillus casei str. NQ2-2 GU299
DQ815681.1 gg_id:166336 mouse cecum clone aab44g06 DQ815
AJ965487.1 gg_id:126988 Lactobacillus arizonensis str. DSM 13273 AJ9654
AB239468.1 gg_id:141834 Lactobacillus casei str. CP1-13 AB239
EU457018.1 gg_id:330111 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU457
GQ030377.1 gg_id:467257 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw877c08c GQ030
EF095994.1 gg_id:186522 mouse cecum clone lean2_aaa01f03 EF0959
FJ682870.1 gg_id:530798 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6828
EU454755.1 gg_id:356144 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75N EU454
EU460235.1 gg_id:295058 polar bear feces clone PB1_aai25b05 EU460
GQ155587.1 gg_id:513479 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
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AB303848.1 gg_id:257805 Monitoring Pickling Bed Fermented Rice Bran Which Dominated S-Growing Lactobac AB3038
EU439433.1 gg_id:267700 Lactobacillus plantarum str. 1L48P35 EU439
EF097557.1 gg_id:196803 mouse cecum clone SWPT19_aaa04c12 EF0975
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DQ015553.1 gg_id:135934 mouse cecum clone M3_e03_2 DQ015
EU460783.1 gg_id:296454 short-beaked echidna feces clone ECH_aai37h09 EU460
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FJ678780.1 gg_id:521424 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6787
EU465367.1 gg_id:302089 lion feces clone LI3_aah76b05 EU465
AB332024.2 gg_id:246232 Lactobacillus nodaensis str. IZ4B AB332
EU526816.1 gg_id:276202 Lactobacillus plantarum str. Z6 EU526
GQ900606.1 gg_id:550314 Lactobacillus plantarum str. F34 GQ900
EU505359.1 gg_id:276978 cecal contents Mus musculus strain C57BL/6J; myd4 clone myd4_aaa03b09 EU505
GQ131153.1 gg_id:385174 Lactobacillus casei str. IMAU70037; BM10307 GQ131
AJ242968.1 gg_id:15128 Lactobacillus gallinarum str. ATCC 33199 AJ2429

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AF243151.1 gg_id:22892 Lactobacillus gasseri str. KC36a AF2431
DQ815389.1 gg_id:164758 mouse cecum clone aab47d05 DQ815
EU451364.1 gg_id:346613 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N EU4513
GQ156345.1 gg_id:575537 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
AM292799.1 gg_id:187763 Lactobacillus ceti str. 142 AM292
AY253660.1 gg_id:84798 Lactobacillus ultunensis str. Kx146C1; LMG 22117T; DSM 16047T; CCUG 48460T AY2536
EU451966.1 gg_id:333408 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N EU4519
EU161635.1 gg_id:239571 Lactobacillus murinus str. LR EU1616
GU191837.1 gg_id:581162 Lactobacillus reuteri str. BR11 GU191
AB303841.1 gg_id:236486 Lactobacillus acetotolerans str. JCM 3825 AB3038
EU511690.1 gg_id:263080 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_aaf07a08 EU5116
EU504504.1 gg_id:276180 cecal contents Mus musculus strain C57BL/6J; myd1 clone myd1_aaa01e09 EU5045
EU547306.1 gg_id:545371 Lactobacillus delbrueckii subsp. bulgaricus str. BCS113 EU5473
EU505043.1 gg_id:263220 cecal contents Mus musculus strain C57BL/6J; myd3 clone myd3_aaa02a11 EU5050
GQ155476.1 gg_id:593810 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
AM236150.1 gg_id:177499 Lactobacillus amylotrophicus str. NRRL B-4435 AM236
EU455693.1 gg_id:305429 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H74N EU4556
AF515229.1 gg_id:56475 Pediococcus acidilactici str. RO17 AF5152
AB018214.1 gg_id:15157 Pediococcus acidilactici str. LA 35 AB0182
FJ915623.1 gg_id:538273 Pediococcus acidilactici str. IMAU20090; mgh10-7-2 FJ9156
AB018212.1 gg_id:27815 Pediococcus acidilactici str. E 7 AB0182
EU331307.1 gg_id:244766 Pediococcus damnosus str. Bpe233 EU3313
AB258357.1 gg_id:158048 Pediococcus siamensis MCH3-2 AB2583
GU125433.1 gg_id:560139 Pediococcus ethanolidurans str. IMAU80011 GU125
AJ271383.1 gg_id:19307 Pediococcus inopinatus str. DSM 20285 AJ2713
EU331259.1 gg_id:239673 Pediococcus parvulus str. Bpe301 EU3312
FM878597.1 gg_id:589816 Pediococcus parvulus str. LA1110 FM878
AY675245.1 gg_id:105170 Pediococcus pentosaceus str. LM2632 AY6752
AB018215.1 gg_id:15152 Pediococcus pentosaceus str. LS 5 AB0182
AJ305321.1 gg_id:38120 Pediococcus pentosaceus str. DSM 20336 (T) AJ3053
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AB362987.1 gg_id:242063 Pediococcus pentosaceus str. NGRI 0305 AB3629
EU483113.1 gg_id:265290 Pediococcus pentosaceus str. MY-800 EU4831
EU878171.1 gg_id:328309 Pediococcus pentosaceus str. SH 740 EU8781
AJ973157.1 gg_id:147407 Pediococcus stilesii str. LMG 23082 = FAIR-E AJ9731
FJ378890.1 gg_id:359769 Pediococcus pentosaceus str. B-38 FJ3788
AJ621555.1 gg_id:113414 Pediococcus claussenii str. DSM 14800 AJ6215
FJ405228.1 gg_id:366574 Pediococcus claussenii str. ZJ5 FJ4052
AY675243.1 gg_id:104878 Pediococcus pentosaceus str. SL4 AY6752
AM279764.2 gg_id:161185 Lactobacillus plantarum 7.8.2 AM279

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AB240455.1 gg_id:145715 Lactobacillus halophilus str. KG34 AB240
EU460734.1 gg_id:303093 short-beaked echidna feces clone ECH_aai37b12 EU460
EU460924.1 gg_id:300991 short-beaked echidna feces clone ECH_aai40e11 EU460
EU626008.1 gg_id:277639 Lactobacillus coryniformis str. KLDS 1.0723 EU626
EU460820.1 gg_id:297646 short-beaked echidna feces clone ECH_aai38g03 EU460
AF360737.1 gg_id:67685 Leuconostoc fructosum str. DSM 20349 AF360
DQ837629.1 gg_id:163654 structures honeybee intestines and their response insecticidal proteins gut clone HB DQ837
AY169967.1 gg_id:101369 Leuconostoc pseudoficulneum str. LC51 AY169
AM157423.1 gg_id:141780 Leuconostoc citreum mother C3 AM157
AM157430.1 gg_id:143322 Leuconostoc citreum mother C4 AM157
GQ392137.1 gg_id:553432 Leuconostoc citreum str. CJGN34 GQ392
FJ040200.1 gg_id:535439 Leuconostoc citreum str. C16 FJ0402
EU074846.1 gg_id:245787 Leuconostoc citreum str. TM319 EU074
AM157444.1 gg_id:141773 Leuconostoc citreum mother V4 AM157
AM600682.1 gg_id:226092 Leuconostoc holzapfelii str. LMG 23990 = BFE 700 AM600
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EU074837.1 gg_id:240308 Leuconostoc mesenteroides str. CM160 EU074
GQ351321.1 gg_id:533637 Leuconostoc mesenteroides str. OR2P-2 GQ351
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FJ040199.1 gg_id:550853 Leuconostoc mesenteroides str. C12 FJ0401
GQ915096.1 gg_id:539665 Leuconostoc mesenteroides str. AaD8 GQ915
FJ215674.1 gg_id:312330 Leuconostoc mesenteroides str. IMAU60052 FJ2156
EU074838.1 gg_id:238676 Leuconostoc mesenteroides str. PC216 EU074
EU074836.1 gg_id:252222 Leuconostoc mesenteroides str. CM135 EU074
EU074841.1 gg_id:247929 Leuconostoc mesenteroides str. CC317 EU074
EU177638.1 gg_id:341233 Leuconostoc mesenteroides str. ANN12 EU177
EU074839.1 gg_id:248008 Leuconostoc mesenteroides str. PM249 EU074
AF515228.1 gg_id:64385 Leuconostoc pseudomesenteroides str. RO1 AF515
EU177631.1 gg_id:337944 Leuconostoc pseudomesenteroides str. NS28 EU177
EU074840.1 gg_id:253688 Leuconostoc mesenteroides str. PM141 EU074
EU177632.1 gg_id:345546 Leuconostoc pseudomesenteroides str. NS33 EU177
FJ015056.1 gg_id:315407 Leuconostoc pseudomesenteroides str. FL6 FJ0150
EU337117.1 gg_id:546379 Leuconostoc pseudomesenteroides str. MC EU337
EF121354.2 gg_id:249922 Leuconostoc citreum str. GJ7 EF1213
EU574896.1 gg_id:267454 Leuconostoc mesenteroides str. NRRL B-1355 EU574
FJ749310.1 gg_id:547101 Leuconostoc lactis str. IMAU40034; QH4-6-2 FJ7493
FJ480207.1 gg_id:592022 Leuconostoc mesenteroides str. WCP907 FJ4802
AB362723.1 gg_id:238348 Leuconostoc citreum str. NRIC 1581 AB362
AB362719.1 gg_id:244448 Leuconostoc garlicum str. NRIC 1577 AB362
AB470239.1 gg_id:365285 Leuconostoc gelidum str. GD AB470

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AM940225.1 gg_id:349734 Leuconostoc palmae str. TMW 2.694 AM940
AB362720.1 gg_id:252701 Leuconostoc garlicum str. NRIC 1578 AB3627
AF111948.1 gg_id:15110 Leuconostoc citreum str. ATCC49370; KCTC3526 AF1119
AB362722.1 gg_id:256844 Leuconostoc garlicum str. NRIC 1580 AB3627
EU463822.1 gg_id:290159 Seba's short-tailed bat feces clone bat_aaj05d07 EU4638
AY165007.4 gg_id:75964 Leuconostoc citreum str. CY2 AY1650
AB022921.1 gg_id:24935 Leuconostoc gelidum str. NRIC 1778 AB0229
AB362682.1 gg_id:246692 Leuconostoc mesenteroides str. NRIC 0587 AB3626
AB470240.1 gg_id:363305 Leuconostoc gasicomitatum str. GC AB4702
AB054806.1 gg_id:43827 Oenococcus oeni str. 95 St.Mer-2-4 AB0548
CP000411.1 gg_id:175948 Oenococcus oeni str. PSU-1 CP0004
FM878590.1 gg_id:571983 Oenococcus oeni str. LA126 FM878
AB221475.1 gg_id:159865 Oenococcus kitaharae str. NRIC 0645 AB2214
GU138518.1 gg_id:568005 Weissella confusa str. LSBM3-1 GU138
AB022926.1 gg_id:45087 Weissella halotolerans str. NRIC 1627 AB0229
EU465515.1 gg_id:292431 lion feces clone LI3_aah78f11 EU4655
AB022922.1 gg_id:43687 Weissella kandleri str. NRIC 1628 AB0229
AM157446.1 gg_id:144619 Weissella confusa mother V4 AM157
EU855224.1 gg_id:352468 Weissella paramesenteroides str. CTSPL5 EU8552
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AM157435.1 gg_id:142903 Weissella cibaria mother C4 AM157
AB015642.1 gg_id:15084 Weissella hellenica str. DS-12 AB0156
EU439435.2 gg_id:560064 Weissella sp. str. 2L24P13 EU4394
AM882997.1 gg_id:241383 Weissella ghanensis str. LMG 24286 AM882
EU177641.1 gg_id:320990 Weissella paramesenteroides str. NS74 EU1776
EU869290.1 gg_id:331921 Weissella sp. str. JZ-1L EU8692
DQ294962.1 gg_id:143027 Weissella cibaria str. Uga57 DQ294
EU074829.1 gg_id:251397 Weissella cibaria str. BC48 EU0748
DQ294964.1 gg_id:142786 Weissella cibaria str. Uga69 DQ294
AF477495.1 gg_id:23573 Weissella confusa str. PL9001 AF4774
AF477498.1 gg_id:36439 Lactobacillus fermentum str. PL9005 AF4774
AF312874.1 gg_id:22775 Weissella cibaria str. CHJ3 AF3128
FJ429974.1 gg_id:565622 Weissella confusa str. C3-7 FJ4299
GU369772.1 gg_id:530233 Weissella confusa str. JS-7-1 GU369
FJ263453.1 gg_id:366705 Weissella confusa str. XW1 FJ2634
AB257595.1 gg_id:158275 Weissella salipiscis str. FS55-1 AB2575
X95981.1 gg_id:15090 Weissella hellenica str. NCFB 2973 X95981
FJ654456.1 gg_id:537058 Weissella hellenica str. 138 FJ6544
FJ654465.1 gg_id:511014 Weissella hellenica str. 1507 FJ6544
DQ883229.1 gg_id:163888 Weissella koreensis str. 405 DQ883
EU180607.1 gg_id:335281 Weissella soli str. NS26 EU1806

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EU775634.1 gg_id:315664 Hedgehog feces clone HH_d06 EU775
EU777721.1 gg_id:330069 Polar bear feces clone PB1_aai28f10 EU777
EU460570.1 gg_id:298506 polar bear feces clone PB2_aai22g09 EU460
EU460926.1 gg_id:299075 short-beaked echidna feces clone ECH_aai40f04 EU460
EU791208.1 gg_id:455671 Enteric Defensins are Essential Regulators Intestinal Microbial Ecology MMP7++ mou EU791
AB018211.1 gg_id:42931 Lactococcus garvieae str. E 1 AB018
EU460718.1 gg_id:302924 polar bear feces clone PB2_aai24h07 EU460
EU467542.1 gg_id:296207 southern three-banded armadillo feces clone arma_f03 EU467
EU775705.1 gg_id:333803 Hedgehog feces clone HH_aai36e07 EU775
EU460397.1 gg_id:302882 polar bear feces clone PB1_aai28a07 EU460
AF283499.1 gg_id:45250 Lactococcus garvieae AF283
EU775674.1 gg_id:336969 Hedgehog feces clone HH_d10 EU775
EU460462.1 gg_id:293407 polar bear feces clone PB2_aai21b11 EU460
EU458153.1 gg_id:297489 North American black bear feces clone BB2_f02 EU458
AB244446.1 gg_id:257338 Lactococcus garvieae str. An10-2 AB244
EU460864.1 gg_id:292600 short-beaked echidna feces clone ECH_aai39e07 EU460
DQ223877.1 gg_id:173259 Lactococcus sp. str. RT5 DQ223
DQ223876.1 gg_id:167936 Lactococcus lactis str. RT4 DQ223
AM490366.1 gg_id:203331 Lactococcus lactis str. C22 AM490
AM157445.1 gg_id:141784 Lactococcus lactis mother V4 AM157
AJ488176.1 gg_id:66046 Lactococcus lactis str. 04 AJ488
AY348313.1 gg_id:93048 Lactococcus lactis str. Akira2 AY348
AM157424.1 gg_id:141720 Lactococcus lactis mother C3 AM157
EU203156.1 gg_id:251182 Lactococcus lactis str. WH11-1 EU203
GQ337889.1 gg_id:594031 Lactococcus lactis str. KLDS4.0352 GQ337
AY762104.1 gg_id:108349 Lactococcus sp. str. MKRL19 AY762
AJ133479.1 gg_id:69992 Lactococcus sp. TmLO5 AJ1334
EU073957.2 gg_id:240865 Lactococcus sp. Da-18 EU073
AB234513.1 gg_id:150304 termite gut homogenate clone MgMjW-44 AB234
AJ439543.2 gg_id:110020 Lactovum miscens str. anNAG3 AJ4395
DQ856510.1 gg_id:253776 intestinal microflora Chinese mitten crab (Eriocheir sinensis) clone C1N DQ856
AB089063.1 gg_id:78015 termite gut homogenate clone Rs-C68 sp. AB089
DQ343754.1 gg_id:146404 Lactococcus piscium str. CCUG 32732 DQ343
EF204369.1 gg_id:201186 Lactococcus sp. G23 EF2043
EU460490.1 gg_id:294254 polar bear feces clone PB2_aai21f02 EU460
AB089061.2 gg_id:78223 termite gut homogenate clone Rs-B70 AB089
AY571411.1 gg_id:114538 termite gut clone RsaM9 AY5714
EF694029.1 gg_id:256029 Lactococcus plantarum str. DSM 20686 EF6940
GQ502570.1 gg_id:555286 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf4- GQ502
AM944736.1 gg_id:270649 Enterococcus sp. str. UNK1 AM944

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NZ_AAJO01000148.1 gg_id:140424 Streptococcus agalactiae str. 18RS21 NZ_AA
AAJO01000006.1 gg_id:139711 Streptococcus agalactiae str. 18RS21 AAJO0
EU473184.1 gg_id:300948 giant panda feces clone GP_1aaa04g12 EU473
AB002519.1 gg_id:15456 Streptococcus alactolyticus str. ATCC 43492 AB002
EU473340.1 gg_id:289833 giant panda feces clone GP_1aaa04h11 EU473
AB355611.1 gg_id:240886 Streptococcus anginosus str. IMU103 AB355
AY691534.1 gg_id:107288 Streptococcus anginosus str. ChDC YA1 AY691
AY986761.1 gg_id:115190 Streptococcus anginosus str. ChDC YA2 AY986
EU075058.1 gg_id:239570 Streptococcus canis str. 3-35MP EU075
FJ557869.1 gg_id:525128 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5578
FJ557854.1 gg_id:527756 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5578
AB182324.1 gg_id:169991 Streptococcus orisuis str. NUM 1001 AB182
AJ853835.1 gg_id:108737 Streptococcus cristatus str. PD01A5 AJ8538
AY281090.1 gg_id:90588 Streptococcus cristatus str. ATCC 49999 AY281
AB008313.1 gg_id:15567 Streptococcus cristatus str. NCTC12479 AB008
NR_029015.1 gg_id:589575 Streptococcus devriesei str. CCUG 47156 NR_02
DQ303185.1 gg_id:167230 Streptococcus didelphis str. ATCC 700828 DQ303
AF176107.1 gg_id:15363 Streptococcus didelphis str. 95-3349-1 AF176
AY942561.1 gg_id:133561 Streptococcus downei str. ChDC YD1 AY9425
AY942564.1 gg_id:137388 Streptococcus downei str. ChDC YD4 AY9425
EF405993.1 gg_id:219796 Streptococcus subsp. equi str. Bd 5895/99 EF4059
AB002516.1 gg_id:15355 Streptococcus equi subsp. zooepidemicus str. ATCC 43079 AB002
AB002515.1 gg_id:15354 Streptococcus subsp. equi str. ATCC 33398 NCTC 9682 AB002
AJ420197.1 gg_id:39498 Streptococcus ferus str. 8S1 AJ4201
U87827.1 gg_id:15564 aortic heart valve patient with endocarditis clone v2 U8782
AJ427479.1 gg_id:36023 Streptococcus gordonii str. DL1 AJ4274
AB355602.1 gg_id:243837 Streptococcus gordonii str. NUK38 AB355
AB002518.1 gg_id:15428 Streptococcus hyointestinalis str. ATCC 49169 DSM 20770 AB002
DQ462420.1 gg_id:203615 Streptococcus icataluri LS0706-05 DQ462
GQ050656.1 gg_id:398932 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu488f1 GQ050
GQ115486.1 gg_id:393307 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw686c07 GQ115
EU156759.1 gg_id:331335 Streptococcus infantis str. CCUG 39817 EU156
AB008315.1 gg_id:15551 Streptococcus infantis str. GTC849 AB008
GQ077246.1 gg_id:395569 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw115 GQ077
EU620580.1 gg_id:279591 Streptococcus iniae str. CMS003 EU620
EU467794.1 gg_id:287876 North American black bear feces clone BB1_b04 EU467
AB002482.1 gg_id:15458 Streptococcus bovis str.ATCC 33317 AB002
AJ297214.1 gg_id:30971 Streptococcus luteciae str. NEM 760 AJ2972
EU461863.1 gg_id:299806 white-faced saki feces clone Saki_aaj62e05 EU461
EU467738.1 gg_id:295347 North American black bear feces clone BB1_a07 EU467

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EU467837.1 gg_id:290948 North American black bear feces clone BB1_b03_1 EU467
EU458240.1 gg_id:295954 North American black bear feces clone BB2_e04 EU458
EU467796.1 gg_id:298722 North American black bear feces clone BB1_b07_1 EU467
EU467742.1 gg_id:291695 North American black bear feces clone BB1_b06 EU467
AJ297218.1 gg_id:21570 Streptococcus luteciae str. NEM1603 AJ2972
EU461969.1 gg_id:291625 white-faced saki feces clone Saki_aaj64e12 EU461
EU163444.1 gg_id:253732 Streptococcus lutetiensis str. 644 EU163
EU163501.1 gg_id:251131 Streptococcus macedonicus str. 905 EU163
EU075079.1 gg_id:246776 Streptococcus minor str. 26-59MP EU075
AF227836.1 gg_id:70091 str. 37236 AF227
AJ409287.1 gg_id:55342 Streptococcus entericus str. CECT 5353 AJ4092
FJ769470.1 gg_id:545996 Changes Methanogenic Microbial After Sludge Pre-treatment full-scale municipal ana FJ7694
DQ677768.1 gg_id:162458 Streptococcus mutans str. ChDC YM53; 32111 DQ677
DQ677712.1 gg_id:170656 Streptococcus mutans str. ChDC YM230; PD1163-1 DQ677
DQ677734.1 gg_id:173377 Streptococcus mutans str. ChDC YM204; PD32 DQ677
DQ677782.1 gg_id:169174 Streptococcus mutans str. ChDC YM26; 16235 DQ677
DQ677717.1 gg_id:169011 Streptococcus mutans str. ChDC YM223; PD1063 DQ677
DQ677727.1 gg_id:170005 Streptococcus mutans str. ChDC YM212; PD1026 DQ677
AF139600.1 gg_id:55433 Streptococcus mutans str. UA96 AF139
DQ677716.1 gg_id:164384 Streptococcus mutans str. ChDC YM225; PD1111 DQ677
DQ677783.1 gg_id:170638 Streptococcus mutans str. ChDC YM29; 17135 DQ677
DQ677733.1 gg_id:169266 Streptococcus mutans str. ChDC YM205; PD59 DQ677
AF077835.1 gg_id:81591 Streptococcus mutans str. UA96 AF077
DQ677769.1 gg_id:171585 Streptococcus mutans str. ChDC YM51; 31125 DQ677
DQ677755.1 gg_id:172601 Streptococcus mutans str. ChDC YM14; 9211 DQ677
DQ677736.1 gg_id:164353 Streptococcus mutans str. ChDC YM202; PD9 DQ677
DQ677787.1 gg_id:172359 Streptococcus mutans str. ChDC YM16; 9226 DQ677
DQ677750.1 gg_id:166980 Streptococcus mutans str. ChDC YM79; 49215 DQ677
DQ677777.1 gg_id:172519 Streptococcus mutans str. ChDC YM6; 3217 DQ677
DQ677765.1 gg_id:169834 Streptococcus mutans str. ChDC YM57; 33211 DQ677
DQ677737.1 gg_id:162868 Streptococcus mutans str. ChDC YM201; PD4 DQ677
AY691526.1 gg_id:102599 Streptococcus mutans str. ChDC YM3 AY691
DQ677753.1 gg_id:164446 Streptococcus mutans str. ChDC YM72; 44211 DQ677
DQ677786.1 gg_id:171168 Streptococcus mutans str. ChDC YM20; 10115 DQ677
DQ677779.1 gg_id:167840 Streptococcus mutans str. ChDC YM34; 20235 DQ677
DQ677761.1 gg_id:167048 Streptococcus mutans str. ChDC YM63; 37121 DQ677
DQ677741.1 gg_id:170415 Streptococcus mutans str. ChDC YM96; 62211 DQ677
DQ677758.1 gg_id:163887 Streptococcus mutans str. ChDC YM1; 1211 DQ677
DQ677722.1 gg_id:171075 Streptococcus mutans str. ChDC YM217; PD1047 DQ677
AF139599.1 gg_id:69287 Streptococcus mutans str. UA140 AF139
DQ677718.1 gg_id:162408 Streptococcus mutans str. ChDC YM222; PD1062 DQ677

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AF077836.1 gg_id:82224 Streptococcus mutans str. UA140 AF077
DQ677732.1 gg_id:167860 Streptococcus mutans str. ChDC YM206; PD65 DQ677
GQ112239.1 gg_id:426772 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ112
GQ073529.1 gg_id:430079 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ073
GQ011465.1 gg_id:498201 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw792c07 GQ011
FJ557749.1 gg_id:518996 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5577
GQ111665.1 gg_id:428868 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ111
AY281080.1 gg_id:90116 Streptococcus oralis str. ATCC 700233 AY281
AY880050.1 gg_id:112132 Streptococcus sp. S16-08 AY880
GQ111693.1 gg_id:410090 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ111
AY281087.1 gg_id:90242 Streptococcus parasanguinis str. ATCC 15909 AY281
EU156771.1 gg_id:356452 Streptococcus parasanguinis str. ATCC 15912 EU156
AY485605.1 gg_id:102231 Streptococcus parasanguinis str. ATCC 15912 AY485
AF543299.1 gg_id:58281 Streptococcus parasanguinis str. ChDC OS49 AF543
EU081009.1 gg_id:253153 Streptococcus parauberis str. BMG 149 EU081
AY584477.1 gg_id:99803 Streptococcus parauberis str. DSM 6631 AY584
AJ621053.1 gg_id:102460 Streptococcus phocae str. CCUG 35103 AJ621
EU391530.1 gg_id:534876 Streptococcus pluranimalium str. 219 EU391
NC_011072.1 gg_id:318252 Streptococcus pneumoniae str. G54 NC_01
CP000920.1 gg_id:517593 Streptococcus pneumoniae str. P1031 CP000
NC_010582.1 gg_id:260561 Streptococcus pneumoniae str. CGSP14 NC_01
CP000936.1 gg_id:266609 Streptococcus pneumoniae str. Hungary19A-6 CP000
NC_010582.1 gg_id:260560 Streptococcus pneumoniae str. CGSP14 NC_01
CP000919.1 gg_id:530213 Streptococcus pneumoniae str. JJA CP000
AF003930.1 gg_id:15572 Streptococcus pneumoniae str. ATCC 33400 AF003
DQ303207.1 gg_id:173018 Streptococcus pseudoporcinus str. LQ 559-98 DQ303
GQ011626.1 gg_id:498040 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw794d0 GQ011
GQ019354.1 gg_id:490312 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu189a GQ019
GQ040213.1 gg_id:458178 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw95 GQ040
GQ021941.1 gg_id:487727 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ021
GQ073432.1 gg_id:374596 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ073
GQ000271.1 gg_id:468836 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbu11 GQ000
GQ016796.1 gg_id:492871 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw825f0 GQ016
GQ073552.1 gg_id:376487 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ073
GQ114404.1 gg_id:374477 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw59 GQ114
GQ007970.1 gg_id:501695 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ007
GQ018379.1 gg_id:491290 Topographical and Temporal Human Skin Microbiome skin back clone nbu138d03c1 GQ018
GQ111622.1 gg_id:465964 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ111
GQ103077.1 gg_id:403395 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ103
GQ021669.1 gg_id:487999 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ021
GQ043832.1 gg_id:392907 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw97 GQ043

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GQ095830.1 gg_id:438226 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw4 GQ095
AY053482.1 gg_id:17851 gas hydrate clone AT425_EubB10 AY053
AY281076.1 gg_id:88205 Streptococcus mitis str. ATCC 15914 AY281
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GQ026868.1 gg_id:426596 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ026
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NC_011375.1 gg_id:314875 Streptococcus pyogenes NZ131 str. NZ131; ATCC BAA-1633 NC_01
CP000829.1 gg_id:319062 Streptococcus pyogenes NZ131 str. NZ131; ATCC BAA-1633 CP000
AM157451.1 gg_id:143051 Streptococcus salivarius mother V5 AM157

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FJ154797.1 gg_id:547030 Streptococcus salivarius str. ATCC 25975 FJ1547
GQ032902.1 gg_id:379571 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ032
GQ076850.1 gg_id:445671 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw1154 GQ076
GQ043267.1 gg_id:448280 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ043
GQ074824.1 gg_id:399219 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv GQ074
FJ363284.1 gg_id:367277 feces adult twins and mothers; TS149 clone TS149_a01d10 FJ3632
GQ019319.1 gg_id:490350 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor GQ019
GQ041356.1 gg_id:452091 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ041
FJ154805.1 gg_id:545804 Streptococcus vestibularis str. CCRI 17387 FJ1548
GQ076777.1 gg_id:376055 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw1153 GQ076
GQ073340.1 gg_id:405098 Topographical and Temporal Human Skin Microbiome skin palm clone nbw207h04c1 GQ073
EF463056.1 gg_id:219466 Streptococcus salivarius str. RKA2 EF463C
GQ073226.1 gg_id:417324 Topographical and Temporal Human Skin Microbiome skin palm clone nbw206e07c1 GQ073
GQ076892.1 gg_id:379619 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw1154 GQ076
EF463059.1 gg_id:224298 Streptococcus salivarius str. RKA5 EF463C
GQ078835.1 gg_id:428382 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ078
GQ073204.1 gg_id:424160 Topographical and Temporal Human Skin Microbiome skin palm clone nbw206c08c1 GQ073
GQ073389.1 gg_id:452062 Topographical and Temporal Human Skin Microbiome skin palm clone nbw208e03c1 GQ073
GQ032174.1 gg_id:418733 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw9 GQ032
GQ073349.1 gg_id:468290 Topographical and Temporal Human Skin Microbiome skin palm clone nbw208a01c1 GQ073
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GQ027365.1 gg_id:396642 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw9 GQ027
GQ007920.1 gg_id:501744 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw1 GQ007
AM157419.1 gg_id:141989 Streptococcus salivarius mother C3 AM157
GQ032472.1 gg_id:384506 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw9 GQ032
GQ019505.1 gg_id:490163 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu190g GQ019
GQ073065.1 gg_id:378696 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw204f09c GQ073
GQ088234.1 gg_id:440158 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw1 GQ088
GQ076935.1 gg_id:386247 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw1155 GQ076
DQ801238.1 gg_id:190678 human fecal clone RL116_aaf02c02 DQ801
GQ073241.1 gg_id:451593 Topographical and Temporal Human Skin Microbiome skin palm clone nbw206g03c1 GQ073
GQ019428.1 gg_id:490239 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu189h GQ019
GQ073128.1 gg_id:374338 Topographical and Temporal Human Skin Microbiome skin palm clone nbw205d10c1 GQ073
GQ073291.1 gg_id:376264 Topographical and Temporal Human Skin Microbiome skin palm clone nbw207c12c1 GQ073
GQ057595.1 gg_id:413021 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ057
FJ154803.1 gg_id:549813 Streptococcus salivarius str. CCUG 7215 FJ1548
GQ041484.1 gg_id:426958 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ041
FJ363912.1 gg_id:358274 feces adult twins and mothers; TS14 clone TS14_a04g10 FJ3639
GQ019436.1 gg_id:490234 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu190a GQ019

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GQ027302.1 gg_id:380914 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw! GQ027
FJ365649.1 gg_id:367692 feces adult twins and mothers; TS21 clone TS21_a01d05 FJ3656
GQ995676.1 gg_id:548391 Streptococcus sanguinis str. Hanzhong-A2 GQ995
CP000387.1 gg_id:210400 Streptococcus sanguinis str. SK36 CP000
AB002524.1 gg_id:38234 Streptococcus sanguinis str. ATCC 10556 AB002
U87828.1 gg_id:15570 aortic heart valve patient with endocarditis clone v3 U87828
U87829.1 gg_id:15571 aortic heart valve patient with endocarditis clone v5 U87829
NC_009009.1 gg_id:205756 Streptococcus sanguinis str. SK36 NC_00
NR_028833.1 gg_id:593803 Streptococcus sinensis str. HKU4; DSM 14990 NR_02
AY691533.1 gg_id:107142 Streptococcus sobrinus str. ChDC YS1 AY691
DQ677799.1 gg_id:170824 Streptococcus sobrinus str. ChDC YS13; 40125 DQ677
DQ677794.1 gg_id:167103 Streptococcus sobrinus str. ChDC YS206; PD1017 DQ677
AJ871181.1 gg_id:110876 Streptococcus sp. 1040-02B AJ8711
AF009484.1 gg_id:15515 Streptococcus suis str. 22083 AF009
DQ113766.1 gg_id:136603 dog jejunum clone J5-01 DQ113
GQ101022.1 gg_id:380857 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw48 GQ101
GQ007632.1 gg_id:502032 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ007
X68418.1 gg_id:15434 Streptococcus thermophilus str. DSM 20617 X68418
GQ104143.1 gg_id:374288 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw563g1 GQ104
GQ058136.1 gg_id:376543 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ058
GQ155489.1 gg_id:577395 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ033163.1 gg_id:406397 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ033
GQ101185.1 gg_id:408208 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw49 GQ101
GQ031863.1 gg_id:372703 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ031
GQ021918.1 gg_id:487750 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ021
GQ058145.1 gg_id:416754 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ058
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GQ052795.1 gg_id:404186 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ052
GQ057721.1 gg_id:447223 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ057
GQ031888.1 gg_id:374845 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ031
GQ045675.1 gg_id:449085 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw! GQ045
GQ052810.1 gg_id:451499 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ052
FJ363751.1 gg_id:357648 feces adult twins and mothers; TS14 clone TS14_a02h07 FJ3637
DQ327131.1 gg_id:148345 Metagenomic gut microbiome healthy human stool clone E649 DQ327
DQ176426.1 gg_id:139353 Streptococcus thermophilus DQ176
GU195648.1 gg_id:578630 Streptococcus thermophilus str. M4 GU195
GQ058082.1 gg_id:392901 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ058
GQ069727.1 gg_id:406513 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ069
NC_008532.1 gg_id:197884 Streptococcus thermophilus str. LMD-9 NC_00
GQ052788.1 gg_id:423913 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ052

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FJ749314.1 gg_id:537395 Streptococcus thermophilus str. IMAU40038; QH31-3-2 FJ7493
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GQ073080.1 gg_id:443273 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw204h03 GQ073
DQ804818.1 gg_id:185602 human fecal clone RL385_aao81b02 DQ804
DQ805013.1 gg_id:198675 human fecal clone RL385_aao84a10 DQ805
GQ106050.1 gg_id:398015 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ106
GQ101210.1 gg_id:411772 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw49 GQ101
FJ364706.1 gg_id:358192 feces adult twins and mothers; TS19 clone TS19_a02a11 FJ3647
GQ155517.1 gg_id:557282 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ058019.1 gg_id:372435 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ058
GQ048271.1 gg_id:377521 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbu GQ048
GQ155829.1 gg_id:584000 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ007512.1 gg_id:502151 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ007
GQ101087.1 gg_id:387080 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw49 GQ101
GQ155483.1 gg_id:579474 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
AY675258.1 gg_id:101812 Streptococcus thermophilus str. ST3 AY675
DQ804809.1 gg_id:190074 human fecal clone RL385_aao81a02 DQ804
AF429765.1 gg_id:71159 Streptococcus equinus str. NCDO1037T; ATCC9812 AF429
GQ074419.1 gg_id:371556 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw162f GQ074
GQ032260.1 gg_id:431839 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ032
EU473988.1 gg_id:291047 giant panda feces clone GP_2aaa03g07 EU473
FJ557752.1 gg_id:519951 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5577
GQ041684.1 gg_id:467380 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw931b1 GQ041
GU045381.1 gg_id:587346 Streptococcus oralis str. KCOM 1408 GU045
EU458225.1 gg_id:296232 North American black bear feces clone BB2_b03_2 EU458
EU458269.1 gg_id:292189 North American black bear feces clone BB2_b03_3 EU458
FJ678567.1 gg_id:526324 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6785
AF396922.1 gg_id:46196 Streptococcus bovis str. NCFB 2476 AF396
GQ076772.1 gg_id:459838 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw1153 GQ076
EU458273.1 gg_id:292624 North American black bear feces clone BB2_b09_2 EU458
GQ073147.1 gg_id:404881 Topographical and Temporal Human Skin Microbiome skin palm clone nbw205f05c1 GQ073
EU470279.1 gg_id:294884 Grevy's zebra feces clone GZ_aaa03a08 EU470
AY858648.1 gg_id:148448 Streptococcus gallolyticus str. 329 AY858
EU460756.1 gg_id:289494 short-beaked echidna feces clone ECH_aai37e12 EU460
DQ824742.1 gg_id:187029 human fecal clone RL185_aaj72e07 DQ824
AY769997.1 gg_id:113900 Streptococcus massiliensis str. 4401825 AY769
EU467782.1 gg_id:297236 North American black bear feces clone BB1_h02 EU467
EU467863.1 gg_id:289201 North American black bear feces clone BB1_g04_1 EU467
FJ684768.1 gg_id:529028 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6847

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EU156788.1 gg_id:349229 Streptococcus pseudopneumoniae str. CCUG 50870 EU156
EU458191.1 gg_id:288025 North American black bear feces clone BB2_d10_1 EU458
AJ871184.1 gg_id:110043 Streptococcus sp. 1606-02B AJ8711
GQ156276.1 gg_id:511755 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
EU458233.1 gg_id:300876 North American black bear feces clone BB2_c02_2 EU458
EU463426.1 gg_id:295495 domesticated horse feces clone horsem_aai93f11 EU463
GQ072611.1 gg_id:398533 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw19 GQ072
GQ069087.1 gg_id:426030 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ069
GQ032546.1 gg_id:458384 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ032
EU458204.1 gg_id:291703 North American black bear feces clone BB2_f09 EU458
FJ892877.1 gg_id:574304 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota HM1; ear p FJ8928
EU460889.1 gg_id:296865 short-beaked echidna feces clone ECH_aai40a06 EU460
GQ156133.1 gg_id:509836 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
EU475773.1 gg_id:297422 white-faced saki feces clone Saki_aaj63a10 EU475
EU461988.1 gg_id:300951 white-faced saki feces clone Saki_aaj64h04 EU461
EU474053.1 gg_id:296602 giant panda feces clone GP_2aaa02b11 EU474
EU779059.1 gg_id:316587 Prevost's squirrel feces clone SQ_aah81a03 EU779
EU471387.1 gg_id:303161 spectacled bear feces clone SB_2aaa01e06 EU471
EU772598.1 gg_id:326464 North American Black Bear feces clone BB1_c09_1 EU772
FJ679343.1 gg_id:517628 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6793
EU475742.1 gg_id:290829 white-faced saki feces clone Saki_aaj62d04 EU475
AJ305257.1 gg_id:36122 Streptococcus bovis str. NCTC11436 AJ3052
GQ019432.1 gg_id:490235 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu189h GQ019
GQ057697.1 gg_id:447655 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ057
GQ072785.1 gg_id:440026 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw201b07 GQ072
NR_029025.1 gg_id:590801 Streptococcus halichoeri str. M512/02/1; CCUG 48324 NR_02
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EU458245.1 gg_id:288170 North American black bear feces clone BB2_f04_2 EU458
EU467179.1 gg_id:297263 white-faced saki feces clone Saki_b01 EU467
GQ105172.1 gg_id:446697 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ105
GQ110037.1 gg_id:465867 Topographical and Temporal Human Skin Microbiome skin back clone nbw658a08c1 GQ110
EU458137.1 gg_id:299774 North American black bear feces clone BB2_c11 EU458
GQ032551.1 gg_id:392746 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ032
AF124350.1 gg_id:22640 Streptococcus orisratti str. ATCC700640; A63 AF1243
FJ154804.1 gg_id:561563 Streptococcus salivarius str. K12 FJ1548

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GQ076806.1 gg_id:421906 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw1153 GQ076
EU467824.1 gg_id:302874 North American black bear feces clone BB1_g09_1 EU4678
EU458201.1 gg_id:296761 North American black bear feces clone BB2_f04_1 EU4582
AJ617805.1 gg_id:105608 Streptococcus mitis str. B6 AJ6178
GQ073665.1 gg_id:407180 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ073
GQ073117.1 gg_id:372638 Topographical and Temporal Human Skin Microbiome skin palm clone nbw205c08c1 GQ073
GQ091708.1 gg_id:432165 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ091
EU458275.1 gg_id:294190 North American black bear feces clone BB2_c04_2 EU4582
GQ076774.1 gg_id:419654 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw1153 GQ076
EU471392.1 gg_id:294794 spectacled bear feces clone SB_2aaa03c03 EU4713
EU467785.1 gg_id:297386 North American black bear feces clone BB1_h05 EU4677
EU471507.1 gg_id:301767 spectacled bear feces clone SB_2aaa04f06 EU4715
EU461831.1 gg_id:296458 white-faced saki feces clone Saki_aaj61g11 EU4618
EU467834.1 gg_id:288953 North American black bear feces clone BB1_a10_2 EU4678
EU475853.1 gg_id:295993 white-faced saki feces clone Saki_aaj62e08 EU4758
GQ114957.1 gg_id:414368 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw59 GQ114
FJ558178.1 gg_id:528842 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5581
EU467902.1 gg_id:302209 North American black bear feces clone BB1_f02_2 EU4679
EU461802.1 gg_id:294888 white-faced saki feces clone Saki_aaj61c11 EU4618
AY281084.1 gg_id:88494 Streptococcus pneumoniae str. ATCC 6303 AY2810
GQ082014.1 gg_id:413510 Topographical and Temporal Human Skin Microbiome skin back clone nbw1199a11c GQ082
FJ677072.1 gg_id:523529 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6770
EU156778.1 gg_id:339761 Streptococcus pneumoniae str. CCRI-14666 EU1567
EU467758.1 gg_id:291579 North American black bear feces clone BB1_d10 EU4677
EU458258.1 gg_id:299395 North American black bear feces clone BB2_h04_1 EU4582
GQ086143.1 gg_id:389175 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ086
EU458150.1 gg_id:289299 North American black bear feces clone BB2_e08 EU4581
FJ673591.1 gg_id:518062 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6735
CP000262.1 gg_id:157784 Streptococcus pyogenes str. MGAS10750 CP0002
EU467778.1 gg_id:294914 North American black bear feces clone BB1_g03 EU4677
FJ679590.1 gg_id:525580 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6795
EU483251.1 gg_id:265868 Streptococcus sp. str. 24180-02 EU4832
EU467842.1 gg_id:291050 North American black bear feces clone BB1_c02 EU4678
GQ074394.1 gg_id:395063 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw162c GQ074
FJ558046.1 gg_id:525966 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5580
EU470264.1 gg_id:290919 Grevy's zebra feces clone GZ_aaa01e07 EU4702
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EU461911.1 gg_id:303202 white-faced saki feces clone Saki_aaj63e11 EU4619

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EU467774.1 gg_id:302237 North American black bear feces clone BB1_f09 EU467
FJ673292.1 gg_id:520118 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6732
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EU461849.1 gg_id:294466 white-faced saki feces clone Saki_aaj62b10 EU461
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AB038371.1 gg_id:42006 Streptococcus sp. str. PSH2 AB038
AY525792.1 gg_id:111812 Streptococcus pneumoniae str. SI_P7 AY525
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GQ081650.1 gg_id:437407 Topographical and Temporal Human Skin Microbiome skin back clone nbw1197g04c GQ081
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AJ608938.1 gg_id:107158 Streptococcus pneumoniae str. 101 AJ6089
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EU458305.1 gg_id:290994 North American black bear feces clone BB2_g04_2 EU458
GQ057676.1 gg_id:414752 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ057
AY976601.1 gg_id:124166 human cecum mucosal biopsy clone K155 AY976

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EU473954.1 gg_id:301968 giant panda feces clone GP_2aaa01a05 EU473
EU458115.1 gg_id:292424 North American black bear feces clone BB2_a03 EU458
FJ675711.1 gg_id:529778 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6757
GQ051339.1 gg_id:422100 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu4 GQ051
EU467772.1 gg_id:295379 North American black bear feces clone BB1_f07 EU467
EU772573.1 gg_id:343721 North American Black Bear feces clone BB2_g11_1 EU772
GQ030437.1 gg_id:440962 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw878c02c GQ030
EU461836.1 gg_id:292510 white-faced saki feces clone Saki_aaj61h07 EU461
GQ156121.1 gg_id:569797 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
GQ043851.1 gg_id:396351 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw97 GQ043
EU467836.1 gg_id:299093 North American black bear feces clone BB1_b02_1 EU467
EU467810.1 gg_id:288003 North American black bear feces clone BB1_e09_1 EU467
EU467768.1 gg_id:291502 North American black bear feces clone BB1_e12 EU467
GQ016664.1 gg_id:493003 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw824b0 GQ016
GQ022888.1 gg_id:486781 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu3 GQ022
GU470907.1 gg_id:549026 Streptococcus mitis bv. 2 str. F0392 GU470
EU458155.1 gg_id:287652 North American black bear feces clone BB2_f04 EU458
EU458251.1 gg_id:293413 North American black bear feces clone BB2_g04_1 EU458
GU045386.1 gg_id:558644 Streptococcus oralis str. DSMZ 20395 GU045
GQ072839.1 gg_id:408605 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw201g11c GQ072
FJ679770.1 gg_id:524800 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6797
EU458207.1 gg_id:301617 North American black bear feces clone BB2_g02_1 EU458
FJ673446.1 gg_id:527638 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6734
GQ112397.1 gg_id:449675 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ112
FJ558181.1 gg_id:526804 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5581
FJ678184.1 gg_id:527125 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6781
EU461987.1 gg_id:297081 white-faced saki feces clone Saki_aaj64h03 EU461
AY485604.1 gg_id:102076 Streptococcus australis str. ATCC 700641 AY485
EU458221.1 gg_id:292142 North American black bear feces clone BB2_a07_1 EU458
EU458291.1 gg_id:302636 North American black bear feces clone BB2_e02_3 EU458
EU473431.1 gg_id:301627 giant panda feces clone GP_1aaa02c05 EU473
EU467885.1 gg_id:293888 North American black bear feces clone BB1_c08_3 EU467
FJ684898.1 gg_id:518374 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6848
FJ558211.1 gg_id:525410 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5582
FJ678668.1 gg_id:523145 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6786
GQ116366.1 gg_id:403611 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw692b0 GQ116
EU458192.1 gg_id:302661 North American black bear feces clone BB2_d12 EU458
GQ032269.1 gg_id:391176 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ032
GQ038600.1 gg_id:432587 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu4 GQ038
GQ032521.1 gg_id:396059 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ032

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FJ662826.1 gg_id:551205 Streptococcus pyogenes str. Sp4 FJ6628
EU460892.1 gg_id:302391 short-beaked echidna feces clone ECH_aai40b02 EU460
EU467908.1 gg_id:292450 North American black bear feces clone BB1_g03_1 EU467
GQ068224.1 gg_id:458497 Topographical and Temporal Human Skin Microbiome skin alar crease clone nbw148 GQ068
EU458149.1 gg_id:289551 North American black bear feces clone BB2_e07 EU458
GQ076119.1 gg_id:372054 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ076
EU458116.1 gg_id:296356 North American black bear feces clone BB2_a05 EU458
GQ013235.1 gg_id:496431 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ013
GQ073338.1 gg_id:418360 Topographical and Temporal Human Skin Microbiome skin palm clone nbw207h02c GQ073
GQ057439.1 gg_id:371684 Topographical and Temporal Human Skin Microbiome skin interdigital web space clo GQ057
NC_003485.1 gg_id:129068 Streptococcus pyogenes str. MGAS8232 NC_00
EU535969.1 gg_id:281999 profile human microbiota antecubital fossa (inner elbow) skin clone nbt06g07 EU535
FJ676264.1 gg_id:525392 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6762
EF509615.1 gg_id:225348 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aerug EF5096
GQ101509.1 gg_id:465878 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw495 GQ101
EU467763.1 gg_id:294288 North American black bear feces clone BB1_e06 EU467
EU461902.1 gg_id:295919 white-faced saki feces clone Saki_aaj63d11 EU461
EU156782.1 gg_id:350039 Streptococcus pneumoniae str. CCRI-15796 EU156
FJ678537.1 gg_id:526366 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6785
EU461866.1 gg_id:298094 white-faced saki feces clone Saki_aaj62e09 EU461
EU458187.1 gg_id:302971 North American black bear feces clone BB2_c08_1 EU458
GQ074067.1 gg_id:404983 Topographical and Temporal Human Skin Microbiome skin interdigital web space clo GQ074
EU458210.1 gg_id:292277 North American black bear feces clone BB2_g09_1 EU458
EU458286.1 gg_id:295358 North American black bear feces clone BB2_d06_1 EU458
GQ028155.1 gg_id:406593 Topographical and Temporal Human Skin Microbiome skin interdigital web space clo GQ028
GQ018843.1 gg_id:490825 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu191d GQ018
EU458252.1 gg_id:296907 North American black bear feces clone BB2_g05_1 EU458
GQ018860.1 gg_id:490807 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu191f GQ018
EU458292.1 gg_id:302364 North American black bear feces clone BB2_e03_1 EU458
GQ010556.1 gg_id:499109 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ010
FJ679324.1 gg_id:509856 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6793
EU774903.1 gg_id:319192 Short-beaked Echidna feces clone ECH_aai38d02 EU774
GQ000869.1 gg_id:469434 Topographical and Temporal Human Skin Microbiome skin interdigital web space clo GQ000
EU461949.1 gg_id:297276 white-faced saki feces clone Saki_aaj64c03 EU461
EU467748.1 gg_id:289224 North American black bear feces clone BB1_c07 EU467
AM157421.1 gg_id:141768 Streptococcus parasanguinis mother C3 AM157
GQ058009.1 gg_id:449776 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ058
EU458304.1 gg_id:297241 North American black bear feces clone BB2_f10_2 EU458
FJ894952.1 gg_id:555959 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota BME; ear p FJ8949
EU471452.1 gg_id:295151 spectacled bear feces clone SB_2aaa01f05 EU471

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AB259061.1 gg_id:192739 Streptococcus dentirousetti str. NUM 1303 AB259
EU473378.1 gg_id:303070 giant panda feces clone GP_1aaa03e07 EU473
EU660341.1 gg_id:293142 Streptococcus pyogenes str. Sp30 EU660
GQ060712.1 gg_id:431280 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw04e07 GQ060
EU467898.1 gg_id:291675 North American black bear feces clone BB1_e07_1 EU467
EU460848.1 gg_id:288152 short-beaked echidna feces clone ECH_aai39c04 EU460
AB002510.1 gg_id:15413 Streptococcus dysgalactiae V24 AB002
GU045379.1 gg_id:578793 Streptococcus oralis str. KCOM 1401 GU045
EU458169.1 gg_id:288654 North American black bear feces clone BB2_h04 EU458
EU774892.1 gg_id:353416 Short-beaked Echidna feces clone ECH_aai38e06 EU774
AF184974.1 gg_id:42170 Streptococcus australis str. AI1; ATCC 700641 AF184
GQ074435.1 gg_id:377602 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw162 GQ074
EU534731.1 gg_id:286668 profile human skin microbiota ear punch biopsy female C57BL/6J mouse clone nbt18 EU534
GQ073325.1 gg_id:409438 Topographical and Temporal Human Skin Microbiome skin palm clone nbw207g01c GQ073
GQ032481.1 gg_id:407929 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ032
GQ156288.1 gg_id:582512 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
GQ043370.1 gg_id:446121 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw9 GQ043
EU467891.1 gg_id:290897 North American black bear feces clone BB1_d09_2 EU467
GQ010627.1 gg_id:499038 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ010
EU475847.1 gg_id:298266 white-faced saki feces clone Saki_g03 EU475
GQ088816.1 gg_id:422570 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ088
EU458230.1 gg_id:294980 North American black bear feces clone BB2_b08_2 EU458
GQ073229.1 gg_id:452542 Topographical and Temporal Human Skin Microbiome skin palm clone nbw206e10c GQ073
AF335573.1 gg_id:33357 Streptococcus iniae str. Dan 1 AF335
EU461941.1 gg_id:297117 white-faced saki feces clone Saki_aaj64b06 EU461
GQ092789.1 gg_id:374841 Topographical and Temporal Human Skin Microbiome skin interdigital web space cl GQ092
EU461957.1 gg_id:303168 white-faced saki feces clone Saki_aaj64d06 EU461
GQ003166.1 gg_id:506496 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbu19 GQ003
EU470337.1 gg_id:292055 Grevy's zebra feces clone GZ_aaa03c12 EU470
DQ148957.1 gg_id:139480 Streptococcus bovis SbH8.11 DQ148
GQ156147.1 gg_id:580333 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
GQ096744.1 gg_id:446169 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ096
EU458211.1 gg_id:300882 North American black bear feces clone BB2_g10_1 EU458
EU467816.1 gg_id:298015 North American black bear feces clone BB1_f06_1 EU467
GQ069073.1 gg_id:404627 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ069
EU156767.1 gg_id:325913 Streptococcus oligofermentans str. CCUG 48365 EU156
GQ076979.1 gg_id:425421 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw115 GQ076
EU156773.1 gg_id:342992 Streptococcus pneumoniae str. ATCC 49619 EU156
GQ101197.1 gg_id:419981 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw49 GQ101

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EU458283.1 gg_id:293073 North American black bear feces clone BB2_d03_1 EU458
EU465122.1 gg_id:300671 African elephant feces clone AFYEL_aaj68d04 EU465
GQ101296.1 gg_id:419123 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw493c GQ101
EU467176.1 gg_id:301477 white-faced saki feces clone Saki_a08 EU467
GQ071872.1 gg_id:459330 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw189d0 GQ071
EU458234.1 gg_id:292953 North American black bear feces clone BB2_c04_1 EU458
EU458200.1 gg_id:289631 North American black bear feces clone BB2_f03_1 EU458
FJ975977.1 gg_id:571637 Human gut microbiome adopts alternative state bowel transplantation ileum effluent FJ9759
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FJ662835.1 gg_id:565491 Streptococcus pyogenes str. Sp19 FJ6628
GQ072817.1 gg_id:454091 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw201e08 GQ072
GQ060504.1 gg_id:466552 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw02e10 GQ060
EU467877.1 gg_id:297939 North American black bear feces clone BB1_b06_2 EU467
EU458146.1 gg_id:300972 North American black bear feces clone BB2_e03 EU458
GQ073546.1 gg_id:459692 Topographical and Temporal Human Skin Microbiome skin interdigital web space cl GQ073
FJ662836.1 gg_id:557233 Streptococcus pyogenes str. Sp21 FJ6628
EU458242.1 gg_id:298551 North American black bear feces clone BB2_f01_2 EU458
EU772612.1 gg_id:329630 North American Black Bear feces clone BB1_g02_1 EU772
EU160562.1 gg_id:332405 diagnosis central-venous infections cultivation-dependent and techniques biofilm sc EU160
FJ672424.1 gg_id:519177 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface FJ6724
CU917914.1 gg_id:568929 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU917
EU458167.1 gg_id:291884 North American black bear feces clone BB2_g11 EU458
EU467806.1 gg_id:291430 North American black bear feces clone BB1_d10_1 EU467
DQ824669.1 gg_id:193137 human fecal clone RL185_aaj71d09 DQ824
GQ113281.1 gg_id:456797 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clo GQ113
EU475811.1 gg_id:295833 white-faced saki feces clone Saki_a01_1 EU475
X89237.1 gg_id:135882 Streptococcus pyogenes str. serotype M49 CS101 X89237
EU467843.1 gg_id:297229 North American black bear feces clone BB1_c04_1 EU467
EU473927.1 gg_id:295065 giant panda feces clone GP_2aaa01a01 EU473
EU467830.1 gg_id:299221 North American black bear feces clone BB1_h10 EU467
DQ232533.1 gg_id:179010 Streptococcus mitis str. CIP 104996 DQ232
GQ091667.1 gg_id:417572 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ091
GQ057669.1 gg_id:375780 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ057
AF003933.1 gg_id:15555 Streptococcus parasanguinis str. ATCC 15912 AF003
FJ673895.1 gg_id:518670 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6738
AY691525.1 gg_id:102441 Streptococcus mutans str. ChDC YM2 AY691
FJ558016.1 gg_id:517987 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5580
EU467856.1 gg_id:298009 North American black bear feces clone BB1_e05 EU467
EU458177.1 gg_id:296799 North American black bear feces clone BB2_a07 EU458

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EU458255.1 gg_id:292733 North American black bear feces clone BB2_g11_2 EU458
AY500370.1 gg_id:104134 Streptococcus bovis Sb5 AY500
AB264619.1 gg_id:164145 Streptococcus sp. bSSV21 AB264
EU461840.1 gg_id:294868 white-faced saki feces clone Saki_aaj62a02 EU461
AY485603.1 gg_id:101921 Streptococcus infantis str. ATCC 700779 AY485
EU461967.1 gg_id:297953 white-faced saki feces clone Saki_aaj64e08 EU461
EU467779.1 gg_id:298188 North American black bear feces clone BB1_g08 EU467
AY324611.1 gg_id:90414 Streptococcus bovis str. MPR2 AY324
GQ073778.1 gg_id:391010 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor GQ073
GQ100994.1 gg_id:451940 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw48 GQ100
GQ011458.1 gg_id:498208 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw792b1: GQ011
AJ634751.1 gg_id:111084 Streptococcus marimammalium str. M54/01/1 AJ634
EU458212.1 gg_id:291889 North American black bear feces clone BB2_h01 EU458
GQ018924.1 gg_id:490744 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu192d GQ018
GQ023586.1 gg_id:486084 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu320c12 GQ023
FJ677566.1 gg_id:530906 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ677
AM183037.1 gg_id:253441 and its spatial composts compost clone SMB52 AM183
GQ072181.1 gg_id:391890 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw193b1(GQ072
EU467826.1 gg_id:301858 North American black bear feces clone BB1_h03_1 EU467
NR_027214.1 gg_id:535803 Streptococcus pseudopneumoniae str. 108; ATCC BAA-960 NR_02
EU458243.1 gg_id:296265 North American black bear feces clone BB2_f02_2 EU458
GQ155808.1 gg_id:588046 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ074087.1 gg_id:401778 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ074
FJ673496.1 gg_id:527788 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ673
GQ155734.1 gg_id:592904 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EU467871.1 gg_id:303225 North American black bear feces clone BB1_h05_2 EU467
FJ678041.1 gg_id:518979 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ678
GU045388.1 gg_id:541157 Streptococcus mitis str. KCOM 1350 GU045
AY324610.1 gg_id:89376 Streptococcus bovis str. MPR1 AY324
EU458295.1 gg_id:295303 North American black bear feces clone BB2_e07_2 EU458
EU772625.1 gg_id:349233 North American Black Bear feces clone BB1_a08_1 EU772
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GQ018662.1 gg_id:491006 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu141e05 GQ018
FJ673875.1 gg_id:528552 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ673
GQ027253.1 gg_id:388019 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw! GQ027
EU772603.1 gg_id:349682 North American Black Bear feces clone BB2_c10 EU772
EU772567.1 gg_id:350483 North American Black Bear feces clone BB2_d03 EU772
EU473235.1 gg_id:296749 giant panda feces clone GP_1aaa01e12 EU473
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EU458213.1 gg_id:302190 North American black bear feces clone BB2_h05_1 EU458

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GQ027310.1 gg_id:434159 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ027
GQ006598.1 gg_id:503066 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu85d08c GQ006
GQ010315.1 gg_id:499348 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw736b1 GQ010
GQ104022.1 gg_id:456295 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw562a0 GQ104
EU458216.1 gg_id:293266 North American black bear feces clone BB2_h10 EU458
EU458302.1 gg_id:299685 North American black bear feces clone BB2_f07_1 EU458
EU475848.1 gg_id:293772 white-faced saki feces clone Saki_aaj62b04 EU475
EU460835.1 gg_id:288716 short-beaked echidna feces clone ECH_aai39a03 EU460
DQ294302.1 gg_id:160607 Streptococcus equi Hyena M149 DQ294
AF084832.1 gg_id:15483 Streptococcus sp. str. KN1 AF084
GQ091850.1 gg_id:416768 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ091
AM157428.1 gg_id:142502 Streptococcus mitis mother C4 AM157
FJ678391.1 gg_id:513075 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6783
GQ155781.1 gg_id:550710 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EU473460.1 gg_id:297804 Somali wild ass feces clone WA_aaa03b08 EU473
GQ030486.1 gg_id:407093 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw878h11 GQ030
EU473991.1 gg_id:299801 giant panda feces clone GP_2aaa04a03 EU473
GQ074320.1 gg_id:386466 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw161 GQ074
FJ367135.1 gg_id:361983 feces adult twins and mothers; TS28 clone TS28_a03h09 FJ3671
GQ073355.1 gg_id:434919 Topographical and Temporal Human Skin Microbiome skin palm clone nbw208a09c GQ073
EU467888.1 gg_id:294779 North American black bear feces clone BB1_c11_2 EU467
EU458114.1 gg_id:302527 North American black bear feces clone BB2_a02 EU458
FJ679191.1 gg_id:519599 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6791
GQ021841.1 gg_id:487827 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ021
AB469560.1 gg_id:359502 Streptococcus sp. str. NUM 1529 AB469
EU474107.1 gg_id:290522 giant panda feces clone GP_2aaa03a05 EU474
GQ102163.1 gg_id:457320 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw561g1 GQ102
EU467809.1 gg_id:288523 North American black bear feces clone BB1_e06_1 EU467
EU474171.1 gg_id:289475 western lowland gorilla feces clone GORSD_2aaa04h03 EU474
EU473228.1 gg_id:294997 giant panda feces clone GP_1aaa04d08 EU473
AY442818.1 gg_id:104405 Streptococcus sp. YE54 AY442
GU045389.1 gg_id:578175 Streptococcus mitis str. KCOM 1379 GU045
GU045392.1 gg_id:512763 Streptococcus mitis str. KCOM 1286 GU045
EU458209.1 gg_id:302903 North American black bear feces clone BB2_g06_1 EU458
EU458287.1 gg_id:296176 North American black bear feces clone BB2_d09_2 EU458
FJ675732.1 gg_id:509993 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6757
GQ073629.1 gg_id:413473 Topographical and Temporal Human Skin Microbiome skin interdigital web space cl GQ073

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EU774840.1 gg_id:319809 Short-beaked Echidna feces clone ECH_aai38g08 EU774
EU772577.1 gg_id:308943 North American Black Bear feces clone BB2_g09 EU772
EU461937.1 gg_id:289435 white-faced saki feces clone Saki_aaj64a10 EU461
EU458220.1 gg_id:291672 North American black bear feces clone BB2_a06_2 EU458
EU156779.1 gg_id:334078 Streptococcus pneumoniae str. CCRI-14734 EU156
EU461935.1 gg_id:301946 white-faced saki feces clone Saki_aaj64a07 EU461
EU289129.1 gg_id:245916 microbiome cloacal openings urogenital and anal tracts tammar wallaby Macropus e EU289
FJ893225.1 gg_id:571456 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota HM3; ear p FJ8932
FJ676607.1 gg_id:526041 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6766
GQ079517.1 gg_id:393671 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ079
EU467801.1 gg_id:297452 North American black bear feces clone BB1_d02_1 EU467
EU458173.1 gg_id:301800 North American black bear feces clone BB2_h12 EU458
AY281085.1 gg_id:90432 Streptococcus sanguinis str. ATCC 29667 AY281
EU467151.1 gg_id:298042 white-faced saki feces clone Saki_a06 EU467
EU461955.1 gg_id:301020 white-faced saki feces clone Saki_aaj64c10 EU461
FJ678419.1 gg_id:516100 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6784
GQ032429.1 gg_id:384627 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu542h04 GQ032
FJ677709.1 gg_id:519382 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6777
AJ420199.1 gg_id:27408 Streptococcus macacae str. NCTC11558 AJ4201
EU775424.1 gg_id:336695 Western lowland gorilla feces clone GORSD_2aaa04d03 EU775
EU467754.1 gg_id:299092 North American black bear feces clone BB1_d05 EU467
GQ067186.1 gg_id:394313 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ067
AB501126.1 gg_id:515853 Streptococcus ursoris str. NUM 1615 AB501
GQ019375.1 gg_id:490293 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu189c GQ019
AY273147.1 gg_id:84371 Streptococcus pyogenes AY273
EU467739.1 gg_id:287916 North American black bear feces clone BB1_a08 EU467
GQ023335.1 gg_id:486334 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu317a0 GQ023
GQ076817.1 gg_id:395887 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw1153 GQ076
GQ073289.1 gg_id:421921 Topographical and Temporal Human Skin Microbiome skin palm clone nbw207c10c1 GQ073
GQ018889.1 gg_id:490779 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu192a GQ018
AM420093.1 gg_id:240905 Noma subgingival plaque clone 302F04(oral) AM420
GQ154900.1 gg_id:557859 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
AY324612.1 gg_id:88822 Streptococcus bovis str. MPR4 AY3246
GQ040793.1 gg_id:374127 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw958g01 GQ040
DQ232536.1 gg_id:199646 Streptococcus oralis str. CIP 104985 DQ232
EU461824.1 gg_id:297884 white-faced saki feces clone Saki_aaj61f09 EU461
GQ155776.1 gg_id:585008 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EF364097.1 gg_id:226980 Streptococcus henryi str. 126 EF364
FJ682683.1 gg_id:514572 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6826

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NC_006086.1 gg_id:128611 Streptococcus pyogenes str. MGAS10394 NC_00
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EU467199.1 gg_id:299664 white-faced saki feces clone Saki_g09 EU467
EU779062.1 gg_id:311993 Prevost's squirrel feces clone SQ_aah79h08 EU779
AF396920.1 gg_id:39742 Streptococcus bovis str. B315 AF396
GQ115601.1 gg_id:400616 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw688b1 GQ115
FJ558308.1 gg_id:516966 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5583
EU458307.1 gg_id:289803 North American black bear feces clone BB2_h08_3 EU458
AB002522.1 gg_id:15573 Streptococcus pneumoniae str. MAFF 911410 AB002
GQ156243.1 gg_id:561883 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
GQ076853.1 gg_id:464954 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw1154 GQ076
GQ021817.1 gg_id:487851 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ021
EU467781.1 gg_id:299667 North American black bear feces clone BB1_g10 EU467
GQ023571.1 gg_id:486098 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu320b09 GQ023
EU458196.1 gg_id:292217 North American black bear feces clone BB2_e11 EU458
DQ318881.1 gg_id:150451 -DGGE and sequencing piglet stomachs stomach clone SY6 DQ318
GQ095863.1 gg_id:435368 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ095
EU467163.1 gg_id:301619 white-faced saki feces clone Saki_f02 EU467
GQ102584.1 gg_id:390165 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ102
EU471514.1 gg_id:294127 spectacled bear feces clone SB_2aaa01d12 EU471
EU467165.1 gg_id:300974 white-faced saki feces clone Saki_f06 EU467
EU474059.1 gg_id:302396 giant panda feces clone GP_2aaa01c07 EU474
GQ074646.1 gg_id:464930 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw164f GQ074
AM157442.1 gg_id:142694 Streptococcus pneumoniae mother V4 AM157
GQ021904.1 gg_id:487765 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ021
EU458151.1 gg_id:291631 North American black bear feces clone BB2_e12 EU458
GQ032381.1 gg_id:399032 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu542a07 GQ032
GQ156168.1 gg_id:590723 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
EU460825.1 gg_id:295866 short-beaked echidna feces clone ECH_aai38g10 EU460
AJ307888.1 gg_id:63461 Streptococcus gallinaceus str. CCUG 42692 AJ3078
AF009507.1 gg_id:15367 Streptococcus suis str. EA1172.91 AF009
EU772622.1 gg_id:314465 North American Black Bear feces clone BB2_c10_1 EU772
EU467845.1 gg_id:287347 North American black bear feces clone BB1_c06_2 EU467
EU775569.1 gg_id:324468 Giant Panda feces clone GP_2aaa01h07 EU775
GU045397.1 gg_id:586088 Streptococcus pneumoniae str. CCARM 4033 GU045
EU473918.1 gg_id:293540 giant panda feces clone GP_2aaa04e06 EU473

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EU467869.1 gg_id:296719 North American black bear feces clone BB1_h03_2 EU467
GQ073370.1 gg_id:442986 Topographical and Temporal Human Skin Microbiome skin palm clone nbw208c05c1 GQ073
EU461864.1 gg_id:300903 white-faced saki feces clone Saki_aaj62e06 EU461
GQ040889.1 gg_id:457333 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw959g10c GQ040
AY281079.1 gg_id:89930 Streptococcus oralis str. ATCC 9811 AY281
GQ010954.1 gg_id:498711 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ010
DQ232534.1 gg_id:190717 Streptococcus mitis str. CIP 104997 DQ232
EU475873.1 gg_id:302995 white-faced saki feces clone Saki_aaj62f09 EU475
GQ073509.1 gg_id:431778 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ073
GQ113226.1 gg_id:461942 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor GQ113
GQ155674.1 gg_id:512915 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ073236.1 gg_id:420071 Topographical and Temporal Human Skin Microbiome skin palm clone nbw206f09c1 GQ073
EU467847.1 gg_id:288218 North American black bear feces clone BB1_c09_2 EU467
FJ677289.1 gg_id:509161 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6772
EU660342.1 gg_id:299977 Streptococcus pyogenes str. Sp32 EU660
EU461896.1 gg_id:290594 white-faced saki feces clone Saki_aaj63c10 EU461
EU458288.1 gg_id:295039 North American black bear feces clone BB2_d11 EU458
EU156784.1 gg_id:331800 Streptococcus pseudopneumoniae str. CCRI-8984 EU156
FJ679815.1 gg_id:531369 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6798
GQ082003.1 gg_id:446773 Topographical and Temporal Human Skin Microbiome skin back clone nbw1198h10c GQ082
DQ016843.2 gg_id:149109 subject-specific oral microflora during initial colonization enamel human mouth; indi DQ016
DQ232537.1 gg_id:196966 Streptococcus oralis str. CIP 105158 DQ232
FJ674207.1 gg_id:527106 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6742
AM941160.1 gg_id:259084 Streptococcus sp. 2923-03 AM941
GQ102114.1 gg_id:374555 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw561c0 GQ102
GU045383.1 gg_id:550425 Streptococcus oralis str. KCOM 1416 GU045
NR_029052.1 gg_id:538185 Streptococcus oligofermentans str. 2-4; LMG 21535 NR_02
FJ674309.1 gg_id:509855 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6743
GQ054576.1 gg_id:456757 Topographical and Temporal Human Skin Microbiome skin back clone nbw1092a07c GQ054
EU458193.1 gg_id:294978 North American black bear feces clone BB2_e02_1 EU458
GQ019723.1 gg_id:489945 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu206c09 GQ019
FJ672838.1 gg_id:515480 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6728
GQ011178.1 gg_id:498488 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ011
GQ155339.1 gg_id:546051 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EU458183.1 gg_id:296971 North American black bear feces clone BB2_b12_1 EU458
EU461976.1 gg_id:300448 white-faced saki feces clone Saki_aaj64f08 EU461
EU471475.1 gg_id:302979 spectacled bear feces clone SB_2aaa03d08 EU471
EU458160.1 gg_id:287785 North American black bear feces clone BB2_g02 EU458
GQ073238.1 gg_id:377455 Topographical and Temporal Human Skin Microbiome skin palm clone nbw206f11c1 GQ073
AB008314.1 gg_id:15560 Streptococcus peroris str. GTC848 AB008

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GQ019801.1 gg_id:489867 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu207c04 GQ019
AB023576.1 gg_id:15371 Streptococcus uberis str. HN1 AB0235
FJ679289.1 gg_id:526351 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6792
AF135453.1 gg_id:25587 Streptococcus bovis str. 1276 AF1354
AY525790.1 gg_id:111444 Streptococcus pneumoniae str. HK_P55 AY5257
FJ672957.1 gg_id:511682 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6729
AJ853836.1 gg_id:108738 Streptococcus cristatus str. 0109 93830B AJ8538
FJ677170.1 gg_id:525204 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6771
EU458274.1 gg_id:296367 North American black bear feces clone BB2_c02_3 EU4582
EU458257.1 gg_id:301824 North American black bear feces clone BB2_h02_1 EU4582
EU458189.1 gg_id:303194 North American black bear feces clone BB2_d05_1 EU4581
EF364098.1 gg_id:219115 Streptococcus caballi str. 151 EF3640
EU467867.1 gg_id:288591 North American black bear feces clone BB1_g10_1 EU4678
GQ060702.1 gg_id:420623 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw04d06 GQ060
FJ557366.1 gg_id:524022 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5573
FJ679360.1 gg_id:524008 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6793
AY525791.1 gg_id:111760 Streptococcus pneumoniae str. HK_P116 AY5257
FJ558253.1 gg_id:526846 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5582
DQ303188.1 gg_id:168087 Streptococcus mitis str. ATCC 49456 DQ303
GQ111270.1 gg_id:383764 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ111
FJ676643.1 gg_id:520991 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6766
EU458226.1 gg_id:290193 North American black bear feces clone BB2_b04_2 EU4582
GQ043319.1 gg_id:439032 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ043
EU775741.1 gg_id:309550 Horse feces clone horsem_aai93e09 EU7757
FJ558487.1 gg_id:530902 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5584
DQ303190.1 gg_id:170102 Streptococcus oralis str. CCUG 24891 DQ303
GQ019394.1 gg_id:490274 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu189e GQ019
GQ032401.1 gg_id:406741 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu542d06 GQ032
EU458208.1 gg_id:303353 North American black bear feces clone BB2_g03_1 EU4582
EU774894.1 gg_id:345575 Short-beaked Echidna feces clone ECH_aai40c10 EU7748
EU460725.1 gg_id:302963 short-beaked echidna feces clone ECH_aai37b01 EU4607
EU475871.1 gg_id:298472 white-faced saki feces clone Saki_e02_1 EU4758
EU467833.1 gg_id:301583 North American black bear feces clone BB1_a07_2 EU4678
GQ086202.1 gg_id:388839 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ086
NC_011375.1 gg_id:314877 Streptococcus pyogenes NZ131 str. NZ131; ATCC BAA-1633 NC_011
EU467904.1 gg_id:298775 North American black bear feces clone BB1_f06_2 EU4679
GQ048268.1 gg_id:451556 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbu GQ048
EU458272.1 gg_id:293401 North American black bear feces clone BB2_b08_3 EU4582
GQ156135.1 gg_id:591692 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
Y17358.1 gg_id:26896 Streptococcus ovis str. S369-98-1 Y17358

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DQ805392.1 gg_id:184376 human fecal clone RL203_aai62a07 DQ805
FJ892760.1 gg_id:550176 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota HM1; ear p FJ8927
FJ678216.1 gg_id:521294 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6782
EU458184.1 gg_id:296435 North American black bear feces clone BB2_c02_1 EU458
EU467771.1 gg_id:291232 North American black bear feces clone BB1_f05 EU467
EU772601.1 gg_id:322567 North American Black Bear feces clone BB2_b10 EU772
GQ078830.1 gg_id:423740 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ078
GQ056825.1 gg_id:374781 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ056
EU461930.1 gg_id:299204 white-faced saki feces clone Saki_aaj63h11 EU461
GQ070655.1 gg_id:395351 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw GQ070
EU460784.1 gg_id:287545 short-beaked echidna feces clone ECH_aai37h10 EU460
EU660340.1 gg_id:290080 Streptococcus pyogenes str. Sp12 EU660
GQ077236.1 gg_id:386987 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw115 GQ077
EU467798.1 gg_id:294395 North American black bear feces clone BB1_c05 EU467
EU467191.1 gg_id:289185 white-faced saki feces clone Saki_e06 EU467
FJ675610.1 gg_id:518399 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6756
EU473899.1 gg_id:289643 giant panda feces clone GP_2aaa02a01 EU473
EU475801.1 gg_id:287600 white-faced saki feces clone Saki_aaj64e04 EU475
EU473322.1 gg_id:295789 giant panda feces clone GP_1aaa03a08 EU473
EU458277.1 gg_id:295281 North American black bear feces clone BB2_c07_1 EU458
EU467864.1 gg_id:293154 North American black bear feces clone BB1_g05_1 EU467
FJ683535.1 gg_id:518286 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6835
FJ676479.1 gg_id:521992 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6764
GQ072667.1 gg_id:411298 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw19 GQ072
EU779050.1 gg_id:333155 Prevost's squirrel feces clone SQ_aah82f11 EU779
AY525789.1 gg_id:112327 Streptococcus pneumoniae str. HK_P47 AY525
GQ076939.1 gg_id:377312 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw1155 GQ076
AF543291.1 gg_id:58287 Streptococcus mitis str. ChDC OS41 AF543
GQ115448.1 gg_id:425877 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw685g05 GQ115
EU467812.1 gg_id:303216 North American black bear feces clone BB1_e11_1 EU467
GQ155692.1 gg_id:589905 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
AM396401.1 gg_id:165104 Streptococcus sp. str. DT2005WUE_IHM AM396
EU458148.1 gg_id:298590 North American black bear feces clone BB2_e06 EU458
EU467827.1 gg_id:302755 North American black bear feces clone BB1_h05_1 EU467
EU779446.1 gg_id:309732 Grevy's Zebra feces clone GZ_aaa04g04 EU779
AF323911.1 gg_id:31706 Streptococcus gallolyticus AF323
EU475852.1 gg_id:296662 white-faced saki feces clone Saki_e08 EU475
GQ101164.1 gg_id:430460 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw49 GQ101
GQ073361.1 gg_id:378214 Topographical and Temporal Human Skin Microbiome skin palm clone nbw208b05c GQ073
DQ303194.1 gg_id:167724 Streptococcus urinalis str. CCUG 41590 DQ303
EU475777.1 gg_id:292482 white-faced saki feces clone Saki_aaj61g03 EU475

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GQ076078.1 gg_id:431953 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ076
EU341148.1 gg_id:243231 Evaluation Rapid Technologies Estimate Microbial Burden and Commercial Airline Ca EU341
AJ295853.1 gg_id:46365 Streptococcus mitis str. 209 AJ2958
GQ076899.1 gg_id:409566 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw1154 GQ076
EU461789.1 gg_id:298208 white-faced saki feces clone Saki_aaj61b04 EU461
GQ043419.1 gg_id:429551 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw96 GQ043
EU467196.1 gg_id:299158 white-faced saki feces clone Saki_g01 EU467
EU458284.1 gg_id:297654 North American black bear feces clone BB2_d04_1 EU458
EU467823.1 gg_id:301071 North American black bear feces clone BB1_g07 EU467
FJ678805.1 gg_id:525261 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6788
GQ081009.1 gg_id:395948 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl GQ081
EU458246.1 gg_id:299675 North American black bear feces clone BB2_f06_2 EU458
EU467808.1 gg_id:298882 North American black bear feces clone BB1_e02_1 EU467
EU458139.1 gg_id:298862 North American black bear feces clone BB2_d04 EU458
GQ155683.1 gg_id:551174 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EU458171.1 gg_id:292100 North American black bear feces clone BB2_h08 EU458
FJ680107.1 gg_id:518559 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6801
EU660336.1 gg_id:298908 Streptococcus pyogenes str. Sp8 EU660
EU778418.1 gg_id:323518 Red Panda feces clone RP_2aaa01c07 EU778
EU458198.1 gg_id:288649 North American black bear feces clone BB2_f01_1 EU458
EU458202.1 gg_id:287473 North American black bear feces clone BB2_f06_1 EU458
EU461971.1 gg_id:299458 white-faced saki feces clone Saki_aaj64f02 EU461
Y07601.1 gg_id:15430 Streptococcus sp. str. SHV515 Y07601
EU458117.1 gg_id:294121 North American black bear feces clone BB2_a06 EU458
EU772619.1 gg_id:345747 North American Black Bear feces clone BB2_c03_2 EU772
EU467750.1 gg_id:291931 North American black bear feces clone BB1_c10 EU467
AJ606047.1 gg_id:114860 Streptococcus castoreus str. M60581/03/2 AJ6060
FJ677268.1 gg_id:531460 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6772
GQ069167.1 gg_id:442582 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ069
FJ673358.1 gg_id:520177 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6733
EU458124.1 gg_id:302904 North American black bear feces clone BB2_b05 EU458
GQ073148.1 gg_id:406688 Topographical and Temporal Human Skin Microbiome skin palm clone nbw205f06c1 GQ073
EU458223.1 gg_id:295170 North American black bear feces clone BB2_a10_1 EU458
EU467903.1 gg_id:301865 North American black bear feces clone BB1_f05_2 EU467
GQ101429.1 gg_id:407688 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw495a GQ101
GQ073121.1 gg_id:397965 Topographical and Temporal Human Skin Microbiome skin palm clone nbw205c12c1 GQ073
DQ798234.1 gg_id:194026 human fecal clone RL181_aah39c03 DQ798
EU156776.1 gg_id:325399 Streptococcus pneumoniae str. CCRI-14589 EU156
EU467878.1 gg_id:297820 North American black bear feces clone BB1_b07_3 EU467
EU458244.1 gg_id:289054 North American black bear feces clone BB2_f03_2 EU458

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EU777768.1 gg_id:349666 Polar bear feces clone PB1_aai27f03 EU777
EU461813.1 gg_id:294792 white-faced saki feces clone Saki_aaj61e02 EU461
FJ678126.1 gg_id:520301 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6781
GQ267979.1 gg_id:563263 Surveys lactic acid yak Tibet China method fermented milk product clone IMAU 462 GQ267
GQ087792.1 gg_id:375084 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ087
EU458219.1 gg_id:291040 North American black bear feces clone BB2_a04_1 EU458
AF009508.1 gg_id:15540 Streptococcus suis str. EA1832.92 AF009
AM157420.1 gg_id:142116 Streptococcus mitis mother C3 AM157
EU289036.1 gg_id:238994 microbiome cloacal openings urogenital and anal tracts tammar wallaby Macropus e EU289
GQ018929.1 gg_id:490737 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu192d GQ018
EU461983.1 gg_id:296189 white-faced saki feces clone Saki_aaj64g06 EU461
GQ030493.1 gg_id:459696 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw879a10 GQ030
AM157441.1 gg_id:142633 Streptococcus parasanguinis mother V4 AM157
EF509782.1 gg_id:219258 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aeru EF5097
EU458152.1 gg_id:292449 North American black bear feces clone BB2_f01 EU458
EU467884.1 gg_id:299150 North American black bear feces clone BB1_c06_3 EU467
GQ018857.1 gg_id:490812 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu191f GQ018
EU458161.1 gg_id:293794 North American black bear feces clone BB2_g03 EU458
GQ060042.1 gg_id:441561 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ060
EU461878.1 gg_id:301061 white-faced saki feces clone Saki_aaj62h01 EU461
GQ074530.1 gg_id:394032 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw164c GQ074
AM157443.1 gg_id:143690 Origen y potencial probiotico microbiota de la leche materna breast milk clone 5V4 AM157
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EU638451.1 gg_id:334625 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU638
NR_025355.1 gg_id:534827 Thermicanus aegyptius str. ET-5b; DSM 12793 NR_02
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EU638544.1 gg_id:354384 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU638
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EU638576.1 gg_id:333359 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU638
EU638435.1 gg_id:336118 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU638
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EU638734.1 gg_id:355173 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU638
EU638336.1 gg_id:339047 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU638
EU638556.1 gg_id:303923 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU638
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AY518549.1 gg_id:107665 Bacillus solfatarensis str. Sol1 AY518

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EU638752.1 gg_id:352598 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU638
AF349724.1 gg_id:20396 Turicibacter sanguinis AF349
DQ015579.1 gg_id:202097 Obesity alters gut microbial ecology mouse cecum clone M3_g05_2 DQ015
DQ015594.1 gg_id:202509 Obesity alters gut microbial ecology mouse cecum clone M3_h11_2 DQ015
DQ015619.1 gg_id:201528 Obesity alters gut microbial ecology mouse cecum clone M3_c07_3 DQ015
DQ815845.1 gg_id:171268 mouse cecum clone aab23b04 DQ815
AJ400262.1 gg_id:41555 intestine clone S24-10 AJ4002
DQ815366.1 gg_id:171609 mouse cecum clone aab46f09 DQ815
DQ015045.1 gg_id:134601 mouse cecum clone M2_d06 DQ015
DQ015416.1 gg_id:201837 Obesity alters gut microbial ecology mouse cecum clone M3_g11 DQ015
EU509845.1 gg_id:272578 cecal contents Mus musculus strain C57BL/6J; WD11 clone WD11_aak22d03 EU5098
DQ015488.1 gg_id:201366 Obesity alters gut microbial ecology mouse cecum clone M3_f09_1 DQ015
FJ880353.1 gg_id:379703 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8803
DQ815843.1 gg_id:172983 mouse cecum clone aab23b01 DQ815
DQ815565.1 gg_id:165315 mouse cecum clone aab42g09 DQ815
DQ015666.1 gg_id:200054 Obesity alters gut microbial ecology mouse cecum clone M3_h01_1 DQ015
DQ015508.1 gg_id:202862 Obesity alters gut microbial ecology mouse cecum clone M3_a02_2 DQ015
DQ015025.1 gg_id:200030 Obesity alters gut microbial ecology mouse cecum clone M2_b01 DQ015
EU509846.1 gg_id:268098 cecal contents Mus musculus strain C57BL/6J; WD11 clone WD11_aak22d04 EU5098
DQ015420.1 gg_id:202998 Obesity alters gut microbial ecology mouse cecum clone M3_h03 DQ015
EU369151.1 gg_id:334937 libraries oyster shell clone MBHOS-02 EU369
AM500764.1 gg_id:536014 proof spatial heterogeneity hot composting clone E2 AM500
GU136560.1 gg_id:588822 Bacillus sp. str. S130(6)-2 GU136
AB308475.1 gg_id:240826 Caldaterra yamamurae str. YMO722 AB3084
DQ346500.1 gg_id:153225 during composting libraries compost clone 2B16 DQ346
AB233999.1 gg_id:151965 anaerobic reactor clone B-6 AB2339
EU194835.1 gg_id:267680 Electricity generation thermophilic microorganisms marine Charleston harbor sedim EU1948
EF559058.1 gg_id:248820 Microbial functional groups solid waste digestor stable isotope probing thermophilic EF5590
AB175380.1 gg_id:103425 mesophilic anaerobic BSA digester clone BSA2B-08 AB1753
EU358728.1 gg_id:354523 structure archaeal denaturing gel electrophoresis and sequencing mesophilic biogas EU3587
DQ887928.1 gg_id:167272 thermophilic anaerobic solid waste bioreactor clone GHB3F05 DQ887
AM947553.1 gg_id:275685 Minor changes detected microbial structure and after three week thermophilic dige AM947
DQ887961.1 gg_id:169373 thermophilic anaerobic solid waste bioreactor clone TIBG11 DQ887
AB486136.1 gg_id:559728 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC AB4861
AJ229198.1 gg_id:34224 anoxic bulk soil flooded rice microcosm clone BSV43 clone AJ2291
DQ129364.1 gg_id:138439 microarray level air two cities Texas urban aerosol clone AKIW782 DQ129
FJ196298.1 gg_id:351034 Microbiological floras Cambrian Period Feicheng Shandong edgewise conglomerate cl FJ1962
EF092457.2 gg_id:187815 Carboxydocella ferrireducens str. 019 EF0924
FJ367045.1 gg_id:368252 feces adult twins and mothers; TS28 clone TS28_a02h01 FJ3670
DQ815751.1 gg_id:165529 mouse cecum clone aab21g12 DQ815

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GQ175436.1 gg_id:592913 Chicken intestinal microbiota modulations various feed supplementations DGGE anc GQ175
EF445143.1 gg_id:205846 rabbit cecum clone NED2A2 EF4451
AB192047.1 gg_id:142288 termite gut homogenate clone M2PT2-06 AB192
DQ015494.1 gg_id:133077 mouse cecum clone M3_g04_1 DQ015
AY426451.1 gg_id:101401 full-scale anaerobic UASB bioreactor treating paper mill wastewater clone B7 AY4264
AB234456.1 gg_id:146392 termite gut homogenate clone MgMjD-038 AB234
EF604609.1 gg_id:227821 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6046
DQ800941.1 gg_id:197539 human fecal clone RL387_aao89f10 DQ800
AB062822.1 gg_id:18245 termite gut homogenate clone BCf4-09 AB062
EU472310.1 gg_id:291318 francois langur feces clone FL_2aaa03d08 EU472
EF454103.1 gg_id:221121 termite hindgut clone 290cost002-P3L-1640 EF4541
FJ881172.1 gg_id:416837 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8811
AB243284.1 gg_id:148219 acetone-preserved termite gut clone M2PB4a-024 AB243
AB299541.1 gg_id:237802 Motility Symbiont Termite Gut Flagellate Caduceia versatilis Member 'Synergistes' G AB2995
DQ815908.1 gg_id:161771 mouse cecum clone aab24b02 DQ815
DQ456434.1 gg_id:157545 pre-adolescent turkey cecum clone CFT214E5 DQ456
FJ681080.1 gg_id:528434 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6810
DQ815614.1 gg_id:166791 mouse cecum clone aab43f01 DQ815
EF445166.1 gg_id:216356 rabbit cecum clone NED1H7 EF4451
FJ881210.1 gg_id:418334 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8812
EF604503.1 gg_id:232085 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6045
FJ681260.1 gg_id:525729 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6812
FJ681301.1 gg_id:511624 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6813
EF454637.1 gg_id:220301 termite hindgut clone 290cost002-P3L-2450 EF4546
EF098915.1 gg_id:197478 mouse cecum clone SWPT1_aaa03b11 EF0989
FJ367654.1 gg_id:365731 feces adult twins and mothers; TS2 clone TS2_a02a06 FJ3676
GQ422712.1 gg_id:552928 Human Oral Microbiome dental plaque clone CK059 GQ422
AF371714.1 gg_id:69942 swine intestine clone p-4154-6Wa5 AF3717
DQ456425.1 gg_id:157989 pre-adolescent turkey cecum clone CFT214F4 DQ456
EU508608.1 gg_id:276402 cecal contents Mus musculus strain C57BL/6J; MD2 clone MD2_aap36b11 EU508
AB243285.1 gg_id:149668 acetone-preserved termite gut clone M2PB4a-031 AB243
DQ815372.1 gg_id:161993 mouse cecum clone aab47b03 DQ815
EF604607.1 gg_id:234054 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6046
DQ015370.1 gg_id:135193 mouse cecum clone M3_c05 DQ015
GQ175384.1 gg_id:554511 Chicken intestinal microbiota modulations various feed supplementations DGGE anc GQ175
GQ175467.1 gg_id:585880 Chicken intestinal microbiota modulations various feed supplementations DGGE anc GQ175
AB009208.1 gg_id:16273 rumen clone RFN54 bacterium AB009
EU458602.1 gg_id:299565 European rabbit feces clone RA_c03 EU458
DQ905244.1 gg_id:172163 human fecal clone 013-e8 DQ905

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EF436324.1 gg_id:204369 library-based ruminal water buffalo (Bubalus bubalis) rumen fluid clone BRC38 EF4363
GQ897552.1 gg_id:555547 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ897
EU845633.1 gg_id:346636 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8456
AJ009493.1 gg_id:16086 anaerobic TCB-transforming consortium clone SJA-136 AJ0094
AB487703.1 gg_id:538197 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNSR0 AB4877
EF436352.1 gg_id:208802 library-based ruminal water buffalo (Bubalus bubalis) rumen fluid clone BRC66 EF4363
GU303307.1 gg_id:576911 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU303
EU474551.1 gg_id:288952 bighorn sheep feces clone BHSD_aaa03g05 EU4745
EF063613.1 gg_id:174127 Microbial ecology autotrophic denitrifying anaerobic methanogenic UASB reactor clo EF0636
AY858451.2 gg_id:110439 gastrointestinal tract zebra clone ZEBRA_12 AY8584
EF603775.1 gg_id:230542 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6037
EU842417.1 gg_id:327471 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU8424
CU925649.1 gg_id:569463 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU925
EU843209.1 gg_id:351235 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8432
EF401880.1 gg_id:217109 human fecal clone SJTU_D_15_78 EF4018
EU778048.1 gg_id:344860 Black rhinoceros feces clone RH_aaj90h01 EU778
GU302617.1 gg_id:538833 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU302
FJ416096.1 gg_id:359349 sediments sediment station NEC5 Northern Bering Sea clone 056M55 FJ4160
AB486406.1 gg_id:549867 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC AB4864
CU924768.1 gg_id:550433 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU924
AM278890.2 gg_id:231376 fecal microbiota irritable bowel syndrome patients significantly that healthy subject AM278
CU927708.1 gg_id:571884 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU927
FJ517038.1 gg_id:513057 semiarid 'Tablas de Daimiel National Park' wetland (Central Spain) unravelled water c FJ5170
AF275916.1 gg_id:72230 anaerobic digester clone AA05 AF2759
AY692049.1 gg_id:99789 UASB reactor clone M77 AY692
EU844816.1 gg_id:315276 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8448
DQ800959.1 gg_id:178394 human fecal clone RL387_aao89h10 DQ800
EU842554.1 gg_id:346151 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU8425
EU844348.1 gg_id:330515 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8443
AB062820.1 gg_id:33347 termite gut homogenate clone BCf4-07 AB0628
AY574991.1 gg_id:102360 Catabacter hongkongensis str. HKU16 AY5749
EF434372.1 gg_id:215573 human infant gastrointestinal tract microbiota stool mother babies 13 and 14 7 mont EF4343
AB486418.1 gg_id:584437 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC AB4864
EF688248.1 gg_id:317224 Detection microbial sludge anaerobic wastewater treatment system clone 6D9_cons EF6882
AY985462.1 gg_id:116947 human stool clone C418 AY9854
CU923982.1 gg_id:551149 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU9239
EU774614.1 gg_id:331966 Angola Colobus feces clone EAC_1aaa02d10 EU7746
CU927863.1 gg_id:557576 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU9278
DQ326341.1 gg_id:145236 Metagenomic gut microbiome healthy human stool clone C332 DQ326
FJ535031.1 gg_id:592702 Enhancement protein conversion volatile fatty acids accumulation during addition: ef FJ5350

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AY854309.1 gg_id:110388 herbivore gastrointestinal tract clone Thompsons14 AY8543
EU259437.1 gg_id:255950 Rumen yak (Bos grunniens) sequences rumen fluid clone YRC61 EU2594
DQ797645.1 gg_id:189301 human fecal clone RL206_aaj14b09 DQ797
AJ576334.1 gg_id:105672 hindgut homogenate Pachnoda ephippiata larva clone PeH17 AJ5763
AF129865.1 gg_id:16131 anaerobic digestor clone HA16 AF1298
EU844475.1 gg_id:338166 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8444
AM275604.2 gg_id:231952 fecal microbiota irritable bowel syndrome patients significantly that healthy subject AM275
FN563365.1 gg_id:582043 Impact changing HRT OLR on prokaryotes involved biomethanizitaion and fuzzy logic FN5633
AF129867.1 gg_id:16130 anaerobic digestor clone HB69 AF1298
DQ805386.1 gg_id:177600 human fecal clone RL203_aai62a01 DQ805
EU508399.1 gg_id:274619 cecal contents Mus musculus strain C57BL/6J; MD2 clone MD2_aap33a04 EU5083
DQ800020.1 gg_id:188183 human fecal clone RL247_aaj23b09 DQ800
AB175358.1 gg_id:107322 mesophilic anaerobic BSA digester clone BSA1B-04 AB1753
AB185741.1 gg_id:107464 rumen clone U29-A02 AB1857
AB486816.1 gg_id:578501 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCOR(AB4868
EU844677.1 gg_id:338831 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8446
EU771507.1 gg_id:320073 Hamadryas Baboon feces clone AFBAB_aai01h10 EU7715
EU475386.1 gg_id:290991 rock hyrax feces clone RHSD_aaa02g08 EU4753
AB294304.1 gg_id:205022 Microbial structure deep coal seem groundwater clone YWB35 AB2943
EU844902.1 gg_id:350834 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8449
EF434357.1 gg_id:213762 human infant gastrointestinal tract microbiota stool mother babies 13 and 14 7 mont EF4343
U81761.2 gg_id:14133 fluidized bed anaerobic digestor fed vinasses (waste wine distillery) clone vadinBB35 U81761
DQ809166.1 gg_id:180585 human fecal clone RL308_aal82f10 DQ809
EU844060.1 gg_id:339645 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8440
EU774645.1 gg_id:322962 Angola Colobus feces clone EAC_2_aaa02f05 EU7746
AB486582.1 gg_id:571348 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCOR(AB4865
DQ798367.1 gg_id:177179 human fecal clone RL181_aah41f03 DQ798
EU466370.1 gg_id:302115 bighorn sheep feces clone BH2_aao22f06 EU4663
EU509200.1 gg_id:270441 cecal contents Mus musculus strain C57BL/6J; MD8 clone MD8_aap45g05 EU5092
FJ366040.1 gg_id:368527 feces adult twins and mothers; TS25 clone TS25_a02a06 FJ3660
AB192038.1 gg_id:142190 termite gut homogenate clone M2PB4-86 AB1920
AB089007.1 gg_id:78174 termite gut homogenate clone Rs-G06 AB0890
AB243282.1 gg_id:149631 acetone-preserved termite gut clone M2PB4a-013 AB2432
AB192021.1 gg_id:143863 termite gut homogenate clone M2PB4-35 AB1920
AB192048.1 gg_id:144142 termite gut homogenate clone M2PT2-23 AB1920
AB255919.1 gg_id:169989 Localization Cell Morphologies Members Candidate TG3 and Subphylum Phylum Fibr AB2559
CP000853.1 gg_id:239100 Alkaliphilus oremlandii str. OhILAs CP0008
DQ128252.1 gg_id:137817 Unique Microbial Fluids Chinese Continental Scientific Drilling drilling fluid clone CCS DQ128
EF125434.1 gg_id:176156 mangrove soil clone MSB-2D5 EF1254

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g__Alkaliphilus
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s__Alkaliphilus transvaalensis	70581
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s__Clostridium acetobutylicum	72762
s__Clostridium baratii	44362
s__Clostridium baratii	45139
s__Clostridium bifermentans	71017
s__Clostridium bifermentans	71133
s__Clostridium bowmanii	71871
s__Clostridium bowmanii	71878
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s__Clostridium butyricum	44423
s__Clostridium butyricum	44938
s__Clostridium butyricum	45218
s__Clostridium butyricum	45831
s__Clostridium cellulolyticum	27653

AY569285.1 gg_id:101611 pink microbial mat clone YJQ-8 AY569
EF559033.1 gg_id:235642 Microbial functional groups solid waste digestor stable isotope probing thermophilic EF559
AM183354.1 gg_id:169422 genetic physiological d deep-biosphere Equatorial Pacific and Peru Margin marine s AM183
X75788.1 gg_id:16108 Caloramator indicus str. IndiB4 X75788
NR_026265.1 gg_id:564401 Caloramator proteoclasticus str. Uruguayensis; DSM 10124 NR_02
AF104215.1 gg_id:16110 Caloramator coolhaasii str. Z AF1042
L09187.1 gg_id:16111 Caloramator fervidus str. RT4. B1 L09187
AF489534.1 gg_id:68459 Caloramator uzoniensis str. JW/VK-KU2 AF4895
AF181848.1 gg_id:34407 Caloramator viterbiensis str. JW/MS-VS5 AF1818
DQ676295.1 gg_id:220054 Archaeal sediment and plankton freshwater pond suboxic freshwater-pond clone M DQ676
GQ906581.1 gg_id:584933 Clostridium sp. str. SW003 GQ906
AB486915.1 gg_id:558768 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCOR AB486
AB486702.1 gg_id:575035 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCOR AB486
AB487603.1 gg_id:536237 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNSR AB487
GQ906580.1 gg_id:558972 Clostridium sp. str. SW002 GQ906
AB488197.1 gg_id:548100 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSSUR AB488
DQ129398.1 gg_id:151986 microarray level air two cities Texas urban aerosol clone AKIW1006 DQ129
AB486298.1 gg_id:554614 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBAR AB486
Y18179.1 gg_id:32182 Clostridium cylindrosporum str. DSM 605 Y18179
DQ129395.1 gg_id:138500 microarray level air two cities Texas urban aerosol clone AKIW981 DQ129
AJ431243.1 gg_id:102801 Clostridium sp. str. Dex60-61 AJ4312
FN356335.1 gg_id:590922 Prokaryotic structure sulfate reducer activity -temperature reservoirs and without ni FN356
AJ431244.1 gg_id:79318 Clostridium sp. str. Dex60-75 AJ4312
FN356332.1 gg_id:563046 Prokaryotic structure sulfate reducer activity -temperature reservoirs and without ni FN356
FN356242.1 gg_id:583876 Prokaryotic structure sulfate reducer activity -temperature reservoirs and without ni FN356
AM231183.1 gg_id:151509 Clostridium acetobutylicum str. 7 MSU AM231
AB240207.1 gg_id:141357 Clostridium baratii str. T8 AB240
AB240209.1 gg_id:142276 Clostridium baratii str. T10 AB240
EU547723.1 gg_id:271569 Clostridium bifermentans str. SL186 EU547
EU460327.1 gg_id:299386 polar bear feces clone PB1_aai26f05 EU460
AB539899.1 gg_id:535555 Clostridium sp. str. C5S3 AB5398
EF589987.2 gg_id:227564 changes structure sediments Songhua River contaminated nitrobenzene -DGGE cloni EF5899
AJ506120.1 gg_id:60735 Clostridium bowmanii str. DSM 14206 AJ5061
EF063634.1 gg_id:191245 Microbial ecology autotrophic anaerobic denitrifying UASB reactor clone R1Cb41 EF0636
EF570920.1 gg_id:231269 Clostridium frigoriphilum str. 14F EF5709
AJ297443.1 gg_id:29618 Clostridium psychrophilum str. -1/C-/I AJ2974
DQ831126.1 gg_id:170961 Clostridium butyricum str. W4 DQ831
ABDT01000025.2 gg_id:262123 Clostridium butyricum str. 5521 ABDT0
AJ289705.1 gg_id:21382 Clostridium butyricum str. IBUN 125C AJ2897
AM930366.1 gg_id:541328 gradual cooling stage mass and its spatial composting clone SMR62 AM930
NC_011898.1 gg_id:471235 Clostridium cellulolyticum H10 str. H10; ATCC 35319 NC_01

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s__Clostridium cellulovorans	72712
s__Clostridium colicanis	45774
s__Clostridium difficile	70879
s__Clostridium glycolicum	70664
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X73438.1 gg_id:16231 Clostridium cellulovorans str. DSM 3052
FJ957870.1 gg_id:454680 Clostridium colicanis str. JPL_15
NZ_ABHE02000055.1 gg_id:559187 Clostridium difficile QCD-76w55
AY007244.1 gg_id:40074 Clostridium glycolicum str. CIN5
FJ384385.1 gg_id:359641 Clostridium glycolicum str. BG-C128
EU887819.1 gg_id:340525 Clostridium glycolicum str. SN10
L37590.1 gg_id:16126 Clostridium botulinum
AB035087.3 gg_id:22235 Clostridium novyi str. ATCC25758
EU458365.1 gg_id:288771 spotted hyena feces clone HY1_e01
FJ978743.1 gg_id:414789 feces clone CL_F_446
EU772684.1 gg_id:319770 Bush dog feces clone bdog1_aai77a07
EU776210.1 gg_id:308823 Spotted hyena feces clone HY1_d03_1
EU776124.1 gg_id:345246 Spotted hyena feces clone HY1_h10
EU772930.1 gg_id:326430 Bush dog feces clone bdog1_aai78c05
DQ800516.1 gg_id:197510 human fecal clone RL183_aah27g08
DQ800626.1 gg_id:185590 human fecal clone RL183_aao01c05
EU468360.1 gg_id:299843 lion feces clone LI2_aae48c06
EU465520.1 gg_id:287479 lion feces clone LI3_aah78g11
EU772771.1 gg_id:318578 Bush dog feces clone bdog1_d07
EU465499.1 gg_id:302610 lion feces clone LI3_aah78d08
EU772822.1 gg_id:319652 Bush dog feces clone bdog1_aai77f11
EU772713.1 gg_id:344553 Bush dog feces clone bdog1_aai80g01
EU458402.1 gg_id:290404 spotted hyena feces clone HY1_d09_2
EU776059.1 gg_id:306891 Spotted hyena feces clone HY1_f06
EU468383.1 gg_id:295187 lion feces clone LI2_aae49a09
EU467616.1 gg_id:297934 southern three-banded armadillo feces clone arma_g12_1
EU459388.1 gg_id:289373 cheetah feces clone CE3_aai06g06
EU776726.1 gg_id:305526 Lion feces clone LI1_c05_1
EU778549.1 gg_id:312781 Ring-tailed lemur feces clone RT_aai09b05
EU468210.1 gg_id:288094 lion feces clone LI1_f02_2
EU463367.1 gg_id:300475 bush dog feces clone bdog1_aai80b06
EU772883.1 gg_id:320308 Bush dog feces clone bdog1_aai79c02
EU458351.1 gg_id:301967 spotted hyena feces clone HY1_b05_1
EU773971.1 gg_id:322366 Cheetah feces clone CE3_aai06a11
EU465484.1 gg_id:293823 lion feces clone LI3_aah78b07
EU772860.1 gg_id:347235 Bush dog feces clone bdog1_aai77b09
EU772796.1 gg_id:355548 Bush dog feces clone bdog1_aai79e10
EU774859.1 gg_id:324938 Short-beaked Echidna feces clone ECH_aai37g08
EU772948.1 gg_id:310880 Bush dog feces clone bdog1_aai80a09
EU773973.1 gg_id:341829 Cheetah feces clone CE3_aai07f08
EU458412.1 gg_id:295090 spotted hyena feces clone HY1_g02_2

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FJ9787
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EU4655
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EU4654
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k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
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g__Clostridium
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s__Clostridium hiranonis	71225
s__Clostridium hiranonis	71251
s__Clostridium hiranonis	71259
s__Clostridium hiranonis	71296
s__Clostridium intestinale	72438
s__Clostridium intestinale	72650
s__Clostridium irregulare	70655
s__Clostridium irregulare	71037
s__Clostridium kluyveri	72080
s__Clostridium kluyveri	72379
s__Clostridium ljungdahlii	72049
s__Clostridium metallolevans	70778
s__Clostridium metallolevans	70819
s__Clostridium metallolevans	70856
s__Clostridium metallolevans	71079
s__Clostridium metallolevans	71237
s__Clostridium neonatale	45495
s__Clostridium neonatale	45891
s__Clostridium novyi	72260
s__Clostridium paradoxum	71205
s__Clostridium paradoxum	71217
s__Clostridium paraputrificum	45270
s__Clostridium pasteurianum	71786
s__Clostridium pasteurianum	71837
s__Clostridium pasteurianum	71935
s__Clostridium perfringens	71846
s__Clostridium perfringens	72153
s__Clostridium perfringens	72179
s__Clostridium perfringens	72181
s__Clostridium perfringens	72305
s__Clostridium perfringens	72505
s__Clostridium perfringens	72587
s__Clostridium perfringens	72718
s__Clostridium perfringens	72764
s__Clostridium perfringens	72823
s__Clostridium septicum	45419
s__Clostridium sordellii	70640
s__Clostridium sordellii	70768
s__Clostridium sordellii	70802
s__Clostridium sordellii	70954
s__Clostridium sordellii	70977

EU467710.1 gg_id:290179 bush dog feces clone bdog1_g09 EU467
EU772864.1 gg_id:306149 Bush dog feces clone bdog1_aai78h05 EU772
EU773792.1 gg_id:326083 Cheetah feces clone CE3_aai06h01 EU773
EU773797.1 gg_id:339350 Cheetah feces clone CE3_aai05c02 EU773
AY781385.1 gg_id:108384 Clostridium intestinale AY781
NR_029263.1 gg_id:578541 Clostridium intestinale str. Catt39; DSM 6191 NR_02
EU887817.1 gg_id:303972 Clostridium irregulare str. SN8 EU887
X73447.1 gg_id:14214 Clostridium irregulare str. DSM 2635 X7344
CP000673.1 gg_id:254073 Clostridium kluyveri str. DSM 555 CP000
ABAJ01000001.1 gg_id:219164 Clostridium kluyveri str. DSM 555 ABAJ0
EU828402.1 gg_id:560739 Microbial effects changeover without CO2 sparging two-stage biological and methan EU828
EU887818.1 gg_id:342268 Clostridium metallolevans str. SN9 EU887
DQ133569.1 gg_id:138329 Clostridium metallolevans str. ASI1 DQ133
EU887815.1 gg_id:324891 Clostridium metallolevans str. SN1 EU887
EU887823.1 gg_id:338957 Clostridium metallolevans str. SN16 EU887
EU887820.1 gg_id:315305 Clostridium glycolicum str. SN12 EU887
AF275949.1 gg_id:73000 Clostridium neonatale str. LCDC no.99--005 AF275
EU869244.1 gg_id:349217 Clostridium neonatale str. CM-C98 EU869
AB045606.1 gg_id:29673 Clostridium novyi str. JCM1406 AB045
Z69928.1 gg_id:14186 Clostridium paradoxum str. DSM 7308T Z69928
Z69933.1 gg_id:14196 Clostridium paradoxum str. DSM 7308T Z69933
X75907.1 gg_id:16215 Clostridium paraputrificum str. ATCC 25780 X7590
EF656616.1 gg_id:248740 Clostridium pasteurianum str. AFBR-G EF656
EF140980.1 gg_id:175357 Clostridium pasteurianum str. CH1 EF140
AB536773.1 gg_id:572490 Clostridium pasteurianum str. JCM 1408 AB536
EU459335.1 gg_id:294957 hedgehog feces clone HH_aai36f06 EU459
AM889034.1 gg_id:237367 Clostridium perfringens JS9 AM889
FJ215327.1 gg_id:577392 Clostridium perfringens str. MOTB3 FJ2153
ABDU01000051.2 gg_id:270573 Clostridium perfringens C str. JGS1495 ABDU0
NC_003366.1 gg_id:128673 Clostridium perfringens str. 13 NC_00
EU773814.1 gg_id:323142 Cheetah feces clone CE2_c01 EU773
NZ_ABOO01000021.1 gg_id:267792 Clostridium perfringens D str. JGS1721 NZ_AB
FJ215350.1 gg_id:559845 Clostridium perfringens str. ME1 FJ2153
EU775668.1 gg_id:304779 Hedgehog feces clone HH_aai35d06 EU775
EU772738.1 gg_id:315982 Bush dog feces clone bdog1_aai80b01 EU772
FJ424478.1 gg_id:363985 Clostridium septicum str. SH-C24 FJ4244
FJ375896.1 gg_id:308996 and prevalence blaTEM genes polar bear feces clone PBF_d34 FJ3758
FJ375897.1 gg_id:334569 and prevalence blaTEM genes polar bear feces clone PBF_d35 FJ3758
FJ375892.1 gg_id:325217 and prevalence blaTEM genes polar bear feces clone PBF_d30 FJ3758
FJ375783.1 gg_id:354513 and prevalence blaTEM genes polar bear feces clone PBF_b12 FJ3757
FJ375820.1 gg_id:320883 and prevalence blaTEM genes polar bear feces clone PBF_c1 FJ3758