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GQ038497.1 gg_id:465769 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu4 GQ038
AY288517.2 gg_id:130587 Eggerthella hongkongensis str. HKU10 1 AY288
FJ676592.1 gg_id:512048 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6765
AM277970.2 gg_id:232823 fecal microbiota irritable bowel syndrome patients significantly that healthy subject AM277
DQ014875.1 gg_id:129970 mouse cecum clone M1_g04_3 DQ014
FJ880734.1 gg_id:419024 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8807
EF099432.1 gg_id:188581 mouse cecum clone SWPT3_aaa03b05.Contig2 EF0994
EU509230.1 gg_id:274856 cecal contents Mus musculus strain C57BL/6J; MD8 clone MD8_aap46b12 EU509
EF099352.1 gg_id:190487 mouse cecum clone SWPT3_aaa02b06 EF0993
DQ015493.1 gg_id:132749 mouse cecum clone M3_g02_1 DQ015
DQ799106.1 gg_id:195061 human fecal clone RL205_aaj17f08 DQ799
EU766266.1 gg_id:336863 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU766
S44206.1 gg_id:11382 Atopobium parvulum S44206
S44205.1 gg_id:11381 Atopobium rimae S44205
NR_029349.1 gg_id:585058 Atopobium vaginae str. 961*00022/98; CCUG 38953 NR_02
FJ833382.1 gg_id:577349 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J1Q101_16H02 FJ8333
AY278623.1 gg_id:87668 Olsenella genomosp. C1 AY278
GU303148.1 gg_id:566154 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU303
AF287760.1 gg_id:25658 human subgingival plaque clone C019 AF287
X67148.1 gg_id:11380 Atopobium minutum str. NCFB 2751 X67148
GU304476.1 gg_id:582069 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU304
AB270088.1 gg_id:173195 Influence temperature and humidity on heifers rumen contents Holstein heifer (Bos AB270
DQ793412.1 gg_id:196712 human fecal clone RL199_aaj43d09 DQ793
DQ798056.1 gg_id:194244 human fecal clone RL302_aal95a07 DQ798
FJ370884.1 gg_id:366874 feces adult twins and mothers; TS5 clone TS5_a02d04 FJ3708
DQ797662.1 gg_id:182774 human fecal clone RL206_aaj14d03 DQ797
DQ802697.1 gg_id:176814 human fecal clone RL188_aan95d04 DQ802
DQ799950.1 gg_id:196639 human fecal clone RL247_aaj22c03 DQ799
DQ798566.1 gg_id:178750 human fecal clone RL181_aan98d04 DQ798
DQ797345.1 gg_id:183310 human fecal clone RL248_aai98b10 DQ797
DQ794703.1 gg_id:194613 human fecal clone RL240_aaj31d03 DQ794
EU763926.1 gg_id:344582 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A5 EU763
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DQ795524.1 gg_id:195737 human fecal clone RL178_aan65f09 DQ795
DQ823720.1 gg_id:180558 human fecal clone RL250_aaj78b06 DQ823
DQ798532.1 gg_id:184171 human fecal clone RL181_aan97h06 DQ798
FJ371155.1 gg_id:359277 feces adult twins and mothers; TS6 clone TS6_a01e12 FJ3711
DQ794737.1 gg_id:198377 human fecal clone RL240_aaj31g03 DQ794
FJ362732.1 gg_id:365444 feces adult twins and mothers; TS13 clone TS13_a02e02 FJ3627
FJ366710.1 gg_id:369629 feces adult twins and mothers; TS27 clone TS27_a02h08 FJ3667

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AB031060.1 gg_id:38088 Collinsella stercoris str. RCA55-34 AB031
EU462966.1 gg_id:293536 southern three-banded armadillo feces clone arma_aaj55g11 EU462
AB031063.1 gg_id:46935 Collinsella intestinalis str. RCA56-68 AB031
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EU458526.1 gg_id:290335 spotted hyena feces clone HY2_c10_1 EU458

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EU467589.1 gg_id:290365 southern three-banded armadillo feces clone arma_f04 EU4675
EU467581.1 gg_id:288978 southern three-banded armadillo feces clone arma_b09_2 EU4675
EU463038.1 gg_id:301713 southern three-banded armadillo feces clone arma_aaj56h02 EU4630
EU458449.1 gg_id:299641 spotted hyena feces clone HY1_f02_3 EU4584
EU465368.1 gg_id:303310 lion feces clone LI3_aah76b06 EU4653
EU462795.1 gg_id:290060 southern three-banded armadillo feces clone arma_aaj53c04 EU4627
EU467594.1 gg_id:297680 southern three-banded armadillo feces clone arma_g06 EU4675
FJ369496.1 gg_id:368705 feces adult twins and mothers; TS51 clone TS51_a01c06 FJ3694
EU465475.1 gg_id:291808 lion feces clone LI3_aah78a09 EU4654
EU468367.1 gg_id:298806 lion feces clone LI2_aae48e02 EU4683
EU462873.1 gg_id:301874 southern three-banded armadillo feces clone arma_aaj54c09 EU4628
EU468133.1 gg_id:301499 bush dog feces clone bdog3_aad70b08 EU4681
EU458538.1 gg_id:297687 spotted hyena feces clone HY2_f07_1 EU4585
FJ554834.1 gg_id:554988 Coriobacterium glomerans str. KP20W4 FJ5548
FJ554836.1 gg_id:585313 Coriobacterium sp. str. Dys2 FJ5548
X79048.1 gg_id:11367 Coriobacterium glomerans X79048
AF227849.1 gg_id:72748 str. 82345 AF2278
AB011817.1 gg_id:11372 Eggerthella lenta str. JCM9979 AB0118
AY321958.1 gg_id:89460 Eggerthella sinensis str. HKU14 AY3219
FN178466.2 gg_id:515726 Olsenella profusa str. CCUG 45371 FN1784
FN178464.2 gg_id:517887 Olsenella uli str. DSM 7084 FN1784
EU592965.1 gg_id:262803 Olsenella sp. str. F0206 EU5929
AF371712.1 gg_id:27160 swine intestine clone p-3423-SwA2 AF3717
EU592964.1 gg_id:266446 Olsenella sp. str. F0004 EU5929
GU395300.1 gg_id:514331 Slackia exigua str. 07-1951 GU395
NZ_ACUX02000006.1 gg_id:484407 Slackia exigua str. ATCC 700122 NZ_AC
AF101241.1 gg_id:11364 Slackia heliotrinireducens str. ATCC 29202 AF1012
FJ368484.1 gg_id:359299 feces adult twins and mothers; TS3 clone TS3_a04h09 FJ3684
DQ808704.1 gg_id:188520 human fecal clone RL239_aaj12b03 DQ808
AM276076.2 gg_id:231940 fecal microbiota irritable bowel syndrome patients significantly that healthy subject AM276
FJ366775.1 gg_id:361191 feces adult twins and mothers; TS27 clone TS27_a03f12 FJ3667
EU776114.1 gg_id:320999 Spotted hyena feces clone HY2_g04_1 EU7761
AJ608686.1 gg_id:125665 Slackia sp. str. CCUG 48399 AJ6086
FJ368806.1 gg_id:359418 feces adult twins and mothers; TS49 clone TS49_a04g09 FJ3688
EU776099.1 gg_id:350120 Spotted hyena feces clone HY2_g11_1 EU7760
EU776136.1 gg_id:333194 Spotted hyena feces clone HY2_e02_3 EU7761
EU776230.1 gg_id:343195 Spotted hyena feces clone HY2_b06_2 EU7762
AJ583196.1 gg_id:94574 radioactive site ground water clone S15B-MN49 AJ5831
AX003092.1 gg_id:51091 Enterococcus casseliflavus AX0030
DQ353921.1 gg_id:147031 Fecal Wild Gorilla (Gorilla beringei) wild gorilla feces clone Z43 DQ353
AF371713.1 gg_id:32126 swine intestine clone p-275-o5 AF3717

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AJ518870.1 gg_id:136127 Denitrobacterium sp. str. CCUG 45665 AJ5188
AB269995.1 gg_id:172895 Influence temperature and humidity on heifers rumen contents Holstein heifer (Bos AB2699
FJ368467.1 gg_id:370166 feces adult twins and mothers; TS3 clone TS3_a04g03 FJ3684
EU592966.1 gg_id:269678 Atopobium sp. str. F0209 EU5929
DQ794471.1 gg_id:175508 human fecal clone RL197_aah88c11 DQ794
AB089077.1 gg_id:78283 termite gut homogenate clone Rs-J59 bacterium AB0890
DQ824215.1 gg_id:185472 human fecal clone RL304_aal73a03 DQ824
EU748234.1 gg_id:349532 neotropical folivorous flying bird adult hoatzin crop clone hoa32_07G01.F EU7482
AM405723.2 gg_id:563304 percent G+C fraction libraries number Actinobacteria human faecal clone AP14K.90 AM405
AY160874.1 gg_id:128261 termite intestinal tract clone COB P3-21 AY1608
GQ502467.1 gg_id:580258 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf1- GQ502
FJ363677.1 gg_id:362064 feces adult twins and mothers; TS14 clone TS14_a02a06 FJ3636
DQ800788.1 gg_id:192875 human fecal clone RL183_aao03e01 DQ800
FJ880340.1 gg_id:398239 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8803
FJ982998.1 gg_id:410239 Aspects Oral Microbiome root canal clone OPEN_ROOT_34 FJ9829
EU773489.1 gg_id:337884 Bonobo feces clone BNO_aaa02g12 EU7734
AB189698.1 gg_id:135349 alkaline segment among various species er termites termite gut homogenate clone 1 AB1896
FJ363734.1 gg_id:358914 feces adult twins and mothers; TS14 clone TS14_a02f07 FJ3637
AB269993.1 gg_id:163566 Influence temperature and humidity on heifers rumen contents Holstein heifer (Bos AB2699
AB269994.1 gg_id:166474 Influence temperature and humidity on heifers rumen contents Holstein heifer (Bos AB2699
EU009849.1 gg_id:241290 intestinal microbiota domestic and wild turkeys turkey cecum clone WTB_U34 EU0098
EF097195.1 gg_id:189082 mouse cecum clone SWPT18_aaa02h08 EF0971
EU773494.1 gg_id:351744 Bonobo feces clone BNO_aaa03d11 EU7734
FJ879101.1 gg_id:410423 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8791
AM278923.2 gg_id:227819 fecal microbiota irritable bowel syndrome patients significantly that healthy subject AM278
EU761755.1 gg_id:315006 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1 EU7617
AB288919.1 gg_id:200827 termite gut homogenate clone BOf8-15 AB2889
AJ534681.1 gg_id:75442 ground water deep-well injection disposal site radioactive wastes Tomsk-7 clone S15A AJ5346
DQ168842.1 gg_id:139221 Fermentative biohydrogen production heated anaerobic sludge clone J26 DQ168
AB192289.1 gg_id:143031 termite gut homogenate clone RPK-25 AB1922
AF079505.1 gg_id:11374 Denitrobacterium detoxificans str. NPOH2 AF0795
EU475540.1 gg_id:301038 springbok feces clone SBSD_aaa02a10 EU4755
EU475037.1 gg_id:292011 visayam warty pig feces clone VWP_aaa04h12 EU4750
AJ534678.1 gg_id:76995 ground water deep-well injection disposal site radioactive wastes Tomsk-7 clone S15A AJ5346
AM275775.2 gg_id:232800 fecal microbiota irritable bowel syndrome patients significantly that healthy subject AM275
AB034096.1 gg_id:42186 rumen clone 4C3d-3 AB0340
AB234517.1 gg_id:149443 termite gut homogenate clone MgMjR-011 AB2345
AY053479.1 gg_id:48363 gas hydrate clone AT425_EubY10 AY0534
FJ152635.1 gg_id:354168 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX1A_ FJ1526
AB478418.1 gg_id:464059 marine actinobacterium F10 AB4784
GQ263040.1 gg_id:585361 Structure Simulated Level Waste Site simulated level waste site clone F2_162X GQ263

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DQ432396.1 gg_id:156755 prokaryotic alkaline hypersaline lakes Wadi Natrun Egypt Lake Hamra water clone W DQ432
FJ152964.1 gg_id:328890 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX4CI FJ1529
FJ152905.1 gg_id:312275 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX4CI FJ1529
AF448192.1 gg_id:80775 actinobacterium clone ML615J-2 AF448
AB038407.1 gg_id:41242 Chibacore 1500 AB038
EF573094.1 gg_id:227879 Coco's Island site 23 marine clone S23_1193 EF573
EU268121.1 gg_id:247055 summer Dalian and Liaodong bay determined sea water clone ZL1711 EU268
EU802784.1 gg_id:320796 It's all ranking aquatic Northeast Colon Panama clone 4C230159 EU802
EU237434.1 gg_id:257745 Genes transcripts Eastern and Western Equatorial North Atlantic Ocean microbial as EU237
FJ745217.1 gg_id:549390 Transporter genes expressed coastal response dissolved organic carbon surface wate FJ7452
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EU804962.1 gg_id:339859 It's all ranking aquatic 250 miles Panama City clone 6C232942 EU804
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GQ347831.1 gg_id:590302 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ347
EU804538.1 gg_id:335721 It's all ranking aquatic 250 miles Panama City clone 6C232484 EU804
AY907794.1 gg_id:136985 identification picoplankton contrasting waters Arabian Sea water clone A713807 AY907
GU119457.1 gg_id:587280 Threatened Corals Provide Microbial Habitats reef water clone Reef_A17 GU119
GU119401.1 gg_id:589405 Threatened Corals Provide Microbial Habitats reef water clone Reef_J24 GU119
GQ347951.1 gg_id:593286 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ347
EU805386.1 gg_id:324898 It's all ranking aquatic 250 miles Panama City clone 6C233394 EU805
EU801503.1 gg_id:332548 It's all ranking aquatic Chesapeake Bay MD clone 3C002811 EU801
EU268088.1 gg_id:254966 summer Dalian and Liaodong bay determined sea water clone L2513 EU268
EU802902.1 gg_id:342436 It's all ranking aquatic Northeast Colon Panama clone 4C230294 EU802
GU061499.1 gg_id:591657 and function microbial mesoscale eddy perturbations South China Sea clone CE1-DC GU061
EU237446.1 gg_id:240327 Genes transcripts Eastern and Western Equatorial North Atlantic Ocean microbial as EU237
EU804365.1 gg_id:350248 It's all ranking aquatic 250 miles Panama City clone 6C232275 EU804
GQ348362.1 gg_id:590344 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ348
AJ224541.1 gg_id:12752 trickling filter biofilm clone koll13 AJ2245
FJ205356.1 gg_id:570905 Prokaryotic deep-sea hydrothermal region East Lau Spreading Centre deep marine se FJ2053
EU491057.1 gg_id:261391 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount South Rift X EU491
FN396746.1 gg_id:557965 constant flux thermophilic cold seabed Arctic marine surface sediment clone s5_8_II FN396
EU374108.1 gg_id:268245 southern Cretan margin (eastern Mediterranean Sea) canyon and slope sediment clc EU374

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AF154093.1 gg_id:11881 hydrocarbon seep clone BPC063 AF154
EU491246.1 gg_id:266087 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak EU491
FJ712450.1 gg_id:530060 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) k FJ7124
AB015267.1 gg_id:12003 deepest cold-seep area Japan Trench clone JTB31 AB015
GU118752.1 gg_id:536016 Threatened Corals Provide Microbial Habitats clone Mfra_A07 GU118
AM259898.1 gg_id:210533 Spatial sponge- Mediterranean Tethya aurantia sponge cortex clone TAA-10-01 AM259
EU491180.1 gg_id:266970 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak EU491
AY225655.1 gg_id:98009 Mid-Atlantic Ridge hydrothermal sediment clone AT-s2-33 AY225
EU328054.1 gg_id:277684 dynamics during bioremediation crude oil contaminated moderate saline soil clone B EU328
AM997746.1 gg_id:566820 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A AM997
AY592138.1 gg_id:101549 marine ANAMMOX sediment clone AY592138 AY592
GQ263100.1 gg_id:551448 Structure Simulated Level Waste Site simulated level waste site clone F2_51X GQ263
GQ263243.1 gg_id:533342 Structure Simulated Level Waste Site simulated level waste site clone F3_62X GQ263
GU056091.1 gg_id:587273 Biologic Techniques Applied Microbial Prospecting China: Ban 876 Gas Oil Field Bein GU056
GQ866098.1 gg_id:571157 Seasonal changes Norway lobster (Nephrops norvegicus) gut clone F1-26 GQ866
EU374095.1 gg_id:260834 southern Cretan margin (eastern Mediterranean Sea) canyon and slope sediment clc EU374
GQ262901.1 gg_id:559440 Structure Simulated Level Waste Site simulated level waste site clone F1_58X GQ262
FJ229926.1 gg_id:509146 Microbes marine sponges Indonesia: Manado clone XA2G07F FJ2299
FJ229962.1 gg_id:564142 Microbes marine sponges USA: Key Largo Florida clone XE1E03 FJ2299
FJ229942.1 gg_id:549301 Microbes marine sponges USA: Key Largo Florida clone XB2G09F FJ2299
EF076145.1 gg_id:255203 Sponge- microorganisms: ecology and biotechnological potential Bahamas: Little San EF0761
EU491602.1 gg_id:262676 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU491
EU491785.1 gg_id:273839 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU491
FJ229955.1 gg_id:510651 Microbes marine sponges USA: Key Largo Florida clone XB3H12F FJ2299
GQ406192.1 gg_id:575324 Benthic submerged sinkhole ecosystems sediment clone BK-45-9 GQ406
DQ811922.1 gg_id:169682 mangrove soil clone MSB-3D10 DQ811
EF632945.1 gg_id:250138 Unique microbial contrasting aquatic altitude Andean Altiplano (northern Chile) fresh EF6329
EU542491.1 gg_id:271885 Effects chemical structure concentration on pathways microbial during dechlorinatio EU542
EF540423.1 gg_id:222313 Impact phytoremediation on structure solid waste oil-shale chemical industry semi-c EF5404
GQ214120.1 gg_id:584943 China loess clone P936 GQ214
GQ246337.1 gg_id:583854 Temporal and spatial China North Yel Sea sediments clone Sd1-56 GQ246
DQ395394.1 gg_id:153946 deep-sea octacoral clone ctg_BRRAA49 DQ395
EU132592.1 gg_id:239247 tallgrass prarie soil clone FFCH10091 EU132
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EU132562.1 gg_id:254092 tallgrass prarie soil clone FFCH5337 EU132
EU133242.1 gg_id:239952 tallgrass prarie soil clone FFCH9801 EU133
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FJ478846.1 gg_id:579019 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4788

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EF019300.1 gg_id:207037 aspen rhizosphere clone Elev_16S_491 EF0193
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EF516264.1 gg_id:217980 grassland soil clone FCPU621 EF5162
EU132678.1 gg_id:250652 tallgrass prarie soil clone FFCH11021 EU132
GQ396935.1 gg_id:541701 Functional unvegetated perhumid recently-deglaciated soils do not correlate shifts s GQ396
GQ396927.1 gg_id:593718 Functional unvegetated perhumid recently-deglaciated soils do not correlate shifts s GQ396
EU132553.1 gg_id:253490 tallgrass prarie soil clone FFCH16258 EU132
DQ129581.1 gg_id:137600 urban aerosol clone AKIW543 DQ129
EU132699.1 gg_id:254009 tallgrass prarie soil clone FFCH11256 EU132
EU881117.1 gg_id:303466 Karst region primary forest soil clone KPF200711-035 EU881
EF492926.1 gg_id:236252 Iron-manganese Nodule and Its Surrounding Soil soil around iron-manganese nodule EF4929
FJ415661.1 gg_id:356779 black loam soil soybean field pH 8.0-9.1 elevation approximately 142.7 m clone SOY4 FJ4156
GQ263223.1 gg_id:589383 Structure Simulated Level Waste Site simulated level waste site clone F3_30X GQ263
DQ347883.1 gg_id:200046 Specificity Soil-Feeding Termite Mounds and Putative Origin these soil-feeding termi DQ347
FJ479080.1 gg_id:584453 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4790
EU490277.1 gg_id:562566 Microbial biodiversity thermophilic mineral soils Tramway Ridge Mount Erebus Anta EU490
EU132758.1 gg_id:239095 tallgrass prarie soil clone FFCH12203 EU132
EF516257.1 gg_id:227361 grassland soil clone FCPN401 EF5162
AJ536866.1 gg_id:78720 uranium mining waste pile soil sample clone JG30-KF-A23 AJ5368
EU861970.1 gg_id:305385 effects chronic fertilization on alpine tundra microbial implications carbon and cyclin EU861
EU133228.1 gg_id:253774 tallgrass prarie soil clone FFCH9064 EU133
FJ479208.1 gg_id:590667 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4792
EU132506.1 gg_id:247552 tallgrass prarie soil clone FFCH9080 EU132
FJ478504.1 gg_id:584366 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4785
EF612368.1 gg_id:244063 historic semiarid lead-zinc mine tailings site soil clone OS-C108 EF6123
DQ906785.1 gg_id:242006 Oman subsurface soil clone 2B-7 DQ906
EU132960.1 gg_id:250840 tallgrass prarie soil clone FFCH17064 EU132
EU132861.1 gg_id:240169 tallgrass prarie soil clone FFCH14388 EU132
EU132554.1 gg_id:251112 tallgrass prarie soil clone FFCH16505 EU132
FJ479287.1 gg_id:572125 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4792
FJ152732.1 gg_id:318193 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX5A_ FJ1527
AJ863234.1 gg_id:121120 poplar tree microcosm bulk soil flooded clone 21BSF48 AJ8632
FJ478941.1 gg_id:539978 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4789
EU132930.1 gg_id:240349 tallgrass prarie soil clone FFCH16272 EU132
EU644096.1 gg_id:282759 and Samoylov Island Lena active layer -centred polygon near permafrost table; Rim_ EU644
EU132703.1 gg_id:248033 tallgrass prarie soil clone FFCH11295 EU132
DQ125846.1 gg_id:134038 uranium contaminated soil clone AKAU4075 DQ125
EU881145.1 gg_id:322589 Karst region primary forest soil clone KPF200711-126 EU881
FJ478898.1 gg_id:563350 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4788
AY326618.1 gg_id:136785 Amazon soil clone 15-1 AY3266

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EU132608.1 gg_id:255406 tallgrass prarie soil clone FFCH10233 EU132
EU133156.1 gg_id:253677 tallgrass prarie soil clone FFCH692 EU133
EF019542.1 gg_id:216189 aspen rhizosphere clone Elev_16S_1047 EF0195
FJ479570.1 gg_id:513760 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4795
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FJ479015.1 gg_id:572569 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4790
FJ478770.1 gg_id:591906 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4787
EU491469.1 gg_id:258935 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X4 clone EU491
GQ014787.1 gg_id:494879 Topographical and Temporal Human Skin Microbiome skin palm clone nbw764c01c1 GQ014
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DQ129290.1 gg_id:138194 microarray level air two cities Texas urban aerosol clone AKIW700 DQ129
FJ479592.1 gg_id:593325 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4795
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GQ263082.1 gg_id:534856 Structure Simulated Level Waste Site simulated level waste site clone F2_31X GQ263
EU132905.1 gg_id:243586 tallgrass prarie soil clone FFCH1535 EU132
DQ906908.1 gg_id:240172 Oman subsurface soil clone 12B-8 DQ906
EU335260.1 gg_id:247772 Changes microbial metabolic and along hydrogeochemically variable profile unsatura EU335
AY395356.1 gg_id:102490 pasture soil clone EB1037 AY395
GQ263259.1 gg_id:583767 Structure Simulated Level Waste Site simulated level waste site clone F3_87X GQ263
AY395379.1 gg_id:104049 pasture soil clone EB1060 AY395
FJ478603.1 gg_id:591747 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4786
EU132557.1 gg_id:235807 tallgrass prarie soil clone FFCH17938 EU132
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AF479791.1 gg_id:32106 Rubrobacter taiwanensis str. LS-286 AF479
CP000386.1 gg_id:160994 Rubrobacter xylanophilus str. DSM 9941 CP000
FJ595575.1 gg_id:536634 rock Black Canyon New Mexico: and Geochemistry rocks no varnish clone NV64_10b FJ5955
DQ129336.1 gg_id:138573 microarray level air two cities Texas urban aerosol clone AKIW774 DQ129
DQ532248.1 gg_id:168709 Geographical Variation Microbial Burden and Spacecraft Assembly Johnson Space C DQ532
AM746686.1 gg_id:247678 etiology rosy discoloration ancient wall paintings rosy-discoloured mural clone A8 AM746

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FJ790551.1 gg_id:510654 Chasmolithic microbial niches -altitude arid tuff Tibet desert clone VB3 FJ7905
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DQ366004.1 gg_id:155707 Dominant soils Marble Point and Wright Valley Victoria Land Antarctica soil clone DQ366
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EU407208.1 gg_id:275285 household biogas digester clone GW-24 EU4072
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AF443586.1 gg_id:89763 semiarid soil clone C-F-15 AF4435
FJ592862.1 gg_id:576320 Fumarole-supported islands biodiversity within hyperarid -elevation landscape on Puı FJ5928
AF443578.1 gg_id:90198 semiarid soil clone C-F-12 AF4435
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EU132753.1 gg_id:235293 tallgrass prarie soil clone FFCH12178 EU1327
EU335168.1 gg_id:236596 Changes microbial metabolic and along hydrogeochemically variable profile saturate EU3351
EF516896.1 gg_id:217448 grassland soil clone FCPU744 EF5168
EU132567.1 gg_id:236583 tallgrass prarie soil clone FFCH8929 EU1325
X92694.1 gg_id:11359 peat bog clone TM36 X92694

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EF516364.1 gg_id:217392 grassland soil clone FCPN720 EF5163
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FJ542906.1 gg_id:521099 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone A FJ5429
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EU093079.1 gg_id:251712 Phytoplasma sp. RYL-GD EU0930
EU223946.1 gg_id:250637 -RFLP microbes Qinghai-Tin rail soil clone 69 EU223
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EU104342.1 gg_id:314357 Evidence Comamonadaceae determinants settling performance activated sludge clo EU1043
EU132917.1 gg_id:239059 tallgrass prarie soil clone FFCH15597 EU1329
FJ592848.1 gg_id:556756 Fumarole-supported islands biodiversity within hyperarid -elevation landscape on Pu FJ5928
GQ094365.1 gg_id:452924 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ094
FJ592851.1 gg_id:533434 Fumarole-supported islands biodiversity within hyperarid -elevation landscape on Pu FJ5928
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EF516706.1 gg_id:219427 grassland soil clone FCPP507 EF5167
AB374386.1 gg_id:267851 sequences Weissenstein (white rock) / few millimeters be surface rock called 'Weiss AB3743
EF019414.1 gg_id:216330 aspen rhizosphere clone Elev_16S_658 EF0194
EU024345.1 gg_id:247938 intestinal microflora Hepialus gonggaensis larvae RFLP larval gut clone Hg22 EU0243
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DQ347845.1 gg_id:203420 Specificity Soil-Feeding Termite Mounds and Putative Origin these soil-feeding term DQ347
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DQ347867.1 gg_id:203418 Specificity Soil-Feeding Termite Mounds and Putative Origin these soil-feeding term DQ347
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EU289476.1 gg_id:252979 metagenomic approach biosynthesis ansamycin endophytes or symbionts enriched s EU2894
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FJ905750.1 gg_id:535482 s Tonga-Kermadec iron oxide sediments Volcano 1 Tonga Arc clone V1F128b FJ9057
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GQ249482.1 gg_id:583433 Microbial anaerobic sediments Bay Cadiz (Spain) marine sediment: 0-2 cm layer clor GQ249
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AF027014.1 gg_id:11591 hot spring clone OPB41 AF0270
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EF520360.1 gg_id:235064 structure lakes: what controls ? acid-impacted lake clone ADK-MOh02-15 EF5203
EU290722.1 gg_id:246054 microbial structure biogeochemical contrasting shelf sediments Namibian upwelling EU2907
EU488303.1 gg_id:545186 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU4883
DQ394972.1 gg_id:154687 harbor sediment clone VHS-B3-91 DQ394
AJ853543.1 gg_id:110776 landfill leachate clone GZKB49 AJ8535
DQ394962.1 gg_id:156539 harbor sediment clone VHS-B3-77 DQ394
EU644115.1 gg_id:286244 and Samoylov Island Lena active layer -centred polygon near permafrost table; Rim_ EU6441
AJ536836.1 gg_id:97060 chemocline clone 122 AJ5368
AB300103.1 gg_id:226025 Wide ancient microbial DNAs Quaternary sediments holocene mud sediment clone K AB3001

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CU922408.1 gg_id:566723 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU922
DQ465405.1 gg_id:223296 Bacillus decisifrondis str. E5HC-32 DQ465
EU373414.1 gg_id:276582 Bacillus pumilus str. TPR11 EU3734
EF492969.1 gg_id:238291 Iron-manganese Nodule and Its Surrounding Soil soil around iron-manganese nodule EF4929
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EF018972.1 gg_id:211351 aspen rhizosphere clone Amb_16S_1487 EF0189
AM749753.1 gg_id:255961 Isolation ing candidate division soils New Zealand steam-affected geothermal soil cl AM749
EU044415.1 gg_id:236245 uences structure fosters richness subtropical Altamaha Ohopee River Valley inland d EU044
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DQ450735.1 gg_id:161224 Microbial Alpine Tundra Wet Meadow Soil: Chloroflexi Cold Water-Saturated satura DQ450
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DQ924737.1 gg_id:177890 Microbial Norris Geyser Basin Yellowstone National Park Echinus Hot Spring clone B DQ924
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DQ834087.1 gg_id:171779 Geochemical Controls on Microbial Rainbow and Springs Yellowstone National Park DQ834
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EF156548.1 gg_id:180187 Microbial Norris Geyser Basin Yellowstone National Park Koz Spring clone KOZ107 EF1565

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AY882803.2 gg_id:112203 hot spring clone SK254 AY8828
EF156603.1 gg_id:189504 Microbial Norris Geyser Basin Yellowstone National Park Koz Spring clone KOZ163 EF1566
DQ924760.1 gg_id:192474 Microbial Norris Geyser Basin Yellowstone National Park Echinus Hot Spring clone B DQ924
DQ832031.1 gg_id:169346 Geochemical Controls on Microbial Rainbow and Springs Yellowstone National Park . DQ832
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DQ832030.1 gg_id:166090 Geochemical Controls on Microbial Rainbow and Springs Yellowstone National Park . DQ832
EF156465.1 gg_id:176781 Microbial Norris Geyser Basin Yellowstone National Park Beowulf Yel Mat clone BY10 EF1564
AF255599.1 gg_id:38815 Thermocrinis-like str. SRI-48 AF2555
DQ833788.1 gg_id:161844 Geochemical Controls on Microbial Rainbow and Springs Yellowstone National Park . DQ833
DQ924688.1 gg_id:196562 Microbial Norris Geyser Basin Yellowstone National Park Cistern Hot Spring clone BV DQ924
AY862041.1 gg_id:112459 Washburn Spring 1 community clone WB1B011 AY8620
EU924258.1 gg_id:348543 Microbiology and geochemistry Little Hot Creek hot spring sediment temperature 8C EU9242
EU635954.1 gg_id:277901 Microbiology geochemistry great boiling and mud springs sediment hot spring; temp EU6359
DQ490016.1 gg_id:158831 Microbial Great Boiling Spring sediment hot spring; temperature 80 C clone GBS_L1_ DQ490
EU924254.1 gg_id:346758 Microbiology and geochemistry Little Hot Creek hot spring sediment temperature 8C EU9242
DQ924678.1 gg_id:198052 Microbial Norris Geyser Basin Yellowstone National Park Cistern Hot Spring clone BV DQ924
EF100635.1 gg_id:194035 Prokaryotic Heated Arsenic-Rich Sediments Shal Submarine Hydrothermal System An EF1006
AB462553.1 gg_id:326675 Microbial production and energy source hyperthermophilic prokaryotes geothermal AB4625
AF301908.1 gg_id:25858 Hydrogenobacter-like str. SS5H1 AF3019
AB199564.1 gg_id:110416 hot spring Japan clone NHS-03 AB1995
AB105049.1 gg_id:98942 Balnearium lithotrophicum str. 17S AB1050
AJ001049.1 gg_id:1260 Desulfurobacterium thermolithotrophum AJ0010
AJ507320.2 gg_id:85051 Desulfurobacterium crinifex str. NE1206 FK10 AJ5073
AJ316619.2 gg_id:104045 Thermovibrio ruber str. DSM 14644 AJ3166
AF068811.2 gg_id:13779 hydrothermal vent clone VC2.1Bac48 AF0688
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AB278143.1 gg_id:191103 hydrothermal vent prokaryotes trapped 0.2- and 0.1-micro-m-filtrates obtained Mar AB2781
AY268936.1 gg_id:104531 Desulfurobacterium sp. str. SL17 AY2689
AJ969464.1 gg_id:157331 Microbial black smoker s Mid Atlantic Ridge ecological implications rock fragments ch AJ9694
AY263403.1 gg_id:83837 Thermovibrio ammoniificans str. HB-1 AY2634
AY268938.1 gg_id:104841 Desulfurobacterium sp. str. SL20 AY2689
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AY861818.1 gg_id:112664 Obsidian Pool prime community clone OPPB088 AY8618
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AM778960.1 gg_id:249144 Sulfurihydrogenibium kristjanssoni str. I6628 AM778
FJ638563.1 gg_id:537415 Temperature dependent succession sulfate reducing muddy southwestern Taiwan hc FJ6385
DQ243783.1 gg_id:142593 Archaeal and Geochemically Hot Springs Yellowstone National Park USA Sylvan Sprir DQ243
DQ645250.1 gg_id:173214 Microbial and oxidation activity biofilms within Alvord Desert Basin Southeastern Or DQ645
AY882746.2 gg_id:111873 hot spring clone SK191 AY8827
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AY686713.1 gg_id:138074 Sulfurihydrogenibium yellowstonense str. SS-5 AY6867
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AY862053.1 gg_id:112485 Washburn Spring 3 community clone WB3B018 AY8620
EU156150.1 gg_id:236881 thermal spring microbial and functional genes Coffee Pots Hot Spring clone pCOF_65 EU1561
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EU134979.1 gg_id:239599 tallgrass prarie soil clone FFCH5249 EU1349
EU135015.1 gg_id:255679 tallgrass prarie soil clone FFCH3880 EU1350
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EU335337.1 gg_id:241653 Changes microbial metabolic and along hydrogeochemically variable profile unsatura EU3353
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EU135011.1 gg_id:246743 tallgrass prarie soil clone FFCH17123 EU1350
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AJ867895.1 gg_id:141847 Fluctuations Significantly Influence Microbial Present Nival Lakes lake water clone A2 AJ8678
AY212563.1 gg_id:112133 manure-contaminated water clone 111ds10 AY2125
EU676408.1 gg_id:296956 rhizosphere pioneer plants (Bahia xylopoda and Viguiera linearis) growing on metals· EU6764
EF683077.1 gg_id:247439 Eastern Mediterranean atmosphere clone F14_4H_FL EF6830
AY948040.1 gg_id:143151 Synchrony and seasonality two temperate rivers USA: Massachusetts Parker River cl AY9480
EF516651.1 gg_id:224566 grassland soil clone FCPT595 EF5166
EU861928.1 gg_id:321601 effects chronic fertilization on alpine tundra microbial implications carbon and cyclin EU8619
GQ402731.1 gg_id:550111 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
AJ292686.1 gg_id:32254 PCB-polluted soil clone WD294 AJ2926
EU861934.1 gg_id:348576 effects chronic fertilization on alpine tundra microbial implications carbon and cyclin EU8619
EU861949.1 gg_id:319724 effects chronic fertilization on alpine tundra microbial implications carbon and cyclin EU8619
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EU332819.1 gg_id:369522 FACS assist identification TFO present aerobic enhanced biological phosphorus remo EU3328
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GQ264378.1 gg_id:584471 Structure Simulated Level Waste Site simulated level waste site clone WW2_58 GQ264
EF515998.1 gg_id:221811 grassland soil clone FCPT516 EF5159
DQ975217.1 gg_id:249601 Iron sulfide and pyrite potential electron donors microbial nitrate reduction fresh w DQ975
AM749746.1 gg_id:247969 Isolation ing candidate division soils New Zealand steam-affected geothermal soil cl AM749
AJ009456.1 gg_id:1435 chlorobenzene-degrading consortium clone SJA-22 AJ0094
EU134994.1 gg_id:238881 tallgrass prarie soil clone FFCH4697 EU1349
FM866305.1 gg_id:362406 Microbial several mining wastes Bulgaria uranium mill tailings clone BuhC-22 FM866
GU198500.1 gg_id:569984 Acid-tolerant microaerophilic enhance Fe(III) accumulation Fe(II) oxidizing enrichme GU198
AJ306784.1 gg_id:66917 DCP-dechlorinating consortium clone SHA-37 AJ3067
DQ330652.1 gg_id:159278 Guerrero Negro hypersaline microbial mat clone 04D2Z29 DQ330
DQ833816.1 gg_id:171283 Geochemical Controls on Microbial Rainbow and Springs Yellowstone National Park DQ833
FM164957.3 gg_id:450088 two Bulgarian geothermal springs hot spring clone S1-133 FM164
DQ645248.1 gg_id:169378 Microbial and oxidation activity biofilms within Alvord Desert Basin Southeastern Or DQ645
DQ324867.1 gg_id:146321 Geochemical and bioenergetic variability across systems Yellowstone National Park DQ324
GQ022437.1 gg_id:487233 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbu31 GQ022
GQ264442.1 gg_id:568015 Structure Simulated Level Waste Site simulated level waste site clone WW3_141 GQ264
AY289459.1 gg_id:88820 soil clone ABS-629 AY2894
CU923234.1 gg_id:537151 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU923
AJ009490.1 gg_id:1430 chlorobenzene-degrading consortium clone SJA-121 AJ0094
FJ793161.1 gg_id:519788 Archaea and Hot Spring Thailand Tao Dam hot spring clone TDB22 FJ7931
EU887975.1 gg_id:314492 Microbial structure hydrolytic stage two-stage anaerobic digestion grass silage leach EU8879
EU246197.1 gg_id:250645 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-P5-B02 EU2461
EU843463.1 gg_id:352273 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8434
DQ404796.1 gg_id:153870 contaminated sediment clone 661250 DQ404
AM490693.1 gg_id:576477 Linking and functional nutrient spiraling mats (USA) microbial mat sulfidic cave sprir AM490

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AB510697.1 gg_id:541942 Bacteroides caccae str. JCM 9498 AB510
EU765625.1 gg_id:352289 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B3 EU765
EU136688.1 gg_id:246247 Bacteroides coprocola str. JCM12979 EU136
FJ363034.1 gg_id:356763 feces adult twins and mothers; TS148 clone TS148_a02b09 FJ3630
AB200225.1 gg_id:130849 Bacteroides coprocola str. M158 AB200
AY985803.1 gg_id:126815 human stool clone D057 AY9858
AB260026.1 gg_id:207799 Bacteroides coprophilus str. CB42 (= JCM 13818 = DSM 18228) AB260
AB510699.1 gg_id:536389 Bacteroides coprosuis str. JCM 13475 AB510
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EU764957.1 gg_id:322715 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2 EU764
EU764442.1 gg_id:314192 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1 EU764
EU766509.1 gg_id:332311 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU766
AB222700.1 gg_id:144954 Bacteroides finegoldii str. JCM 13346 176 AB222
DQ057444.1 gg_id:130819 str. ic1252 DQ057
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EU136691.1 gg_id:243642 Bacteroides intestinalis str. JCM13266 EU136
FJ372297.1 gg_id:357023 feces adult twins and mothers; TS9 clone TS9_a04a03 FJ3722
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AB510703.1 gg_id:536606 Bacteroides massiliensis str. JCM 13223 AB510
EU765962.1 gg_id:305072 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B4 EU765
EU764452.1 gg_id:342305 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1 EU764
EU766455.1 gg_id:332300 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU766

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s__Bacteroides massiliensis	68583
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s__Bacteroides plebeius	68539

EU764317.1 gg_id:352365 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1 EU764
EU764401.1 gg_id:345289 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1 EU764
EU766538.1 gg_id:340694 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU766
EU764456.1 gg_id:342150 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1 EU764
EU765095.1 gg_id:304136 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2 EU765
EU765852.1 gg_id:348178 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B4 EU765
EU765803.1 gg_id:340562 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B4 EU765
EU766386.1 gg_id:355400 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU766
EU765932.1 gg_id:353539 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B4 EU765
EU765043.1 gg_id:309304 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2 EU765
EU766317.1 gg_id:313020 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU766
EU764392.1 gg_id:306362 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1 EU764
EU766114.1 gg_id:322222 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU766
AB200226.1 gg_id:136630 Bacteroides massiliensis str. EG4-8-2 AB200
EU764425.1 gg_id:346002 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1 EU764
EU766314.1 gg_id:351455 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU766
EU765977.1 gg_id:310598 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B4 EU765
EU763365.1 gg_id:319923 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A4 EU763
EU766331.1 gg_id:317897 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU766
EU763920.1 gg_id:339965 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A5 EU763
DQ799335.1 gg_id:179763 human fecal clone RL305aal85a10 DQ799
EU766112.1 gg_id:322303 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU766
DQ798822.1 gg_id:176388 human fecal clone RL242_aaj97g08 DQ798
FJ369010.1 gg_id:363625 feces adult twins and mothers; TS4 clone TS4_a03c03 FJ3690
DQ805617.1 gg_id:176185 human fecal clone RL306aal89a05 DQ805
AB050108.1 gg_id:37022 Bacteroides ovatus str. JCM 5824T AB050
GQ492617.1 gg_id:539888 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
GQ491656.1 gg_id:577651 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
EU768716.1 gg_id:303636 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C5 EU768
EU768196.1 gg_id:318509 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C4 EU768
FJ365436.1 gg_id:362940 feces adult twins and mothers; TS20 clone TS20_a02h02 FJ3654
EU762338.1 gg_id:345835 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A9 EU762
EU763065.1 gg_id:356294 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A9 EU763
GQ079152.1 gg_id:377892 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1229b GQ079
DQ100446.1 gg_id:141994 Bacteroides ovatus str. SDG-Mt85-3Cy DQ100
FJ368826.1 gg_id:367134 feces adult twins and mothers; TS4 clone TS4_a01a11 FJ3688
FJ363281.1 gg_id:365909 feces adult twins and mothers; TS149 clone TS149_a01d07 FJ3632
AY982129.1 gg_id:119221 human sigmoid colon mucosal biopsy clone P716 AY982
DQ799104.1 gg_id:186140 human fecal clone RL205_aaj17f06 DQ799
DQ824367.1 gg_id:187751 human fecal clone RL304_aal75b05 DQ824
DQ823862.1 gg_id:174475 human fecal clone RL250_aaj80a12 DQ823

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AB200217.1 gg_id:131236 Bacteroides plebeius str. M12 AB200
AB200219.1 gg_id:134286 Bacteroides plebeius str. M35 AB200
EU766635.1 gg_id:318833 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU766
EF400653.1 gg_id:216960 human fecal clone SJTU_E_16_63 EF4006
EU767622.1 gg_id:315932 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C3 EU767
EF403124.1 gg_id:210025 human fecal clone SJTU_A1_1_22 EF4031
EU136690.1 gg_id:236480 Bacteroides salyersiae str. JCM12988 EU136
DQ905050.1 gg_id:162723 human fecal clone 2-002-d8 DQ905
DQ905008.1 gg_id:164088 human fecal clone 2-002-a10 DQ905
ABFZ02000010.1 gg_id:266138 Bacteroides stercoris str. ATCC 43183 ABFZ0
EU136684.1 gg_id:245615 Chromaphyosemion bivittatum str. JCM9496 EU136
FJ371227.1 gg_id:365084 feces adult twins and mothers; TS6 clone TS6_a02d09 FJ3712
DQ905097.1 gg_id:164178 human fecal clone 2-002-h9 DQ905
FJ370549.1 gg_id:359417 feces adult twins and mothers; TS57 clone TS57_a02d05 FJ3705
NZ_ABFZ02000011.1 gg_id:469826 Bacteroides stercoris str. ATCC 43183 NZ_AB
DQ905028.1 gg_id:165847 human fecal clone 2-002-c10 DQ905
X83953.1 gg_id:2030 Bacteroides stercoris str. ATCC 43183T X83953
DQ805722.1 gg_id:184209 human fecal clone RL306aal90c06 DQ805
GQ491307.1 gg_id:544341 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
EU765106.1 gg_id:354895 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2 EU765
EU766220.1 gg_id:347407 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU766
EU765541.1 gg_id:337684 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B3 EU765
EU765881.1 gg_id:355109 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B4 EU765
AB117563.1 gg_id:112035 Bacteroides uniformis str. NB-13 AB117
AB021157.1 gg_id:2045 Bacteroides acidofaciens str. AB021
EU766171.1 gg_id:331754 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU766
EU765282.1 gg_id:308188 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B3 EU765
DQ456111.1 gg_id:158663 pre-adolescent turkey cecum clone CFT114E8 DQ456
EU511533.1 gg_id:271150 cecal contents Mus musculus strain C57BL/6J; WD9 clone WD9_aak06b03 EU511
EU763339.1 gg_id:315474 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A4 EU763
FJ371809.1 gg_id:362127 feces adult twins and mothers; TS8 clone TS8_a02d10 FJ3718
AY978878.1 gg_id:124255 human transverse colon mucosal biopsy clone NE82 AY978
DQ798203.1 gg_id:191479 human fecal clone RL302_aal96g09 DQ798
DQ824385.1 gg_id:197052 human fecal clone RL304_aal75d09 DQ824
AY895194.1 gg_id:111383 Bacteroides sp. str. 4072 AY895
EU681979.1 gg_id:301746 microflora imbalances intestine dogs inflammatory bowel disease duodenum dog IBI EU681
EU136689.1 gg_id:246004 Bacteroides tectus str. JCM10003 EU136
AY981662.1 gg_id:115480 human sigmoid colon mucosal biopsy clone L940 AY981
DQ456025.1 gg_id:158651 pre-adolescent turkey cecum clone CFT112D6 DQ456
EU764615.1 gg_id:320837 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1 EU764

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AF227834.1 gg_id:48647 str. 31285 AF227
GQ867554.1 gg_id:564616 and prevalence blaTEM genes Arctic seals colon content clone CSH59 GQ867
FJ362922.1 gg_id:361680 feces adult twins and mothers; TS13 clone TS13_a04g09 FJ3629
FJ371985.1 gg_id:365192 feces adult twins and mothers; TS8 clone TS8_a04d11 FJ3719
EU767678.1 gg_id:332031 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C3 EU767
EU764074.1 gg_id:305008 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A5 EU764
EU766032.1 gg_id:336559 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B4 EU766
EU766963.1 gg_id:319413 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU766
DQ793958.1 gg_id:174194 human fecal clone RL176_aah45g09 DQ793
EU767532.1 gg_id:345989 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C2 EU767
FJ681103.1 gg_id:526303 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6811
AM275521.2 gg_id:234488 fecal microbiota irritable bowel syndrome patients significantly that healthy subject AM275
GQ492318.1 gg_id:562721 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
GQ867293.1 gg_id:551593 and prevalence blaTEM genes Arctic seals colon content clone WSp23 GQ867
AB437413.1 gg_id:358550 Bacteroides intestinalis str. AM-1 AB437
FJ683108.1 gg_id:523989 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6831
EU505150.1 gg_id:276484 cecal contents Mus musculus strain C57BL/6J; myd3 clone myd3_aaa03e12 EU505
EF434324.1 gg_id:205290 gastrointestinal tract microbiota microarray reference pool created pooling products EF4343
FJ372367.1 gg_id:370102 feces adult twins and mothers; TS9 clone TS9_a04g08 FJ3723
EU768090.1 gg_id:332404 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C4 EU768
EU768640.1 gg_id:348832 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C5 EU768
AY986070.1 gg_id:125534 human stool clone D394 AY986
FJ366443.1 gg_id:366374 feces adult twins and mothers; TS26 clone TS26_a03c11 FJ3664
EU767318.1 gg_id:329732 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C2 EU767
AM420078.1 gg_id:242308 Noma subgingival plaque clone 301H11(oral) AM420
AY977553.1 gg_id:119557 human cecum mucosal biopsy clone W359 AY977
AY975360.1 gg_id:117724 human ascending colon mucosal biopsy clone N653 AY975
AY975485.1 gg_id:125748 human ascending colon mucosal biopsy clone N919 AY975
GQ492611.1 gg_id:588825 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
DQ807063.1 gg_id:189614 human fecal clone RL244_aaj45g04 DQ807
EU761916.1 gg_id:340637 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1 EU761
FJ440088.1 gg_id:512957 Megamonas hypermegale colonization correlates Campylobacter jejuni exclusion pou FJ4400
EU531945.1 gg_id:271214 Predominant role host genetics controlling gut microbiota FMF remission stool clone EU531
AY977810.1 gg_id:124192 human cecum mucosal biopsy clone LF01 AY977
EU762766.1 gg_id:311251 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU762
FJ363423.1 gg_id:366083 feces adult twins and mothers; TS149 clone TS149_a03b02 FJ3634
AY985214.1 gg_id:127000 human stool clone C078 AY985
EU766954.1 gg_id:320670 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU766
FJ672191.1 gg_id:516365 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6721
EU768032.1 gg_id:306991 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C4 EU768

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EU768154.1 gg_id:356616 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C4 EU768
EU655886.1 gg_id:283641 influence dietary flavonoid-containing extracts on gut microbiota mouse feces clone EU655
EU766456.1 gg_id:333475 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU766
DQ905076.1 gg_id:172060 human fecal clone 2-002-g11 DQ905
EU761699.1 gg_id:327096 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1 EU761
EU765443.1 gg_id:345104 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B3 EU765
EU768406.1 gg_id:344420 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C5 EU768
EU531963.1 gg_id:261878 Predominant role host genetics controlling gut microbiota FMF remission stool clone EU531
EU472048.1 gg_id:299461 francois langur feces clone FL_1aaa04f05 EU472
EU767197.1 gg_id:315993 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C2 EU767
DQ807484.1 gg_id:195157 human fecal clone RL307_aam07b09 DQ807
EU763736.1 gg_id:323812 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A4 EU763
GQ867518.1 gg_id:536429 and prevalence blaTEM genes Arctic seals colon content clone CSH15 GQ867
FJ371434.1 gg_id:360815 feces adult twins and mothers; TS6 clone TS6_a04h08 FJ3714
EU764091.1 gg_id:329028 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A5 EU764
AB490801.1 gg_id:570110 Bacteroides clarus str. YIT 12056 AB490
DQ905928.1 gg_id:172994 human fecal clone 29c-h5 DQ905
GQ448371.1 gg_id:550814 Microbiome neonatal calves: shedding microorganisms fecal clone calf783_2wks_gr GQ448
DQ805840.1 gg_id:196926 human fecal clone RL306aal91g04 DQ805
AB499846.1 gg_id:556126 Bacteroides sp. str. TP-5 AB499
FJ366345.1 gg_id:366626 feces adult twins and mothers; TS26 clone TS26_a01f09 FJ3663
EU772744.1 gg_id:356052 Bush dog feces clone bdog1_aai78e02 EU772
EU768028.1 gg_id:353215 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C4 EU768
EU767916.1 gg_id:313565 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C3 EU767
GQ043048.1 gg_id:407354 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1012e GQ043
GQ492204.1 gg_id:591783 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
AY981521.1 gg_id:124731 human sigmoid colon mucosal biopsy clone L650 AY981
EU136696.1 gg_id:244304 Bacteroides massiliensis str. JCM12982 EU136
EU763175.1 gg_id:342782 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A3 EU763
FJ363523.1 gg_id:358503 feces adult twins and mothers; TS149 clone TS149_a04c02 FJ3635
EU768386.1 gg_id:310386 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C5 EU768
FJ978549.1 gg_id:375393 feces clone CL_F_093 FJ9785
DQ441261.1 gg_id:192907 human intestinal biopsy clone CD10 DQ441
EU761595.1 gg_id:311500 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1 EU761
EU764768.1 gg_id:316580 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2 EU764
GQ492338.1 gg_id:591967 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
AY980883.1 gg_id:119266 human rectum mucosal biopsy clone LQ19 AY980
EU767175.1 gg_id:306006 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU767
EU764895.1 gg_id:335758 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2 EU764
EU761967.1 gg_id:313373 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1 EU761

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EU458543.1 gg_id:292388 spotted hyena feces clone HY2_h02_1 EU458
GQ492812.1 gg_id:574579 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
EU768519.1 gg_id:320344 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C5 EU768
AY082451.1 gg_id:73751 Bacteroides sp. str. 265d AY082
EU459616.1 gg_id:298021 ring-tailed lemur feces clone RT_aai09c10 EU459
EU761599.1 gg_id:318214 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1 EU761
EU768407.1 gg_id:315901 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C5 EU768
AY976899.1 gg_id:123455 human cecum mucosal biopsy clone K545 AY976
DQ803835.1 gg_id:196080 human fecal clone RL200_aai58h11 DQ803
DQ456053.1 gg_id:158706 pre-adolescent turkey cecum clone CFT112H3 DQ456
FJ978637.1 gg_id:466274 feces clone CL_F_309 FJ9786
FJ372099.1 gg_id:369529 feces adult twins and mothers; TS9 clone TS9_a01g04 FJ3720
EU768092.1 gg_id:308644 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C4 EU768
X89217.1 gg_id:1988 Bacteroides sp str. BV-1 X89217
EU768194.1 gg_id:350389 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C4 EU768
EU722740.1 gg_id:334393 Bacteroides finegoldii str. B16 EU722
EU767054.1 gg_id:355760 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU767
GQ492136.1 gg_id:583117 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
EU766982.1 gg_id:307849 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU766
DQ456041.1 gg_id:158667 pre-adolescent turkey cecum clone CFT112F11 DQ456
EU530393.1 gg_id:268332 mucosa adherent and invasive microbes adenoma colorectal cancer profile non-ader EU5303
AY979572.1 gg_id:121549 human transverse colon mucosal biopsy clone M241 AY979
FJ363227.1 gg_id:359702 feces adult twins and mothers; TS148 clone TS148_a04g03 FJ3632
EU768143.1 gg_id:355581 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C4 EU768
FJ370558.1 gg_id:363236 feces adult twins and mothers; TS57 clone TS57_a02e03 FJ3705
DQ806375.1 gg_id:197731 human fecal clone RL186_aan91d07 DQ806
AY549431.1 gg_id:113854 Bacteroides denticanoris str. B78 AY549
EU768015.1 gg_id:314364 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C4 EU768
AY895191.1 gg_id:111421 Bacteroides thetaiotaomicron str. 3731 AY895
FJ363131.1 gg_id:358493 feces adult twins and mothers; TS148 clone TS148_a03e01 FJ3631
EU764778.1 gg_id:322273 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2 EU764
EU763101.1 gg_id:319092 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A9 EU763
EF604959.1 gg_id:228420 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6049
EU764460.1 gg_id:345223 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1 EU764
AB253731.1 gg_id:172821 Bacteroides salanitronis str. JCM 13657 BL78 AB253
DQ799526.1 gg_id:192839 human fecal clone RL305aal87c11 DQ799
EU772839.1 gg_id:333981 Bush dog feces clone bdog1_aai77e11 EU772
FJ978508.1 gg_id:433947 feces clone CL_F_038 FJ9785
EU766840.1 gg_id:347808 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU766
EU764666.1 gg_id:307730 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1 EU764

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EU763007.1 gg_id:315093 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A› EU763
GQ867528.1 gg_id:568757 and prevalence blaTEM genes Arctic seals colon content clone CSH32 GQ867
EU764580.1 gg_id:341721 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1 EU764
EF071154.1 gg_id:187179 library survey and quantitative measurement major mucosa- IBD human colonic muc EF0711
AJ811981.1 gg_id:186113 human biopsies Human ulcerative colitis biopsy clone UC9-44 AJ8119
EU762570.1 gg_id:321669 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A› EU762
GQ492505.1 gg_id:582063 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
DQ797137.1 gg_id:195781 human fecal clone RL386_aao87d11 DQ797
AY981632.1 gg_id:126962 human sigmoid colon mucosal biopsy clone L880 AY9816
AB253733.1 gg_id:169036 Bacteroides gallinarum str. JCM 13659 C43 AB253
EU763053.1 gg_id:310481 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A› EU763
EU764049.1 gg_id:312952 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU764
EU764629.1 gg_id:340796 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1 EU764
EU763817.1 gg_id:315105 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU763
EU766989.1 gg_id:331197 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU766
FJ879857.1 gg_id:466785 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8798
GQ079282.1 gg_id:430193 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1230g(GQ079
EU768441.1 gg_id:336580 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C EU768
DQ456092.1 gg_id:158906 pre-adolescent turkey cecum clone CFT114C11 DQ456
FJ978643.1 gg_id:418340 feces clone CL_F_315 FJ9786
DQ456331.1 gg_id:158660 pre-adolescent turkey cecum clone CFT212B1 DQ456
EU767474.1 gg_id:355274 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C EU767
EU767881.1 gg_id:315203 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C EU767
FJ363181.1 gg_id:358119 feces adult twins and mothers; TS148 clone TS148_a04b04 FJ3631
DQ824075.1 gg_id:187574 human fecal clone RL204_aaj59a07 DQ824
AY895200.1 gg_id:112005 Bacteroides thetaiotaomicron str. 8669 AY895
EU768687.1 gg_id:354209 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C EU768
EU762810.1 gg_id:339814 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A› EU762
FJ978484.1 gg_id:451077 feces clone CL_F_007 FJ9784
EU764663.1 gg_id:347381 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1 EU764
EU765769.1 gg_id:331820 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B4 EU765
EU767849.1 gg_id:307633 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C EU767
EU766915.1 gg_id:336052 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU766
FJ368848.1 gg_id:365266 feces adult twins and mothers; TS4 clone TS4_a01c10 FJ3688
EU762885.1 gg_id:342841 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A› EU762
EU009790.1 gg_id:258109 intestinal microbiota domestic and wild turkeys turkey cecum clone DTB_X30 EU009
GQ079223.1 gg_id:456662 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1230a(GQ079
FJ681664.1 gg_id:530494 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6816
DQ456114.1 gg_id:158839 pre-adolescent turkey cecum clone CFT114E11 DQ456
EU622718.1 gg_id:279192 -feed administered sub-therapeutic chlorotetracycline alters structure and but not a EU622
GQ897967.1 gg_id:563880 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ897

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o__Bacteroidales	f__Marinilabiaceae

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FJ363125.1 gg_id:367489 feces adult twins and mothers; TS148 clone TS148_a03d07 FJ3631
GQ448989.1 gg_id:577170 Microbiome neonatal calves: shedding microorganisms fecal clone calf783_2wks_gr GQ448
ABJL02000007.1 gg_id:350694 Bacteroides intestinalis str. DSM 17393 ABJL02
FJ363537.1 gg_id:361984 feces adult twins and mothers; TS149 clone TS149_a04d05 FJ3635
EU768677.1 gg_id:321309 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C5 EU768
AY975458.1 gg_id:122208 human ascending colon mucosal biopsy clone N861 AY9754
EU762666.1 gg_id:329247 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A> EU762
AB264079.1 gg_id:196778 Fecal microbial (dugong dugon) determined genes Dugong feces clone dgD-156 AB2640
EU468119.1 gg_id:303158 bush dog feces clone bdog3_aad68e04 EU468
EU763236.1 gg_id:349090 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A> EU763
EU762605.1 gg_id:341587 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A> EU762
AY895199.1 gg_id:111709 Bacteroides thetaiotaomicron str. 7330 AY895
EU763549.1 gg_id:308453 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A4 EU763
FJ372113.1 gg_id:363282 feces adult twins and mothers; TS9 clone TS9_a01h06 FJ3721
AF132263.1 gg_id:71331 adult human fecal matter clone adhufec355 AF1322
FJ683852.1 gg_id:531412 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6838
GQ898079.1 gg_id:583769 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ898
DQ807525.1 gg_id:174868 human fecal clone RL307_aam07f12 DQ807
FJ371831.1 gg_id:365819 feces adult twins and mothers; TS8 clone TS8_a02f10 FJ3718
GQ496623.1 gg_id:561253 Bacteroides faecis str. MAJ26 GQ496
AB050109.1 gg_id:46476 Bacteroides thetaiotaomicron str. JCM 5827T AB050
FJ366386.1 gg_id:361304 feces adult twins and mothers; TS26 clone TS26_a02d07 FJ3663
EU009829.1 gg_id:240992 intestinal microbiota domestic and wild turkeys turkey cecum clone WTB_M48 EU009
EU768350.1 gg_id:353533 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C5 EU768
EU767940.1 gg_id:342174 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C4 EU767
AB490802.1 gg_id:563616 Bacteroides fluxus str. YIT 12057 AB490
AJ608232.1 gg_id:145315 human biopsies ulcerative colitis biopsy clone UC7-16 AJ6082
EU766579.1 gg_id:341436 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU766
FJ366424.1 gg_id:366744 feces adult twins and mothers; TS26 clone TS26_a03a05 FJ3664
EU768600.1 gg_id:333709 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C5 EU768
EU766592.1 gg_id:319657 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU766
DQ806938.1 gg_id:187639 human fecal clone RL198_aaj75g03 DQ806
EU763003.1 gg_id:346904 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A> EU763
DQ793722.1 gg_id:182419 human fecal clone RL246_aai76b11 DQ793
GQ493546.1 gg_id:551340 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
EU762582.1 gg_id:343759 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A> EU762
EU763718.1 gg_id:349576 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A4 EU763
EU290711.1 gg_id:240737 microbial structure biogeochemical contrasting shelf sediments Namibian upwelling EU290
DQ647061.1 gg_id:238065 Anaerophaga sp. str. TC371 DQ647
FJ231145.1 gg_id:342042 Microbial Laguna Lejia Salar de Aguas Calientes and summit Simba volcano three altit FJ2311
FJ202953.1 gg_id:349548 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2029

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AJ784993.1 gg_id:108748 Alkaliflexus imshenetskii str. Z-7010 AJ7849
FJ675203.1 gg_id:522481 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6752
AF449260.1 gg_id:61849 Riftia pachyptila's tube clone R76-B58 AF4492
EF559098.1 gg_id:226425 mesophilic anaerobic digester clone C35_D7_L_B_F05 EF5590
AB237697.1 gg_id:139833 microorganisms deep subsurface groundwater sedimentary rock milieu clone HDBW AB2376
FJ716917.1 gg_id:540416 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United Kingc FJ7169
FJ202485.1 gg_id:350582 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2024
EU052266.1 gg_id:251381 degradation kinetics and current efficiency cells supplied anode microbial fuel cell fe EU052
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AJ441218.1 gg_id:57462 hydrothermal vent polychaete mucous clone P. palm C/A 221 AJ4412
DQ517535.1 gg_id:161206 Anaerophaga sp. str. HS1 DQ517
GQ261777.1 gg_id:549338 shifts taxa and response localized organic loading deep sea sediment whale falls clo GQ261
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AJ418048.1 gg_id:51657 Anaerophaga thermohalophila str. Fru22 AJ4180
EF590038.2 gg_id:228045 changes structure sediments Songhua River contaminated nitrobenzene -DGGE cloni EF5900
DQ141183.1 gg_id:138582 Ruminofilibacter xylanolyticum str. S1 DQ141
DQ676403.1 gg_id:224027 Archaeal and plankton freshwater pond suboxic freshwater-pond sediment clone M DQ676
FJ024713.1 gg_id:310419 Copper affects reduction and genetic enriched sulfate reducing coastal sediments exp FJ0247
NC_011565.1 gg_id:363475 Candidatus Azobacteroides pseudotrichonymphae genomovar. CFP2 NC_01
AB231289.1 gg_id:149530 Bacteroidales symbiotic Oxymonas sp. gut termite Neotermes kosunensis flagellatec AB2312
AB231016.1 gg_id:148689 termite gut wall clone HsW01-025 AB2310
AB231023.1 gg_id:148038 termite gut wall clone HsW01-044 AB2310
AB462742.1 gg_id:540265 Complex coevolutionary history symbiotic Bacteroidales various protists termites fla AB4627
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AB088922.1 gg_id:78150 termite gut homogenate clone Rs-B92 bacterium AB0889
AB192159.1 gg_id:144700 termite gut homogenate clone RsTz-18 AB1921
AB299533.1 gg_id:243363 Motility Symbiont Termite Gut Flagellate Caduceia versatilis Member 'Synergistes' G AB2995
AB088936.2 gg_id:77941 termite gut homogenate clone Rs-B48 bacterium AB0889
AB231049.1 gg_id:148392 termite gut wall clone NkW01-005 AB2310
AB198444.1 gg_id:135574 termite gut wall fraction clone RsW01-002 AB1984
AB192208.1 gg_id:143532 termite gut homogenate clone RsTu1-13 AB1922
AB062838.1 gg_id:39177 termite gut homogenate clone BCf7-17 AB0628
DQ009684.2 gg_id:143053 termite gut homogenate clone R38A14 DQ009
AB192204.1 gg_id:141732 termite gut homogenate clone RsTu1-35 AB1922
AB088932.1 gg_id:77928 termite gut homogenate clone Rs-J02 bacterium AB0889
AB194938.1 gg_id:142402 Identification ectosymbionts distinct lineages Bacteroidales attached protists termit AB1949
AB062835.1 gg_id:38316 termite gut homogenate clone BCf7-02 AB0628
GQ502506.1 gg_id:535826 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf2- GQ502
AB194939.1 gg_id:143775 Identification ectosymbionts distinct lineages Bacteroidales attached protists termit AB1949

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g__Parabacteroides

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s__Parabacteroides distasonis	69646
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AB231017.1 gg_id:146610 termite gut wall clone HsW01-007 AB2310
AB088923.2 gg_id:77598 termite gut homogenate clone Rs-D66 bacterium AB0889
AB231290.1 gg_id:150115 Bacteroidales symbiotic Oxymonas sp. Neotermes kosunensis flagellated protist gut AB2312
AB192206.1 gg_id:141613 termite gut homogenate clone RsTu1-23 AB1922
AB088943.1 gg_id:78288 termite gut homogenate clone Rs-D29 bacterium AB0889
AB088935.1 gg_id:78052 termite gut homogenate clone Rs-M16 bacterium AB0889
AB262559.1 gg_id:186572 Cospeciation triplex symbiosis protists (Pseudotrichonympha spp.) hosts and their er AB2625
AB262557.1 gg_id:186877 Cospeciation triplex symbiosis protists (Pseudotrichonympha spp.) hosts and their er AB2625
AB262558.1 gg_id:191537 Cospeciation triplex symbiosis protists (Pseudotrichonympha spp.) hosts and their er AB2625
AB262556.1 gg_id:193546 Cospeciation triplex symbiosis protists (Pseudotrichonympha spp.) hosts and their er AB2625
AB548675.1 gg_id:524197 Dysgonomonas gadei str. JCM 16698 AB5486
NR_025484.1 gg_id:570833 Dysgonomonas mossii str. CCUG 43457 NR_025
GQ502485.1 gg_id:593371 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf2- GQ502
AY643492.1 gg_id:107721 Dysgonomonas wimpennyi str. ANFA2 AY6434
FJ823922.1 gg_id:524743 Controlling accumulation fermentation inhibitors biorefinery recycle water microbial FJ8239
AB234423.1 gg_id:147708 termite gut homogenate clone MgMjD-090 AB2344
AB199571.1 gg_id:110974 river water Japan clone RVW-04 AB1995
EF608552.1 gg_id:227900 predatory Poecilus chalcites their response lab rearing and antibiotic treatment diges EF6085
GQ502504.1 gg_id:535685 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf2- GQ502
AB288912.1 gg_id:202454 termite gut homogenate clone BOf7-08 AB2889
DQ856517.1 gg_id:239708 intestinal microflora Chinese mitten crab (Eriocheir sinensis) clone C1O DQ856
AB234397.1 gg_id:148589 termite gut homogenate clone MgMjD-025 AB2343
AB288875.1 gg_id:203234 termite gut homogenate clone BOf1-02 AB2888
AY953156.1 gg_id:114705 anaerobic swine lagoon clone B-1AL AY9531
AJ576373.1 gg_id:98890 hindgut homogenate Pachnoda ephippiata larva clone PeH10 AJ5763
AB548674.1 gg_id:530785 Dysgonomonas capnocytophagoides str. JCM 16697 AB5486
EF602792.1 gg_id:233332 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6027
AY916310.1 gg_id:112884 human sigmoid colon biopsy clone NX93 AY9163
AY916145.1 gg_id:113167 human transverse colon biopsy clone M048 AY9161
DQ815520.1 gg_id:164344 mouse cecum clone aab42b08 DQ815
EU728709.1 gg_id:347862 Odoribacter splanchnicus str. DJF_B089 EU7287
GQ402138.1 gg_id:544305 alpacas and sheep forestomach clone SH12 GQ402
AF001749.1 gg_id:1923 rumen clone RF17 AF0017
AB009214.1 gg_id:1943 rumen clone RFN67 bacterium AB0092
EU794157.1 gg_id:341926 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_P8 EU7941
AB009202.1 gg_id:2037 rumen clone RFN46 bacterium AB0092
EU469046.1 gg_id:288192 Speke's gazelle feces clone SP2_d12_3 EU4690
AB009197.1 gg_id:1969 rumen clone RFN41 bacterium AB0091
EU794092.1 gg_id:330762 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_O3 EU7940
EF403021.1 gg_id:210264 human fecal clone SJTU_B_15_68 EF4030
GQ016637.1 gg_id:493030 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw GQ016

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EU939404.1 gg_id:308165 Fecal wild pygmy loris feces clone WF16S_117 EU939
DQ799651.1 gg_id:194286 human fecal clone RL305aal88f12 DQ799
AB470345.1 gg_id:570230 Parabacteroides gordonii str. JCM 15726 MS-3 AB470
NZ_ABYH01000014.1 gg_id:470761 Parabacteroides johnsonii str. DSM 18315 NZ_AB
FJ681504.1 gg_id:529639 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6815
FJ673756.1 gg_id:520075 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6737
AF371918.1 gg_id:28974 swine intestine clone p-1862-c3 AF371
FJ366812.1 gg_id:357610 feces adult twins and mothers; TS27 clone TS27_a04b09 FJ3668
FJ684517.1 gg_id:515739 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6845
AF371917.1 gg_id:35721 swine intestine clone p-816-a5 AF371
EU774994.1 gg_id:347974 Francois Langur feces clone FL_2aaa01d07 EU774
FJ677705.1 gg_id:531069 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6777
FJ674079.1 gg_id:528653 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6740
EU771909.1 gg_id:306330 Southern three-banded armadillo feces clone arma_aaj53e03 EU771
FJ680516.1 gg_id:514875 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6805
FJ681022.1 gg_id:529102 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6810
FJ677437.1 gg_id:514220 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6774
DQ071528.1 gg_id:230553 microbial cecum captive and free-living capercaillies (Tetrao urogallus) clone TuCw7 DQ071
FJ680728.1 gg_id:532407 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6807
FJ677309.1 gg_id:532192 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6773
FJ681057.1 gg_id:523933 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6810
FJ677094.1 gg_id:522582 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6770
DQ801512.1 gg_id:199622 human fecal clone RL388_aao96e03 DQ801
EU136685.1 gg_id:245932 Parabacteroides merdae str. JCM9497 EU136
DQ456138.1 gg_id:157481 pre-adolescent turkey cecum clone CFT114H3 DQ456
FJ677490.1 gg_id:529708 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6774
FJ671638.1 gg_id:526025 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6716
AY975949.1 gg_id:122815 human ascending colon mucosal biopsy clone LS60 AY975
GQ448451.1 gg_id:592097 Microbiome neonatal calves: shedding microorganisms fecal clone calf783_10wks_g GQ448
FJ683073.1 gg_id:531353 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6830
FJ676802.1 gg_id:516933 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6768
AB430829.1 gg_id:263317 Porphyromonas crevioricanis str. ATCC 55563 AB430
NZ_ACNN01000021.1 gg_id:470807 Porphyromonas endodontalis str. ATCC 35406 NZ_AC
GU233445.1 gg_id:524704 Porphyromonas gingivicanis str. NUM 301 GU233
EU845219.1 gg_id:340509 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU845
AP009380.1 gg_id:294930 Porphyromonas gingivalis str. ATCC 33277 AP009
FJ792536.1 gg_id:560360 Porphyromonas levii str. ATCC 29147 FJ7925
GU454798.1 gg_id:522507 Porphyromonas levii str. Israel GU454
GQ112407.1 gg_id:423451 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ112
GQ074579.1 gg_id:407491 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ074
X76259.1 gg_id:1941 Porphyromonas cangingivalis str. VPB 4874 X76259

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FJ848556.1 gg_id:542665 Porphyromonas sp. str. 2014 FJ8485
EU289097.1 gg_id:254483 microbiome cloacal openings urogenital and anal tracts tammar wallaby Macropus e EU289
GQ081345.1 gg_id:462094 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl GQ081
EF511866.1 gg_id:221666 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aerug EF5118
EU557014.1 gg_id:308956 Detection microorganisms involved infectious endocarditis cultivation techniques inf EU557
FJ848566.1 gg_id:564437 Porphyromonas sp. str. 2121 FJ8485
X76261.1 gg_id:1951 Porphyromonas canoris str. VPB 4882 X76261
FJ976295.1 gg_id:591163 Interindividual healthy human oral microbiota mouth clone 10B051 FJ9762
GQ075596.1 gg_id:387445 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ075
CU923280.1 gg_id:543028 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU923
AY570514.1 gg_id:108520 Porphyromonas uenonis str. WAL 9902; ATCC BAA-906; CCUG 48615 AY5705
EU414673.1 gg_id:268540 Porphyromonas sp. str. WAL 1926C EU414
GQ115447.1 gg_id:397693 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw685g04 GQ115
AF287986.1 gg_id:42871 Porphyromonas gulae str. coyote 1.5.1 AF2879
AB053945.1 gg_id:46214 Tannerella forsythensis str. L7 AB0539
DQ344915.1 gg_id:161737 Tannerella forsythensis str. RMA 8286 DQ344
AB053939.1 gg_id:40709 Tannerella forsythensis str. G9 AB0539
AB053942.1 gg_id:34893 Tannerella forsythensis str. KM3 AB0539
AB191996.1 gg_id:143551 termite gut homogenate clone M2PB4-84 AB1919
AF385565.1 gg_id:43915 crevicular epithelial cells clone BU045 AF3855
AB191987.1 gg_id:142913 termite gut homogenate clone M1PL1-34 AB1919
FJ374177.1 gg_id:360716 Inter- and intraspecific humivorous scarab beetle larvae (Pachnoda spp.) larval hindgu FJ3741
AB088937.1 gg_id:78297 termite gut homogenate clone Rs-E83 bacterium AB0889
AY160850.1 gg_id:97947 termite intestinal tract clone COB P5-27 AY1608
AB189687.1 gg_id:113389 termite gut homogenate clone Tc-42 AB1896
AB243256.1 gg_id:149284 acetone-preserved termite gut clone M2PB4a-054 AB2432
FJ374176.1 gg_id:368029 Inter- and intraspecific humivorous scarab beetle larvae (Pachnoda spp.) larval hindgu FJ3741
AJ576344.1 gg_id:101861 hindgut homogenate Pachnoda ephippiata larva clone PeH27 AJ5763
AJ576330.1 gg_id:105053 hindgut homogenate Pachnoda ephippiata larva clone PeH12 AJ5763
AB062826.1 gg_id:19082 termite gut homogenate clone BCf5-08 AB0628
AM420141.1 gg_id:247976 Noma subgingival plaque clone 402C09(oral) AM420
AB189685.1 gg_id:113096 termite gut homogenate clone Tc-38 AB1896
AB255914.1 gg_id:166153 Localization Cell Morphologies Members Candidate TG3 and Subphylum Phylum Fibr AB2559
EU470470.1 gg_id:292037 Grevy's zebra feces clone GZ_aaa04f04 EU4704
FJ671888.1 gg_id:511761 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6718
DQ988275.1 gg_id:198436 Microbial lab-scale A1-A2-O fixed biofilm system coking wastewater treatment with DQ988
FJ672767.1 gg_id:532401 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6727
FJ672819.1 gg_id:510506 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6728
EF559223.1 gg_id:221775 mesophilic anaerobic digester clone A35_D28_L_B_D06 EF5592
FJ672904.1 gg_id:521556 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6729

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AJ853526.1 gg_id:111183 landfill leachate clone GZKB32 AJ8535
FN563309.1 gg_id:565774 Impact changing HRT OLR on prokaryotes involved biomethanizitaion and fuzzy logic FN563
FJ675576.1 gg_id:521274 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6755
FJ205819.1 gg_id:347868 microbial integrating library sequences and metagenome data obtained 454-pyroseq FJ2058
EF559172.1 gg_id:218156 mesophilic anaerobic digester clone G35_D8_H_B_A04 EF5591
FJ664781.1 gg_id:552684 Quantitative dynamics cells plankton-fed microbial fuel cell clone PFC_3_peak_D10 FJ6647
FJ202203.1 gg_id:354185 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2022
GQ052695.1 gg_id:460594 Topographical and Temporal Human Skin Microbiome skin back clone nbu539g04c1 GQ052
EU469149.1 gg_id:298915 Speke's gazelle feces clone SP3_c06 EU469
GQ052715.1 gg_id:404267 Topographical and Temporal Human Skin Microbiome skin back clone nbu540a05c1 GQ052
AJ318147.1 gg_id:45562 Waste-gas biofilter clone BIhiii38 AJ3181
FJ675463.1 gg_id:530837 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6754
EU794304.1 gg_id:339564 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_R22 EU794
AB100456.1 gg_id:81498 termite gut clone Rs-003 AB100
EU052241.1 gg_id:242269 degradation kinetics and current efficiency cells supplied anode microbial fuel cell fe EU052
CR933297.1 gg_id:109632 Evry municipal wastewater treatment plant clone 060H11_B_SD_P93 CR933
FJ664818.1 gg_id:512016 Quantitative dynamics cells plankton-fed microbial fuel cell clone PFC_3_peak_A10 FJ6648
AY977440.1 gg_id:115908 human cecum mucosal biopsy clone W144 AY977
CT574073.1 gg_id:155288 Evry municipal wastewater treatment plant clone 053H07_B_DI_P58 CT574
CU926729.1 gg_id:569056 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU926
FJ672406.1 gg_id:524949 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6724
FJ716926.1 gg_id:563763 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United King FJ7169
CT573875.1 gg_id:151413 Evry municipal wastewater treatment plant clone 013B08_B_SD_P15 CT5738
AY976380.1 gg_id:122025 human ascending colon mucosal biopsy clone LY65 AY9763
AM420225.1 gg_id:254175 Noma subgingival plaque clone 601G07(oral) AM420
AY983350.1 gg_id:121452 human descending colon mucosal biopsy clone A451 AY9833
EF559178.1 gg_id:220350 mesophilic anaerobic digester clone G35_D8_H_B_A02 EF5591
AY005072.1 gg_id:46885 subgingival dental plaque clone AU126 AY005
EF559129.1 gg_id:222811 mesophilic anaerobic digester clone C35_D63_H_B_H09 EF5591
EU470429.1 gg_id:290027 Grevy's zebra feces clone GZ_aaa01c12 EU470
FJ497484.1 gg_id:571407 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun FJ4974
EU052252.1 gg_id:251724 degradation kinetics and current efficiency cells supplied anode microbial fuel cell fe EU052
EU461317.1 gg_id:287569 red kangaroo feces clone KO2_aai17a01 EU461
EF157125.1 gg_id:237787 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon EF1571
AM420248.1 gg_id:237717 Noma subgingival plaque clone 701B08(oral) AM420
FJ672462.1 gg_id:511079 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6724
FJ674493.1 gg_id:526084 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6744
FJ439854.1 gg_id:536271 Investigation estrogen-degrading bioreactors membrane bioreactor biofilm clone M3 FJ4398

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U81722.2 gg_id:1975 fluidized bed anaerobic digestor fed vinasses (waste wine distillery) clone vadinHA54 U8172
FJ374186.1 gg_id:368153 Inter- and intraspecific humivorous scarab beetle larvae (Pachnoda spp.) larval hindgu FJ3741
FJ672447.1 gg_id:516031 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6724
EU721787.1 gg_id:567204 microbial production water Alaskan mesothermic petroleum reservoir two methods EU7217
EU794159.1 gg_id:355683 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_AF37 EU7941
AF371914.1 gg_id:102513 swine intestine clone p-238-o5 AF3719
FJ672854.1 gg_id:514271 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6728
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AY571432.1 gg_id:114637 termite gut clone RsaP168 AY5714
AB088927.2 gg_id:77707 termite gut homogenate clone Rs-N56 bacterium AB0889
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AB186895.1 gg_id:101957 polychlorinated dioxin dechlorinating microcosm clone TSAI15 AB1868
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FJ374185.1 gg_id:361949 Inter- and intraspecific humivorous scarab beetle larvae (Pachnoda spp.) larval hindgu FJ3741
EU465580.1 gg_id:297581 argali sheep feces clone AS1_aao38f01.Contig1 EU4655
EF559156.1 gg_id:219368 mesophilic anaerobic digester clone G35_D8_L_B_E07 EF5591
FJ671936.1 gg_id:529973 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6719
EU358697.1 gg_id:323312 structure archaeal denaturing gel electrophoresis and sequencing mesophilic biogas EU3586
AY953229.1 gg_id:114483 anaerobic swine lagoon clone A-2X AY9532
DQ860019.1 gg_id:240669 anchovy intestinal microflora clone F1P DQ860
AF349759.2 gg_id:49573 reductive TCE-dehalogenating enrichment clone TCE5 AF3497
AB355049.1 gg_id:235348 Monitoring and archaeal two heavy polluted areas lake Egypt based on surface wate AB3550
DQ003623.1 gg_id:119392 human mouth clone MB3_P19 DQ003
FJ202527.1 gg_id:314487 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2025
DQ205192.1 gg_id:150369 acid-tolerant H2/CO2-utilizing methanogenic s New York State enrichment acidic pe DQ205
AJ582209.1 gg_id:93925 soil near uranium mill tailings clone Gitt-GS-109 AJ5822
AY991817.1 gg_id:131239 mouse cecum clone C20_f23 AY9918
AB237700.1 gg_id:140394 microorganisms deep subsurface groundwater sedimentary rock milieu clone HDBW AB2377
AY134906.1 gg_id:59562 oral periodontitis clone FX069 AY1349

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AB088941.1 gg_id:78217 termite gut homogenate clone Rs-P01 bacterium AB088
FJ672436.1 gg_id:516239 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6724
EU467655.1 gg_id:298534 naked mole-rat feces clone molerat_2b05_1 EU467
FJ167452.1 gg_id:315404 microbiology granular sludge under autotrophic mixotrophic and heterotrophic denit FJ1674
AF132281.1 gg_id:70461 adult human fecal matter clone adhufec84 AF132
FJ167475.1 gg_id:355592 microbiology granular sludge under autotrophic mixotrophic and heterotrophic denit FJ1674
AF550591.1 gg_id:75791 Bacteroidetes Ko710 AF550
EU472295.1 gg_id:288734 francois langur feces clone FL_2aaa01a02 EU472
CU923533.1 gg_id:565061 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU923
DQ178248.1 gg_id:139320 Ruminobacillus xylanolyticum str. G1 DQ178
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EU573101.1 gg_id:279304 and Dependent Microbial Oil Reservoir North Sea Ekofisk oil field Norwegian sector c EU573
CU920278.1 gg_id:551524 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU920
CU919616.1 gg_id:551763 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU919
DQ447167.1 gg_id:156592 Microbial long-term performance full-scale synthesis gas fed bioreactor treating sulf DQ447
AY571436.1 gg_id:114716 termite gut clone RsaHw540 AY571
AB288898.1 gg_id:201673 termite gut homogenate clone BOf3-21 AB288
CU926773.1 gg_id:573887 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU926
AY949860.1 gg_id:114497 Bacteroides sp. strain str. Z4 AY9498
AB234434.1 gg_id:149277 termite gut homogenate clone MgMjR-061 AB2344
CU925579.1 gg_id:545453 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU925
EF559149.1 gg_id:222737 mesophilic anaerobic digester clone G35_D8_L_B_D04 EF5591
AB198454.1 gg_id:135866 termite gut wall fraction clone RsW01-016 AB1984
AB194940.1 gg_id:144765 Identification ectosymbionts distinct lineages Bacteroidales attached protists termit AB1949
FJ940882.1 gg_id:590552 Prevotella baroniae str. DSM 16972 FJ9408
AJ006457.1 gg_id:2048 Prevotella bryantii str. B14 (DSM 11371 species) AJ0064
EU469476.1 gg_id:300636 black lemur feces clone BKLE_e08_2 EU469
FJ677429.1 gg_id:512581 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6774
EU475181.1 gg_id:298789 bonobo feces clone BNO_aaa03f04 EU475
EU461975.1 gg_id:301191 white-faced saki feces clone Saki_aaj64f07 EU461
EU461664.1 gg_id:287914 mongoose lemur feces clone ML_aaj26f03 EU461
DQ795990.1 gg_id:188367 human fecal clone RL202_aai49h10 DQ795
FJ677392.1 gg_id:524100 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6773
ACBX02000017.1 gg_id:563962 Prevotella copri str. DSM 18205 ACBX0
AY979496.1 gg_id:126721 human transverse colon mucosal biopsy clone M138 AY9794
FJ678036.1 gg_id:518418 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6780
AY983808.1 gg_id:127263 human descending colon mucosal biopsy clone M868 AY9838
EU728712.1 gg_id:338913 Prevotella sp. str. DJF_B112 EU728
EU774935.1 gg_id:320044 Flying Fox feces clone FF_a09 EU774
EU462001.1 gg_id:298154 black-handed spider monkey feces clone SPIM_aaj33b06 EU462

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EU776839.1 gg_id:348750 Mongoose lemur feces clone ML_aaj27h07 EU776
FJ674146.1 gg_id:531121 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6741
EU461720.1 gg_id:289257 mongoose lemur feces clone ML_aaj27f09 EU461
NZ_ACBX02000014.1 gg_id:484333 Prevotella copri str. DSM 18205 NZ_AC
DQ796037.1 gg_id:195851 human fecal clone RL202_aai50e11 DQ796
AY984075.1 gg_id:120238 human descending colon mucosal biopsy clone ME85 AY984
EU775444.1 gg_id:351341 Western lowland gorilla feces clone GOR_aad33f07 EU775
AB429508.1 gg_id:292064 Prevotella falsenii str. 04161(= JCM 15128) AB429
X73965.1 gg_id:2197 Prevotella intermedia X73965
AF414831.1 gg_id:70556 Prevotella intermedia str. 23-PIN AF414
NZ_ACSI01000003.1 gg_id:471122 Prevotella melaninogenica str. ATCC 25845 NZ_AC
NZ_ACSI01000031.1 gg_id:471123 Prevotella melaninogenica str. ATCC 25845 NZ_AC
AB182485.1 gg_id:108139 Prevotella multiformis str. PPPA28 AB182
EF405530.1 gg_id:216693 Prevotella nanceiensis str. LBN 298 EF405
AY689228.1 gg_id:107476 Prevotella nigrescens str. ChDC KB6 AY689
ACUZ02000034.1 gg_id:557672 Prevotella oris str. F0302 ACUZ0
L16472.2 gg_id:2185 Prevotella oulorum str. ATCC43324 L16472
Y13106.1 gg_id:72060 Prevotella pallens str. 9423 Y13106
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AF183402.1 gg_id:30384 Prevotella tannerae str. 131-9-1 AF183
AY836507.1 gg_id:111357 Prevotella veroralis str. ATCC 33779 AY836
EU850489.1 gg_id:308966 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF255 EU850
AY980990.1 gg_id:123369 human rectum mucosal biopsy clone V110 AY980
FJ683706.1 gg_id:526349 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6837
FJ679759.1 gg_id:528783 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6797
FJ680505.1 gg_id:526641 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6805
FJ677502.1 gg_id:528859 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6775
FJ676728.1 gg_id:525468 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6767
AJ581354.1 gg_id:151386 Prevotella sp. str. BI-42 AJ5813
FJ681718.1 gg_id:519244 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6817
FJ675763.1 gg_id:515100 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6757
EU467352.1 gg_id:294044 chimpanzee feces clone CHIMP12_a12 EU467
FJ364596.1 gg_id:368761 feces adult twins and mothers; TS15 clone TS15_a04h02 FJ3645
FJ682151.1 gg_id:530650 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6821
GQ492287.1 gg_id:554830 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
AY978047.1 gg_id:127644 human cecum mucosal biopsy clone LH92 AY978
FJ682990.1 gg_id:531754 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6829
FJ674177.1 gg_id:523578 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6741
AF018455.1 gg_id:2191 rumen clone 12-7 AF018

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EF445275.1 gg_id:211356 dairy cow rumen clone NED5F5 EF4452
EF097566.1 gg_id:178558 mouse cecum clone SWPT19_aaa04e03 EF0975
FJ684982.1 gg_id:529185 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6849
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FJ682998.1 gg_id:528890 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6829
FJ557802.1 gg_id:522669 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5578
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FJ365605.1 gg_id:360621 feces adult twins and mothers; TS20 clone TS20_a04h03 FJ3656
GQ491765.1 gg_id:581537 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
EU460026.1 gg_id:287974 mammals their gut microbes eastern black and white colobus feces clone COL_aai13 EU460
L16483.1 gg_id:2193 Prevotella disiens L16483
EU461736.1 gg_id:291589 mongoose lemur feces clone ML_aaj28a06 EU461
GQ448975.1 gg_id:578219 Microbiome neonatal calves: shedding microorganisms fecal clone calf783_2wks_gr GQ448
EU748460.1 gg_id:348149 neotropical folivorous flying bird adult hoatzin crop clone hoa61_09b11 EU7484
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AY836508.1 gg_id:109626 Prevotella loescheii str. NCTC 11321 AY8365
AF371877.1 gg_id:28413 swine intestine clone p-1310-a5 AF3718
FJ673401.1 gg_id:520866 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6734
GQ491454.1 gg_id:539050 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
FJ363048.1 gg_id:367089 feces adult twins and mothers; TS148 clone TS148_a02d02 FJ3630
EU467386.1 gg_id:291328 chimpanzee feces clone CHIMP12_g09_1 EU467
EF445259.1 gg_id:212167 dairy cow rumen clone NED5D8 EF4452
AB185757.1 gg_id:104511 rumen clone U29-B08 AB185
DQ801361.1 gg_id:187628 human fecal clone RL388_aao94e03 DQ801
EU747951.1 gg_id:339093 neotropical folivorous flying bird adult hoatzin crop clone hoa11_70F09 EU747
FJ671740.1 gg_id:532041 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6717
DQ801635.1 gg_id:180138 human fecal clone RL117_aae93b10 DQ801
FJ681316.1 gg_id:519417 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6813
FJ684766.1 gg_id:529366 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6847
FJ681390.1 gg_id:531139 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6813
DQ797096.1 gg_id:186007 human fecal clone RL386_aao86h09 DQ797
FJ679785.1 gg_id:510855 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6797
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EU467084.1 gg_id:303306 mongoose lemur feces clone ML_aae87f08 EU467
GQ491976.1 gg_id:573810 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491

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FJ365580.1 gg_id:357467 feces adult twins and mothers; TS20 clone TS20_a04e08 FJ3655
FJ681551.1 gg_id:515734 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6815
EU773702.1 gg_id:340238 Capybara feces clone CAP_aah97c05 EU773
FJ365485.1 gg_id:368449 feces adult twins and mothers; TS20 clone TS20_a03d11 FJ3654
FJ681706.1 gg_id:516236 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6817
FJ678113.1 gg_id:509724 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6781
EU459803.1 gg_id:296515 Prevost's squirrel feces clone SQ_aah79b04 EU459
AB270064.1 gg_id:170559 Influence temperature and humidity on heifers rumen contents Holstein heifer (Bos AB270
FJ674011.1 gg_id:532013 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6740
EU461722.1 gg_id:301626 mongoose lemur feces clone ML_aaj27g01 EU461
EU467113.1 gg_id:292253 mongoose lemur feces clone ML_aae88e08 EU467
FJ681046.1 gg_id:521640 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6810
AB185633.1 gg_id:105738 rumen clone F24-F12 AB185
EU748247.1 gg_id:304355 neotropical folivorous flying bird adult hoatzin crop clone hoa45_54F07 EU748
GU302809.1 gg_id:536141 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU302
EU771540.1 gg_id:321723 Hamadryas Baboon feces clone AFBAB_aai01e04 EU771
GQ493961.1 gg_id:561151 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
GU303821.1 gg_id:570979 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU303
EU531871.1 gg_id:272155 Predominant role host genetics controlling gut microbiota FMF remission stool clone EU531
GQ025673.1 gg_id:396867 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ025
EF445225.1 gg_id:204190 dairy cow rumen clone NED5D2 EF445
FJ679994.1 gg_id:528287 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6799
EU777529.1 gg_id:324283 Sumatran orangutan feces clone orang1_b04 EU777
FJ682571.1 gg_id:516854 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6825
FJ673303.1 gg_id:515870 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6733
FJ673617.1 gg_id:525511 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6736
AJ009933.1 gg_id:2170 Prevotella aff. ruminicola Tc2-24 AJ0099
FJ364399.1 gg_id:360425 feces adult twins and mothers; TS15 clone TS15_a02d11 FJ3643
GQ492549.1 gg_id:545761 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
EU461619.1 gg_id:300684 mongoose lemur feces clone ML_aaj25f10 EU461
FJ364599.1 gg_id:358738 feces adult twins and mothers; TS15 clone TS15_a04h05 FJ3645
GQ449130.1 gg_id:544926 Microbiome neonatal calves: shedding microorganisms fecal clone calf784_6wks_gr GQ449
AB269968.1 gg_id:171872 Influence temperature and humidity on heifers rumen contents Holstein heifer (Bos AB269
GQ491322.1 gg_id:582462 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
GQ867327.1 gg_id:573688 and prevalence blaTEM genes Arctic seals colon content clone WSp68 GQ867
EU463137.1 gg_id:295917 naked mole-rat feces clone molerat_aai70d12 EU463
GQ493782.1 gg_id:588929 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
FJ673118.1 gg_id:521450 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6731
FJ678505.1 gg_id:523335 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6785
GU302532.1 gg_id:587640 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU302
EU459683.1 gg_id:299215 ring-tailed lemur feces clone RT_aai10g09 EU459

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EU458702.1 gg_id:290109 Goeldi's marmoset feces clone CAL_f02 EU458
DQ308594.1 gg_id:150163 sheep rumen enrichment clone 196.F11 DQ308
AF018486.1 gg_id:2208 rumen clone 12-109 AF0184
EU748085.1 gg_id:303751 neotropical folivorous flying bird adult hoatzin crop clone hoa2_44f02 EU748
EU469471.1 gg_id:297749 black lemur feces clone BKLE_d11_1 EU469
FJ684964.1 gg_id:523901 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6849
EU850591.1 gg_id:329927 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF415 EU850
GU302651.1 gg_id:549174 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU302
GQ493350.1 gg_id:583870 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
FJ557580.1 gg_id:520942 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5575
EU462060.1 gg_id:292785 black-handed spider monkey feces clone SPIM_aaj34b09 EU462
FJ680644.1 gg_id:518150 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6806
FJ364333.1 gg_id:357026 feces adult twins and mothers; TS15 clone TS15_a01f12 FJ3643
EU460000.1 gg_id:301320 Prevost's squirrel feces clone SQ_aah82f08 EU460
FJ681471.1 gg_id:524449 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6814
FJ678726.1 gg_id:516894 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6787
FJ682499.1 gg_id:521915 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6824
FJ673331.1 gg_id:524827 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6733
EU773472.1 gg_id:356372 Bonobo feces clone BNO_aaa04h04 EU773
EU462114.1 gg_id:301147 black-handed spider monkey feces clone SPIM_aaj35c02 EU462
GU302758.1 gg_id:581246 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU302
GQ179741.1 gg_id:453900 Heterogeneity vaginal microbial within individuals vagina clone VE62D04 GQ179
FJ674220.1 gg_id:513326 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6742
EU778215.1 gg_id:304851 feces clone RL388_aao93e08 EU778
AY244911.1 gg_id:84913 cow rumen clone BF33 AY244
GU302695.1 gg_id:542879 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU302
FJ365296.1 gg_id:367816 feces adult twins and mothers; TS20 clone TS20_a01c03 FJ3652
EU531869.1 gg_id:261330 Predominant role host genetics controlling gut microbiota FMF remission stool clone EU531
FJ557908.1 gg_id:522663 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5579
EU462176.1 gg_id:289542 black-handed spider monkey feces clone SPIM_aaj36e11 EU462
GQ493115.1 gg_id:581089 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
DQ801307.1 gg_id:195099 human fecal clone RL388_aao93g04 DQ801
EU259409.1 gg_id:251069 Rumen yak (Bos grunniens) sequences rumen fluid clone YRC33 EU259
EU774357.1 gg_id:319810 Chimpanzee feces clone CHIMP1_aaj39a04 EU774
FJ683112.1 gg_id:516530 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6831
EU463602.1 gg_id:300061 domesticated horse feces clone horsej_aai89e10 EU463
FJ674149.1 gg_id:516591 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6741
AY977838.1 gg_id:120596 human cecum mucosal biopsy clone LF34 AY977
FJ681877.1 gg_id:532296 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6818
DQ518919.1 gg_id:181627 Prevotella sp. str. 4401737 DQ518

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FJ684931.1 gg_id:516464 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6849
EU467101.1 gg_id:291438 mongoose lemur feces clone ML_aae88c02 EU467
FJ684855.1 gg_id:524957 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6848
EU774233.1 gg_id:335566 Chimpanzee feces clone CHIMP1_aaj37h12 EU774
FJ673972.1 gg_id:520856 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6739
AY979519.1 gg_id:120419 human transverse colon mucosal biopsy clone M167 AY979
FJ684201.1 gg_id:528619 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6842
EU776852.1 gg_id:341421 Mongoose lemur feces clone ML_aaj27a05 EU776
EF603058.1 gg_id:235046 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF603
FJ674046.1 gg_id:530392 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6740
FJ683175.1 gg_id:510416 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6831
FJ673465.1 gg_id:532179 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6734
EF445226.1 gg_id:211557 dairy cow rumen clone NED5H5 EF4452
FJ684873.1 gg_id:529031 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6848
EU467249.1 gg_id:296720 black-handed spider monkey feces clone SPIM_h08 EU467
AY982301.1 gg_id:117207 human sigmoid colon mucosal biopsy clone MI62 AY982
FJ673599.1 gg_id:530725 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6735
EF097294.1 gg_id:187934 mouse cecum clone SWPT18_aaa04e10 EF0972
DQ797179.1 gg_id:190072 human fecal clone RL386_aao88a06 DQ797
DQ796159.1 gg_id:198715 human fecal clone RL202_aai52d10 DQ796
EF097208.1 gg_id:180282 mouse cecum clone SWPT18_aaa03b07 EF0972
DQ796142.1 gg_id:187055 human fecal clone RL202_aai52b12 DQ796
EU459673.1 gg_id:299368 ring-tailed lemur feces clone RT_aai10f06 EU459
GU470887.1 gg_id:539347 Prevotella sp. oral taxon 302 str. F0323 GU470
FJ676106.1 gg_id:515850 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6761
FJ682447.1 gg_id:520581 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6824
FJ834265.1 gg_id:510667 Microbial Ecology Crop Folivorous Hoatzin crop contents clone A2Q401_48H06 FJ8342
EU459943.1 gg_id:290924 Prevost's squirrel feces clone SQ_aah81f06 EU459
AM422125.1 gg_id:245050 Prevotella amniotica str. CCUG 53648 AM422
DQ795906.1 gg_id:178860 human fecal clone RL245_aai84e05 DQ795
EU778318.1 gg_id:347953 feces clone RL388_aao93f08 EU778
FJ678522.1 gg_id:512781 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6785
EU776927.1 gg_id:316941 Naked mole-rat feces clone molerat_aai71d05 EU776
FJ673642.1 gg_id:520686 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6736
EU850466.1 gg_id:338302 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF44 EU850
GQ492508.1 gg_id:571918 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
FJ681312.1 gg_id:527502 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6813
FJ684758.1 gg_id:524124 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6847
EU473087.1 gg_id:299362 douc langur feces clone DL_1aaa02g12 EU473
DQ801633.1 gg_id:198472 human fecal clone RL117_aae93b07 DQ801

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DQ308599.1 gg_id:149030 sheep rumen enrichment clone 196.G09 DQ308
EF445249.1 gg_id:211987 dairy cow rumen clone NED6C6 EF4452
EU842865.1 gg_id:313080 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU8428
FJ682084.1 gg_id:529577 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6820
AF018460.1 gg_id:2051 rumen clone 12-16 AF0184
EF510668.1 gg_id:220889 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aerug EF5106
FJ673367.1 gg_id:519509 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6733
AY278625.1 gg_id:88035 Prevotella genomosp. C2 AY2786
FJ673762.1 gg_id:516492 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6737
AM420076.1 gg_id:244669 Noma subgingival plaque clone 301G11(oral) AM420
AF001777.1 gg_id:2121 rumen clone RFN1 AF0017
AF018482.1 gg_id:2143 rumen clone 12-103 AF0184
AB185747.1 gg_id:99412 rumen clone U29-A10 AB1857
FJ364552.1 gg_id:363513 feces adult twins and mothers; TS15 clone TS15_a04c09 FJ3645
DQ801414.1 gg_id:198573 human fecal clone RL388_aao95c01 DQ801
DQ796381.1 gg_id:187532 human fecal clone RL179_aah26e05 DQ796
GQ492443.1 gg_id:547386 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
EU843990.1 gg_id:353232 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8439
GQ448254.1 gg_id:587185 Microbiome neonatal calves: shedding microorganisms fecal clone calf783_2wks_gr GQ448
FJ680952.1 gg_id:529311 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6809
GQ006634.1 gg_id:503030 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu85h01c GQ006
AM420252.1 gg_id:237394 Noma subgingival plaque clone 701D05(oral) AM420
EU467139.1 gg_id:291194 mongoose lemur feces clone ML_aae89d04 EU4671
DQ796032.1 gg_id:189776 human fecal clone RL202_aai50e04 DQ796
FJ685231.1 gg_id:526617 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6852
GQ491487.1 gg_id:582564 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
AB009184.1 gg_id:2073 rumen clone RFN26 bacterium AB0091
FJ558104.1 gg_id:526949 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5581
FJ682743.1 gg_id:516402 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6827
FJ674157.1 gg_id:520484 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6741
EU775095.1 gg_id:334392 Francois Langur feces clone FL_2aaa01e10 EU7750
FJ679127.1 gg_id:525990 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6791
AY093462.1 gg_id:63123 deep marine sediment clone MB-A2-107 AY0934
FJ674138.1 gg_id:520780 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6741
FJ682119.1 gg_id:528609 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6821
FJ364458.1 gg_id:364074 feces adult twins and mothers; TS15 clone TS15_a03b11 FJ3644
EF510483.1 gg_id:222154 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aerug EF5104
EU461603.1 gg_id:294196 mongoose lemur feces clone ML_aaj25d04 EU4616
AB270111.1 gg_id:168200 Influence temperature and humidity on heifers rumen contents Holstein heifer (Bos AB2701
FJ674044.1 gg_id:525357 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6740

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AY981001.1 gg_id:117786 human rectum mucosal biopsy clone V138 AY981
DQ015308.1 gg_id:132494 mouse cecum clone M2_1e09 DQ015
EU774114.1 gg_id:349352 Chimpanzee feces clone CHIMP1_aaj40h10 EU774
FJ683316.1 gg_id:509294 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6833
EU537408.1 gg_id:285626 profile human microbiota antecubital fossa (inner elbow) skin clone nbt78a03 EU537
FJ674193.1 gg_id:521199 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6741
DQ796131.1 gg_id:186388 human fecal clone RL202_aai52a06 DQ796
EU774309.1 gg_id:329650 Chimpanzee feces clone CHIMP1_aaj37f03 EU774
FJ673054.1 gg_id:524193 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6730
FJ676833.1 gg_id:527419 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6768
GQ492186.1 gg_id:581344 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
AF018469.1 gg_id:2140 rumen clone 12-51 AF018
FJ683139.1 gg_id:522450 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6831
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AY978001.1 gg_id:117426 human cecum mucosal biopsy clone LH36 AY978
FJ674154.1 gg_id:520593 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6741
DQ797117.1 gg_id:189432 human fecal clone RL386_aao87b12 DQ797
GQ491991.1 gg_id:546549 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
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AY979701.1 gg_id:121507 human transverse colon mucosal biopsy clone M435 AY979
FJ681462.1 gg_id:519347 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6814
GQ037615.1 gg_id:374568 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu4 GQ037
FJ364593.1 gg_id:361488 feces adult twins and mothers; TS15 clone TS15_a04g10 FJ3645
GQ448313.1 gg_id:541579 Microbiome neonatal calves: shedding microorganisms fecal clone calf783_2wks_gr GQ448
FJ676933.1 gg_id:530238 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6769
EU467121.1 gg_id:293143 mongoose lemur feces clone ML_aae88g03 EU467
DQ801565.1 gg_id:194357 human fecal clone RL117_aae91e01 DQ801
EU778580.1 gg_id:339374 Ring-tailed lemur feces clone RT_aai09f10 EU778
FJ976203.1 gg_id:544617 Interindividual healthy human oral microbiota mouth clone 3083 FJ9762
FJ679660.1 gg_id:520962 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6796
GU302821.1 gg_id:582218 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU302
EU850584.1 gg_id:334521 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF403 EU850
EU459856.1 gg_id:299317 Prevost's squirrel feces clone SQ_aah80c01 EU459
EF445247.1 gg_id:214336 dairy cow rumen clone NED6C4 EF4452
AY976237.1 gg_id:123765 human ascending colon mucosal biopsy clone LW67 AY976
FJ557771.1 gg_id:528457 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5577
FJ680456.1 gg_id:530706 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6804

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DQ795033.1 gg_id:185560 human fecal clone RL310_aam39d05 DQ795
GQ493530.1 gg_id:580564 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
EU748168.1 gg_id:329933 neotropical folivorous flying bird adult hoatzin crop clone hoa33_17A03.F EU748
EU778985.1 gg_id:307174 Prevost's squirrel feces clone SQ_aah82a04 EU778
EU887831.1 gg_id:321459 and RFLP slurry Nisargruna biogas plant aerobic predigester clone 9B EU887
EU472954.1 gg_id:295831 douc langur feces clone DL_1aaa02f02 EU472
FJ684479.1 gg_id:523276 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6844
FJ683769.1 gg_id:530979 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6837
EU531892.1 gg_id:272726 Predominant role host genetics controlling gut microbiota FMF remission stool clone EU531
GQ044807.1 gg_id:375044 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw GQ044
EU462153.1 gg_id:302183 black-handed spider monkey feces clone SPIM_aaj36a09 EU462
AY978038.1 gg_id:117846 human cecum mucosal biopsy clone LH81 AY978
AY976203.1 gg_id:123983 human ascending colon mucosal biopsy clone LW22 AY976
FJ673016.1 gg_id:519306 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6730
AB270095.1 gg_id:164946 Influence temperature and humidity on heifers rumen contents Holstein heifer (Bos AB270
EU773649.1 gg_id:336924 Capybara feces clone CAP_aah97f08 EU773
FJ683145.1 gg_id:527471 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6831
EF534315.1 gg_id:224539 Prevotella genomosp. T3 str. W1609 EF5343
DQ797184.1 gg_id:174975 human fecal clone RL386_aao88b01 DQ797
FJ685119.1 gg_id:526943 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6851
GQ492563.1 gg_id:538485 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
FJ673913.1 gg_id:520460 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6739
FJ685238.1 gg_id:528077 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6852
EU461757.1 gg_id:292547 mongoose lemur feces clone ML_aaj28d02 EU461
FJ673610.1 gg_id:532039 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6736
FJ364375.1 gg_id:357830 feces adult twins and mothers; TS15 clone TS15_a02b10 FJ3643
GQ006801.1 gg_id:502863 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu87h07c GQ006
EU475110.1 gg_id:301251 visayam warty pig feces clone VWP_aaa01c09 EU475
FJ362948.1 gg_id:364157 feces adult twins and mothers; TS148 clone TS148_a01b05 FJ3629
FJ678342.1 gg_id:522618 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6783
AY982503.1 gg_id:118916 human sigmoid colon mucosal biopsy clone MN09 AY982
EU461703.1 gg_id:295287 mongoose lemur feces clone ML_aaj27d08 EU461
EU775112.1 gg_id:326403 Francois Langur feces clone FL_2aaa02g04 EU775
FJ679733.1 gg_id:518773 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6797
FJ685476.1 gg_id:517719 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6854
FJ684568.1 gg_id:529076 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6845
EU778816.1 gg_id:336769 Black-handed Spider Monkey feces clone SPIM_aaj35h09 EU778
FJ685495.1 gg_id:530925 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6854
FJ674081.1 gg_id:513870 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6740
EF401398.1 gg_id:214549 human fecal clone SJTU_D_09_79 EF4013
FJ680457.1 gg_id:516274 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6804

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EU773152.1 gg_id:333756 BigHorn sheep feces clone BHSD_aaa03c01 EU773
EU467242.1 gg_id:288050 black-handed spider monkey feces clone SPIM_d08_1 EU467
EU462271.1 gg_id:294573 chimpanzee feces clone CHIMP1_aaj38g12 EU462
FJ685406.1 gg_id:523949 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6854
GQ031818.1 gg_id:370841 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ031
EU467643.1 gg_id:299524 naked mole-rat feces clone molerat_2d12_1 EU467
DQ795931.1 gg_id:174318 human fecal clone RL202_aai49b03 DQ795
FJ685510.1 gg_id:515077 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6855
DQ796855.1 gg_id:185708 human fecal clone RL179_aao55e05 DQ796
EU778070.1 gg_id:328035 feces clone RL388_aao93b02 EU778
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EU458766.1 gg_id:296943 Goeldi's marmoset feces clone CAL_a04_1 EU458
EU461954.1 gg_id:299764 white-faced saki feces clone Saki_aaj64c08 EU461
EU459724.1 gg_id:300135 ring-tailed lemur feces clone RT_aai11f02 EU459
GQ072794.1 gg_id:381205 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw201c04c GQ072
AM420217.1 gg_id:247034 Noma subgingival plaque clone 601D02(oral) AM420
AY979721.1 gg_id:121586 human transverse colon mucosal biopsy clone M462 AY979
FJ673616.1 gg_id:525181 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6736
AY979544.1 gg_id:123488 human transverse colon mucosal biopsy clone M201 AY979
FJ684156.1 gg_id:525306 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6841
DQ801513.1 gg_id:174844 human fecal clone RL388_aao96e04 DQ801
EU461652.1 gg_id:288795 mongoose lemur feces clone ML_aaj26d01 EU461
FJ685070.1 gg_id:518228 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6850
FJ673390.1 gg_id:513417 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6733
DQ794957.1 gg_id:183105 human fecal clone RL310_aam38d09 DQ794
EU469446.1 gg_id:298451 black lemur feces clone BKLE_a06_2 EU469
EF510408.1 gg_id:219995 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aerug EF5104
DQ796298.1 gg_id:186364 human fecal clone RL179_aah25d08 DQ796
GQ493728.1 gg_id:588151 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
EF436381.1 gg_id:216511 library-based ruminal water buffalo (Bubalus bubalis) rumen fluid clone BRC95 EF4363
EU773561.1 gg_id:334610 Goeldi's Marmoset feces clone CAL_g04_1 EU773
GQ021950.1 gg_id:487718 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ021
FJ683508.1 gg_id:515712 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6835
EU562293.1 gg_id:267244 Prevotella genomosp. E3 str. 4D22 EU562
EU381837.1 gg_id:271262 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU381
EU462041.1 gg_id:296442 black-handed spider monkey feces clone SPIM_aaj33g08 EU462
FJ674185.1 gg_id:527333 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6741

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EU774533.1 gg_id:305603 Douc langur feces clone DL_2aaa02f12 EU774
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EU843543.1 gg_id:352418 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
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FJ673559.1 gg_id:521157 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6735
FJ683451.1 gg_id:513649 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6834
FJ982992.1 gg_id:393419 Aspects Oral Microbiome root canal clone OPEN_ROOT_39 FJ9829
EU469550.1 gg_id:303304 western lowland gorilla feces clone GOR_aad32f07 EU469
AY980771.1 gg_id:120305 human rectum mucosal biopsy clone LN69 AY980
FJ684111.1 gg_id:531103 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6841
FJ678631.1 gg_id:522413 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6786
FJ677781.1 gg_id:520447 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6777
FJ674195.1 gg_id:520294 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6741
FJ678568.1 gg_id:517889 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6785
GQ492008.1 gg_id:540051 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
GQ491649.1 gg_id:589891 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
EU475447.1 gg_id:302303 springbok feces clone SBSD_aaa03e02 EU475
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AF481227.1 gg_id:68339 Prevotella sp. str. E9_34 AF481
FJ683584.1 gg_id:519069 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6835
FJ678992.1 gg_id:526388 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6789
DQ797126.1 gg_id:188652 human fecal clone RL386_aao87c11 DQ797
GQ492677.1 gg_id:588173 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
FJ683185.1 gg_id:517978 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6831

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FJ676640.1 gg_id:522859 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6766
AF385515.1 gg_id:73324 tongue dorsa clone DO045 AF3855
AB009237.1 gg_id:2081 rumen clone RFN90 bacterium AB0092
EU469378.1 gg_id:292751 black lemur feces clone BKLE_f01 EU4693
FJ674026.1 gg_id:522462 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6740
GQ402134.1 gg_id:512265 alpacas and sheep forestomach clone SH17 GQ402
EU776030.1 gg_id:305514 Spotted hyena feces clone HY1_h05_2 EU7760
EU748036.1 gg_id:321154 neotropical folivorous flying bird adult hoatzin crop clone hoa2_43f07 EU7480
DQ797187.1 gg_id:195206 human fecal clone RL386_aao88b05 DQ797
EU778991.1 gg_id:341295 Prevost's squirrel feces clone SQ_aah82h08 EU7789
FJ681588.1 gg_id:517965 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6815
FJ683293.1 gg_id:524838 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6832
EU432416.1 gg_id:261404 variation and endosymbiotic phenotypically- sea urchin Strongylocentrotus intermec EU4324
FJ684258.1 gg_id:510384 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6842
FJ685374.1 gg_id:512261 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6853
FJ673204.1 gg_id:517714 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6732
EF510603.1 gg_id:227118 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aerug EF5106
AF414823.1 gg_id:72550 Prevotella intermedia str. 6-PIN AF4148
FJ557883.1 gg_id:531961 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5578
EF445236.1 gg_id:210346 dairy cow rumen clone NED4D2 EF4452
EU462076.1 gg_id:300872 black-handed spider monkey feces clone SPIM_aaj34e01 EU4620
AB078826.2 gg_id:147308 Bacteroidales str. KB3 AB0788
EU850530.1 gg_id:314206 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF318 EU8505
FJ681842.1 gg_id:518692 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6818
FJ440093.1 gg_id:554296 Megamonas hypermegale colonization correlates Campylobacter jejuni exclusion pou FJ4400
DQ801108.1 gg_id:176761 human fecal clone RL387_aao92c09 DQ801
FJ879770.1 gg_id:455452 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8797
EU774591.1 gg_id:327684 Douc langur feces clone DL_1aaa03a10 EU7745
FJ674210.1 gg_id:510200 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6742
FJ678888.1 gg_id:525355 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6788
AF371882.1 gg_id:46017 swine intestine clone p-408-o3 AF3718
EU458688.1 gg_id:291144 Goeldi's marmoset feces clone CAL_b09 EU4586
AB185507.1 gg_id:103209 rumen clone F23-A04 AB1855
FJ684554.1 gg_id:529883 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6845
FJ683093.1 gg_id:519998 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6830
AB185648.1 gg_id:102695 rumen clone F24-H04 AB1856
EU461639.1 gg_id:301048 mongoose lemur feces clone ML_aaj26b02 EU4616
GQ004014.1 gg_id:505648 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu67e0 GQ004
AY349397.1 gg_id:92496 human oral cavity clone GI059 AY3493
EU461584.1 gg_id:287542 mongoose lemur feces clone ML_aaj25a06 EU4615
EU774976.1 gg_id:323239 Flying Fox feces clone FF_c03 EU7749

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EU778908.1 gg_id:317337 Black-handed Spider Monkey feces clone SPIM_aaj36f08 EU778
FJ683280.1 gg_id:521175 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6832
GU302957.1 gg_id:553043 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU302
GQ000713.1 gg_id:469277 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ000
DQ801533.1 gg_id:196806 human fecal clone RL388_aao96g03 DQ801
AB185623.1 gg_id:100680 rumen clone F24-F01 AB185
EU461508.1 gg_id:290453 black rhinoceros feces clone RH_aaj91c02 EU461
EF445269.1 gg_id:214082 dairy cow rumen clone NED4H12 EF4452
FJ679524.1 gg_id:527726 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6795
FJ672981.1 gg_id:511974 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6729
FJ676996.1 gg_id:524240 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6769
AB286442.1 gg_id:205607 Reducing production and domination comamonadaceae reducing oxygen supply was AB286
DQ801283.1 gg_id:185287 human fecal clone RL388_aao93d08 DQ801
DQ797016.1 gg_id:190025 human fecal clone RL386_aao85g10 DQ797
EU871411.1 gg_id:351351 Genetic Bovine (Bos taurus) Rumen Thailand clone CF383 EU871
AF371903.1 gg_id:20534 swine intestine clone p-817-a5 AF371
GQ491301.1 gg_id:593822 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
AM420031.1 gg_id:252889 Noma subgingival plaque clone 201F12(oral) AM420
FJ673999.1 gg_id:517123 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6739
FJ679715.1 gg_id:530240 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6797
FJ685341.1 gg_id:526489 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6853
EU458726.1 gg_id:289980 Goeldi's marmoset feces clone CAL_d03 EU458
FJ685375.1 gg_id:525880 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6853
DQ801483.1 gg_id:177789 human fecal clone RL388_aao96b05 DQ801
FJ673420.1 gg_id:523261 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6734
FJ673272.1 gg_id:515189 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6732
EU472979.1 gg_id:301030 douc langur feces clone DL_1aaa03f03 EU472
EU459530.1 gg_id:294458 capybara feces clone CAP_aah99c08 EU459
FJ678717.1 gg_id:526104 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6787
GQ492292.1 gg_id:583770 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
DQ796504.1 gg_id:192562 human fecal clone RL179aan73e10 DQ796
EU463048.1 gg_id:296766 naked mole-rat feces clone molerat_aai69a04 EU463
GQ458218.1 gg_id:577260 Microbial structure co-digestion anaerobic bioreactors treating cassava pulp and pig GQ458
AY977971.1 gg_id:125607 human cecum mucosal biopsy clone LH01 AY977
EU777022.1 gg_id:352470 Naked mole-rat feces clone molerat_2b06 EU777
DQ801587.1 gg_id:188149 human fecal clone RL117_aae92a12 DQ801
GU174055.1 gg_id:586099 Microbial Bactrian camel estimated rumen clone XJC84 GU174
FJ673023.1 gg_id:521137 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6730
FJ680545.1 gg_id:511256 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6805
EU843073.1 gg_id:329796 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
GQ448611.1 gg_id:572743 Microbiome neonatal calves: shedding microorganisms fecal clone calf784_6wks_gr GQ448

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GQ492269.1 gg_id:587839 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
FJ682799.1 gg_id:526362 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6827
GQ448340.1 gg_id:545061 Microbiome neonatal calves: shedding microorganisms fecal clone calf783_2wks_gr GQ448
FJ674237.1 gg_id:516332 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6742
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EU344585.1 gg_id:277290 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU3445
EU459966.1 gg_id:292284 Prevost's squirrel feces clone SQ_aah82a11 EU4599
AY983899.1 gg_id:116299 human descending colon mucosal biopsy clone MA96 AY9838
AB009236.1 gg_id:2128 rumen clone RFN9 bacterium AB0092
FJ678725.1 gg_id:523005 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6787
FJ674139.1 gg_id:523308 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6741
FJ681767.1 gg_id:526763 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6817
GQ491722.1 gg_id:579740 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
FJ825149.1 gg_id:546934 Prevotella genomosp. T1 str. D033B-12-2 FJ8251
EU473721.1 gg_id:290880 douc langur feces clone DL_2aaa03h08 EU4737
EU777602.1 gg_id:342638 Sumatran orangutan feces clone orang1_aai53g06 EU7776
FJ673613.1 gg_id:523947 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6736
EU459973.1 gg_id:301649 Prevost's squirrel feces clone SQ_aah82b10 EU4599
DQ797212.1 gg_id:189542 human fecal clone RL386_aao88d09 DQ797
EU532001.1 gg_id:275566 Predominant role host genetics controlling gut microbiota FMF remission stool clone EU5320
FJ673603.1 gg_id:517360 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6736
FJ676526.1 gg_id:518330 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6765
EU344676.1 gg_id:273149 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU3446
FJ684906.1 gg_id:524143 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6849
FJ683408.1 gg_id:514719 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6834
EU871373.1 gg_id:307197 Genetic Bovine (Bos taurus) Rumen Thailand clone CF192 EU8713
EU850476.1 gg_id:328246 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF64 EU8504
AY028443.1 gg_id:70217 mpn-isolate group 2 AY0284
EU842796.1 gg_id:346503 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU8427
FJ557915.1 gg_id:517411 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5579
EU773693.1 gg_id:346189 Capybara feces clone CAP_aai00e05 EU7736
FJ685108.1 gg_id:516580 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6851
GQ492062.1 gg_id:589329 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
EU344418.1 gg_id:264746 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU3444
DQ797162.1 gg_id:198733 human fecal clone RL386_aao87g05 DQ797
FJ684477.1 gg_id:515660 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6844
FJ685323.1 gg_id:524619 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6853
GQ073309.1 gg_id:441328 Topographical and Temporal Human Skin Microbiome skin palm clone nbw207e09c1 GQ073
EU381895.1 gg_id:261646 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU3818
AB278593.1 gg_id:192814 Prevotella pleuritidis str. JCM 14110 AB2785

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AB009187.1 gg_id:2074 rumen clone RFN29 bacterium AB009
GQ493694.1 gg_id:583126 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
FJ673887.1 gg_id:528706 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6738
DQ113737.1 gg_id:132480 dog colon clone C5-17 DQ113
FJ683202.1 gg_id:532413 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6832
FJ673229.1 gg_id:523833 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6732
FJ678986.1 gg_id:517816 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6789
AY976458.1 gg_id:124114 human ascending colon mucosal biopsy clone LZ62 AY9764
EU777604.1 gg_id:326108 Sumatran orangutan feces clone orang1_aai53c03 EU777
AY981014.1 gg_id:126778 human rectum mucosal biopsy clone V184 AY981
FJ682579.1 gg_id:523551 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6825
AF001759.1 gg_id:2118 rumen clone RF27 AF001
EU463171.1 gg_id:303058 naked mole-rat feces clone molerat_aai71a10 EU463
EU844794.1 gg_id:332263 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
FJ978771.1 gg_id:436201 feces clone CL_F_479 FJ9787
EU774243.1 gg_id:319679 Chimpanzee feces clone CHIMP1_aaj38d06 EU774
NZ_ACKS01000100.1 gg_id:470823 Prevotella bergensis str. DSM 17361 NZ_AC
GU303916.1 gg_id:532681 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU303
AB269970.1 gg_id:170418 Influence temperature and humidity on heifers rumen contents Holstein heifer (Bos AB269
FJ673304.1 gg_id:526031 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6733
EU774217.1 gg_id:342890 Chimpanzee feces clone CHIMP1_b03 EU774
FJ673265.1 gg_id:530447 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6732
EU467085.1 gg_id:291677 mongoose lemur feces clone ML_aae87f09 EU467
FJ682897.1 gg_id:516731 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6828
GQ493224.1 gg_id:582888 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
FJ684189.1 gg_id:519697 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6841
EU773408.1 gg_id:356625 Black lemur feces clone BKLE_e03_2 EU773
EU778865.1 gg_id:347831 Black-handed Spider Monkey feces clone SPIM_c03 EU778
FJ675931.1 gg_id:529907 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6759
AB477014.2 gg_id:528418 Prevotella dentasini str. NUM 1903 AB477
FJ684108.1 gg_id:511379 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6841
DQ797074.1 gg_id:197763 human fecal clone RL386_aao86f07 DQ797
FJ673773.1 gg_id:519762 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6737
FJ673620.1 gg_id:521737 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6736
EU467225.1 gg_id:300603 black-handed spider monkey feces clone SPIM_g12 EU467
EU778888.1 gg_id:339561 Black-handed Spider Monkey feces clone SPIM_c02 EU778
FJ681726.1 gg_id:509358 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6817
FJ682972.1 gg_id:521760 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6829
GQ101478.1 gg_id:457738 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw495f GQ101
EU473086.1 gg_id:293009 douc langur feces clone DL_1aaa02f01 EU473

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EU845194.1 gg_id:335548 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU845
FJ679778.1 gg_id:528866 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6797
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GQ493811.1 gg_id:556757 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
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FJ681232.1 gg_id:530653 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6812
FJ364421.1 gg_id:357005 feces adult twins and mothers; TS15 clone TS15_a02g04 FJ3644
FJ172820.1 gg_id:312373 Qinghai Yak Ruminal and Fungi China rumen clone RB-5B5 FJ1728
AF132249.1 gg_id:72142 adult human fecal matter clone adhufec235 AF1322
FJ681368.1 gg_id:510300 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6813
DQ801321.1 gg_id:194164 human fecal clone RL388_aao93h08 DQ801
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FJ680901.1 gg_id:511091 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6809
DQ801556.1 gg_id:181943 human fecal clone RL117_aae91a12 DQ801
FJ674135.1 gg_id:524891 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6741
DQ797023.1 gg_id:188921 human fecal clone RL386_aao85h09 DQ797
FJ683138.1 gg_id:515532 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6831
AF371875.1 gg_id:24907 swine intestine clone p-2190-s959-3 AF3718
FJ673391.1 gg_id:530487 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6733
FJ680203.1 gg_id:518851 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6802
FJ678765.1 gg_id:517558 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6787
AF018480.1 gg_id:2142 rumen clone 12-101 AF0184
AY244930.1 gg_id:100068 cow rumen clone BE13 AY2449
DQ456110.1 gg_id:157597 pre-adolescent turkey cecum clone CFT114E7 DQ456
FJ674173.1 gg_id:524836 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6741
FJ683154.1 gg_id:516852 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6831
FJ684879.1 gg_id:525835 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6848
FJ028800.1 gg_id:567752 Microbial Taiwan water buffalo rumen fluid clone TWBRB87 FJ0288
DQ795861.1 gg_id:178434 human fecal clone RL245_aai83e09 DQ795
FJ558443.1 gg_id:518217 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5584
DQ796011.1 gg_id:196481 human fecal clone RL202_aai50c04 DQ796
EU871377.1 gg_id:322023 Genetic Bovine (Bos taurus) Rumen Thailand clone CF199 EU871
EU778079.1 gg_id:316570 feces clone RL388_aao93f04 EU778
FJ678203.1 gg_id:509498 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6782
EU467097.1 gg_id:288393 mongoose lemur feces clone ML_aae88b06 EU467

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EU459941.1 gg_id:300536 Prevost's squirrel feces clone SQ_aah81f03 EU459
EU459830.1 gg_id:294537 Prevost's squirrel feces clone SQ_aah79f05 EU459
GQ897764.1 gg_id:585756 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ897
EU778293.1 gg_id:325046 feces clone RL388_aao96b06 EU778
EU458706.1 gg_id:296262 Goeldi's marmoset feces clone CAL_f10 EU458
FJ679626.1 gg_id:524036 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6796
EU461627.1 gg_id:296932 mongoose lemur feces clone ML_aaj25g09 EU461
FJ675967.1 gg_id:515381 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6759
EU473861.1 gg_id:292246 douc langur feces clone DL_2aaa02g03 EU473
FJ685261.1 gg_id:514444 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6852
GQ047279.1 gg_id:377975 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1010h GQ047
FJ683431.1 gg_id:520737 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6834
AY244912.1 gg_id:83758 cow rumen clone BF34 AY244
AJ315483.1 gg_id:26715 human colonic sample clone AJ3154
AY977626.1 gg_id:124820 human cecum mucosal biopsy clone LC71 AY977
GQ491841.1 gg_id:538267 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
DQ801569.1 gg_id:192124 human fecal clone RL117_aae91f01 DQ801
FJ681522.1 gg_id:532396 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6815
GQ433639.1 gg_id:577211 Prevotella sp. str. WAL 2039G GQ433
EU531920.1 gg_id:259433 Predominant role host genetics controlling gut microbiota FMF remission stool clone EU531
GQ030288.1 gg_id:463032 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw876a GQ030
GQ422744.1 gg_id:532929 Prevotella sp. oral taxon 781 str. F0055 GQ422
EU459927.1 gg_id:299240 Prevost's squirrel feces clone SQ_aah81d02 EU459
FJ364568.1 gg_id:360096 feces adult twins and mothers; TS15 clone TS15_a04e03 FJ3645
FJ684510.1 gg_id:517196 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6845
EU469364.1 gg_id:293011 black lemur feces clone BKLE_b11 EU469
FJ684867.1 gg_id:523851 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6848
FJ673336.1 gg_id:515720 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6733
FJ685365.1 gg_id:511813 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6853
EU462253.1 gg_id:294521 chimpanzee feces clone CHIMP1_aaj38e05 EU462
AM420262.1 gg_id:236167 Noma subgingival plaque clone 701G08(oral) AM420
EF510678.1 gg_id:224575 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aerug EF5106
FJ557727.1 gg_id:521268 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5577
FJ673253.1 gg_id:511743 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6732
EU462056.1 gg_id:293402 black-handed spider monkey feces clone SPIM_aaj34a11 EU462
FJ675551.1 gg_id:531487 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6755
FJ684653.1 gg_id:528818 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6846
FJ680910.1 gg_id:518747 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6809
GU303995.1 gg_id:542145 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU303
AY982518.1 gg_id:117749 human sigmoid colon mucosal biopsy clone MN41 AY982
FJ674199.1 gg_id:527095 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6741

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EU472622.1 gg_id:294714 Angola colobus feces clone EAC_2_aaa02c04 EU472
FJ681868.1 gg_id:530508 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6818
FJ683006.1 gg_id:516303 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6830
EU850571.1 gg_id:339973 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF383 EU850
FJ364385.1 gg_id:357152 feces adult twins and mothers; TS15 clone TS15_a02c08 FJ3643
EU850455.1 gg_id:313890 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF24 EU850
EU473048.1 gg_id:292699 douc langur feces clone DL_1aaa03e11 EU473
FJ557945.1 gg_id:521803 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5579
FJ365334.1 gg_id:364193 feces adult twins and mothers; TS20 clone TS20_a01f07 FJ3653
EU773458.1 gg_id:321145 Black lemur feces clone BKLE_e03_3 EU773
FJ673184.1 gg_id:524964 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6731
GQ493590.1 gg_id:564755 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
FJ365512.1 gg_id:362089 feces adult twins and mothers; TS20 clone TS20_a03g02 FJ3655
AY977674.1 gg_id:117761 human cecum mucosal biopsy clone LD28 AY977
EU381854.1 gg_id:271680 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU381
FJ684203.1 gg_id:519003 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6842
EU777028.1 gg_id:323411 Naked mole-rat feces clone molerat_aai72d04 EU777
FJ683074.1 gg_id:509587 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6830
DQ796936.1 gg_id:185170 human fecal clone RL179_aao56f06 DQ796
FJ682022.1 gg_id:511530 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6820
EU462168.1 gg_id:296780 black-handed spider monkey feces clone SPIM_aaj36c09 EU462
FJ680885.1 gg_id:527286 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6808
EF096023.1 gg_id:190522 mouse cecum clone lean2_aaa02c05 EF096
GQ402129.1 gg_id:584509 alpacas and sheep forestomach clone ALP23 GQ402
EF096104.1 gg_id:180524 mouse cecum clone lean2_aaa04c04 EF0961
FJ673318.1 gg_id:517304 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6733
FJ685049.1 gg_id:512224 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6850
EU473854.1 gg_id:292234 douc langur feces clone DL_2aaa04b06 EU473
AY244933.1 gg_id:86315 cow rumen clone BE15 AY244
FJ674171.1 gg_id:510530 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6741
GQ422745.1 gg_id:570119 Prevotella sp. oral taxon 782 str. F0012 GQ422
FJ363234.1 gg_id:366561 feces adult twins and mothers; TS148 clone TS148_a04g10 FJ3632
DQ794918.1 gg_id:191249 human fecal clone RL310_aam37h08 DQ794
AY980875.1 gg_id:116049 human rectum mucosal biopsy clone LQ01 AY980
EU462285.1 gg_id:302389 chimpanzee feces clone CHIMP1_aaj39c08 EU462
GQ492017.1 gg_id:581481 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
AB270138.1 gg_id:168429 Influence temperature and humidity on heifers rumen contents Holstein heifer (Bos AB270
FJ683497.1 gg_id:511597 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6834
AY349394.1 gg_id:92629 human oral cavity clone FW035 AY349
FJ558099.1 gg_id:521761 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5580
FJ673305.1 gg_id:524963 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6733

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AF153866.1 gg_id:2190 faecal clone adhufec41.25 AF153
EU462594.1 gg_id:297847 Sumatran orangutan feces clone orang2_aai65g11 EU462
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FJ682169.1 gg_id:517050 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6821
FJ684805.1 gg_id:531509 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6848
FJ674182.1 gg_id:528488 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6741
EU381939.1 gg_id:259544 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU381
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EU462333.1 gg_id:299235 chimpanzee feces clone CHIMP1_aaj40c12 EU462
EU462125.1 gg_id:298189 black-handed spider monkey feces clone SPIM_aaj35d03 EU462
FJ673154.1 gg_id:512933 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6731
EU467184.1 gg_id:298007 white-faced saki feces clone Saki_c01 EU467
EU776856.1 gg_id:313152 Mongoose lemur feces clone ML_aaj27h04 EU776
FJ684967.1 gg_id:523945 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6849
FJ363033.1 gg_id:368725 feces adult twins and mothers; TS148 clone TS148_a02b08 FJ3630
AY976024.1 gg_id:117319 human ascending colon mucosal biopsy clone LT70 AY976
EU381986.1 gg_id:260514 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU381
FJ684292.1 gg_id:515980 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6842
FJ364562.1 gg_id:357744 feces adult twins and mothers; TS15 clone TS15_a04d08 FJ3645
AB034103.1 gg_id:31669 rumen clone 4C3d-5 AB034
FJ684836.1 gg_id:521597 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6848
EU467230.1 gg_id:289953 black-handed spider monkey feces clone SPIM_a09 EU467
FJ673684.1 gg_id:519820 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6736
DQ801406.1 gg_id:175562 human fecal clone RL388_aao95b04 DQ801
GQ493827.1 gg_id:550372 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
FJ677459.1 gg_id:527153 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6774
FJ364488.1 gg_id:366536 feces adult twins and mothers; TS15 clone TS15_a03e09 FJ3644
AB269982.1 gg_id:165485 Influence temperature and humidity on heifers rumen contents Holstein heifer (Bos AB269
FJ685211.1 gg_id:521837 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6852
AF414822.1 gg_id:70907 Prevotella intermedia str. 5-PIN AF414
AB009225.1 gg_id:2079 rumen clone RFN78 bacterium AB009
FJ364288.1 gg_id:364886 feces adult twins and mothers; TS15 clone TS15_a01b09 FJ3642
AY944134.1 gg_id:114813 Prevotella genomosp. P4 str. P4P_53 AY944
FJ685000.1 gg_id:512387 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6850
EU462169.1 gg_id:297270 black-handed spider monkey feces clone SPIM_aaj36d01 EU462
AB185513.1 gg_id:107586 rumen clone F23-A10 AB185
FJ673935.1 gg_id:531755 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6739
AY980608.1 gg_id:116069 human rectum mucosal biopsy clone LK41 AY980

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EU382007.1 gg_id:270749 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU382
EU462051.1 gg_id:291409 black-handed spider monkey feces clone SPIM_aaj34a03 EU462
EU462357.1 gg_id:287476 chimpanzee feces clone CHIMP1_aaj40h06 EU462
FJ684936.1 gg_id:523487 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6849
EU794130.1 gg_id:343453 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_B15 EU794
FJ685499.1 gg_id:525684 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6854
GU303863.1 gg_id:576321 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU303
FJ678990.1 gg_id:531015 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6789
FJ558006.1 gg_id:524930 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5580
EF510785.1 gg_id:221716 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aerug EF5107
AY244942.1 gg_id:82965 cow rumen clone BE28 AY244
DQ113761.1 gg_id:130336 dog ileum clone I8-18 DQ113
AY323522.1 gg_id:89232 Prevotella oralis str. ATCC 33269 AY323
FJ880100.1 gg_id:432904 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8801
AJ011683.1 gg_id:2200 Prevotella albensis str. M384 AJ0116
DQ795952.1 gg_id:196360 human fecal clone RL202_aai49d04 DQ795
FJ676816.1 gg_id:523904 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6768
EU776890.1 gg_id:327728 Mongoose lemur feces clone ML_aaj26a07 EU776
FJ682269.1 gg_id:518097 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6822
EU461706.1 gg_id:294811 mongoose lemur feces clone ML_aaj27e01 EU461
EU531921.1 gg_id:270686 Predominant role host genetics controlling gut microbiota FMF remission stool clone EU531
AF385509.1 gg_id:70671 tongue dorsa clone DO014 AF385
FJ684180.1 gg_id:531562 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6841
FJ685141.1 gg_id:514801 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6851
EF510841.1 gg_id:224824 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aerug EF5108
FJ364461.1 gg_id:368482 feces adult twins and mothers; TS15 clone TS15_a03c04 FJ3644
EU461648.1 gg_id:298929 mongoose lemur feces clone ML_aaj26c05 EU461
GQ491758.1 gg_id:590857 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
EF510440.1 gg_id:218082 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aerug EF5104
FJ681717.1 gg_id:511017 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6817
GQ491904.1 gg_id:567987 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
FJ674037.1 gg_id:530649 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6740
EU344275.1 gg_id:260187 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU344
FJ677005.1 gg_id:523019 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6770
EU475262.1 gg_id:299882 bonobo feces clone BNO_aaa03c06 EU475
FJ557663.1 gg_id:525105 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5576
FJ680794.1 gg_id:517921 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6807
FJ673656.1 gg_id:513815 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6736
GQ010629.1 gg_id:499036 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ010
FJ028784.1 gg_id:510871 Microbial Taiwan water buffalo rumen fluid clone TWBRB69 FJ0287

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FJ677433.1 gg_id:519738 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6774
EU778264.1 gg_id:304166 feces clone RL388_aao96b11 EU778
FJ678298.1 gg_id:526911 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6782
FJ683687.1 gg_id:517784 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6836
GQ491551.1 gg_id:570360 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
DQ797060.1 gg_id:176028 human fecal clone RL386_aao86d10 DQ797
GQ493297.1 gg_id:536652 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
GQ491577.1 gg_id:577157 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
EU473009.1 gg_id:300879 douc langur feces clone DL_1aaa03d07 EU473
EU778133.1 gg_id:337656 feces clone RL117_aae91e03 EU778
FJ684992.1 gg_id:519598 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6849
AY982422.1 gg_id:118345 human sigmoid colon mucosal biopsy clone ML25 AY9824
FJ673340.1 gg_id:526514 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6733
EU475054.1 gg_id:295322 visayam warty pig feces clone VWP_aaa04a01 EU475
EU871406.1 gg_id:351650 Genetic Bovine (Bos taurus) Rumen Thailand clone CF367 EU8714
EU467067.1 gg_id:296772 mongoose lemur feces clone ML_aae87a02 EU467
AF001708.1 gg_id:2172 rumen clone RC17 AF0017
DQ794897.1 gg_id:197293 human fecal clone RL310_aam37f10 DQ794
FJ683479.1 gg_id:514486 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6834
AB009178.1 gg_id:2124 rumen clone RFN19 AB009
AY978052.1 gg_id:115991 human cecum mucosal biopsy clone LI04 AY978
GU303838.1 gg_id:534756 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU303
CU926909.1 gg_id:558189 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU926
FJ678284.1 gg_id:525581 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6782
GQ493375.1 gg_id:592705 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
EU468932.1 gg_id:290509 Speke's gazelle feces clone SP2_d12_1 EU468
FJ675854.1 gg_id:525223 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6758
FJ674162.1 gg_id:530021 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6741
DQ794878.1 gg_id:189711 human fecal clone RL310_aam37d12 DQ794
AB270080.1 gg_id:163689 Influence temperature and humidity on heifers rumen contents Holstein heifer (Bos AB270
EU843355.1 gg_id:336569 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
EU469846.1 gg_id:294896 western lowland gorilla feces clone GOR_aag72d07 EU469
EU467431.1 gg_id:295620 chimpanzee feces clone CHIMP12_g01 EU467
FJ577255.2 gg_id:588912 Prevotella sp. oral taxon 317 str. F0108 FJ5772
FJ365600.1 gg_id:364196 feces adult twins and mothers; TS20 clone TS20_a04g08 FJ3656
FJ684735.1 gg_id:517701 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6847
DQ795814.1 gg_id:185522 human fecal clone RL245_aai82g09 DQ795
EU850541.1 gg_id:326121 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF335 EU850
FJ673386.1 gg_id:510064 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6733
FJ681684.1 gg_id:526867 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6816

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GQ491516.1 gg_id:582363 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
DQ797245.1 gg_id:197149 human fecal clone RL386_aao88h03 DQ797
EU344463.1 gg_id:266559 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU344
EU461321.1 gg_id:302729 red kangaroo feces clone KO2_aai17a11 EU461
FJ683039.1 gg_id:523539 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6830
FJ680423.1 gg_id:529428 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6804
DQ801086.1 gg_id:192723 human fecal clone RL387_aao91h11 DQ801
EU461617.1 gg_id:288217 mongoose lemur feces clone ML_aaj25f05 EU461
EU473029.1 gg_id:288876 douc langur feces clone DL_1aaa02c09 EU473
FJ681266.1 gg_id:519342 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6812
FJ684520.1 gg_id:521258 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6845
EU773471.1 gg_id:318181 Bonobo feces clone BNO_aaa02b05 EU773
EU381791.1 gg_id:262164 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU381
GQ054111.1 gg_id:429229 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1098g GQ054
AB185521.1 gg_id:103448 rumen clone F23-B08 AB185
FJ365568.1 gg_id:360196 feces adult twins and mothers; TS20 clone TS20_a04d07 FJ3655
EU461697.1 gg_id:300106 mongoose lemur feces clone ML_aaj27c11 EU461
FJ681358.1 gg_id:517926 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6813
DQ796007.1 gg_id:193455 human fecal clone RL202_aai50b11 DQ796
FJ792538.1 gg_id:535359 Prevotella melaninogenica str. ATCC 43982 FJ7925
FJ676936.1 gg_id:519070 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6769
AY916271.1 gg_id:113370 human rectum biopsy clone N064 AY916
EU381908.1 gg_id:276131 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU381
FJ557682.1 gg_id:529630 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5576
EU773685.1 gg_id:312051 Capybara feces clone CAP_aah97b02 EU773
FJ365308.1 gg_id:361498 feces adult twins and mothers; TS20 clone TS20_a01d03 FJ3653
EU469497.1 gg_id:295421 black lemur feces clone BKLE_h09_2 EU469
AB009235.1 gg_id:2080 rumen clone RFN89 bacterium AB009
GU302844.1 gg_id:575618 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU302
EU794188.1 gg_id:321621 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_D02 EU794
EU462042.1 gg_id:301550 black-handed spider monkey feces clone SPIM_aaj33g10 EU462
FJ364538.1 gg_id:361284 feces adult twins and mothers; TS15 clone TS15_a04b06 FJ3645
DQ795899.1 gg_id:191319 human fecal clone RL245_aai84c09 DQ795
EU776846.1 gg_id:343094 Mongoose lemur feces clone ML_aaj26g04 EU776
FJ679787.1 gg_id:515802 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6797
AY982452.1 gg_id:117045 human sigmoid colon mucosal biopsy clone ML81 AY982
EU461621.1 gg_id:295934 mongoose lemur feces clone ML_aaj25f12 EU461
EU773517.1 gg_id:354322 Bonobo feces clone BNO_aaa02g04 EU773
EU778818.1 gg_id:336258 Black-handed Spider Monkey feces clone SPIM_aaj33e11 EU778
EU472955.1 gg_id:295175 douc langur feces clone DL_1aaa03d10 EU472

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AY323524.1 gg_id:88701 Prevotella denticola str. ATCC 35308 AY3235
EU469385.1 gg_id:295406 black lemur feces clone BKLE_g01 EU4693
FJ673578.1 gg_id:527874 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6735
GQ402133.1 gg_id:562683 alpacas and sheep forestomach clone ALP25 GQ402
EU531893.1 gg_id:274980 Predominant role host genetics controlling gut microbiota FMF remission stool clone EU5318
EU850503.1 gg_id:311462 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF273 EU8505
FJ684973.1 gg_id:520181 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6849
FJ680670.1 gg_id:509720 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6806
FJ363100.1 gg_id:370036 feces adult twins and mothers; TS148 clone TS148_a03a10 FJ3631
AY992930.1 gg_id:135660 mouse cecum clone C22_j09 AY9929
FJ684658.1 gg_id:517908 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6846
AF371884.1 gg_id:42406 swine intestine clone p-185-o5 AF3718
FJ028751.1 gg_id:552400 Microbial Taiwan water buffalo rumen fluid clone TWBRB27 FJ0287
AY984123.1 gg_id:122625 human descending colon mucosal biopsy clone MF93 AY9841
GQ493958.1 gg_id:568261 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
FJ673365.1 gg_id:510239 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6733
FJ676140.1 gg_id:520810 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6761
FJ680416.1 gg_id:509703 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6804
FJ682033.1 gg_id:518528 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6820
EU842487.1 gg_id:351813 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU8424
EU842548.1 gg_id:326333 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU8425
FJ681995.1 gg_id:522422 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6819
FJ679583.1 gg_id:528902 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6795
FJ676423.1 gg_id:523360 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6764
FJ681009.1 gg_id:525734 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6810
EF510457.1 gg_id:226400 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aerug EF5104
FJ675976.1 gg_id:509430 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6759
EU461709.1 gg_id:292318 mongoose lemur feces clone ML_aaj27e04 EU4617
FJ685142.1 gg_id:514269 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6851
EU469532.1 gg_id:298360 black lemur feces clone BKLE_f09_3 EU4695
GQ493814.1 gg_id:592612 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
DQ278861.1 gg_id:154641 Prevotella sp. 152R-1a DQ278
FJ678573.1 gg_id:526174 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6785
AY983829.1 gg_id:119916 human descending colon mucosal biopsy clone M919 AY9838
GQ038538.1 gg_id:412937 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu4 GQ038
FJ684244.1 gg_id:513431 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6842
EU531891.1 gg_id:276145 Predominant role host genetics controlling gut microbiota FMF remission stool clone EU5318
FJ673624.1 gg_id:513335 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6736
DQ796978.1 gg_id:195574 human fecal clone RL386_aao85c07 DQ796
EU773521.1 gg_id:340253 Bonobo feces clone BNO_aaa02c12 EU7735

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FJ172825.1 gg_id:337278 Qinghai Yak Ruminal and Fungi China rumen clone RB-5E1 FJ1728
EU779070.1 gg_id:331015 Prevost's squirrel feces clone SQ_aah79c10 EU779
AB264070.1 gg_id:196997 Fecal microbial (dugong dugon) determined genes Dugong feces clone dgD-75 AB264
EU773564.1 gg_id:354491 Goeldi's Marmoset feces clone CAL_g07_1 EU773
EU778855.1 gg_id:305145 Black-handed Spider Monkey feces clone SPIM_a10 EU778
DQ797036.1 gg_id:188089 human fecal clone RL386_aao86b06 DQ797
FJ683399.1 gg_id:513249 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6833
EU774602.1 gg_id:328946 Douc langur feces clone DL_1aaa01f04 EU774
FJ683172.1 gg_id:514517 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6831
FJ685379.1 gg_id:515705 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6853
EF096662.1 gg_id:198204 mouse cecum clone SWPT11_aaa02g08 EF0966
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AF371896.1 gg_id:45645 swine intestine clone p-1933-s962-3 AF371
EF436315.1 gg_id:213152 library-based ruminal water buffalo (Bubalus bubalis) rumen fluid clone BRC29 EF4363
GQ074351.1 gg_id:438260 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw161h GQ074
EU467104.1 gg_id:288753 mongoose lemur feces clone ML_aae88c11 EU467
FJ364571.1 gg_id:364967 feces adult twins and mothers; TS15 clone TS15_a04e06 FJ3645
AY244928.1 gg_id:86283 cow rumen clone BE11 AY244
GQ491858.1 gg_id:576234 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
FJ684133.1 gg_id:516225 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6841
EU381758.1 gg_id:267845 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU381
EU778194.1 gg_id:351168 feces clone RL117_aae92b12 EU778
FJ685436.1 gg_id:521152 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6854
GQ073116.1 gg_id:415792 Topographical and Temporal Human Skin Microbiome skin palm clone nbw205c07c1 GQ073
FJ674116.1 gg_id:529679 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6741
FJ673357.1 gg_id:521841 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6733
FJ676939.1 gg_id:520450 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6769
FJ676966.1 gg_id:519529 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6769
FJ679668.1 gg_id:530373 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6796
AF218619.1 gg_id:69910 Prevotella ruminicola str. TC2-28 AF218
FJ684336.1 gg_id:509425 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6843
EU531867.1 gg_id:269138 Predominant role host genetics controlling gut microbiota FMF remission stool clone EU531
FJ673775.1 gg_id:531273 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6737
EU774268.1 gg_id:335697 Chimpanzee feces clone CHIMP1_aaj40g11 EU774
FJ685256.1 gg_id:523620 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6852
AY244914.1 gg_id:82967 cow rumen clone BF36 AY244
EU473005.1 gg_id:296243 douc langur feces clone DL_1aaa02e07 EU473
FJ684814.1 gg_id:528993 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6848
FJ684515.1 gg_id:525810 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6845
FJ673375.1 gg_id:523090 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6733

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FJ681799.1 gg_id:520235 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6817
AB009191.1 gg_id:2174 rumen clone RFN35 bacterium AB009
GQ493040.1 gg_id:543667 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
FJ683495.1 gg_id:523862 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6834
EU461634.1 gg_id:300957 mongoose lemur feces clone ML_aaj25h12 EU461
EU777984.1 gg_id:304278 Rock hyrax feces clone RHSD_aaa01h11_1 EU777
FJ682963.1 gg_id:525654 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6829
GQ448332.1 gg_id:585048 Microbiome neonatal calves: shedding microorganisms fecal clone calf783_2wks_gr GQ448
FJ684257.1 gg_id:530209 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6842
EU472972.1 gg_id:287921 douc langur feces clone DL_1aaa04f11 EU472
EU469531.1 gg_id:293939 black lemur feces clone BKLE_f08_2 EU469
GQ492787.1 gg_id:563840 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
AJ005635.1 gg_id:2181 Prevotella enoeca str. ATCC 51261 AJ0056
EU843354.1 gg_id:334051 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
EU461752.1 gg_id:301489 mongoose lemur feces clone ML_aaj28c05 EU461
FJ363067.1 gg_id:368969 feces adult twins and mothers; TS148 clone TS148_a02f01 FJ3630
EU774603.1 gg_id:353551 Douc langur feces clone DL_2aaa02f02 EU774
GU304031.1 gg_id:539999 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU304
FJ684484.1 gg_id:531065 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6844
EU467281.1 gg_id:298841 black-handed spider monkey feces clone SPIM_g05_2 EU467
GU303561.1 gg_id:541984 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU303
FJ370118.1 gg_id:362555 feces adult twins and mothers; TS55 clone TS55_a04f03 FJ3701
EU777261.1 gg_id:308029 Okapi feces clone OK3_h06_2 EU777
EU461552.1 gg_id:298770 black rhinoceros feces clone RH_aaj92c09 EU461
EU777995.1 gg_id:326540 Black rhinoceros feces clone RH_aaj91c03 EU777
EU475391.1 gg_id:293472 springbok feces clone SBSD_aaa04f08 EU475
AB034021.1 gg_id:34809 rumen clone 4C0d-8 AB034
EU463261.1 gg_id:295357 naked mole-rat feces clone molerat_aai72e06 EU463
EU871385.1 gg_id:304289 Genetic Bovine (Bos taurus) Rumen Thailand clone CF231 EU871
EU459498.1 gg_id:293135 capybara feces clone CAP_aah98e04 EU459
EU474589.1 gg_id:302013 bighorn sheep feces clone BHSD_aaa04a07 EU474
AB009211.1 gg_id:2201 rumen clone RFN64 bacterium AB009
AB331897.1 gg_id:362169 Paraprevotella xylaniphila str. YIT 11841 (= JCM 14860 = DSM 19 AB331
EU468730.1 gg_id:302334 okapi feces clone OK3_b01 EU468
EU773683.1 gg_id:347680 Capybara feces clone CAP_aah98f08 EU773
EU461370.1 gg_id:300691 red kangaroo feces clone KO2_aai19b05 EU461
EU462623.1 gg_id:299230 Sumatran orangutan feces clone orang2_aai66c05 EU462
FJ880903.1 gg_id:379362 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8809
AJ518874.1 gg_id:109956 Alistipes finegoldii str. ANH 2437 AJ5188
NZ_ABFK02000016.1 gg_id:469639 Alistipes putredinis str. DSM 17216 NZ_AB

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EU655882.1 gg_id:286948 influence dietary flavonoid-containing extracts on gut microbiota mouse feces clone EU655
AY979218.1 gg_id:122365 human transverse colon mucosal biopsy clone Z358 AY979
FJ680633.1 gg_id:518598 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6806
EU452123.1 gg_id:324193 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K79S EU452
AY643082.1 gg_id:128182 Alistipes finegoldii str. 4401054 AY643
EF098147.1 gg_id:185451 mouse cecum clone SWPT14_aaa02b11 EF0981
EU468718.1 gg_id:301755 okapi feces clone OK2_e10_2 EU468
EU456567.1 gg_id:320525 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K79S EU456
DQ456413.1 gg_id:158550 pre-adolescent turkey cecum clone CFT214G5 DQ456
AY992622.1 gg_id:135560 mouse cecum clone C23_l20 AY992
AY547271.1 gg_id:107044 Alistipes massiliensis str. 3302398 AY547
EU469334.1 gg_id:296168 springbok feces clone SBK_f08_1 EU469
EF603936.1 gg_id:227834 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF603
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EF096138.1 gg_id:175375 mouse cecum clone obob1_aaa01b08 EF0961
EU655761.1 gg_id:286907 influence dietary flavonoid-containing extracts on gut microbiota mouse feces clone EU655
EU453026.1 gg_id:329877 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H74 EU453
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EU456350.1 gg_id:319372 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K77S EU456
EU773364.1 gg_id:323400 BigHorn sheep feces clone BH1_aao27a03 EU773
EU655981.1 gg_id:286067 influence dietary flavonoid-containing extracts on gut microbiota mouse feces clone EU655
EU505566.1 gg_id:259196 cecal contents Mus musculus strain C57BL/6J; myd5 clone myd5_aaa02g06 EU505
EU455346.1 gg_id:316883 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83 EU455
DQ798086.1 gg_id:179688 human fecal clone RL302_aal95d02 DQ798
EU468557.1 gg_id:298464 okapi feces clone OK1_f10_1 EU468
EU655977.1 gg_id:283716 influence dietary flavonoid-containing extracts on gut microbiota mouse feces clone EU655
AJ518876.1 gg_id:104780 Bacteroides sp. str. DSM 12148 AJ5188
AY974072.1 gg_id:138006 Alistipes sp. WAL 8301 AY974
GQ043010.1 gg_id:396409 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1012a GQ043
EU655719.1 gg_id:282072 influence dietary flavonoid-containing extracts on gut microbiota mouse feces clone EU655
EU468653.1 gg_id:288382 okapi feces clone OK2_e11_1 EU468
EU468891.1 gg_id:296840 Speke's gazelle feces clone SP2_f11 EU468
GQ493426.1 gg_id:579595 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
AY993266.1 gg_id:129437 mouse cecum clone C21_l17 AY993
AY991744.1 gg_id:133452 mouse cecum clone C20_b22 AY991
AY991932.1 gg_id:133674 mouse cecum clone C20_l18 AY991
EU505322.1 gg_id:262704 cecal contents Mus musculus strain C57BL/6J; myd4 clone myd4_aaa02e02 EU505
DQ794029.1 gg_id:192724 human fecal clone RL176_aah46h06 DQ794
AY992915.1 gg_id:134775 mouse cecum clone C22_i11 AY992
EF402636.1 gg_id:213671 human fecal clone SJTU_B_10_51 EF402
FJ681251.1 gg_id:515059 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6812

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EU764925.1 gg_id:337670 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2 EU764
EF602837.1 gg_id:227692 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6028
EU453554.1 gg_id:317407 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N EU453
DQ815959.1 gg_id:173573 mouse cecum clone aab24g11 DQ815
EU452946.1 gg_id:316354 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU452
AY992841.1 gg_id:131061 mouse cecum clone C22_e18 AY992
EF603815.1 gg_id:256742 Salmonella enterica serovar typhimurium exploits inflammation compete intestinal m EF6038
FJ681306.1 gg_id:520462 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6813
EF099892.1 gg_id:198614 mouse cecum clone SWPT5_aaa01h03 EF0998
DQ800969.1 gg_id:197995 human fecal clone RL387_aao90b01 DQ800
EF100039.1 gg_id:190844 mouse cecum clone SWPT5_aaa03g11 EF100
EF096012.1 gg_id:194490 mouse cecum clone lean2_aaa01h09 EF096
EU656031.1 gg_id:284620 influence dietary flavonoid-containing extracts on gut microbiota mouse feces clone EU656
EU655858.1 gg_id:286968 influence dietary flavonoid-containing extracts on gut microbiota mouse feces clone EU655
EU452427.1 gg_id:322395 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU452
EU505657.1 gg_id:270391 cecal contents Mus musculus strain C57BL/6J; myd5 clone myd5_aaa04c04 EU505
EF603125.1 gg_id:230784 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6031
EU510227.1 gg_id:267812 cecal contents Mus musculus strain C57BL/6J; WD3 clone WD3_aak03c01 EU510
GQ031018.1 gg_id:465433 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ031
EF097211.1 gg_id:190026 mouse cecum clone SWPT18_aaa03b10 EF0972
AB234408.1 gg_id:149167 termite gut homogenate clone MgMjD-026 AB234
DQ307714.1 gg_id:143926 termite intestinal tract clone MTG-47 DQ307
GQ175524.1 gg_id:569030 Chicken intestinal microbiota modulations various feed supplementations DGGE and GQ175
EF400613.1 gg_id:205226 human fecal clone SJTU_E_15_74 EF4006
DQ307718.1 gg_id:144574 termite intestinal tract clone MTG-60 DQ307
EU655943.1 gg_id:282931 influence dietary flavonoid-containing extracts on gut microbiota mouse feces clone EU655
EU656070.1 gg_id:283288 influence dietary flavonoid-containing extracts on gut microbiota mouse feces clone EU656
EU009842.1 gg_id:251257 intestinal microbiota domestic and wild turkeys turkey cecum clone WTB_S10 EU0098
AB088945.1 gg_id:77794 termite gut homogenate clone Rs-F73 bacterium AB088
GQ175488.1 gg_id:512098 Chicken intestinal microbiota modulations various feed supplementations DGGE and GQ175
EU791148.1 gg_id:418501 Enteric Defensins are Essential Regulators Intestinal Microbial Ecology MMP7++ mou EU791
EU760448.1 gg_id:355301 Mouse fecal microbiota feces clone 3E1 EU760
EF401874.1 gg_id:211541 human fecal clone SJTU_D_11_42 EF4018
EU655844.1 gg_id:281630 influence dietary flavonoid-containing extracts on gut microbiota mouse feces clone EU655
DQ307715.1 gg_id:144995 termite intestinal tract clone MTG-56 DQ307
FJ374191.1 gg_id:366302 Inter- and intraspecific humivorous scarab beetle larvae (Pachnoda spp.) larval hindgu FJ3741
AB234412.1 gg_id:149950 termite gut homogenate clone MgMjD-045 AB234
AB234442.1 gg_id:150403 termite gut homogenate clone MgMjW-42 AB234
FJ362627.1 gg_id:362179 feces adult twins and mothers; TS13 clone TS13_a01c04 FJ3626
CU927011.1 gg_id:565304 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU927

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EU655868.1 gg_id:285292 influence dietary flavonoid-containing extracts on gut microbiota mouse feces clone EU6558
GQ175465.1 gg_id:569831 Chicken intestinal microbiota modulations various feed supplementations DGGE and GQ175
AB288900.1 gg_id:203209 termite gut homogenate clone BOf4-04 AB2889
AB234381.1 gg_id:147812 termite gut homogenate clone MgMjD-085 AB2343
AB234430.1 gg_id:145163 termite gut homogenate clone MgMjR-034 AB2344
DQ307694.1 gg_id:143794 termite intestinal tract clone MTG-1 DQ307
AB234413.1 gg_id:148704 termite gut homogenate clone MgMjD-055 AB2344
AB234444.1 gg_id:146402 termite gut homogenate clone MgMjW-65 AB2344
AB234440.1 gg_id:147387 termite gut homogenate clone MgMjW-41 AB2344
DQ307716.1 gg_id:144084 termite intestinal tract clone MTG-58 DQ307
DQ307722.1 gg_id:144258 termite intestinal tract clone MTG-85 DQ307
EU778281.1 gg_id:307742 feces clone RL117_aae92a01 EU7782
EF515393.1 gg_id:226691 Electricigen Enrichment MFC upf microbial fuel cell anode clone 23g10 EF5153
FJ825571.1 gg_id:562180 Microbial during start-up mesophilic biogas plant clone 43_BS5_8 FJ8255
EF436336.1 gg_id:212713 library-based ruminal water buffalo (Bubalus bubalis) rumen fluid clone BRC50 EF4363
EU771218.1 gg_id:352631 Asiatic elephant feces clone AE3_aaa01a05 EU7712
AY188307.1 gg_id:80463 marine? clone KD3-67 AY1883
GQ502510.1 gg_id:558040 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf2- GQ502
EU850557.1 gg_id:306219 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF365 EU8505
AM086105.1 gg_id:145424 Abundance and archaea mesotrophic Lake Kinneret lake profundal sediment clone AM086
CT574141.1 gg_id:152067 Evry municipal wastewater treatment plant clone 061A06_B_SD_P93 CT5741
EU358741.1 gg_id:310915 structure archaeal denaturing gel electrophoresis and sequencing mesophilic biogas EU3587
AB244308.1 gg_id:143645 Microbial mesophilic chemostat cultivation long-chain fatty acids-degrading methan AB2443
FM179909.1 gg_id:315021 Biogeochemical processes microbial Gullfaks and Tommeliten methane seeps (Nortl FM179
EU871403.1 gg_id:343959 Genetic Bovine (Bos taurus) Rumen Thailand clone CF343 EU8714
U81709.2 gg_id:1878 fluidized bed anaerobic digestor fed vinasses (waste wine distillery) clone vadinHA21 U81709
DQ330455.1 gg_id:159438 Guerrero Negro hypersaline microbial mat clone 062DZ68 DQ330
FJ484700.1 gg_id:535284 microbial autonomous rover world's deepest phreatic sinkhole wall biomat El Zacator FJ4847
EU662616.1 gg_id:592227 Productivity- Chemolithoautotrophically Based Sulfidic Karst Systems floating microb EU6626
AY838556.1 gg_id:109402 fruiting body Pleurotus eryngii clone PE01 AY8385
EU407205.1 gg_id:258955 household biogas digester clone GW-20 EU4072
CT573994.1 gg_id:154079 Evry municipal wastewater treatment plant clone 009A01_B_SD_P15 CT5739
DQ395033.1 gg_id:151832 harbor sediment clone VHS-B5-15 DQ395
EF454472.2 gg_id:219599 termite hindgut clone 290cost002-P3L-2184 EF4544
FJ230923.1 gg_id:329546 under Level Antibiotic Selection Pressures river water clone F12 FJ2309
AJ534684.1 gg_id:75921 ground water deep-well injection disposal site radioactive wastes Tomsk-7 clone S15A AJ5346
GQ377114.1 gg_id:590965 structure two reactive PCE degrading enrichment s stimulated OU Duck Pond Norm GQ377
FJ437992.1 gg_id:548813 Benthic okenone production Fayetteville New York Green Lake surface sediments 16. FJ4379
CT574155.1 gg_id:152565 Evry municipal wastewater treatment plant clone 060G05_B_SD_P93 CT5741
CT573934.1 gg_id:154809 Evry municipal wastewater treatment plant clone 012A08_B_SD_P15 CT5739

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AM162485.1 gg_id:151096 and situ identification acidic sphagnum peat bog clone B114 AM162
AY571426.1 gg_id:114648 termite gut clone RsaHf415 AY5714
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AJ431253.1 gg_id:107777 Cytophaga sp. str. Dex80-37 AJ4312
AY188300.1 gg_id:80683 marine? clone KD2-33 AY1883
AB088921.1 gg_id:77751 termite gut homogenate clone Rs-E47 bacterium AB0889
AY216454.1 gg_id:81597 temperate estuarine mud clone KM66 AY2164
EU475307.1 gg_id:299959 rock hyrax feces clone RHSD_aaa03e02 EU4753
CT574192.1 gg_id:151076 Evry municipal wastewater treatment plant clone 060C01_B_SD_P93 CT5741
FJ901804.1 gg_id:584556 phreatic limestone sinkholes northeastern Mexico water column surface cenote La Pa FJ9018
DQ206420.1 gg_id:150564 Sulfide oxidation coupled arsenate reduction microbial soda lake water clone ML-S-1 DQ206
EF648025.1 gg_id:241699 dynamics during produced water treatment aerobic activated sludge clone HB14 EF6480
AB255913.1 gg_id:165659 Localization Cell Morphologies Members Candidate TG3 and Subphylum Phylum Fibr AB2559
FJ712490.1 gg_id:518764 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) k FJ7124
CU922535.1 gg_id:537422 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU9225
EF648023.1 gg_id:242143 dynamics during produced water treatment aerobic activated sludge clone HB12 EF6480

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AB447626.1 gg_id:587106 Microbial Structure and Dynamics Granules Expanded Granular Sludge Bed (EGSB) R AB447
EU778007.1 gg_id:340733 Black rhinoceros feces clone RH_aaj91g09 EU778
AB234373.1 gg_id:148765 termite gut homogenate clone MgMjD-040 AB234
GU196223.1 gg_id:593277 Bioaugmentation improved recovery digesters after toxicant exposure lab-scale ana GU196
AB288897.1 gg_id:202388 termite gut homogenate clone BOf3-20 AB288
EU381867.1 gg_id:274261 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU381
EF648053.1 gg_id:248589 dynamics during produced water treatment aerobic activated sludge clone HB45 EF648
EU461561.1 gg_id:296651 black rhinoceros feces clone RH_aaj92e07 EU461
EU461511.1 gg_id:301495 black rhinoceros feces clone RH_aaj91c11 EU461
FJ437917.1 gg_id:564635 Benthic okenone production Fayetteville New York Green Lake 25 m water depth clo FJ4379
AY548930.1 gg_id:99570 ANAMMOX sludge clone 1-1 AY548
EF562574.1 gg_id:239593 stable microbial consortia capable degrading complex organic matter paper pulp colu EF5625
AF449768.1 gg_id:80791 CFB group clone ML1228J-9 AF449
EU777479.1 gg_id:350728 Sumatran orangutan feces clone orang1_aai53c10 EU777
AB530243.1 gg_id:570855 Monitoring Suez and Tokyo bays based on analyses marine sediment clone Tokyo..B AB530
AJ306736.1 gg_id:66951 DCP-dechlorinating consortium clone SHA-5 AJ3067
EU459441.1 gg_id:297220 capybara feces clone CAP_aah97a09 EU459
AJ488097.1 gg_id:66167 chlorobenzene-degrading consortium clone IIIB-1 AJ488
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EF148839.1 gg_id:187075 sp. str. OF1 EF1488
EU778256.1 gg_id:323736 feces clone RL388_aao96a11 EU778
CR933168.1 gg_id:109928 Evry municipal wastewater treatment plant clone 009C01_B_SD_P15 CR933
EU871349.1 gg_id:340817 Genetic Bovine (Bos taurus) Rumen Thailand clone CF24 EU871
EU778270.1 gg_id:347138 feces clone RL388_aao94a06 EU778
EU843687.1 gg_id:344506 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
EU463641.1 gg_id:294443 domesticated horse feces clone horsej_aai90c05 EU463
FJ172810.1 gg_id:336477 Qinghai Yak Ruminal and Fungi China rumen clone RB-4G9 FJ1728
EU473846.1 gg_id:300815 douc langur feces clone DL_2aaa02f04 EU473
EF436357.1 gg_id:204894 library-based ruminal water buffalo (Bubalus bubalis) rumen fluid clone BRC71 EF4363
EU458001.1 gg_id:326858 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83 EU458
DQ777884.1 gg_id:162338 rat feces clone R-1153 DQ777
EU748358.1 gg_id:327696 neotropical folivorous flying bird adult hoatzin crop clone hoa5_05g04 EU748
EU461240.1 gg_id:288278 hamadryas baboon feces clone BAZ_aah91c04 EU461
EU453832.1 gg_id:339637 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75 EU453
EU006270.1 gg_id:245595 Salmonella enterica serovar typhimurium exploits inflammation compete intestinal r EU006
EU791114.1 gg_id:437229 Enteric Defensins are Essential Regulators Intestinal Microbial Ecology HD5-- mouse EU791
DQ823995.1 gg_id:198761 human fecal clone RL204_aaj57h05 DQ823
EU504520.1 gg_id:275108 cecal contents Mus musculus strain C57BL/6J; myd1 clone myd1_aaa01g06 EU504
FJ880426.1 gg_id:443609 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8804

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EF603052.1 gg_id:232866 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6030
EF098294.1 gg_id:193974 mouse cecum clone SWPT14_aaa04c11 EF0982
EF100060.1 gg_id:190816 mouse cecum clone SWPT5_aaa04b05 EF1000
AY990250.1 gg_id:129831 mouse cecum clone C3_E23 AY9902
EF604853.1 gg_id:235135 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6048
FJ879160.1 gg_id:460476 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8791
FJ880190.1 gg_id:447761 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8801
EU455049.1 gg_id:335280 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU4550
EU452048.1 gg_id:319794 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N EU4520
EU474325.1 gg_id:290142 western lowland gorilla feces clone GORSD_aaa04b01 EU4743
EU344221.1 gg_id:276488 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU3442
EU461555.1 gg_id:291173 black rhinoceros feces clone RH_aaj92d08 EU4615
EU454885.1 gg_id:308212 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N EU4548
EU451421.1 gg_id:318052 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU4514
FJ674167.1 gg_id:518896 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6741
EF099942.1 gg_id:187037 mouse cecum clone SWPT5_aaa02e06 EF0999
DQ015647.1 gg_id:133444 mouse cecum clone M3_f04_3 DQ015
EU748033.1 gg_id:333767 neotropical folivorous flying bird adult hoatzin crop clone hoa2_44d08 EU7480
EF603021.1 gg_id:232374 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6030
EF098597.1 gg_id:191252 mouse cecum clone SWPT16_aaa01h11 EF0985
EU843235.1 gg_id:324417 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8432
EF614890.1 gg_id:235223 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o EF6148
EF604748.1 gg_id:228472 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6047
EF096266.1 gg_id:192712 mouse cecum clone obob1_aaa03g06 EF0962
DQ809192.1 gg_id:182039 human fecal clone RL308_aal83b07 DQ809
EF400350.1 gg_id:211699 human fecal clone SJTU_E_11_94 EF4003
FJ880902.1 gg_id:439512 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8809
EF096823.1 gg_id:186342 mouse cecum clone SWPT13_aaa01c04 EF0968
EU452288.1 gg_id:355245 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N EU4522
EU505008.1 gg_id:272333 cecal contents Mus musculus strain C57BL/6J; myd3 clone myd3_aaa01e09 EU5050
EU510319.1 gg_id:259347 cecal contents Mus musculus strain C57BL/6J; WD3 clone WD3_aak04f07 EU5103
FJ880449.1 gg_id:379255 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8804
EF603912.1 gg_id:228791 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6039
EU622716.1 gg_id:278265 -feed administered sub-therapeutic chlorotetracycline alters structure and but not a EU6227
EF603985.1 gg_id:233000 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6039
EU474208.1 gg_id:288634 western lowland gorilla feces clone GORSD_aaa01a08 EU4742
EF603044.1 gg_id:227767 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6030
AF371911.1 gg_id:45604 swine intestine clone p-2445-18B5 AF3719
EU456979.1 gg_id:314956 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N EU4569
DQ014909.1 gg_id:130514 mouse cecum clone M1_1c08 DQ014
EF604467.1 gg_id:231927 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6044

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EU743928.1 gg_id:325933 Mouse fecal microbiota feces clone 3B6 EU743
FJ879269.1 gg_id:416233 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8792
EU656018.1 gg_id:282023 influence dietary flavonoid-containing extracts on gut microbiota mouse feces clone EU656
EF097726.1 gg_id:189531 mouse cecum clone SWPT20_aaa02g09 EF0977
EU474718.1 gg_id:300665 takin feces clone TAK_aaa03g01.Contig2 EU474
EF099096.1 gg_id:174741 mouse cecum clone SWPT2_aaa02b08.Contig2 EF0990
EU504956.1 gg_id:259835 cecal contents Mus musculus strain C57BL/6J; myd2 clone myd2_aaa04g08 EU504
EF099937.1 gg_id:178306 mouse cecum clone SWPT5_aaa02e01 EF0999
FJ879522.1 gg_id:402704 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8795
EF097748.1 gg_id:184865 mouse cecum clone SWPT20_aaa03b05 EF0977
EU622752.1 gg_id:279579 -feed administered sub-therapeutic chlorotetracycline alters structure and but not a EU622
EU765785.1 gg_id:309629 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B4 EU765
EF603581.1 gg_id:229522 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6035
FJ673460.1 gg_id:516479 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6734
EF100007.1 gg_id:191621 mouse cecum clone SWPT5_aaa03d12 EF1000
EU510274.1 gg_id:264605 cecal contents Mus musculus strain C57BL/6J; WD3 clone WD3_aak03h10 EU510
EU504962.1 gg_id:267331 cecal contents Mus musculus strain C57BL/6J; myd2 clone myd2_aaa04h04 EU504
EF097884.1 gg_id:193106 mouse cecum clone SWPT12_aaa01c08 EF0978
EF603896.1 gg_id:231210 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6038
EU458061.1 gg_id:321671 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H79 EU458
EU504777.1 gg_id:276032 cecal contents Mus musculus strain C57BL/6J; myd2 clone myd2_aaa02a05 EU504
FJ880859.1 gg_id:420373 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8808
EU622655.1 gg_id:278105 -feed administered sub-therapeutic chlorotetracycline alters structure and but not a EU622
EF097203.1 gg_id:192034 mouse cecum clone SWPT18_aaa03b01 EF0972
EU463064.1 gg_id:291639 naked mole-rat feces clone molerat_aai69c07 EU463
EF097265.1 gg_id:195543 mouse cecum clone SWPT18_aaa04a12 EF0972
EU464141.1 gg_id:288655 reticulated giraffe feces clone gir_aah94g07 EU464
EU843556.1 gg_id:341053 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
EF096036.1 gg_id:182345 mouse cecum clone lean2_aaa02e05 EF0960
FJ880763.1 gg_id:387968 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8807
EU504616.1 gg_id:266075 cecal contents Mus musculus strain C57BL/6J; myd1 clone myd1_aaa03c07 EU504
EU459736.1 gg_id:298057 ring-tailed lemur feces clone RT_aai11h09 EU459
EF099380.1 gg_id:189985 mouse cecum clone SWPT3_aaa02e04 EF0993
DQ014612.1 gg_id:131899 mouse cecum clone M1_f05 DQ014
EF614858.1 gg_id:228861 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o EF6148
EF604593.1 gg_id:230920 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6045
EF097497.1 gg_id:187537 mouse cecum clone SWPT19_aaa03e02 EF0974
EU457205.1 gg_id:307427 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77 EU457
EU504683.1 gg_id:264752 cecal contents Mus musculus strain C57BL/6J; myd1 clone myd1_aaa04e01 EU504
FJ880214.1 gg_id:424255 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8802
EF603737.1 gg_id:233584 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6037

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EU453593.1 gg_id:339017 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75N EU453
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EU455009.1 gg_id:325057 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H74N EU455
EU381853.1 gg_id:262581 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU381
EU622648.1 gg_id:278171 -feed administered sub-therapeutic chlorotetracycline alters structure and but not a EU622
EF603749.1 gg_id:230641 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF603
EF603903.1 gg_id:233923 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF603
EF097895.1 gg_id:196913 mouse cecum clone SWPT12_aaa01e08 EF097
EU777326.1 gg_id:326627 Okapi feces clone OK1_f07_1 EU777
EU655810.1 gg_id:284926 influence dietary flavonoid-containing extracts on gut microbiota mouse feces clone EU655
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EU510694.1 gg_id:269241 cecal contents Mus musculus strain C57BL/6J; WD5 clone WD5_aak39e04 EU510
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EU748352.1 gg_id:310634 neotropical folivorous flying bird adult hoatzin crop clone hoa5_07d02 EU748
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EU467659.1 gg_id:300634 naked mole-rat feces clone molerat_2c03_2 EU467
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EU455289.1 gg_id:326297 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83N EU455
EU471874.1 gg_id:293854 Asiatic elephant feces clone AE3_aaa04c09 EU471
GQ492835.1 gg_id:552779 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
EF099271.1 gg_id:176215 mouse cecum clone SWPT2_aaa04h04 EF099
AY993118.1 gg_id:132569 mouse cecum clone C21_e21 AY993
EF099246.1 gg_id:185948 mouse cecum clone SWPT2_aaa04e07 EF099
EF097178.1 gg_id:180387 mouse cecum clone SWPT18_aaa02e07 EF097
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EU453748.1 gg_id:305789 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU453
EF604468.1 gg_id:229055 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF604
EF614680.1 gg_id:234291 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o EF614
EF096743.1 gg_id:179168 mouse cecum clone SWPT11_aaa04a05 EF096
EU505586.1 gg_id:263664 cecal contents Mus musculus strain C57BL/6J; myd5 clone myd5_aaa03b02 EU505
FJ684583.1 gg_id:517722 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ684
EF406717.1 gg_id:204158 mouse colon clone infected_14days-B10 EF406
EU463180.1 gg_id:290181 naked mole-rat feces clone molerat_aai71c03 EU463
EF096320.1 gg_id:188845 mouse cecum clone obob1_aaa04h02 EF096
EU461002.1 gg_id:288628 red kangaroo feces clone KO1_aai42a08 EU461

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EF406445.1 gg_id:209552 mouse colon clone control_7days-H4 EF4064
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FJ879109.1 gg_id:396796 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8791
EU622642.1 gg_id:279248 -feed administered sub-therapeutic chlorotetracycline alters structure and but not a EU622

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DQ815337.1 gg_id:168732 mouse cecum clone aab45h10 DQ815
DQ815534.1 gg_id:167078 mouse cecum clone aab42d05 DQ815
EF100100.1 gg_id:189237 mouse cecum clone SWPT5_aaa04f10 EF1001
EU452919.1 gg_id:338076 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU452
EF099201.1 gg_id:192206 mouse cecum clone SWPT2_aaa03g08 EF0992
EU453409.1 gg_id:314284 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H79S EU453
DQ815707.1 gg_id:168880 mouse cecum clone aab21c02 DQ815
EF097001.1 gg_id:196067 mouse cecum clone SWPT13_aaa04a06 EF0970
EU469598.1 gg_id:302042 flying fox feces clone FF_e10 EU469
EU456444.1 gg_id:346997 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU456
EF406463.1 gg_id:214715 mouse colon clone control_14days-B6 EF4064
EF096007.1 gg_id:197522 mouse cecum clone lean2_aaa01g12 EF0960
EF098272.1 gg_id:191723 mouse cecum clone SWPT14_aaa04a04 EF0982
EU504985.1 gg_id:263232 cecal contents Mus musculus strain C57BL/6J; myd3 clone myd3_aaa01b12 EU504
EU344438.1 gg_id:272858 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU344
EU510551.1 gg_id:274125 cecal contents Mus musculus strain C57BL/6J; WD5 clone WD5_aak37a08 EU510
AF371913.1 gg_id:49015 swine intestine clone p-251-o5 AF371
DQ905202.1 gg_id:173773 human fecal clone 013-b11 DQ905
EU463693.1 gg_id:294182 domesticated horse feces clone horsej_aai91b06 EU463
EU451397.1 gg_id:344901 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU451
EU456545.1 gg_id:329371 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83N EU456
DQ015199.1 gg_id:133109 mouse cecum clone M2_h12_2 DQ015
EU794078.1 gg_id:345791 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_O4 EU794
EF603895.1 gg_id:228588 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6038
EF098910.1 gg_id:177453 mouse cecum clone SWPT1_aaa03b06 EF0989
EU510197.1 gg_id:259625 cecal contents Mus musculus strain C57BL/6J; WD3 clone WD3_aak02g09 EU510
EU771635.1 gg_id:351900 African elephant feces clone AFEL3_aao16g05 EU771
EU457393.1 gg_id:356389 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU457
EF099960.1 gg_id:180240 mouse cecum clone SWPT5_aaa02g11 EF0999
EF097016.1 gg_id:186680 mouse cecum clone SWPT13_aaa04c04 EF0970
EF604781.1 gg_id:228568 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6047
EF603098.1 gg_id:228267 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6030
EF406790.1 gg_id:214904 mouse colon clone infected_14days-H6 EF4067
EU510156.1 gg_id:264835 cecal contents Mus musculus strain C57BL/6J; WD3 clone WD3_aak02b12 EU510
EU453039.1 gg_id:321735 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N EU453
AY239399.1 gg_id:97196 rat feces clone rc3-52 AY2393
EU510721.1 gg_id:265939 cecal contents Mus musculus strain C57BL/6J; WD5 clone WD5_aak40a04 EU510
EF096055.1 gg_id:198382 mouse cecum clone lean2_aaa03a09 EF0960
EF097021.1 gg_id:192035 mouse cecum clone SWPT13_aaa04d01 EF0970
EU775301.1 gg_id:343616 Reticulated giraffe feces clone gir_aah96d03 EU775
EF098930.1 gg_id:190976 mouse cecum clone SWPT1_aaa03d08 EF0989

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EU453264.1 gg_id:335050 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU453
EU510491.1 gg_id:263168 cecal contents Mus musculus strain C57BL/6J; WD4 clone WD4_aal39f05 EU510
EF096961.1 gg_id:175646 mouse cecum clone SWPT13_aaa03d04 EF0969
AY239412.1 gg_id:97151 rat feces clone rc2-4(2) AY2394
EU456177.1 gg_id:322237 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU456
EU748162.1 gg_id:305473 neotropical folivorous flying bird adult hoatzin crop clone hoa33_63G08.F EU748
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AY993727.1 gg_id:135206 mouse cecum clone C15_J03 AY9937
EU457424.1 gg_id:320200 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K79S EU457
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EF604564.1 gg_id:230346 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6045
EF099086.1 gg_id:174420 mouse cecum clone SWPT2_aaa02a08 EF0990
EU777229.1 gg_id:313410 Okapi feces clone OK2_c05_1 EU777
EU779037.1 gg_id:334720 Prevost's squirrel feces clone SQ_aah81f10 EU779
EF445234.1 gg_id:206507 dairy cow rumen clone NED4C7 EF4452
EU455879.1 gg_id:307731 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83N EU455
EU474278.1 gg_id:294646 western lowland gorilla feces clone GORSD_aaa04g10 EU474
EU510141.1 gg_id:265808 cecal contents Mus musculus strain C57BL/6J; WD3 clone WD3_aak01h09 EU510
EF097720.1 gg_id:186508 mouse cecum clone SWPT20_aaa02g03 EF0977
EU457872.1 gg_id:327559 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83N EU457
EU510115.1 gg_id:258247 cecal contents Mus musculus strain C57BL/6J; WD3 clone WD3_aak01e12 EU510
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DQ014936.1 gg_id:135808 mouse cecum clone M1_1g10 DQ014
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EF604753.1 gg_id:231289 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6047
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EU775557.1 gg_id:311186 Western lowland gorilla feces clone GORSD_aaa02g11 EU775
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FJ880357.1 gg_id:386729 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8803
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EU458102.1 gg_id:336454 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU458
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EU505050.1 gg_id:263586 cecal contents Mus musculus strain C57BL/6J; myd3 clone myd3_aaa02b08 EU505
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EU454725.1 gg_id:312854 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N EU454
FJ879812.1 gg_id:419444 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8798
EU453931.1 gg_id:334800 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU453
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EU452889.1 gg_id:338324 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N EU452
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EF603107.1 gg_id:232033 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6031
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EF604835.1 gg_id:231806 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6048

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EU006217.1 gg_id:240633 Salmonella enterica serovar typhimurium exploits inflammation compete intestinal r EU006
EF603916.1 gg_id:228458 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF603
EF097679.1 gg_id:189127 mouse cecum clone SWPT20_aaa02b09 EF0976
EF100062.1 gg_id:196923 mouse cecum clone SWPT5_aaa04b07 EF100
EF602770.1 gg_id:230836 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6027
EU504920.1 gg_id:269859 cecal contents Mus musculus strain C57BL/6J; myd2 clone myd2_aaa04b11 EU504
EF098360.1 gg_id:193807 mouse cecum clone SWPT15_aaa01e07 EF0983
EU463191.1 gg_id:294221 naked mole-rat feces clone molerat_aai71d07 EU463
EF604640.1 gg_id:230453 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6046
EF604939.1 gg_id:231349 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6049
EU776950.1 gg_id:309676 Naked mole-rat feces clone molerat_aai70b02 EU776
EU467647.1 gg_id:289805 naked mole-rat feces clone molerat_2g10 EU467
FJ880096.1 gg_id:442846 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8800
GU302930.1 gg_id:550070 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU302
FJ880583.1 gg_id:426735 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8805
EU622730.1 gg_id:278940 -feed administered sub-therapeutic chlorotetracycline alters structure and but not a EU622
EU843395.1 gg_id:312272 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
EU455328.1 gg_id:320024 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU455
EU505320.1 gg_id:271280 cecal contents Mus musculus strain C57BL/6J; myd4 clone myd4_aaa02d10 EU505
EU381897.1 gg_id:275175 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU381
AM265425.1 gg_id:159925 Oligonucleotide Probes intestinal flora BB-DP rat colon clone ratAD060301 AM265
GQ896847.1 gg_id:578799 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do GQ896
DQ015356.1 gg_id:135834 mouse cecum clone M3_b02 DQ015
EF099751.1 gg_id:195475 mouse cecum clone SWPT4_aaa03g10 EF0997
EU456256.1 gg_id:304541 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU456
EF406449.1 gg_id:211595 mouse colon clone control_7days-H9 EF4064
EU779312.1 gg_id:354876 Visayam Warty Pig feces clone VWP_aaa04h02 EU779
EF406819.1 gg_id:217096 mouse colon clone infected_28days-C3 EF4068
EF097253.1 gg_id:181680 mouse cecum clone SWPT18_aaa03h02 EF0972
DQ015015.1 gg_id:131469 mouse cecum clone M1_1g04_2 DQ015
EU474374.1 gg_id:292591 western lowland gorilla feces clone GORSD_aaa03h06 EU474
AY239406.1 gg_id:98683 rat feces clone rc3-37 AY239
DQ015629.1 gg_id:133346 mouse cecum clone M3_d06_3 DQ015
EU006237.1 gg_id:247154 Salmonella enterica serovar typhimurium exploits inflammation compete intestinal r EU006
EU468776.1 gg_id:290077 okapi feces clone OK3_f06 EU468
AY993195.1 gg_id:131253 mouse cecum clone C21_i12 AY993
AY990304.1 gg_id:132871 mouse cecum clone C3_F09 AY990
EU474328.1 gg_id:297768 western lowland gorilla feces clone GORSD_aaa02h05 EU474
EF096109.1 gg_id:187153 mouse cecum clone lean2_aaa04c11 EF0961
EF097070.1 gg_id:190752 mouse cecum clone SWPT18_aaa01a03 EF0970

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EU452936.1 gg_id:319699 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K79S EU452
EU760449.1 gg_id:329026 Mouse fecal microbiota feces clone 3H3 EU760
EF097246.1 gg_id:194729 mouse cecum clone SWPT18_aaa03f12 EF0972
EU504203.1 gg_id:264534 cecal contents Mus musculus strain C57BL/6J; CRWD5 clone CRWD5_aaa04b01 EU504
EF406703.1 gg_id:204375 mouse colon clone infected_7days-H7 EF4067
EU506168.1 gg_id:259557 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aaa01h02 EU506
EF099144.1 gg_id:189700 mouse cecum clone SWPT2_aaa02h11 EF0991
EU453346.1 gg_id:337004 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU453
EU504144.1 gg_id:265567 cecal contents Mus musculus strain C57BL/6J; CRWD5 clone CRWD5_aaa02b07 EU504
EU507923.1 gg_id:260460 cecal contents Mus musculus strain C57BL/6J; MD24 clone MD24_aaa03e08 EU507
EU510603.1 gg_id:268107 cecal contents Mus musculus strain C57BL/6J; WD5 clone WD5_aak38a07 EU510
EU381784.1 gg_id:273277 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU381
EF097715.1 gg_id:187391 mouse cecum clone SWPT20_aaa02f10 EF0977
EF604469.1 gg_id:228370 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6044
EU775447.1 gg_id:307242 Western lowland gorilla feces clone GORSD_aaa02h07 EU775
EF099844.1 gg_id:175658 mouse cecum clone SWPT5_aaa01b12 EF0998
EU622740.1 gg_id:278240 -feed administered sub-therapeutic chlorotetracycline alters structure and but not a EU622
EF604644.1 gg_id:233540 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6046
EF406383.1 gg_id:211771 mouse colon clone control_7days-B5 EF4063
EF602759.1 gg_id:231387 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6027
EU504036.1 gg_id:277555 cecal contents Mus musculus strain C57BL/6J; CRWD4 clone CRWD4_aaa04d01 EU504
EU471547.1 gg_id:288578 Asiatic elephant feces clone AE1_aaa03g07 EU471
EF099334.1 gg_id:176935 mouse cecum clone SWPT3_aaa01h05 EF0993
EF603018.1 gg_id:231681 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6030
EF096871.1 gg_id:184698 mouse cecum clone SWPT13_aaa02a03 EF0968
FJ368943.1 gg_id:369063 feces adult twins and mothers; TS4 clone TS4_a02d06 FJ3689
EU474297.1 gg_id:299687 western lowland gorilla feces clone GORSD_aaa03g11 EU474
AY993275.1 gg_id:134248 mouse cecum clone C21_m04 AY9932
EF097825.1 gg_id:183755 mouse cecum clone SWPT20_aaa04d06 EF0978
EF097844.1 gg_id:194048 mouse cecum clone SWPT20_aaa04f09 EF0978
EF097131.1 gg_id:180152 mouse cecum clone SWPT18_aaa01g11 EF0971
AB370251.1 gg_id:274244 Barnesiella intestinihominis str. YIT 11860 AB370
EF603725.1 gg_id:229158 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6037
DQ015238.1 gg_id:133103 mouse cecum clone M2_f09_1 DQ015
EF096489.1 gg_id:180290 mouse cecum clone obob2_aaa03f10 EF0964
EF096452.1 gg_id:192586 mouse cecum clone obob2_aaa03a10 EF0964
FJ678385.1 gg_id:528459 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6783
EU504803.1 gg_id:262102 cecal contents Mus musculus strain C57BL/6J; myd2 clone myd2_aaa02d08 EU504
EF098085.1 gg_id:193878 mouse cecum clone SWPT14_aaa01c07 EF0980
EF099615.1 gg_id:198966 mouse cecum clone SWPT4_aaa01h05 EF0996

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EU451626.1 gg_id:316383 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H74N EU4516
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EU459488.1 gg_id:288014 capybara feces clone CAP_aah98c03 EU459
AB192163.1 gg_id:142693 termite gut homogenate clone RsTz-83 AB192
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EU474844.1 gg_id:298225 takin feces clone TAK_aaa03c10 EU4748
AB447622.1 gg_id:582590 Microbial Structure and Dynamics Granules Expanded Granular Sludge Bed (EGSB) R AB447
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GU322884.1 gg_id:568069 Metaproteomics -temperature anaerobic granular sludge cultivated temperatures c GU322
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AB240349.1 gg_id:143752 microbial structure Phragmites rhizosphere biofilm reed bed reactor laboratory clon AB240
EU101168.1 gg_id:241983 Sulfide/oxygen supply ratio predicts outcome competition among sulfur-oxidizing wa EU101
EU887841.1 gg_id:344827 Bacteroides nordii str. H6 EU8878
AJ249101.1 gg_id:16567 SHA-25 clone AJ2491
EU777142.1 gg_id:308111 Okapi feces clone OK3_c06_2 EU777
EU775257.1 gg_id:312978 Reticulated giraffe feces clone gir_aah93g11 EU775
DQ168847.1 gg_id:139337 Fermentative biohydrogen production heated anaerobic sludge clone J3 DQ168
EF467522.1 gg_id:215462 situ microelectrode voltammetry sulfur-oxidizing biofilms Frasassi sulfidic cave strear EF4675
EU626628.1 gg_id:277641 variation and endosymbiotic phenotypically- sea urchin Strongylocentrotus intermec EU626
AM086143.1 gg_id:149805 Abundance and archaea mesotrophic Lake Kinneret lake profundal sediment clone AM086
EU626717.1 gg_id:278621 variation and endosymbiotic phenotypically- sea urchin Strongylocentrotus intermec EU626
EU469991.1 gg_id:299307 trancaspain urial feces clone TU1_aaa03a07 EU469
EU344633.1 gg_id:265199 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU344
GU454901.1 gg_id:524763 Understanding short-chain fatty acids accumulation enhanced alkaline digestion: kir GU454
FJ612117.1 gg_id:573374 and Biogeochemistry Dongping Lake Ecosystems lake water clone DP3.1.10 FJ6121
DQ330407.2 gg_id:159129 Guerrero Negro hypersaline microbial mat clone 02N1A277 DQ330
FJ672357.1 gg_id:518436 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6723
GQ844375.1 gg_id:562395 Microbial anoxic tank full-scale water treatment plant influent produced wastewate GQ844
AB447707.1 gg_id:587341 Microbial Structure and Dynamics Granules Expanded Granular Sludge Bed (EGSB) R AB447
AJ969457.1 gg_id:157758 Microbial black smoker s Mid Atlantic Ridge ecological implications rock fragments ch AJ9694
EU358743.1 gg_id:311025 structure archaeal denaturing gel electrophoresis and sequencing mesophilic biogas EU358
FJ680373.1 gg_id:509073 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6803
EU283476.1 gg_id:278938 Model Early Earth Harbors Deeply Divergent Divisions Anderson Lake clone A840 EU2834
EU775874.1 gg_id:344007 Horse feces clone horsem_aai94d01 EU7758

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EU617865.1 gg_id:334161 Seasonal variation microbial Yel Sea sediment clone C13S-108 EU6178
EU234211.1 gg_id:237249 receiving river and un techniques effluent WWTP treating penicillin G production wa EU2342
GU174049.1 gg_id:566383 Microbial Bactrian camel estimated rumen clone XJC123 GU174
AM086153.1 gg_id:149981 Abundance and archaea mesotrophic Lake Kinneret lake profundal sediment clone AM086
AB189373.1 gg_id:113650 cold seep sediment clone JT75-304 AB1893
EU488084.1 gg_id:533148 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU4880
EF632714.1 gg_id:237093 Unique microbial contrasting aquatic altitude Andean Altiplano (northern Chile) wate EF6327
GU180191.1 gg_id:592210 Impact coplanar PCBs on microbial activity anaerobic estuarine sediments sediment GU180
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AJ249107.1 gg_id:27268 SHA-54 clone AJ2491
GQ354965.1 gg_id:592485 structure between two geochemically distinct springs Alum Rock Park spring clone 4 GQ354
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EF515716.1 gg_id:225096 Electricigen Enrichment MFC full-scale anaerobic bioreactor sludge treating brewery EF5157
AB062847.1 gg_id:22095 termite gut homogenate clone BCf9-17 AB0628
EU460992.1 gg_id:301069 red kangaroo feces clone KO1_aai41g02 EU4609
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GU061301.1 gg_id:534403 Evaluation culturing methods cultivate previously Yel Sea intertidal beach seawater GU061
AJ007873.1 gg_id:1909 cytophagales clone LD21 AJ0078
EU344456.1 gg_id:259929 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU3444
EU283479.1 gg_id:278289 Model Early Earth Harbors Deeply Divergent Divisions Anderson Lake clone A1892 EU2834
GQ339154.1 gg_id:525962 Comprehensive Investigation on Iron Cycling Freshwater Seep ing Microscopy Cultiv GQ339
EU468706.1 gg_id:290252 okapi feces clone OK2_a07 EU4687
EF208683.1 gg_id:202437 Vertical and horizontal structure microbial sandy carbonate sediment clone CI5cm.C EF2086
CU927762.1 gg_id:550552 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU9277
EU644260.1 gg_id:281260 and Samoylov Island Lena active layer -centred polygon near surface horizon; Rim_T EU6442
CU927382.1 gg_id:569229 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU9273
FJ374189.1 gg_id:361803 Inter- and intraspecific humivorous scarab beetle larvae (Pachnoda spp.) larval hindg FJ3741
EU468800.1 gg_id:300785 okapi feces clone OK3_d07 EU4688
FJ716481.1 gg_id:511725 Uncultivated archaea sulfate-reducing biofilm Frasassi cave system anoxic lake water FJ7164
AY340833.1 gg_id:91285 sulfate-reducing fluidized-bed reactor clone SR_FBR_E99 AY3408
AJ441238.1 gg_id:57446 hydrothermal vent polychaete mucous clone P. palm A/C 22 AJ4412
FN396675.1 gg_id:537712 constant flux thermophilic cold seabed Arctic marine surface sediment clone s5_0_V FN3966
AJ633981.1 gg_id:114657 hlpd: Llgnd and Idspd) hst's accssr ndmntl glnd cln T66ANG1 AJ6339
EF687372.1 gg_id:281446 Biogeochemistry iron- and sulfur-precipitating microbial mats (Nile Mediterranean) s EF6873
FJ670687.1 gg_id:523843 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface FJ6706
EU794308.1 gg_id:347016 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_H34 EU7943
GQ449224.1 gg_id:537070 Microbiome neonatal calves: shedding microorganisms fecal clone calf784_10wks_ GQ449
FJ672548.1 gg_id:515828 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface FJ6725

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EU474496.1 gg_id:302981 bighorn sheep feces clone BHSD_aaa04g01 EU474
AM883180.1 gg_id:349092 Endosymbioses between and deep-sea siboglinid tubeworms arctic cold seep (Haak AM883
AY082459.1 gg_id:69791 neutral pH mine biofilm clone 44a-B1-14 AY0824
GQ360012.1 gg_id:559138 Microbial intestinal contents and yel catfish (Pelteobagrus fulvidraco) intestine muc GQ360
EU773616.1 gg_id:354389 Capybara feces clone CAP_aah97h09 EU773
EU775144.1 gg_id:341051 Francois Langur feces clone FL_1aaa01g03 EU775
EU775249.1 gg_id:321527 Reticulated giraffe feces clone gir_aah93b08 EU775
AB240242.1 gg_id:141996 microbial structure rhizosphere Phragmites bulk soil reed bed reactor laboratory clo AB240
EU245226.1 gg_id:246041 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-H4-D0 EU245
FJ674366.1 gg_id:514574 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface FJ6743
AB195895.1 gg_id:109183 Anaerobic sludge clone S15 AB195
EU472280.1 gg_id:289823 francois langur feces clone FL_2aaa04a07 EU472
AB186817.1 gg_id:106460 polychlorinated dioxin dechlorinating microcosm clone TSBX12 AB186
AB191998.1 gg_id:142777 termite gut homogenate clone M1PL1-52 AB191
AF419687.1 gg_id:72909 Guaymas Basin hydrothermal sediment clone CS_B045 AF419
AB504929.1 gg_id:554505 structure microorganisms reddish-brown iron-rich snow clone oze05B24 AB504
FJ202099.1 gg_id:342229 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata FJ2020
EU644099.1 gg_id:284431 and Samoylov Island Lena active layer -centred polygon near permafrost table; Rim_ EU644
EU777992.1 gg_id:335513 Black rhinoceros feces clone RH_aaj92b02 EU777
DQ394963.1 gg_id:152831 harbor sediment clone VHS-B3-78 DQ394
EU772007.1 gg_id:310931 Argali sheep feces clone AS2_aao33a07 EU772
AJ011042.1 gg_id:1910 strain clone R1 AJ0110
AF371924.1 gg_id:16915 swine intestine clone p-2534-18B5 AF371
EU472140.1 gg_id:300246 francois langur feces clone FL_1aaa03b03 EU472
EF454492.2 gg_id:227458 termite hindgut clone 290cost002-P3L-2216 EF4544
FM955631.1 gg_id:551607 Study Prokaryotic Some Selected Niches Western Ghats India water clone BCWCSP1 FM955
EU475381.1 gg_id:296470 rock hyrax feces clone RHSD_aaa02b12 EU475
EF420217.1 gg_id:211333 Mature fine processing harbour methanogenic oil sands tailings pond clone 24-9G EF4202
GQ448662.1 gg_id:509560 Microbiome neonatal calves: shedding microorganisms fecal clone calf784_10wks_ GQ448
EU474792.1 gg_id:291587 takin feces clone TAK_aaa02d05 EU474
AB363973.1 gg_id:236772 Bacteroides sp. str. XDT-1 AB363
AF320926.1 gg_id:70586 Lake Michigan sediment clone LMBA49 AF320
GQ448729.1 gg_id:557275 Microbiome neonatal calves: shedding microorganisms fecal clone calf784_10wks_ GQ448
EF688234.1 gg_id:338749 Detection microbial sludge anaerobic wastewater treatment system clone 5F10_con EF6882
EF420216.1 gg_id:204265 Mature fine processing harbour methanogenic oil sands tailings pond clone 12-3C EF4202
EU472043.1 gg_id:297059 francois langur feces clone FL_1aaa03a10 EU472
AM176862.1 gg_id:160787 Recovery mangrove sediment clone SZB26 AM176
FJ516976.1 gg_id:546673 semiarid 'Tablas de Daimiel National Park' wetland (Central Spain) unravelled upper FJ5169
EU101284.1 gg_id:238631 Sulfide/oxygen supply ratio predicts outcome competition among sulfur-oxidizing EU101
AB192158.1 gg_id:142988 termite gut homogenate clone RsTz-24 AB192

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EU700166.1 gg_id:302703 Study on Shantou Bay Marine Sediments Microorganisms sediment clone STU24 EU700
EU842222.1 gg_id:356426 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
FJ484663.1 gg_id:548668 microbial autonomous rover world's deepest phreatic sinkhole wall biomat El Zacator FJ4846
AJ306737.1 gg_id:101390 DCP-dechlorinating consortium clone SHA-13 AJ3067
FJ462124.1 gg_id:544483 Microbial ecology industrial digestor mesophilic anaerobic reactor fed effluent chemi FJ4621
EF097027.1 gg_id:177669 mouse cecum clone SWPT13_aaa04d07 EF097
DQ676360.1 gg_id:225388 Archaeal sediment and plankton freshwater pond suboxic freshwater-pond clone M DQ676
EU644165.1 gg_id:284946 and Samoylov Island Lena active layer -centred polygon near permafrost table; Rim_ EU644
EU468504.1 gg_id:294848 okapi feces clone OK1_d05_1 EU468
AF029039.1 gg_id:1921 Benzene mineralizing consortium complete clone SB-1 consortium AF029
AF050539.1 gg_id:1896 contaminated aquifer clone WCHB1-53 AF050
CU918213.1 gg_id:558606 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU918
AJ240979.1 gg_id:1914 Norway:(Svalbard)Hornsund clone Sva1038 AJ2409
FJ672351.1 gg_id:525055 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6723
FJ172812.1 gg_id:312412 Qinghai Yak Ruminal and Fungi China rumen clone RB-4G11 FJ1728
EU463478.1 gg_id:291681 domesticated horse feces clone horsem_aai94f08 EU463
EU592422.1 gg_id:561608 Seasonal changes Salton Sea hypersaline sediment clone SSS23N EU592
AY572027.1 gg_id:114774 termite gut clone RsaPv13 AY572
EU234164.1 gg_id:244201 receiving river and un techniques effluent WWTP treating penicillin G production wa EU234
DQ824495.1 gg_id:183618 human fecal clone RL304_aal76g04 DQ824
AY168724.2 gg_id:76102 arsenite-oxidizing biofilm clone Hot Creek 27 AY168
DQ799357.1 gg_id:178148 human fecal clone RL305aal85c11 DQ799
AB234433.1 gg_id:145246 termite gut homogenate clone MgMjR-050 AB2344
AM490701.1 gg_id:584987 Linking and functional nutrient spiraling mats (USA) microbial mat sulfidic cave sprir AM490
GQ461682.1 gg_id:588344 Coupling -ITS Clone Libraries and Automated Intergenic Spacer Microbial Bioremedi GQ461
EU245060.1 gg_id:240986 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-H1-C07 EU245
EU925908.1 gg_id:325319 sediments sediment station DBS1 northern Bering Sea clone 137I1 EU925
EU644161.1 gg_id:282325 and Samoylov Island Lena active layer -centred polygon near permafrost table; Rim_ EU644
FJ680730.1 gg_id:521139 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6807
AB191984.1 gg_id:141874 termite gut homogenate clone M1NP1-14 AB191
EU461421.1 gg_id:288259 black rhinoceros feces clone RH_aaj89a08 EU461
EU644268.1 gg_id:282750 and Samoylov Island Lena active layer -centred polygon near surface horizon; Rim_T EU644
EU828421.1 gg_id:564444 Microbial effects changeover without CO2 sparging two-stage biological and methan EU828
EU773667.1 gg_id:333804 Capybara feces clone CAP_aah97h05 EU773
EU528260.1 gg_id:285668 Seasonal Dynamics Mudflat Mouth Major Kentucky Lake Reservoir Tributary sedime EU528
AB426186.1 gg_id:277035 -situ identification study benzene-degrading s under methanogenic condition anaerc AB426
AB234394.1 gg_id:147476 termite gut homogenate clone MgMjR-007 AB2343
EF520436.1 gg_id:228557 structure lakes: what controls ? acid-impacted lake clone ADK-MOh02-18 EF5204
EU473455.1 gg_id:288119 Somali wild ass feces clone WA_aaa02g08 EU473
EU573107.1 gg_id:279087 and Dependent Microbial Oil Reservoir North Sea Ekofisk oil field Norwegian sector c EU573

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AB240489.1 gg_id:144918 microbial structure rhizosphere biofilm Sapporo root-tip (0 40 mm) Phragmites Sosei AB240
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EU779171.1 gg_id:314276 Trancaspian Urial feces clone TU2_aaa02c08 EU779
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CU925689.1 gg_id:559384 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU925
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EF436442.1 gg_id:216099 library-based ruminal water buffalo (Bubalus bubalis) rumen fluid clone BRC156 EF4364
AM420249.1 gg_id:237268 Noma subgingival plaque clone 701B10(oral) AM420
AM086109.1 gg_id:146275 Abundance and archaea mesotrophic Lake Kinneret lake profundal sediment clone AM086
EU794185.1 gg_id:351627 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_B46 EU794
CT573907.1 gg_id:153033 Evry municipal wastewater treatment plant clone 012F02_B_SD_P15 CT573
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EU842960.1 gg_id:308429 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU842
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AB487860.1 gg_id:579376 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNSR0 AB4878
EU467513.1 gg_id:292321 Sumatran orangutan feces clone orang1_f02_2 EU467
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DQ394647.1 gg_id:156519 on -Arctic peninsula Svalbard Norway determined genes and rumen isolates reindee DQ394
GU174038.1 gg_id:578661 Microbial Bactrian camel estimated rumen clone XJC75 GU174
EU771109.1 gg_id:319120 Asiatic elephant feces clone AE2_aaa02b11 EU771
DQ811911.1 gg_id:169882 mangrove soil clone MSB-5A10 DQ811
AB307635.1 gg_id:271588 clay wall used Japanese traditional buildings clone B22 AB307
GQ347420.1 gg_id:568514 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ347
GQ402123.1 gg_id:591233 alpacas and sheep forestomach clone ALP16 GQ402
FJ832931.1 gg_id:574718 Microbial Ecology Crop Folivorous Hoatzin crop contents clone A1Q101_43C06 FJ8329
AB299528.1 gg_id:248049 Motility Symbiont Termite Gut Flagellate Caduceia versatilis Member 'Synergistes' G AB299
DQ394583.1 gg_id:156411 -Arctic peninsula Svalbard Norway determined genes and rumen isolates reindeer o DQ394
EU779386.1 gg_id:326906 Somali Wild Ass feces clone WA_aaa02e05 EU779
AJ535255.1 gg_id:77623 marine sediment above hydrate ridge clone Hyd89-65 AJ5352
AF001701.1 gg_id:1880 rumen clone RC9 AF001
EF208704.1 gg_id:201885 Vertical and horizontal structure microbial sandy carbonate sediment clone CI75cm.2 EF2087
FJ833658.1 gg_id:578259 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J1Q402_75C10 FJ8336
EU468305.1 gg_id:294655 domesticated horse feces clone horsem_d07 EU468
AB255907.1 gg_id:167008 Localization Cell Morphologies Members Candidate TG3 and Subphylum Phylum Fibr AB255

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EU470252.1 gg_id:295171 Grevy's zebra feces clone GZ_aaa02g09 EU4702
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EU774538.1 gg_id:305859 Douc langur feces clone DL_1aaa01a05 EU7745
EU734985.1 gg_id:343763 assemblages sediment station DBSE Northern Bering Sea clone 079B21 EU7349
FJ534992.1 gg_id:559276 Enhancement protein conversion volatile fatty acids accumulation during addition: ef FJ5349
EU748041.1 gg_id:337169 neotropical folivorous flying bird adult hoatzin crop clone hoa2_41a11 EU7480
DQ018802.1 gg_id:129393 anaerobic swine lagoon clone C-102 DQ018
AB240491.1 gg_id:143744 microbial structure rhizosphere biofilm Sapporo root-tip (0 40 mm) Phragmites Sosei AB2404
EU344372.1 gg_id:276301 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU3443
EU779130.1 gg_id:331919 Trancaspian Urial feces clone TU2_aaa01a05 EU7791
EF559197.1 gg_id:217858 mesophilic anaerobic digester clone A35_D28_L_B_D03 EF5591
FJ202260.1 gg_id:337337 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2022
EU773072.1 gg_id:314825 Banteng feces clone BG_aaa02h03.Contig1 EU7730
AB177222.1 gg_id:133354 seafloor methane hydrate clone ODP1230B6.31 AB1772
AB185691.1 gg_id:99984 rumen clone U28-D05 AB1856
GQ347553.1 gg_id:558459 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ347

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AB191989.1 gg_id:142446 termite gut homogenate clone M2PB4-72 AB191
EU473576.1 gg_id:298864 Somali wild ass feces clone WA_aaa01e11 EU473
DQ456031.1 gg_id:159032 pre-adolescent turkey cecum clone CFT112E7 DQ456
FJ172845.1 gg_id:345477 Qinghai Yak Ruminal and Fungi China rumen clone RB-2B7 FJ1728
EU463760.1 gg_id:303347 domesticated horse feces clone horsej_aai92d02 EU463
EU463415.1 gg_id:291060 domesticated horse feces clone horsem_aai93e04 EU463
CU925021.1 gg_id:563507 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU925
EU469023.1 gg_id:297758 Speke's gazelle feces clone SP2_b01_3 EU469
CT574143.1 gg_id:156107 Evry municipal wastewater treatment plant clone 061A01_B_SD_P93 CT574
AB234243.1 gg_id:149156 Biotransformation Polychlorinated Dioxins Microbial Dynamics Sediment Microcosm AB234
AM157648.1 gg_id:141722 Cytophaga sp. str. -BI4 AM157
EF436314.1 gg_id:207085 library-based ruminal water buffalo (Bubalus bubalis) rumen fluid clone BRC28 EF4363
DQ673498.1 gg_id:166526 rumen fluid clone GRC33 DQ673
FJ203657.1 gg_id:351676 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h FJ2036
FJ716343.1 gg_id:513117 Chlorobi dominate shal chemocline Bahamas Sawmill Sink column 10.3 m water dept FJ7163
EU259441.1 gg_id:254541 Rumen yak (Bos grunniens) sequences rumen fluid clone YRC65 EU259
AB231048.1 gg_id:150102 termite gut wall clone NkW01-004 AB231
GQ347492.1 gg_id:544518 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ347
AB240481.1 gg_id:142435 microbial structure rhizosphere biofilm Sapporo root-tip (0 40 mm) Phragmites Sosei AB240
DQ673480.1 gg_id:173669 rumen fluid clone GRC15 DQ673
EU843787.1 gg_id:342384 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
EU463453.1 gg_id:289260 domesticated horse feces clone horsem_aai94c04 EU463
DQ330518.1 gg_id:159207 Guerrero Negro hypersaline microbial mat clone 09D2Z20 DQ330
EU468496.1 gg_id:294059 okapi feces clone OK1_b09 EU468
AB494915.1 gg_id:563403 Fibrobacter succinogenes dominated consortium on hay stems sheep rumen clone N AB494
EU469327.1 gg_id:301613 springbok feces clone SBK_f02 EU469
EU626625.1 gg_id:278732 variation and endosymbiotic phenotypically- sea urchin Strongylocentrotus intermec EU626
AF001746.1 gg_id:1956 rumen clone RF14 AF001
FJ832802.1 gg_id:585003 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J3Q201_30F04 FJ8328
FJ832848.1 gg_id:548307 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J3Q301_49A07 FJ8328
DQ856504.1 gg_id:245820 intestinal microflora Chinese mitten crab (Eriocheir sinensis) clone C1G DQ856
EU471879.1 gg_id:291143 Asiatic elephant feces clone AE3_aaa01c04 EU471
EU843500.1 gg_id:308739 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
GQ347395.1 gg_id:591978 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ347
EF562552.1 gg_id:257527 stable microbial consortia capable degrading complex organic matter paper pulp colu EF5625
EU470313.1 gg_id:299488 Grevy's zebra feces clone GZ_aaa02a08 EU470
GU174039.1 gg_id:556899 Microbial Bactrian camel estimated rumen clone XJC76 GU174
EU748062.1 gg_id:313687 neotropical folivorous flying bird adult hoatzin crop clone hoa2_44b05 EU748
FJ834259.1 gg_id:512857 Microbial Ecology Crop Folivorous Hoatzin crop contents clone A2Q401_31G04 FJ8342
DQ351806.1 gg_id:149262 Microbial Adherent Sediment Particles Heavy Metal Contaminated North Sea Surfac DQ351
EU779179.1 gg_id:328981 Trancaspian Urial feces clone TU2_aaa02c10 EU779

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AB231046.1 gg_id:150318 termite gut wall clone NkW01-010 AB231
EU776268.1 gg_id:335713 Red Kangaroo feces clone KO1_aai43e05 EU776
EU461047.1 gg_id:302016 red kangaroo feces clone KO1_aai43a10 EU461
EU468838.1 gg_id:296958 okapi feces clone OK3_f06_2 EU468
AB494857.1 gg_id:588984 Fibrobacter succinogenes dominated consortium on hay stems sheep rumen clone N AB494
FJ832825.1 gg_id:536508 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J3Q201_76D10 FJ8328
FJ497383.1 gg_id:549719 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun FJ4973
EF445286.1 gg_id:207764 dairy cow rumen clone NED4H2 EF445
EU850526.1 gg_id:341942 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF312 EU850
EU259388.1 gg_id:247308 Rumen yak (Bos grunniens) sequences rumen fluid clone YRC12 EU259
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AM420001.1 gg_id:250872 Noma subgingival plaque clone 102F04(oral) AM420
GU302721.1 gg_id:549765 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU302
DQ018790.1 gg_id:130880 anaerobic swine lagoon clone C-16 DQ018
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EU358698.1 gg_id:317871 structure archaeal denaturing gel electrophoresis and sequencing mesophilic biogas EU358
EU461939.1 gg_id:293725 white-faced saki feces clone Saki_aaj64b03 EU461
EU473583.1 gg_id:291747 Somali wild ass feces clone WA_aaa04h08 EU473
EU470042.1 gg_id:300082 trancaspain urial feces clone TU1_aaa01c10 EU470
EU464195.1 gg_id:299917 reticulated giraffe feces clone gir_aah96a03 EU464
AB185695.1 gg_id:100612 rumen clone U28-D09 AB185
EU465542.1 gg_id:291169 argali sheep feces clone AS1_aao37c10.Contig1 EU465
EU771187.1 gg_id:348911 Asiatic elephant feces clone AE3_aaa01d12 EU771
AB243257.1 gg_id:148372 acetone-preserved termite gut clone M2PB4a-094 AB243
EU344342.1 gg_id:260440 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU344
EU462709.1 gg_id:295701 Sumatran orangutan feces clone orang2_aai67f12 EU462
EF436305.1 gg_id:214424 library-based ruminal water buffalo (Bubalus bubalis) rumen fluid clone BRC19 EF4363
EU470020.1 gg_id:288652 trancaspain urial feces clone TU1_aaa04a04 EU470
EU748102.1 gg_id:305543 neotropical folivorous flying bird adult hoatzin crop clone hoa2_43b07 EU748
EF436356.1 gg_id:209931 library-based ruminal water buffalo (Bubalus bubalis) rumen fluid clone BRC70 EF4363
EU842409.1 gg_id:332099 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
CT573886.1 gg_id:152026 Evry municipal wastewater treatment plant clone 013A02_B_SD_P15 CT5738
EU464524.1 gg_id:301331 African elephant feces clone AFEL_aai30e11 EU464

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EU245179.1 gg_id:243547 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-H3-F07 EU2451
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CU466749.1 gg_id:341960 Evry wastewater treatment plant anoxic basin clone CU466
EU777829.1 gg_id:311444 European rabbit feces clone RA_f05_3 EU7778
GQ357018.1 gg_id:509437 Metal Dependent Marine Methane Oxidation methane seep sediment clone FeOrig_ GQ357
DQ330405.1 gg_id:159414 Guerrero Negro hypersaline microbial mat clone 02N1A225 DQ330
EU662472.1 gg_id:533502 Productivity- Chemolithoautotrophically Based Sulfidic Karst Systems microbial mat EU6624
CR933139.1 gg_id:110799 Evry municipal wastewater treatment plant clone 012E05_B_SD_P15 CR9331
AB494948.1 gg_id:583826 Fibrobacter succinogenes dominated consortium on hay stems sheep rumen clone N AB4949
AB185523.1 gg_id:103729 rumen clone F23-B11 AB1855
EU465836.1 gg_id:289466 argali sheep feces clone AS2_aao36e06 EU4658

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AF029041.1 gg_id:2476 Benzene mineralizing consortium complete clone SB-5 AF0290
EU779275.1 gg_id:303504 Trancaspian Urial feces clone TU2_aaa02g06 EU7792
FJ172867.1 gg_id:356189 Qinghai Yak Ruminal and Fungi China rumen clone RB-3B2 FJ1728
EF436379.1 gg_id:211575 library-based ruminal water buffalo (Bubalus bubalis) rumen fluid clone BRC93 EF4363
FJ832615.1 gg_id:510752 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P3Q302_51C07 FJ8326
FJ497446.1 gg_id:534938 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun FJ4974
EU472504.1 gg_id:299841 Angola colobus feces clone EAC_2_aaa03b12 EU4725
EU644103.1 gg_id:280540 and Samoylov Island Lena active layer -centred polygon near permafrost table; Rim_ EU6441
FJ833777.1 gg_id:581418 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J2Q301_45E06 FJ8337
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EU794094.1 gg_id:342089 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_O10 EU7940
EU843760.1 gg_id:342684 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8437
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AB121104.1 gg_id:100286 cold seep sediment clone JS624-9 AB1211
EU850501.1 gg_id:311418 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF271 EU8505
EU843362.1 gg_id:347678 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8433
FJ517042.1 gg_id:565133 semiarid 'Tablas de Daimiel National Park' wetland (Central Spain) unravelled water c FJ5170
AY667260.1 gg_id:101918 TCE-dechlorinating groundwater clone TANB53 AY6672
CU924843.1 gg_id:567660 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU9248
EU655924.1 gg_id:285831 influence dietary flavonoid-containing extracts on gut microbiota mouse feces clone EU6559
EU843935.1 gg_id:336049 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8439
AJ534683.1 gg_id:75351 ground water deep-well injection disposal site radioactive wastes Tomsk-7 clone S15A AJ5346
EU779491.1 gg_id:330732 Grevy's Zebra feces clone GZ_aaa04h10 EU7794
FJ679020.1 gg_id:524048 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6790
EU748268.1 gg_id:347900 neotropical folivorous flying bird adult hoatzin crop clone hoa45_25A04 EU7482
EU246065.1 gg_id:250662 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-P2-F12 EU2460
EU772481.1 gg_id:307991 Hamadryas Baboon feces clone BAZ_aah90e10 EU7724
GU455026.1 gg_id:529619 Understanding short-chain fatty acids accumulation enhanced alkaline digestion: kir GU455
AB185756.1 gg_id:104352 rumen clone U29-B07 AB1857
DQ673584.1 gg_id:161764 rumen fluid clone GRC119 DQ673
EU382048.1 gg_id:264591 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU3820
EU472952.1 gg_id:302010 douc langur feces clone DL_1aaa03h01 EU4729
DQ415754.1 gg_id:157385 Dominant microbial limestone-corroding biofilms system Italy Frasassi sulfidic cave s DQ415
FJ516916.1 gg_id:554336 semiarid 'Tablas de Daimiel National Park' wetland (Central Spain) unravelled upper s FJ5169
AB243255.1 gg_id:148852 acetone-preserved termite gut clone M2PB4a-023 AB2432
EU461358.1 gg_id:300177 red kangaroo feces clone KO2_aai18f05 EU4613
AB240370.1 gg_id:141173 microbial structure Phragmites rhizosphere biofilm reed bed reactor laboratory clone AB2403
EU468998.1 gg_id:302775 Speke's gazelle feces clone SP2_e12_2 EU4689
DQ334621.1 gg_id:175084 Impact metals on sediments heavy metal polluted marine sediment clone HB2-15-3(DQ334

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FJ497505.1 gg_id:539608 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun FJ4975
EU259389.1 gg_id:237728 Rumen yak (Bos grunniens) sequences rumen fluid clone YRC13 EU259
DQ394624.1 gg_id:152221 -Arctic peninsula Svalbard Norway determined genes and rumen isolates reindeer o DQ394
CT573936.1 gg_id:153085 Evry municipal wastewater treatment plant clone 012A05_B_SD_P15 CT5739
EU474777.1 gg_id:292120 takin feces clone TAK_aaa04h09 EU474
AY244968.1 gg_id:83719 cow rumen clone BS14 AY2449
EU245071.1 gg_id:242715 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-H1-E01 EU2450
EU468816.1 gg_id:301037 okapi feces clone OK3_h07_1 EU4688
EU843666.1 gg_id:305138 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8436
GQ347477.1 gg_id:536407 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ347
EU981245.1 gg_id:334455 sulfate reducing living bench scale aquifer packed bed clone D23_FB EU981
GQ350920.1 gg_id:583859 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ350
EU472521.1 gg_id:299958 Angola colobus feces clone EAC_2_aaa02d03 EU4725
AB198479.1 gg_id:135780 termite gut wall fraction clone RsW01-047 AB1984
EU778712.1 gg_id:343538 Springbok feces clone SBSD_aaa03f04 EU7787
AB100009.1 gg_id:79430 inactive deep-sea hydrothermal vent chimneys clone IndB4-4 AB1000
X75622.1 gg_id:2243 Blattabacterium species X75622
Z35665.1 gg_id:2237 Mastotermes darwiniensis endosymbiont Z35665
X96730.1 gg_id:2236 Blattabacterium sp X96730
Y13889.1 gg_id:2240 Coleomegilla maculata male-killing endosymbiont male-killing Y13889
AJ009687.1 gg_id:2241 Flavobacterium sp AJ0096
AJ318122.1 gg_id:28868 Waste-gas biofilter clone BIfcii9 AJ3181
DQ395551.1 gg_id:154321 deep-sea octacoral clone ctg_CGOCA86 DQ395
U87105.1 gg_id:2252 Ornithobacterium rhinotracheale str. LMG 14578 U87105
GQ350671.1 gg_id:573049 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ350
FJ710777.1 gg_id:544037 Abundance and microbial long-term operated anammox biofilm reactors initiated ino FJ7107
AM930294.1 gg_id:539275 gradual cooling stage mass and its spatial composting clone SMG46 AM930
AY947955.1 gg_id:141673 Synchrony and seasonality two temperate rivers USA: Massachusetts Ipswich River c AY9479
EU801225.1 gg_id:356497 It's all ranking aquatic Chesapeake Bay MD clone 3C002472 EU801
EU005803.1 gg_id:271719 Major activity inside and outside natural iron-fertilized phytoplankton bloom 3 micro EU0058
AY948068.1 gg_id:141750 Synchrony and seasonality two temperate rivers USA: Massachusetts Parker River cl AY9480
AY225660.1 gg_id:95582 organic-rich substrate exposed to Mid-Atlantic Ridge vent clone AT-co1 AY2256
AF314421.1 gg_id:49398 aerobic phosphorus-removal ecosystem clone PHOS-HE28 AF3144
DQ071117.1 gg_id:132660 marine surface water clone SJC3.17 DQ071
AB125062.1 gg_id:100077 Owenweeksia hongkongensis str. UST20020801 AB1250
GQ351219.1 gg_id:590041 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Eastern GQ351
AY947978.1 gg_id:141856 Synchrony and seasonality two temperate rivers USA: Massachusetts Ipswich River c AY9479
GU230411.1 gg_id:585843 Multilevel approach along Rio de la Plata-South Atlantic Ocean coastal water clone A GU230
EU283529.1 gg_id:278327 Model Early Earth Harbors Deeply Divergent Divisions Anderson Lake clone A1856 EU2835
EU544839.1 gg_id:276455 free-living particle- aggregate- archaeal and Laptev Sea 1.0-60 um size fraction (susp EU5448

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GQ350649.1 gg_id:556934 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ350
FJ152979.1 gg_id:319175 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX4CI FJ1529
GQ349547.1 gg_id:572077 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ349
EU801442.1 gg_id:326250 It's all ranking aquatic Chesapeake Bay MD clone 3C002735 EU801
EF108212.1 gg_id:192107 Coccinistipes vermicola str. IMCC1411 EF1082
EF572500.1 gg_id:231342 Coco's Island site 23 marine clone S23_599 EF5725
EF659422.1 gg_id:240929 mixed granule anammox reactor clone KIST-JJY049 EF6594
GQ350126.1 gg_id:563364 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ350
GQ037609.1 gg_id:374923 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu4 GQ037
EF648062.1 gg_id:254309 dynamics during produced water treatment aerobic activated sludge clone BH58 EF6480
AF468278.1 gg_id:80562 Arctic pack ice; northern Fram Strait; 80 31.1 N; 01 deg 59.7 min E clone ARKIA-105 AF4682
EU133759.1 gg_id:256454 tallgrass prarie soil clone FFCH3291 EU1337
EF646134.1 gg_id:243514 Potential interactions particle- anammox and archaeal partners namibian Namibian u EF6461
AM279205.1 gg_id:171966 Cytophaga-Flavobacterium-Bacteroides coastal North Sea marine water clone NorS AM279
EF572825.1 gg_id:232976 Coco's Island site 23 marine clone S23_924 EF5728
EF645943.1 gg_id:257079 Potential interactions particle- anammox and archaeal partners namibian Namibian u EF6459
AY907766.1 gg_id:136952 identification picoplankton contrasting waters Arabian Sea water clone A712014 AY9077
EF572198.1 gg_id:228608 Coco's Island site 23 marine clone S23_297 EF5721
GQ349023.1 gg_id:567825 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ349
GQ350545.1 gg_id:579668 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ350
DQ395555.1 gg_id:156530 deep-sea octacoral clone ctg_CGOCA81 DQ395
GQ350398.1 gg_id:589627 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ350
EU005823.1 gg_id:265044 Major activity inside and outside natural iron-fertilized phytoplankton bloom 3 micrc EU0058
AB239762.1 gg_id:146507 isotopic evidence ectosymbiosis between filamentous and stalked barnacle (Cirriped AB2397
AY693832.1 gg_id:103624 anaerobic sludge clone EUB72-2 AY6938
GQ350620.1 gg_id:537682 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ350
DQ071031.1 gg_id:131321 marine surface water clone Chl1.10 DQ071
GQ349831.1 gg_id:535025 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ349
AY922203.1 gg_id:113227 whalefall clone 131637 AY9222
AF452594.1 gg_id:63864 CFB group clone ML110J-8 AF4525
GQ259251.1 gg_id:511108 Microbial activities coastal marine sediments and column Svalbard surface water clc GQ259
EU801471.1 gg_id:337438 It's all ranking aquatic Chesapeake Bay MD clone 3C002767 EU801
AM279183.1 gg_id:163266 Cytophaga-Flavobacterium-Bacteroides coastal North Sea marine water clone NorS AM279
GQ340290.1 gg_id:571029 Prokaryotic Marathonas Reservoir Greece water column clone B08-115-BAC GQ340
EF645942.1 gg_id:245184 Potential interactions particle- anammox and archaeal partners namibian Namibian u EF6459
GQ348600.1 gg_id:561299 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ348
DQ009096.1 gg_id:122966 bacterioplankton clone SPOTSAPR01_5m129 DQ009
GQ356156.1 gg_id:585736 biomarkers ammonia oxidation activity anaerobic ammonium-oxidation (Anammox) GQ356
GQ348151.1 gg_id:549398 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ348
FJ169200.1 gg_id:305331 microbial and polyketide biosynthetic potential palmerolide-producing tunicate Synoi FJ1692
AB189346.1 gg_id:113820 cold seep sediment clone JT58-23 AB1893

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AY344418.1 gg_id:91513 Lake Kauhako 30 m clone K2-30-6 AY344
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EF092242.1 gg_id:268391 Persistent Axinella corrugata Flavobacteriaceae clone B276_B9 EF0922
AF382110.1 gg_id:79316 bacterioplankton clone ZA2515c AF382
FJ403071.1 gg_id:363690 Disease- changes healthy and diseased colonies Caribbean coral Montastrea faveolat FJ4030
FJ203162.1 gg_id:352599 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c FJ2031
EF016472.1 gg_id:196863 Near real-time autonomous detection marine on coastal mooring Monterey Bay Calif EF0164
AY947919.1 gg_id:142782 Synchrony and seasonality two temperate rivers USA: Massachusetts Ipswich River c AY9479
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EU703443.1 gg_id:457098 lakes on Eastern Tin Plateau freshwater lake altitude 4219 masl clone XZXXH35 EU7034
EF471629.1 gg_id:271550 Fast Screening and Estuarine Operon Libraries whole surface water Chesapeake Bay (EF4716
EU394563.1 gg_id:324593 Coccolithophore bloom dynamics shape (NE-Atl) northern Bay Biscay pelagic particle EU3945
FJ615174.1 gg_id:592284 Microbial dynamics seasonally fjord: British Columbia Saanich Inlet depth 10m anoxic FJ6151
AF361205.1 gg_id:20456 mesoeutrophic reservoir clone 06 AF3612
EU010171.1 gg_id:239916 Biogeography Singapore seawaters seawater clone B82 EU0101
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EU801202.1 gg_id:328847 It's all ranking aquatic Chesapeake Bay MD clone 3C002449 EU801
EU236348.1 gg_id:295497 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg91A10 EU236
EU246821.1 gg_id:242251 polyphasic description Pocillopora meandrina Palmyra Atoll Calcinus obscurus abdon EU246
AF521195.1 gg_id:69811 Brumimicrobium glaciale str. ACAM 644 AF521
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FN433447.1 gg_id:588456 patterns and flavobacterial clades contrasting masses North Atlantic marine water cl FN433
EU592398.1 gg_id:564878 Seasonal changes Salton Sea hypersaline water clone SSW85N EU592
EU652656.1 gg_id:277616 Seasonal variation microbial Yel Sea sediment clone B8S-139 EU652
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EU803886.1 gg_id:351352 It's all ranking aquatic Lake Gatun clone 5C231539 EU803
AM930461.1 gg_id:264938 involved Tripneustes gratilla (Echinoidea) cloning and FISH host body wall lesions cl AM930
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FJ889654.1 gg_id:547999 Aequorivita sp. str. ZS1-6 FJ8896
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AY187689.1 gg_id:80619 Algibacter lectus str. KMM 3902 AY187
AY612758.1 gg_id:140533 Formosa sp. str. 18III/A01/079 AY612
AM946640.1 gg_id:265850 Tamlana sp. Aga22 AM946
EU221275.1 gg_id:245619 Tamlana agarivorans str. JW-26 EU221
AY608407.1 gg_id:106561 Aquimarina muelleri str. KMM 6021 AY608
DQ660387.1 gg_id:172234 Aquimarina sp. str. HJ055 DQ660
FJ490365.1 gg_id:547485 Aquimarina sp. str. CNURIC 011 FJ4903
FN554605.2 gg_id:540893 Aquimarina latercula str. HJ5 FN554

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AM113977.1 gg_id:160694 Aquimarina intermedia R-28470 AM113
DQ357763.1 gg_id:149899 Aquimarina sp. SW42 DQ357
AY987367.1 gg_id:122067 Gaetbulimicrobium brevivitae str. SMK-19 AY9873
AM259874.1 gg_id:207314 Spatial sponge- Mediterranean Tethya aurantia sponge cortex clone TAA-10-29 AM259
DQ357758.1 gg_id:146214 Marine Hatchery: Balance Between Pathogenic and Potentially Probiotic Strains adu DQ357
EF536748.1 gg_id:253613 Arenibacter echinorum str. KMM 6032 EF5367
NR_024790.1 gg_id:561384 Arenibacter troitsensis str. KMM 3674 NR_024
AY398697.1 gg_id:99911 Bergeyella sp. h1890 AY3986
AY694005.1 gg_id:102654 Calefactosor saleffrenus str. HFD AY6940
NR_025827.1 gg_id:555628 Bizionia paragorgiae str. KMM 6029 NR_025
AF513399.1 gg_id:55449 Gelidibacter sp. str. 13-4 AF5133
AY694004.1 gg_id:102497 Calefactosor gelidisalsuginis str. IC164 AY6940
AY643075.1 gg_id:129359 Capnocytophaga canimorsus str. CIP 103936 AY6430
DQ009624.2 gg_id:125969 Capnocytophaga haemolytica str. A0404 DQ009
U41350.1 gg_id:2363 Capnocytophaga ochracea str. ATCC 27872 T U41350
GQ000769.1 gg_id:469333 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ000
AM179907.1 gg_id:149379 Identification microflora (Oncorhynchus mykiss) rainbow trout intestine clone G3-1: AM179
FJ976269.1 gg_id:582773 Interindividual healthy human oral microbiota mouth clone 7BB410 FJ9762
AF538853.1 gg_id:59534 Capnocytophaga sp. oral strain str. P4G_35 P4 oral AF5388
AF543298.1 gg_id:56144 Capnocytophaga ochracea str. ChDC OS48 AF5432
X67609.1 gg_id:2373 Capnocytophaga sputigena str. ATCC 33612 X67609
FJ976207.1 gg_id:577305 Interindividual healthy human oral microbiota mouth clone 3405 FJ9762
AY643076.1 gg_id:133677 Capnocytophaga cynodegmi str. CIP 103937 AY6430
AF385494.1 gg_id:71957 subgingival plaque clone DZ074 AF3854
AY429469.1 gg_id:102901 Capnocytophaga sp. P2 oral strain str. P4P_12 AY4294
DQ009623.1 gg_id:125439 Capnocytophaga leadbetteri str. AHN8855 DQ009
AM420201.1 gg_id:249209 Noma subgingival plaque clone 502H07(oral) AM420
AY005076.1 gg_id:70616 subgingival dental plaque clone BB167 AY0050
AF118419.1 gg_id:31284 Coenonia anatina str. 726-82 AF1184
GQ110815.1 gg_id:465094 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ110
EU432438.1 gg_id:270675 variation and endosymbiotic phenotypically- sea urchin Strongylocentrotus intermec EU4324
AY008312.1 gg_id:73803 Capnocytophaga sp. oral clone EL043 AY0083
FJ773364.1 gg_id:530224 biofilm incipient early childhood caries dental plaque clone SK117 FJ7733
AM420168.1 gg_id:245563 Noma subgingival plaque clone 501C07(oral) AM420
X67610.1 gg_id:2370 Capnocytophaga ochracea str. ATCC 33596 X67610
GU410280.1 gg_id:533210 Human Oral Microbiome oral cavity GU410
EU000223.1 gg_id:323900 Cellulophaga algicola str. KOPRI_22146 EU000
NR_028661.1 gg_id:569170 Cellulophaga algicola str. IC166; ACAM 630 NR_028
AB032512.1 gg_id:28162 Cellulophaga lytica str. IFO16021 AB0325
DQ311648.1 gg_id:147086 Cellulophaga sp. str. QY201 DQ311
AB032510.1 gg_id:23812 Cellulophaga lytica str. IFO15986 AB0325

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AB100840.1 gg_id:99263 Cellulophaga pacifica str. KMM 3664 AB100
AB100842.1 gg_id:99572 Cellulophaga pacifica str. KMM 3915 AB100
DQ356486.1 gg_id:145374 Cellulophaga sp. str. CC11 DQ356
DQ357766.1 gg_id:146410 Cellulophaga sp. SED18 DQ357
AF539754.1 gg_id:83115 Cytophaga sp. str. E46 AF5397
EU443205.1 gg_id:272395 Cellulophaga sp. str. EM41 EU443
FJ439599.1 gg_id:362021 Cellulophaga sp. str. KT8 FJ4395
AF235118.1 gg_id:45411 Cytophaga sp. str. KT02ds20 AF235
EU626632.1 gg_id:278303 variation and endosymbiotic phenotypically- sea urchin Strongylocentrotus intermec EU626
DQ357768.1 gg_id:149157 Cellulophaga sp. SED13 DQ357
NR_025287.1 gg_id:568483 Cellulophaga fucicola str. NN015860; LMG 18536 NR_02
EF204446.1 gg_id:201471 Chryseobacterium sp. H9 EF2044
FJ455451.1 gg_id:571052 Chryseobacterium daecheongense str. BF-Y6 FJ4554
NR_028942.1 gg_id:584982 Chryseobacterium defluvii str. B2; DSM 14219 NR_02
FJ887959.1 gg_id:434553 Chryseobacterium gleum FJ8879
AY468478.1 gg_id:102517 Chryseobacterium sp. str. LMG 19914 AY4684
GU296676.1 gg_id:585426 Chryseobacterium sp. str. ANSL GU296
AY770428.1 gg_id:128035 insect gut clone AY7704
DQ117545.1 gg_id:138622 structure (Citrullus vulgaris SCHARD.) -based approaches and terminal fragment len DQ117
AB264127.1 gg_id:162873 Chryseobacterium sp. str. TDMA-39 AB2641
AY468481.1 gg_id:106431 Chryseobacterium indologenes str. LMG 12856; NCTC 11409 AY4684
AJ843132.1 gg_id:102871 Chryseobacterium taichungense str. TWGS-8 AJ8431
EU221399.1 gg_id:256453 Chryseobacterium indologenes str. H2S10 EU2213
EU598809.2 gg_id:580026 Chryseobacterium sp. str. CH8 EU5988
AM232813.1 gg_id:161516 Chryseobacterium indologenes str. LMG 8337 AM232
EU121860.1 gg_id:238528 Chryseobacterium letacus str. CW-H EU1218
AY468467.1 gg_id:106164 Chryseobacterium sp. LDA39 G1966 12a AY4684
AY468479.1 gg_id:102672 Chryseobacterium joostei str. LMG 18208 AY4684
AM489609.1 gg_id:188834 Chryseobacterium aurantiacum str. DSM 18605 = LMG 237 AM489
EU999734.1 gg_id:345921 Chryseobacterium sp. str. KM EU999
DQ673671.1 gg_id:167569 Chryseobacterium sp. str. RHA3-1 DQ673
AY468458.1 gg_id:101293 Chryseobacterium sp. JIP 108/83 AY4684
EU862562.1 gg_id:328172 Chryseobacterium sp. str. ABc1 EU8625
EU057840.1 gg_id:250695 Chryseobacterium sp. WOF18(2)-4 EU0578
AY468460.1 gg_id:105095 Chryseobacterium sp. JIP 16/96 AY4684
EU057841.1 gg_id:251504 Chryseobacterium sp. CH33-3 EU0578
GQ225686.1 gg_id:392179 Chryseobacterium sp. str. HMC6043 GQ225
DQ166169.3 gg_id:155194 Chryseobacterium sp. str. TSBY-67 DQ166
GQ070524.1 gg_id:422863 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ070
GQ098998.1 gg_id:372442 Topographical and Temporal Human Skin Microbiome skin interdigital web space clo GQ098
EF591302.1 gg_id:230912 Chryseobacterium sp. str. JS6-6 EF5913

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AM748691.1 gg_id:254510 Chryseobacterium sp. str. 10-106 AM748
AJ871397.1 gg_id:113156 Chryseobacterium sp. str. R-23566 AJ8713
EU538611.1 gg_id:282420 profile human microbiota antecubital fossa (inner elbow) skin clone nbt233g03 EU5386
AJ715377.1 gg_id:105032 Chryseobacterium formosense str. CC-H3-2 AJ7153
FJ378901.1 gg_id:359773 Chryseobacterium sp. str. PF-45 FJ3789
DQ530068.1 gg_id:161519 Chryseobacterium sp. CI06 DQ530
AY599654.1 gg_id:102549 Chryseobacterium sp. str. TB2-6-I AY5996
EU869190.1 gg_id:318853 Chryseobacterium sp. str. VQ-6316s EU8691
AM232806.1 gg_id:153966 Chryseobacterium sp. F-Fue-04IIIaaaa AM232
EU182844.1 gg_id:242035 Chryseobacterium sp. str. MH15 EU1828
EF077177.1 gg_id:258002 Chryseobacterium daejeonense str. RB-18 EF0771
EF591303.1 gg_id:229762 Chryseobacterium sp. str. JS17-8 EF5913
AY427792.1 gg_id:102191 Chryseobacterium sp. str. UOF CO294 AY4277
EU538930.1 gg_id:284702 profile human microbiota antecubital fossa (inner elbow) skin clone nbt95d09 EU5389
AM773820.1 gg_id:242921 Chryseobacterium gregarium str. DSM 19109 = LMG 240 AM773
GU138380.1 gg_id:549660 Chryseobacterium sp. str. THG 15 GU138
GQ093801.1 gg_id:408201 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ093
EU999735.1 gg_id:345793 Chryseobacterium sp. str. CTM EU9997
GU451165.1 gg_id:519304 Chryseobacterium sp. str. BMC-1 GU451
GU458265.1 gg_id:526859 Chryseobacterium sp. str. HT4B GU458
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DQ301786.1 gg_id:146939 Chryseobacterium sp. str. PHD-9 DQ301
EF077176.1 gg_id:240678 Chryseobacterium moechotypicola str. RB-02 EF0771
EF601827.1 gg_id:232408 Chryseobacterium sp. str. NX12 EF6018
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DQ869047.1 gg_id:243833 Chryseobacterium sp. str. WO DQ869
EU375848.1 gg_id:264030 Elizabethkingia miricola str. L99; CGMCC 2295 EU3758
EU797623.1 gg_id:342882 Chryseobacterium sp. str. DP2 EU7976
DQ673675.1 gg_id:170460 Chryseobacterium sp. str. PSB1-20 DQ673
EU537783.1 gg_id:283836 profile human microbiota antecubital fossa (inner elbow) skin clone nbt79g03 EU5377
EF540483.1 gg_id:219518 Chryseobacterium sp. 12_4K EF5404
DQ530083.1 gg_id:160692 Chryseobacterium sp. CI21 DQ530
EF076759.1 gg_id:185444 Chryseobacterium daeguense str. K105 EF0767
DQ314742.1 gg_id:147749 Chryseobacterium stagni str. 10-59 DQ314
EF601823.1 gg_id:229949 Chryseobacterium sp. str. HX31 EF6018
AB193101.1 gg_id:112081 Chryseobacterium shigense str. GUM-Kaji AB1931
AY751083.1 gg_id:99776 Chryseobacterium sp. AUR9 AY7510
EU598813.2 gg_id:578292 Chryseobacterium sp. str. CH34 EU5988

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AY599653.1 gg_id:102388 Chryseobacterium sp. str. TB2-1-I AY5996
AY050493.1 gg_id:17076 Chryseobacterium indologenes str. SB1 AY0504
AY230767.1 gg_id:82614 Flavobacterium sp. 'Smarlab BioMol-2300973' str. Smarlab BioMol-2300973 'Smarlab AY2307
EF644913.1 gg_id:248031 Chryseobacterium kwangyangense str. CW9 EF6449
DQ673672.1 gg_id:162999 Chryseobacterium sp. str. RHA2-9 DQ673
EU598815.2 gg_id:585876 Chryseobacterium sp. str. CH30 EU5988
AY883415.1 gg_id:143124 Chryseobacterium soldanellicola str. PSD1-4 AY8834
GU385848.1 gg_id:514346 Chryseobacterium sp. str. QT2 GU385
EF608166.1 gg_id:554568 Chryseobacterium sp. str. HT11 EF6081
AB024308.1 gg_id:32882 Flavobacteriaceae str. 2 AB0243
GQ383901.1 gg_id:559864 Chryseobacterium sp. str. M13 GQ383
DQ530065.1 gg_id:161375 Chryseobacterium sp. CI05 DQ530
DQ673676.1 gg_id:168204 Chryseobacterium sp. str. PSB1-1 DQ673
EF204449.1 gg_id:199834 Chryseobacterium sp. H30 EF2044
AM232812.1 gg_id:160223 Chryseobacterium gleum str. CCUG 14555 AM232
FJ671737.1 gg_id:515176 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6717
AY278484.2 gg_id:87806 Chryseobacterium sp. str. jll AY2784
GQ023905.1 gg_id:485764 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbu GQ023
DQ394928.1 gg_id:153040 harbor sediment clone VHS-B3-5 DQ394
AF217562.1 gg_id:32560 Chryseobacterium sp. str. FR2 AF2175
GQ103633.1 gg_id:389542 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ103
AB245373.1 gg_id:149000 Chryseobacterium ginsengisoli str. Gsoil 248 AB2453
DQ256729.1 gg_id:142251 Chryseobacterium wanjuense str. R2A10-2 DQ256
GU353121.1 gg_id:575598 Chryseobacterium sp. str. CH21 GU353
AM159183.2 gg_id:150743 Chryseobacterium hispanicum str. VP48 AM159
GQ069603.1 gg_id:411327 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ069
AY468483.1 gg_id:106749 Chryseobacterium sp. UOF CR4095 AY4684
EU057843.1 gg_id:253242 Chryseobacterium sp. 3Ablue EU0578
AY163576.1 gg_id:75119 Croceibacter atlanticus str. HTCC2559T; KCTC 12090T; ATCC BAA-628T AY1635
DQ811906.1 gg_id:167133 mangrove soil clone MSB-3B12 DQ811
DQ481462.1 gg_id:176649 Dokdonia donghaensis str. MED134 DQ481
AF207075.1 gg_id:27969 Chryseobacterium meningosepticum str. CIP 6057 AF2070
AM945588.1 gg_id:275181 Eudora adriatica AM945
AY154889.1 gg_id:57759 Flavobacterium sp. str. SR1 AY1548
AB016515.1 gg_id:2312 Flavobacterium columnare str. EK-28 (IAM 14820) AB0165
AB010952.1 gg_id:2311 Flavobacterium columnare str. FK 401 AB0109
EU431785.1 gg_id:544271 Troglobitic (Cansiliella) on specialized feeding apparatus calcium carbonate (moonmi EU4317
AB010951.1 gg_id:2310 Flavobacterium columnare str. IAM 14301 (NCMB2248T) AB0109
DQ005505.1 gg_id:129444 Flavobacterium columnare str. Kokanee-94 DQ005
AJ318907.2 gg_id:77276 ED5 earthworm gut AJ3189
EU599190.1 gg_id:278190 Flavobacterium denitrificans str. JS14-1 EU5991

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EU037341.2 gg_id:277429 structure landfill sediments receiving long-term augmentations wastes chromium co EU037
AB455257.1 gg_id:333236 Flavobacterium frigidarium str. NBRC 102676 AB455
AY771738.1 gg_id:144927 Flavobacterium frigidarium S5-15 AY771
AF321008.2 gg_id:37648 Flavobacterium sp. str. GOBB3-C101 AF321
AF235124.1 gg_id:28033 Cytophaga sp. str. KT0234A AF235
AF468425.1 gg_id:80437 Arctic sea ice ARK10164 AF468
AF321019.2 gg_id:19998 Flavobacterium sp. str. GOBB3-C103-3 AF321
AB275999.1 gg_id:222700 Flavobacterium kamogawaensis str. KG12 AB275
GU073293.1 gg_id:580196 Flavobacterium sp. str. LW30 GU073
AB455260.1 gg_id:311116 Flavobacterium psychrolimnae str. NBRC 102679 AB455
AB078060.1 gg_id:58629 Flavobacterium psychrophilum str. IFO 15942 AB078
AM177631.1 gg_id:149279 Flavobacterium sp. str. WB 4.3-34 AM177
AM265623.1 gg_id:159982 Flavobacterium hercynium str. WB 4.2-33 AM265
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EU431710.1 gg_id:544153 Troglobitic (Cansiliella) on specialized feeding apparatus calcium carbonate (moonmi EU431
FJ958328.1 gg_id:418781 Flavobacterium sp. str. Tibet-YD5000-3 FJ9583
EU057853.1 gg_id:237807 Flavobacterium sp. 20I EU057
AJ551174.1 gg_id:93705 Cytophaga sp. An36 AJ5511
AM230488.1 gg_id:152029 Flavobacterium johnsoniae str. DSM 425 AM230
EU707556.1 gg_id:333324 Flavobacterium sp. str. YC6718 EU707
AM921624.1 gg_id:245846 Flavobacterium pectinovorum PhyCEm-99 AM921
DQ640006.1 gg_id:161549 Flavobacterium sp. str. PR01 DQ640
AM934631.1 gg_id:264229 Flavobacterium sp. str. WB2.1-16 AM934
AB496407.1 gg_id:543988 Flavobacterium sp. str. S22202a AB496
AJ557888.1 gg_id:88003 Flavobacterium micromati str. LMG 21919 AJ5578
FN397666.1 gg_id:382056 Flavobacterium sp. str. PON14 FN397
AM230490.1 gg_id:151743 Flavobacterium pectinovorum str. DSM 6368 AM230
DQ778315.1 gg_id:172143 Flavobacterium sp. YO51 DQ778
EU057848.1 gg_id:257608 Flavobacterium sp. 19C EU057
EU636033.1 gg_id:279577 Antarctic str. L10 EU636
AM921621.1 gg_id:250589 Flavobacterium johnsoniae PhyCEm-72 AM921
AM934672.1 gg_id:267882 Flavobacterium sp. str. WB4.3-66 AM934
AY599656.1 gg_id:102856 Flavobacterium sp. str. TB4-4-II AY599
AY550033.1 gg_id:104940 Sporocytophaga cauliformis str. 9726R AY550
EF395377.1 gg_id:222394 Cytophaga sp. str. 4D9 EF3953
FJ786050.1 gg_id:539182 Flavobacterium sp. str. I-111-19 FJ7860
EF640932.1 gg_id:254023 Chryseobacterium sp. str. GR15 EF6409
EU099872.1 gg_id:257508 Flavobacterium sp. str. CJ4 EU099
EU057845.1 gg_id:257586 Flavobacterium sp. CH16-1 EU057
EU057851.1 gg_id:245636 Flavobacterium sp. PR30-9 EU057

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EU104118.1 gg_id:320418 Evidence Comamonadaceae determinants settling performance activated sludge clo EU104
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DQ530073.1 gg_id:161601 Flavobacterium johnsoniae CI04 DQ530
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EF601819.1 gg_id:231100 Flavobacterium sp. str. WX3 EF6018
DQ478946.1 gg_id:158263 Flavobacterium sp. QLX6 DQ478
AB075231.1 gg_id:36697 Flavobacterium limicola str. ST-10 AB075
AB075232.1 gg_id:34165 Flavobacterium limicola str. ST-92 AB075
AJ601392.1 gg_id:95581 Flavobacterium xanthum AJ6013
AF030380.1 gg_id:2327 Flavobacterium xanthum str. ACAM 81(T) AF0303
GQ009789.1 gg_id:499875 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw77 GQ009
EU431833.1 gg_id:561092 Troglobitic (Cansiliella) on specialized feeding apparatus calcium carbonate (moonmi EU4318
DQ228399.1 gg_id:142636 microbial compositions two subglacial possible role microbes chemical weathering p DQ228
EF019396.1 gg_id:211062 aspen rhizosphere clone Elev_16S_629 EF0193
GQ249374.1 gg_id:555934 Research on biodiversity sludge bioflim Biological Aeration Filter clone B16 GQ249
AY212736.1 gg_id:99774 water 5 m downstream manure clone 41ds5 AY2127
EU432473.1 gg_id:266040 variation and endosymbiotic phenotypically- sea urchin Strongylocentrotus intermec EU4324
FJ716000.1 gg_id:588086 Diet- gut microbiota Lumbricus rubellus fingerprinting technique and cloning intestina FJ7160
GQ084774.1 gg_id:445836 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw26 GQ084
GQ249524.1 gg_id:579829 Microbial anaerobic sediments Bay Cadiz (Spain) marine sediment: 6-8 cm layer clor GQ249
AM934667.1 gg_id:268494 Flavobacterium sp. str. WB4.1-56 AM934
AF289165.1 gg_id:71577 freshwater clone PRD01b005B AF2891
DQ264555.1 gg_id:144460 universal microarray broader than typical library when sampling subsurface groundv DQ264
DQ856509.1 gg_id:252738 intestinal microflora Chinese mitten crab (Eriocheir sinensis) clone C1M DQ856
EU431740.1 gg_id:563689 Troglobitic (Cansiliella) on specialized feeding apparatus calcium carbonate (moonmi EU4317
AM934683.1 gg_id:263519 Flavobacterium sp. str. BF134 AM934
EF424395.1 gg_id:210562 Flavobacterium sp. str. IP10 EF4243
DQ628917.1 gg_id:173779 sequences Arctic glacier subglacial water ice or sediment clone BFA 7C DQ628
AM110990.1 gg_id:140778 Flavobacterium sp. str. 3037 AM110
AM230493.1 gg_id:156139 Flavobacterium succinicans str. DSM 4003 AM230
DQ501350.1 gg_id:198748 Seasonal dynamics free-living and particle- four lakes northeastern Germany freshw DQ501

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GQ389164.1 gg_id:509696 quality deterioration drinking system during serious red water outbreak clone D32 GQ389
FJ517669.1 gg_id:510071 Disturbing epithelial homeostasis metazoan Hydra leads drastic changes microbiota e FJ5176
FN421997.1 gg_id:586494 proteogenomics physiology phyllosphere clover clone 5_H09 FN421
EF648152.1 gg_id:250428 dynamics during produced water treatment aerobic activated sludge clone XJ104 EF6481
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EU109724.1 gg_id:248774 Flavobacterium sp. str. H7 EU109
GQ406174.1 gg_id:511461 Benthic submerged sinkhole ecosystems sediment clone -45-4 GQ406
GU305854.1 gg_id:558583 Research on changes structure during algae outbreak oligotrophic lakes (YangHe res GU305
AJ318198.1 gg_id:21369 Waste-gas biofilter clone BIwi5 AJ3181
EU802008.1 gg_id:340945 It's all ranking aquatic Chesapeake Bay MD clone 3C003394 EU802
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AB180738.1 gg_id:102656 Flavobacterium granulensis str. Kw05 AB180
DQ222427.1 gg_id:141129 Flavobacterium sp. str. GH1-10 DQ222
FJ535187.1 gg_id:556344 Contamination risk vegetables Arcobacter during post-harvest processing water carrc FJ5351
AM934669.1 gg_id:274086 Flavobacterium sp. str. WB4.3-36 AM934
EF467491.1 gg_id:204202 situ microelectrode voltammetry sulfur-oxidizing biofilms Frasassi sulfidic cave strear EF4674
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DQ658240.1 gg_id:168113 Flavobacterium arcticum DQ658
DQ256316.1 gg_id:141407 subsurface water clone EV818BHEB5102502SAR27F80 DQ256
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GQ000816.1 gg_id:469382 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ000
GQ079017.1 gg_id:413256 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ079
EF632770.1 gg_id:244921 Unique microbial contrasting aquatic altitude Andean Altiplano (northern Chile) fresh EF6327
FJ593904.2 gg_id:538912 Flavobacterium sp. str. -8 FJ5939
L39067.1 gg_id:73974 Flavobacterium hibernum str. ATCC51468 L39067

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EF520552.1 gg_id:227962 structure lakes: what controls ? acid-impacted lake clone ADK-MOe02-29 EF5205
AM230492.1 gg_id:156027 Flavobacterium succinicans str. DSM 4002 AM230
AM230486.1 gg_id:152630 Flavobacterium flevense str. DSM 1076 AM230
AY212593.1 gg_id:99956 water 20 m downstream manure clone 142ds20 AY2125
GQ395239.1 gg_id:570635 Flavobacterium sp. str. XAS590 GQ395
FJ529995.1 gg_id:510944 Initial ammonia- and nitrite-oxidizing compromises successful nitritation counter-diffu FJ5299
CU466733.1 gg_id:350201 Evry wastewater treatment plant anoxic basin clone CU466
DQ521513.1 gg_id:193156 Antarctic lake ice cover clone ANTLV2_D10 DQ521
FJ716009.1 gg_id:566584 Diet- gut microbiota Lumbricus rubellus fingerprinting technique and cloning intestina FJ7160
AF336355.1 gg_id:32387 Flavobacterium sp. str. Wuba46 AF3363
DQ298763.1 gg_id:143021 Effect Nutrient Periodicity upon Microbial Dynamics exposed 7-day nutrient flux DQ298
AM230494.1 gg_id:156296 Flavobacterium succinicans str. DSM 4001 AM230
FN547416.1 gg_id:574039 Flavobacterium sp. str. WG2 FN5474
AJ786797.1 gg_id:108074 Flavobacterium sp. R-21935 AJ7867
DQ298762.1 gg_id:142500 Effect Nutrient Periodicity upon Microbial Dynamics exposed 7-day nutrient flux DQ298
DQ521514.1 gg_id:186502 Antarctic lake ice cover clone ANTLV2_D11 DQ521
DQ256490.1 gg_id:144140 Flavobacterium johnsoniae Jm162a DQ256
AM934684.1 gg_id:269942 Flavobacterium sp. str. CL1.100 AM934
EF424249.1 gg_id:212836 Isolation and properties alginate-decomposing decomposer alginate rotten algae sun EF4242
AM177633.1 gg_id:148903 Flavobacterium sp. str. WB 4.3-96 AM177
AM412168.1 gg_id:257833 Flavobacterium sp. str. P-131 AM412
EF632769.1 gg_id:253814 Unique microbial contrasting aquatic altitude Andean Altiplano (northern Chile) fresh EF6327
CP000685.1 gg_id:220711 Flavobacterium johnsoniae UW101 str. UW101; ATCC 17061 CP000
DQ264616.1 gg_id:141431 universal microarray broader than typical library when sampling subsurface groundv DQ264
EU340154.1 gg_id:249417 on Aquatic Macrophytes Geothermally Active Area Sedge Bay Yellowstone Lake WY EU3401
AM934651.1 gg_id:267818 Flavobacterium sp. str. WB2.3-68 AM934
EU104097.1 gg_id:348328 Evidence Comamonadaceae determinants settling performance activated sludge clo EU1040
GQ144412.1 gg_id:439710 Flavobacterium sp. str. HMD1045 GQ144
AM934644.1 gg_id:264327 Flavobacterium sp. str. WB2.3-9 AM934
AM934665.1 gg_id:277605 Flavobacterium sp. str. WB3.4-82 AM934
AF090991.1 gg_id:2299 Flavobacterium psychrophilum str. ATCC49418 AF0909
EU703375.1 gg_id:456274 lakes on Eastern Tin Plateau freshwater lake altitude 4298 masl clone XZTSH72 EU7033
FJ362499.1 gg_id:363931 Flavobacterium sp. str. AC17 FJ3624
EU636031.1 gg_id:278951 Antarctic str. N04 EU6360
AM230485.1 gg_id:150856 Flavobacterium aquatile str. DSM 1132 AM230
AJ534682.1 gg_id:76123 ground water deep-well injection disposal site radioactive wastes Tomsk-7 clone S15A AJ5346
DQ659445.1 gg_id:161600 Flavobacterium sp. W6-14 DQ659
GQ281769.1 gg_id:557941 Flavobacterium sp. str. 15C3 GQ281

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EU801647.1 gg_id:320416 It's all ranking aquatic Chesapeake Bay MD clone 3C002993 EU801
EU057846.1 gg_id:252975 Flavobacterium sp. PR6-3-11 EU057
EU340167.1 gg_id:253323 on Aquatic Macrophytes Geothermally Active Area Sedge Bay Yellowstone Lake WY EU340
GQ079944.1 gg_id:429841 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ079
GQ406175.1 gg_id:552287 Benthic submerged sinkhole ecosystems sediment clone CR-36-44 GQ406
AY773135.1 gg_id:109636 swine manure biofilm developed sub-surface f constructed wetland AY773
CU466729.1 gg_id:339084 Evry wastewater treatment plant anoxic basin clone CU466
AY747592.1 gg_id:106211 Flavobacterium columnare AY747
GQ019803.1 gg_id:489865 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu207c06 GQ019
AY947917.1 gg_id:141253 Synchrony and seasonality two temperate rivers USA: Massachusetts Ipswich River c AY947
GQ093968.1 gg_id:395787 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ093
EU801889.1 gg_id:329653 It's all ranking aquatic Chesapeake Bay MD clone 3C003266 EU801
DQ239767.1 gg_id:141821 Flavobacterium sp. str. CC-JY-6 DQ239
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AF321014.2 gg_id:52052 Flavobacterium sp. str. GOBB3-317_2 AF321
DQ372986.1 gg_id:151876 Flavobacterium sp. str. EMB117 DQ372
GU295966.1 gg_id:585224 Flavobacterium sp. str. ARSA-45 GU295
AY947924.1 gg_id:143141 Synchrony and seasonality two temperate rivers USA: Massachusetts Ipswich River c AY947
AF368756.1 gg_id:111856 Flavobacterium sp. str. 3A5 AF368
GQ397015.1 gg_id:559612 Functional unvegetated perhumid recently-deglaciated soils do not correlate shifts s GQ397
AJ440988.1 gg_id:83757 Flavobacterium frigoris str. LMG 21471 AJ4409
GQ018496.1 gg_id:491172 Topographical and Temporal Human Skin Microbiome skin back clone nbu139f08c1 GQ018
GQ144413.1 gg_id:382914 Flavobacterium sp. str. HMD1001 GQ144
EU194891.1 gg_id:368794 Flavobacterium sp. str. B46 EU194
DQ677872.1 gg_id:246431 Flavobacterium sp. BF03-Tho3 DQ677
GQ103400.1 gg_id:465739 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ103
EF632773.1 gg_id:241587 Unique microbial contrasting aquatic altitude Andean Altiplano (northern Chile) fresh EF6327
EF632767.1 gg_id:240042 Unique microbial contrasting aquatic altitude Andean Altiplano (northern Chile) fresh EF6327
DQ889724.1 gg_id:189074 Flavobacterium terrigena str. DS-20 DQ889
EU937955.1 gg_id:318613 Biogeochemistry Iron Oxidation Circumneutral Freshwater Habitat riparian iron oxidi EU937
EU431729.1 gg_id:548887 Troglobitic (Cansiliella) on specialized feeding apparatus calcium carbonate (moonmi EU431
EF523606.1 gg_id:233570 Flavobacterium sp. str. OW3-15-5 EF5236
GQ144414.1 gg_id:442300 Flavobacterium sp. str. HMDW1 GQ144
FJ979836.1 gg_id:426108 Flavobacterium sp. str. tsz03 FJ9798
EU662323.1 gg_id:558797 Productivity- Chemolithoautotrophically Based Sulfidic Karst Systems microbial mat EU662
AB542075.1 gg_id:570482 Formosa sp. str. MA3 AB542
U62915.1 gg_id:17502 Gelidibacter algens str. ACAM 550 A374 U62915
AY694009.1 gg_id:103250 Gelidibacter salicanalis str. IC162 AY694
AJ344133.1 gg_id:25577 Gelidibacter mesophilus str. 2SM29T CECT 5103T AJ3441
AY218549.1 gg_id:81654 penguin droppings sediments clone KD1-108 AY218
AF001369.2 gg_id:39592 Gelidibacter gilvus str. IC158 AF0013

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s__Mesonia algae	65979
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AJ786810.1 gg_id:108084 nitrifying inoculum isolate R-22858 AJ7868
DQ202393.1 gg_id:140497 Gillisia sp. str. UST050418-085 DQ202
AY913287.1 gg_id:114195 forest soil clone DUNssu064 (-2C) (OTU#204) AY9132
AY694007.1 gg_id:102953 Gillisia sandarakina str. IC148 AY6940
DQ365988.1 gg_id:154376 Dominant soils Marble Point and Wright Valley Victoria Land Antarctica soil clone 2C DQ365
EU735632.1 gg_id:315560 archaeal structures and pristine soils China oil contaminated soil Jidong Oilfield clone EU7356
NC_008571.1 gg_id:188892 Gramella forsetii str. KT0803 NC_008
NR_025824.1 gg_id:550580 Gramella echinicola str. KMM 6050 NR_025
AB279985.1 gg_id:223116 Gramella marina str. YM1 AB2799
AB035150.2 gg_id:45877 Haloanella gallinarum str. PS3 AB0351
AY294611.1 gg_id:90366 Kaistella koreensis str. Ko2 AY2946
GQ060011.1 gg_id:452349 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ060
AF385544.1 gg_id:72435 crevicular epithelial cells clone AY017 AF3855
EU104108.1 gg_id:345646 Evidence Comamonadaceae determinants settling performance activated sludge clo EU1041
AY195836.1 gg_id:79767 Kordia algicida str. OT-1 AY1958
AB198086.1 gg_id:140181 Krokinobacter genikus str. Cos-13 AB1980
DQ328321.1 gg_id:155182 Dokdonia donghaensis 2.3 DQ328
AB198087.1 gg_id:140334 Krokinobacter genikus str. CKS-39 AB1980
AY694001.1 gg_id:102038 Lacinutrix copepodicola str. DJ3 AY6940
AY771723.1 gg_id:141174 Psychroserpens burtonensis S3-13 AY7717
AB261015.1 gg_id:166261 Lacinutrix copepodicola str. KMM 3967 AB2610
EU823298.1 gg_id:316012 Leeuwenhoekiella marinoflava str. P37 EU8232
EU823302.1 gg_id:322414 Leeuwenhoekiella marinoflava str. P7 EU8233
DQ294290.1 gg_id:143860 Leeuwenhoekiella blandensis str. MED217 DQ294
AJ780980.1 gg_id:102544 Leeuwenhoekiella aequorea str. LMG 22555 = KMM 6066 AJ7809
AY259509.1 gg_id:94012 Cytophaga sp. 'BSD 22' str. BSD S1 22 AY2595
EU239499.1 gg_id:250747 Aestuariicola saemankumensis str. SMK-142 EU2394
AM712898.1 gg_id:252605 Maribacter forsetii subsp. roscoffensis str. KT02ds18-4=CIP 10950 AM712
EU050897.1 gg_id:238825 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_01_12 EU0508
AY271624.1 gg_id:85665 Maribacter orientalis str. KMM 3947 AY2716
AY271626.1 gg_id:83608 Maribacter ulvicola str. KMM 3951 AY2716
EU287358.1 gg_id:238195 Pacific arctic surface sediment clone S26-58 EU2873
AY271623.1 gg_id:86570 Maribacter sedimenticola str. KMM 3903 AY2716
AF539757.1 gg_id:83542 Cellulophaga sp. str. E6 AF5397
AY258125.1 gg_id:136335 Zobellia sp. str. DG975 AY2581
AF235126.1 gg_id:46683 Cytophaga sp. str. KT02ds18 AF2351
EF536746.1 gg_id:278614 Maribacter sp. str. KMM 6025 EF5367
NR_025263.1 gg_id:543612 Mesonia algae str. KMM 3909 NR_025
DQ367409.1 gg_id:154938 Mesonia motionis str. KMM 6059 DQ367
EU369132.1 gg_id:333131 libraries oyster shell clone MBIOS-16 EU3691
EU328104.1 gg_id:279296 dynamics during bioremediation crude oil contaminated moderate saline soil clone Y EU3281

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g__Psychroserpens
g__Psychroserpens

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s__Psychroserpens burtonensis	66343
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AM403221.1 gg_id:162097 Nitrate-reducing and Denitrifying Marine Aqua Biofilter marine aqua AM403
AB073562.2 gg_id:70926 Cytophaga sp. str. MBIC04684 AB0735
AY576776.1 gg_id:139292 Muricauda sp. str. 3IX/A02/243 AY5767
AY445076.1 gg_id:100173 Muricauda aquimarina str. SW-72 AY4450
AB073566.2 gg_id:101291 Cytophaga sp. I-2029 AB0735
AM990884.1 gg_id:277744 Muricauda sp. MOLA 110 AM990
GQ348772.1 gg_id:582005 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ348
FJ517032.1 gg_id:561872 semiarid 'Tablas de Daimiel National Park' wetland (Central Spain) unravelled water c FJ5170
AY445073.1 gg_id:99698 Muricauda flavescens str. SW-62 AY4450
EU311217.1 gg_id:255094 Myroides odoratimimus str. DB-3 EU3112
GU253339.1 gg_id:579933 Myroides sp. str. MY15 GU253
DQ346455.1 gg_id:154979 during composting libraries compost clone 1B23 DQ346
AY773141.1 gg_id:200923 microbial treated subsurface wetlands swine manure biofilm sub-surface f wetland AY7731
EU000228.1 gg_id:338486 Olleya marilimosa str. KOPRI_22310 EU0002
EF660466.1 gg_id:239512 Olleya marilimosa str. CAM030 EF6604
AY167317.1 gg_id:81957 Polaribacter irgensii str. ANT9210 AY1673
FJ425213.1 gg_id:366819 Polaribacter sp. str. K17-16 FJ4252
U73726.1 gg_id:2357 Polaribacter filamentus str. 215 U73726
GQ349584.1 gg_id:576701 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ349
EU626664.1 gg_id:278366 variation and endosymbiotic phenotypically- sea urchin Strongylocentrotus intermec EU6266
FN433361.1 gg_id:541258 patterns and flavobacterial clades contrasting masses North Atlantic marine water cl FN4333
AF359539.1 gg_id:70110 Alexandrium tamarense PCC 173a AF3595
AM259822.1 gg_id:205919 Spatial sponge- Mediterranean Tethya aurantium sponge endosome clone TAI-8-94 AM259
GQ259215.1 gg_id:563333 Microbial activities coastal marine sediments and column Svalbard deep water clone GQ259
U85884.1 gg_id:2356 Polaribacter sp. str. IC066 U85884
AY922239.1 gg_id:113813 whalefall clone 131792 AY9222
AF468414.1 gg_id:79935 Arctic sea ice ARK10121 AF4684
GQ350084.1 gg_id:536354 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ350
GU061158.1 gg_id:575162 Evaluation culturing methods cultivate previously Yel Sea intertidal beach clone SF1 GU061
DQ356492.1 gg_id:148858 Polaribacter sp. str. AC3 DQ356
U85885.1 gg_id:2355 Polaribacter sp. str. IC063 U85885
FJ425215.1 gg_id:358831 Polaribacter sp. str. K17-17 FJ4252
FJ169204.1 gg_id:329178 microbial and polyketide biosynthetic potential palmerolide-producing tunicate Synoi FJ1692
U14586.1 gg_id:2352 Polaribacter franzmannii str. 301 U14586
AB234297.1 gg_id:141245 Pseudoscourfieldia sp. str. Nak AB2342
AY771712.1 gg_id:108685 Polaribacter irgensii str. S2-53 AY7717
EU703307.1 gg_id:457830 lakes on Eastern Tin Plateau polysaline lake altitude 3204 masl clone XZQH107 EU7033
DQ677858.1 gg_id:241336 Blood Falls Subglacial Outf Taylor Glacier Antarctica subglacial outf clone BF99_C105 DQ677
EU874390.1 gg_id:326705 Psychroflexus sp. str. ISL-14 EU8743
U62911.1 gg_id:2445 Psychroserpens burtonensis str. ACAM167 U62911
EU581702.1 gg_id:277351 Psychroserpens sp. MEBiC05023 EU5817

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AY167341.1 gg_id:81033 Psychroserpens sp. str. ARK10236 AY1673
AM040097.1 gg_id:145548 sandy sediments clone Sylt 1 AM040
EU715009.1 gg_id:313767 Riemerella anatipestifer str. RAf51 EU715
DQ995227.1 gg_id:182298 Riemerella anatipestifer str. RAf34 Minghou/FuZhou DQ995
AY920410.1 gg_id:114330 Riemerella anatipestifer str. RA-T2-122 AY9204
DQ995234.1 gg_id:191124 Riemerella anatipestifer str. RAf28 FuZhou DQ995
EU715007.1 gg_id:332013 Riemerella anatipestifer str. RAf43 EU715
EU715006.1 gg_id:322887 Riemerella anatipestifer str. RAf25 EU715
DQ995231.1 gg_id:184500 Riemerella anatipestifer str. RAf115 Weifang/Shandong DQ995
EU016549.1 gg_id:244701 Riemerella anatipestifer str. RAf46 Fuzhou EU016
DQ078779.1 gg_id:128148 Riemerella anatipestifer str. GDGZ-001 DQ078
DQ995226.1 gg_id:193890 Riemerella anatipestifer str. RAf17 Putian/Fujian DQ995
EU715002.1 gg_id:327523 Riemerella anatipestifer str. RAf10 EU715
AY871827.2 gg_id:112028 Riemerella anatipestifer str. D-28020 AY8718
EF641572.1 gg_id:240665 Riemerella anatipestifer str. RAf75 Fuzhou EF6415
AY871817.2 gg_id:112052 Riemerella anatipestifer str. D-26338 AY8718
U60101.2 gg_id:2261 Riemerella anatipestifer str. ATCC 11845T U6010
DQ995232.1 gg_id:187418 Riemerella anatipestifer str. RAf116 Minghou/FuZhou DQ995
AF181448.1 gg_id:2269 Riemerella columbina str. LMG11607 T AF1814
AF118416.1 gg_id:22221 Riemerella anatipestifer str. 4005 AF1184
EF641573.1 gg_id:243606 Riemerella anatipestifer str. RAf60 Fuzhou EF6415
EF641578.1 gg_id:242618 Riemerella anatipestifer str. RAf63 Fujian EF6415
DQ995233.1 gg_id:189735 Riemerella anatipestifer str. RAf2 Beijin DQ995
AY424899.1 gg_id:98563 Robiginitalea biformata str. HTCC2501 AY4248
DQ330448.1 gg_id:159349 Guerrero Negro hypersaline microbial mat clone 04D2Z14 DQ330
FJ872534.1 gg_id:544563 Robiginitalea sp. str. ZH09 FJ8725
FJ517119.1 gg_id:549936 semiarid 'Tablas de Daimiel National Park' wetland (Central Spain) unravelled water c FJ5171
DQ334626.1 gg_id:187417 Impact metals on sediments heavy metal polluted marine sediment clone HB2-21-1 DQ334
EF612764.1 gg_id:239789 Salegentibacter locisalis str. ISL-4 EF6127
AY682200.1 gg_id:107403 Salegentibacter flavus str. Fg69 AY6822
EF520007.1 gg_id:221915 Salegentibacter sp. str. BH206 EF5200
EU328085.1 gg_id:278201 dynamics during bioremediation crude oil contaminated moderate saline soil clone Y EU3280
FJ425217.1 gg_id:366927 Salinimicrobium sp. str. J14-12 FJ4252
AB206954.1 gg_id:161186 Sandarakinobacter sediminis str. CKA-5 AB2069
DQ514308.1 gg_id:160771 Flavobacterium sp. str. BSs20192 DQ514
EU802116.1 gg_id:323610 It's all ranking aquatic Chesapeake Bay MD clone 3C003523 EU8021
DQ015793.1 gg_id:139885 Antarctic lake water clone ELB16-036 DQ015
FJ203271.1 gg_id:338398 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c FJ2032
AY697923.1 gg_id:107130 Antarctica clone F4C78 AY6979

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EF108215.1 gg_id:190052 Aureimarina marisflavi str. IMCC3054	EF1082
GU345046.1 gg_id:550689 Chryseobacterium sp. str. Sa 1143-06	GU345
FN297836.1 gg_id:558661 Chryseobacterium sp. str. IMMIB L-1519	FN2978
DQ856545.1 gg_id:250944 intestinal microflora Chinese mitten crab (Eriocheir sinensis) clone C3D	DQ856
AJ244696.1 gg_id:70361 Flavobacterium sp. str. V4.ME.09 = MM_2295	AJ2446
AY006468.1 gg_id:45622 Flexibacter echinicida str. F8	AY0064
DQ868688.1 gg_id:165798 Tenacibaculum sp. str. SMB27	DQ868
EU419920.1 gg_id:277347 Tenacibaculum aestuarii str. RW33	EU4199
AY661693.1 gg_id:106077 Tenacibaculum marilutum str. TF-42	AY6616
AB078057.1 gg_id:58630 Tenacibaculum maritimum str. IFO 15946	AB0780
AB032504.1 gg_id:22718 Tenacibaculum mesophilum str. MBIC4357	AB0325
AB078058.1 gg_id:58631 Tenacibaculum ovolyticum str. IFO 15947	AB0780
AM746476.1 gg_id:233273 Tenacibaculum soleae str. LL04 12.1.7	AM746
AM259865.1 gg_id:207908 Spatial sponge- Mediterranean Tethya aurantium sponge cortex clone TAA-10-96	AM259
AM411030.2 gg_id:254395 Tenacibaculum discolor str. LL0411.1.1	AM411
DQ660385.1 gg_id:169324 Tenacibaculum sp. str. HJ103	DQ660
AB078044.1 gg_id:58642 Flexibacter aurantiacus subsp. copepodarum str. IFO 15978 subsp.	AB0780
GU124763.1 gg_id:541877 Tenacibaculum sp. str. 5136_F112_C_98	GU124
AB275606.1 gg_id:216158 Tenacibaculum japonica str. H2M8	AB2756
AM746477.1 gg_id:230495 Tenacibaculum gallaicum str. A37.1	AM746
AF530136.1 gg_id:61125 Tenacibaculum sp. str. MGP-10	AF5301
AM990757.1 gg_id:279493 Tenacibaculum sp. MOLA 533	AM990
EU428783.1 gg_id:259950 Tenacibaculum sp. str. JO-1	EU4287
EF416572.1 gg_id:204367 Tenacibaculum sp. str. a4	EF4165
AY353819.1 gg_id:92882 Flavobacteriaceae G121102s2_2	AY3538
NR_024737.1 gg_id:552292 Tenacibaculum amylolyticum str. MBIC4355	NR_024
GU289641.1 gg_id:562638 Tenacibaculum sp. str. MEBiC06102T	GU289
DQ314760.1 gg_id:145826 Tenacibaculum aestuarii str. SMK-4	DQ314
AF530150.1 gg_id:73960 Tenacibaculum sp. str. MGP-74/AN6	AF5301
DQ395657.1 gg_id:152840 deep-sea octacoral clone ctg_CGOF173	DQ395
FJ457296.1 gg_id:542003 Flexibacter sp. str. S4471	FJ4572
AM412314.1 gg_id:258128 Tenacibaculum adriaticum str. B390	AM412
AF469612.1 gg_id:22873 Tenacibaculum skagerrakense str. D30	AF4696
DQ334344.1 gg_id:150237 Microbial within ornate rock lobster (Panulirus ornatus) water column Panulirus orn	DQ334
AY353820.1 gg_id:92204 Flavobacteriaceae G121102s2_3	AY3538
AF468243.1 gg_id:80559 Arctic pack ice; northern Fram Strait; 80 31.1 N; 01 deg 59.7 min E clone ARKDMS-33	AF4682
AB476295.1 gg_id:542229 Compositional and functional transition epibiotic microbial hydrothermal vent galath	AB4762
DQ660381.1 gg_id:162582 Ulvibacter sp. str. AKS476	DQ660
DQ015799.1 gg_id:140731 Antarctic lake water clone ELB16-117	DQ015
DQ015819.1 gg_id:140527 Antarctic lake water clone ELB19-122	DQ015

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GQ114266.1 gg_id:423764 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw59 GQ114
GQ039046.1 gg_id:391867 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbu41 GQ039
DQ336714.1 gg_id:147046 Chryseobacterium caeni str. N4 DQ336
GQ104291.1 gg_id:381286 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ104
GQ007217.1 gg_id:502446 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ007
EU535726.1 gg_id:286716 profile human microbiota antecubital fossa (inner elbow) skin clone nbt10b01 EU535
GQ114067.1 gg_id:380870 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ114
GQ071987.1 gg_id:396996 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw190g08 GQ071
GQ105856.1 gg_id:425298 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw GQ105

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GQ097152.1 gg_id:423968 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw GQ097
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DQ856530.1 gg_id:248648 intestinal microflora Chinese mitten crab (Eriocheir sinensis) clone C2K DQ856
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GQ098103.1 gg_id:429844 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw40 GQ098
GQ024383.1 gg_id:485287 Topographical and Temporal Human Skin Microbiome skin palm clone nbw121g11c1 GQ024

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EF688382.1 gg_id:244377 soil clone F6-94 EF6883
DQ167246.1 gg_id:139202 Costertonia jungdongjinensis str. KOPRI 13342 DQ167
EU236356.1 gg_id:292328 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg91B11 EU2363
FJ882164.2 gg_id:541534 Aquimarina sp. str. antisso-27 FJ8821

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FJ675086.1 gg_id:515439 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6750
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EU246690.1 gg_id:249383 Zobellia aquimaris str. KMM 3942 EU246
DQ071071.1 gg_id:130971 marine surface water clone PB1.19 DQ071
EU801540.1 gg_id:332561 It's all ranking aquatic Chesapeake Bay MD clone 3C002857 EU801
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GU118604.1 gg_id:588842 Threatened Corals Provide Microbial Habitats clone Mfav_B01 GU118
DQ334647.1 gg_id:175223 Impact metals on sediments heavy metal polluted marine sediment clone HB2-4-7 DQ334
EU735616.1 gg_id:341915 archaeal structures and pristine soils China oil contaminated soil Jidong Oilfield clone EU735
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EU003227.1 gg_id:255704 variation and endosymbiotic phenotypically sea urchin Strongylocentrotus intermedi EU003
EU236412.1 gg_id:287759 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg92F1 EU236
GU369875.1 gg_id:529450 and mats vents Arc white filamentous microbial mat photic shal hydrothermal vent GU369
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DQ530476.1 gg_id:168278 Arenibacter sp. str. gap-e-67 DQ530
DQ009109.1 gg_id:123870 bacterioplankton clone SPOTSDEC01_5m8 DQ009
GQ872423.1 gg_id:590020 Gaetbulibacter sp. str. M1-7 GQ872
AM040105.1 gg_id:147529 sandy sediments clone Sylt 9 AM040
DQ513012.1 gg_id:161548 Microbial life fluids ridge flank crustal fluid clone FS140-164B-02 DQ513
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AY701469.1 gg_id:108543 Bacteroidetes clone GCDE08_K AY701
AM162577.1 gg_id:150733 and role capsules Sepia officinalis host egg clone 3SOMBO82 AM162
AF406541.1 gg_id:56043 bacterioplankton clone AEGEAN_179 AF406
AY682383.1 gg_id:100578 Mesophilibacter yeosuensis str. NC1-5 AY682
FJ889648.1 gg_id:571155 Subsaxibacter sp. str. ZS4-19 FJ8896
EU888117.1 gg_id:321134 Muricauda sp. str. CL-SS4 EU888
EU804390.1 gg_id:314108 It's all ranking aquatic 250 miles Panama City clone 6C232304 EU804
EU464970.1 gg_id:298323 African elephant feces clone AFYEL_aaj66a04 EU464
AY654825.1 gg_id:104306 Oculina mucus isolate 88 AY654
DQ395462.1 gg_id:156104 deep-sea octacoral clone ctg_CGOAA74 DQ395
DQ154838.1 gg_id:139216 Diel Migration Restructures Hypersaline Microbial Mat hypersaline microbial mat cl DQ154
AM292800.1 gg_id:179042 Cetobacillus canariasensis str. 454-2 AM292
EU287304.1 gg_id:251312 Pacific arctic surface sediment clone S26-4 EU287
FN433422.1 gg_id:551808 patterns and flavobacterial clades contrasting masses North Atlantic marine water cl FN433
AM286230.1 gg_id:164896 Tamlana sedimenti str. HST1-43 AM286
AB073564.2 gg_id:69822 Cytophaga sp. str. MBIC04693 AB073
GQ349775.1 gg_id:585849 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ349
AJ535222.1 gg_id:78228 marine sediment above hydrate ridge clone Hyd24-2-2 bacterium AJ5352
EU432414.1 gg_id:263786 variation and endosymbiotic phenotypically- sea urchin Strongylocentrotus intermec EU432

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EU626667.1 gg_id:278558 variation and endosymbiotic phenotypically- sea urchin Strongylocentrotus intermec EU6266
EU369165.1 gg_id:323406 libraries oyster shell clone MBFOS-06 EU3691
EF092235.1 gg_id:267240 Persistent Axinella corrugata Flavobacteriaceae clone B2706_G2 EF0922
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DQ269118.1 gg_id:182252 marine macro-alga surface clone DPC244 DQ269
AF170737.1 gg_id:2313 Gelidibacter sp. str. QSSC1-21 AF1707
EU805333.1 gg_id:328149 It's all ranking aquatic 250 miles Panama City clone 6C233336 EU8053
FJ674613.1 gg_id:531182 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6746
EU003220.1 gg_id:243895 variation and endosymbiotic phenotypically sea urchin Strongylocentrotus intermedi EU0032
GU118755.1 gg_id:554611 Threatened Corals Provide Microbial Habitats clone Mfra_N17 GU118
AY907775.1 gg_id:136893 identification picoplankton contrasting waters Arabian Sea water clone A712034 AY9077
EF208678.1 gg_id:199798 Vertical and horizontal structure microbial sandy carbonate sediment clone CI5cm.A(EF2086
AB294106.1 gg_id:552203 Sediminitalea flava str. Mhi-72 AB2941
FN433418.1 gg_id:581484 patterns and flavobacterial clades contrasting masses North Atlantic marine water cl FN4334
FJ675151.1 gg_id:518527 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6751
EU021293.1 gg_id:252313 Tenacibaculum sp. str. D38BY EU0212
DQ361033.1 gg_id:147647 Flaviramulus basaltis str. H35 DQ361
AF427479.1 gg_id:49407 Cytophaga sp. str. 41-DBG2 AF4274
DQ486480.1 gg_id:217732 Muricauda sp. str. DG1233 DQ486
FM179907.1 gg_id:330803 Biogeochemical processes microbial Gullfaks and Tommeliten methane seeps (Nortl FM179
EU443206.1 gg_id:270202 Maribacter sp. str. EM44 EU4432
FJ674419.1 gg_id:510951 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6744
FJ416110.1 gg_id:356976 sediments sediment station NEC5 Northern Bering Sea clone 089L88 FJ4161
AY922250.1 gg_id:113758 whalefall clone 131854 AY9222
AJ575643.1 gg_id:133240 Pibocella ulvae str. LMG 21972 AJ5756
FJ672842.1 gg_id:527499 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6728
GU369879.1 gg_id:521453 and mats vents Arc white filamentous microbial mat photic shal hydrothermal vent GU369
GU119445.1 gg_id:556808 Threatened Corals Provide Microbial Habitats reef water clone Reef_K14 GU119
EF108217.1 gg_id:190536 Aureimonas pelagi str. HTCC2652 EF1082
EU010132.1 gg_id:236858 Biogeography Singapore seawaters seawater clone A40 EU0101
EU394577.1 gg_id:353843 Coccolithophore bloom dynamics shape (NE-Atl) northern Bay Biscay pelagic particle EU3945
EU626698.1 gg_id:278872 variation and endosymbiotic phenotypically- sea urchin Strongylocentrotus intermec EU6266
AM745157.1 gg_id:299050 Impact oil er hydrocarbons on microbial and activity Gulf Mexico cold seep marine s AM745
EU328022.1 gg_id:278042 dynamics during bioremediation crude oil contaminated moderate saline soil clone B EU3280
FJ674317.1 gg_id:512308 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6743
AM292396.1 gg_id:336602 Microbial investigations anaerobic nitrate-dependent utilization toluene and n-hexa AM292
EU000243.1 gg_id:310620 Donghaeana dokdonensis str. KOPRI_22265 EU0002

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AB244984.1 gg_id:161450 Flavobacterium sp. str. MS-3 AB244
DQ103641.1 gg_id:129412 hypersaline endoevaporitic microbial mat clone E6aH07 DQ103
DQ395624.1 gg_id:151414 deep-sea octacoral clone ctg_CGOF071 DQ395
FJ155065.1 gg_id:348807 seasonal fluctuation coastal Bohai Bay sequencing and RFLP soil clone D FJ1550
GQ848410.1 gg_id:567371 Microbial sediments vents along East Lau Spreading Centre deep sea hydrothermal GQ848
FJ360684.1 gg_id:362896 Gaetbulibacter sp. str. NH57N FJ3606
EF574626.1 gg_id:230145 site S25 near Coco's Island marine clone S25_970 EF5746
EU328020.1 gg_id:277873 dynamics during bioremediation crude oil contaminated moderate saline soil clone B EU328
EU799445.1 gg_id:323173 It's all ranking aquatic Newport Harbour RI clone 1C227044 EU799
EU050901.1 gg_id:249428 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_04_87 EU050
GQ348530.1 gg_id:581353 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ348
EU491703.1 gg_id:268530 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU491
CU467431.1 gg_id:345202 Prokaryotic Tunisian saltern Saltern solar multipond clone CU467
EU369144.1 gg_id:345475 libraries oyster shell clone MBIOS-28 EU369
FJ675599.1 gg_id:515649 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6755
EU434366.1 gg_id:260191 Flavobacterium sp. str. a306 EU434
DQ351761.1 gg_id:148990 Microbial Adherent Sediment Particles Heavy Metal Contaminated North Sea Surfac DQ351
FN433358.1 gg_id:585425 patterns and flavobacterial clades contrasting masses North Atlantic marine water cl FN433
EU626707.1 gg_id:281940 variation and endosymbiotic phenotypically- sea urchin Strongylocentrotus intermec EU626
GU118801.1 gg_id:586182 Threatened Corals Provide Microbial Habitats clone Mfra_M18 GU118
U85886.1 gg_id:2403 marine psychrophile str. ACAM210 U8588
AF286039.1 gg_id:35713 mercury and PCB contaminated saltmarsh sediment clone LCP-72 LCP-72 AF286
DQ070805.1 gg_id:146853 Prokaryotic Structures Seafloor Basalts Varying Age and Juan de Fuca Ridge basalt gl DQ070
DQ514301.1 gg_id:160581 Flexibacter aggregans str. BSs20185 DQ514
AF468407.1 gg_id:80764 Arctic sea ice ARK10007 AF468
AJ704703.1 gg_id:109300 marine sediment clone HMMVCen-36 AJ7047
EU283513.1 gg_id:279132 Model Early Earth Harbors Deeply Divergent Divisions Anderson Lake clone A1530 EU283
AY936177.1 gg_id:113358 Flavobacteriaceae clone F1C24F AY936
AM945545.1 gg_id:267601 Pibocella sp. MOLA:312 AM945
AF406550.1 gg_id:60625 bacterioplankton clone AEGEAN_129 AF406
AF530135.1 gg_id:61127 Polaribacter sp. str. MGP-9 AF530
GQ348250.1 gg_id:581424 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ348
FJ416125.1 gg_id:361177 sediments sediment station NEC5 Northern Bering Sea clone 117O18 FJ4161
EU626639.1 gg_id:279125 variation and endosymbiotic phenotypically- sea urchin Strongylocentrotus intermec EU626
FJ675281.1 gg_id:516393 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6752
EF016467.1 gg_id:176313 Near real-time autonomous detection marine on coastal mooring Monterey Bay Calif EF0164
AM259825.1 gg_id:211011 Spatial sponge- Mediterranean Tethya aurantium sponge endosome clone TAI-2-81 AM259

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FJ196015.1 gg_id:340255 Donghaeana sp. str. ZS1-13 FJ1960
EF092186.1 gg_id:270683 Persistent Axinella corrugata Flavobacteriaceae clone Ax26_E2 EF0921
FJ595484.1 gg_id:543469 Winogradskyella sp. str. 022-2-26 FJ5954
DQ002871.1 gg_id:118184 Gramella portivictoriae str. UST040801-001 DQ002
AY162121.1 gg_id:136017 Cultivating Sargasso Sea clone GMD15A07 AY162
EF123625.1 gg_id:249295 Microbial disease microbial mats on Siderastrea siderea three regions wider Caribbea EF1236
GQ249588.1 gg_id:591430 Microbial anaerobic sediments Bay Cadiz (Spain) marine sediment: 12-14 cm layer cl GQ249
DQ334648.1 gg_id:175076 Impact metals on sediments heavy metal polluted marine sediment clone HB2-6-7 DQ334
AY694003.1 gg_id:102333 Calefactosor algoritergicola str. APA-1 AY694
EU925905.1 gg_id:353655 sediments sediment station DBS1 northern Bering Sea clone 131H30 EU925
AF449259.1 gg_id:61850 Riftia pachyptila's tube clone R103-B20 AF449
FJ791926.1 gg_id:537409 Unexpectedly archaeal species shift between rare and dominant over thousand year FJ7919
FJ675178.1 gg_id:520926 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6751
AY280421.1 gg_id:100925 exterior deep-sea hydrothermal vent sulfide chimney Juan de Fuca Ridge Pacific Oce AY2804
EF157086.1 gg_id:250910 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon EF157
FJ825844.1 gg_id:569124 Succession during spring Sea filtered surface sea water period diatom bloom Yel Sea; FJ8258
EU491694.1 gg_id:267629 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU491
FJ403056.1 gg_id:361407 Disease- changes healthy and diseased colonies Caribbean coral Montastrea faveolat FJ4030
EU491713.1 gg_id:261907 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU491
AJ318193.1 gg_id:20776 Waste-gas biofilter clone BIvi22 AJ3181
EU236427.1 gg_id:293136 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg92H7 EU2364
AB084261.1 gg_id:142361 Zobellia sp. str. KMM 3531 AB084
FJ675009.1 gg_id:517967 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6750
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GU118352.1 gg_id:540288 Threatened Corals Provide Microbial Habitats clone Gven_L09 GU118
EU465137.1 gg_id:295672 African elephant feces clone AFYEL_aaj68f01 EU465
AB362216.1 gg_id:324561 Leptobacterium flavescens str. 04PA2 Co4-8B AB362
EU626675.1 gg_id:277680 variation and endosymbiotic phenotypically- sea urchin Strongylocentrotus intermec EU6266
EU419942.1 gg_id:266863 Formosa sp. str. RW55 EU4199
EU021217.2 gg_id:254152 Bizionia argentinensis str. JUB59 EU0212
AY654759.1 gg_id:105219 Oculina mucus isolate 110 AY6547
EF687174.1 gg_id:286813 Biogeochemistry iron- and sulfur-precipitating microbial mats (Nile Mediterranean) ir EF6871
EF572248.1 gg_id:228698 Coco's Island site 23 marine clone S23_347 EF5722
EF108214.1 gg_id:179639 Croceimarina litoralis str. IMCC1993 EF1082
EU369134.1 gg_id:324541 libraries oyster shell clone MBIOS-18 EU369
AB255696.1 gg_id:186864 Orabacterium aurantiaca str. HSF3 AB2556
GU233518.1 gg_id:578850 Kordia sp. str. IMCC1412 GU233
GQ348644.1 gg_id:583466 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ348
EU443204.1 gg_id:265965 Gaetbulibacter sp. str. EM39 EU443

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EU290161.1 gg_id:237287 Tenacibaculum marinus str. A31 EU290
AM259823.1 gg_id:212421 Spatial sponge- Mediterranean Tethya aurantium sponge endosome clone TAI-8-51 AM259
GQ452872.1 gg_id:586530 Biodiversity planktonic surface water Northern Bering Sea clone s3 GQ452
EF573073.1 gg_id:231756 Coco's Island site 23 marine clone S23_1172 EF5730
EF571947.1 gg_id:232534 Coco's Island site 23 marine clone S23_46 EF5719
AB073573.2 gg_id:66035 Cytophaga sp. I-545 AB0735
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EU512921.1 gg_id:260066 Maribacter sp. str. CL-AP4 EU5129
FM179910.1 gg_id:311773 Biogeochemical processes microbial Gullfaks and Tommeliten methane seeps (Nortl FM179
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DQ015841.1 gg_id:140556 Antarctic lake water clone WLB13-197 DQ015
EU287913.1 gg_id:237293 Lutaonella thermophilus str. CC-MHSW-2 EU2879
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FJ674780.1 gg_id:519316 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6747
EU287319.1 gg_id:243681 Pacific arctic surface sediment clone S26-19 EU2873
AY883939.1 gg_id:112379 Gaetbulibacter saemankumensis str. SMK-45 AY8839
DQ191182.1 gg_id:139623 Muricauda sp. str. DOKDO 023 DQ191
EU328155.1 gg_id:244757 Formosa crassostrea str. KO3 EU3281
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EU626686.1 gg_id:279532 variation and endosymbiotic phenotypically- sea urchin Strongylocentrotus intermec EU6266
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EU564844.1 gg_id:263680 Muricauda sp. str. CC-HSB-11 EU5648
EU735708.1 gg_id:332107 Biological Arsenic Remediation Project Groundwater Aquifer soil clone 1As26 EU7357
AY922244.1 gg_id:113641 whalefall clone 131828 AY9222
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FJ497566.1 gg_id:579831 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun FJ4975
EU287015.1 gg_id:251033 Pacific arctic surface sediment clone B78-51 EU2870
FJ744983.1 gg_id:554802 Transporter genes expressed coastal response dissolved organic carbon surface wate FJ7449

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EU236375.1 gg_id:301867 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg91G5 EU2363
GU118047.1 gg_id:586123 Threatened Corals Provide Microbial Habitats clone Apal_M01 GU118
AM259875.1 gg_id:206791 Spatial sponge- Mediterranean Tethya aurantia sponge cortex clone TAA-10-74 AM259
FJ624452.1 gg_id:555318 Lau Basin hydrothermal vent sediment clone DY2-180 FJ6244
EU050894.1 gg_id:245177 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_03_15 EU0508
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AY372916.1 gg_id:141336 marine sponge Rhabdastrella globostellata symbiont AY3729
AB362815.1 gg_id:552208 Xanthobacillum maris str. Se5-09-15 AB3628
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FJ716956.1 gg_id:539891 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United Kingc FJ7169
AM945558.1 gg_id:260584 Winogradskyella sp. MOLA:326 AM945
AB261012.1 gg_id:165728 Marinoxanthomonas ophiurae str. KMM 3046 AB2610
DQ351766.1 gg_id:145981 Microbial Adherent Sediment Particles Heavy Metal Contaminated North Sea Surfac DQ351
FJ202911.1 gg_id:329636 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2029
EF125443.1 gg_id:191828 mangrove soil clone MSB-2E3 EF1254
DQ064789.1 gg_id:130810 Stenothermobacter spongiae str. UST030701-156 DQ064
EU464885.1 gg_id:291250 Hartmann's mountain zebra feces clone AFZEB_aaj72e02 EU4648
EU626642.1 gg_id:278244 variation and endosymbiotic phenotypically- sea urchin Strongylocentrotus intermec EU6266
FN433333.1 gg_id:547261 patterns and flavobacterial clades contrasting masses North Atlantic marine water cl FN4333
FJ674283.1 gg_id:530154 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6742
FJ203427.1 gg_id:330755 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h FJ2034
EU287285.1 gg_id:243677 Pacific arctic surface sediment clone S11-102 EU2872
AY285940.1 gg_id:87495 Flavobacteriaceae G11A1 AY2859
EU626567.1 gg_id:278602 variation and endosymbiotic phenotypically- sea urchin Strongylocentrotus intermec EU6265
AB017597.1 gg_id:2462 Flavobacterium sp. str. 5N-3 AB0175
AM292405.1 gg_id:308348 Microbial investigations anaerobic nitrate-dependent utilization toluene and n-hexa AM292
EU722656.1 gg_id:346435 Microbial athalassohaline Tirez lagoon (Spain) sediment clone SB80 EU7226
AJ567549.1 gg_id:89871 deep-sea sediment clone MBMPE34 AJ5675
EF123558.1 gg_id:250190 Microbial disease microbial mats on Siderastrea siderea three regions wider Caribbea EF1235
DQ372851.1 gg_id:154027 Pirellula and OM43 are among dominant lineages identified Oregon coast diatom bl DQ372
AB073589.2 gg_id:102971 Cytophaga sp. I-1856 AB0735
FJ674609.1 gg_id:520214 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6746
AY693998.1 gg_id:105007 Subsaximicrobium saxinquilinus str. Y4-5 AY6939
FJ403077.1 gg_id:362103 Disease- changes healthy and diseased colonies Caribbean coral Montastrea faveolat FJ4030

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EU624432.1 gg_id:284011 str. AMSU EU624
FJ545547.1 gg_id:509482 Diveristy Seawater and Sediment Northern North Yel Sea sediment clone S2-2 FJ5455
EU005774.1 gg_id:259717 Major activity inside and outside natural iron-fertilized phytoplankton bloom 3 micrc EU005
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AM982605.1 gg_id:279056 microbial and slurry pig saw dust spent bedding clone PISD-AIA05 AM982
FJ744837.1 gg_id:564502 Transporter genes expressed coastal response dissolved organic carbon surface wate FJ7448
AM279180.1 gg_id:171189 Cytophaga-Flavobacterium-Bacteroides coastal North Sea marine water clone NorS AM279
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AF419681.1 gg_id:26293 Guaymas Basin hydrothermal sediment clone CS_B009 AF4196
EF572790.1 gg_id:234993 Coco's Island site 23 marine clone S23_889 EF5727
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AF052742.1 gg_id:39004 Arenibacter latericius str. KMM 426; LMG 19694; CIP 106861 AF0527
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AY654766.1 gg_id:100882 Oculina mucus isolate 20 AY6547
EU465134.1 gg_id:288740 African elephant feces clone AFYEL_aaj68e07 EU465
FM958432.1 gg_id:544536 olive flies and its major symbiont 'Candidatus Erwinia dacicola adult female headless FM958
FM162560.1 gg_id:540441 Wautersiella falsenii str. MT2 FM162
AJ853512.1 gg_id:110915 landfill leachate clone GZKB17 AJ8535
DQ346496.1 gg_id:155685 during composting libraries compost clone 2B12 DQ346
DQ129251.1 gg_id:137948 microarray level air two cities Texas urban aerosol clone AKIW644 DQ129
EU794729.1 gg_id:330265 Empedobacter sp. str. FM-1 EU794
AM177497.1 gg_id:147208 Empedobacter brevis str. LMG 4011 AM177
EU779437.1 gg_id:337303 Hartmann's Mountain Zebra feces clone AFZEB_aaj72h08 EU7794
FJ999733.1 gg_id:525497 Wautersiella falsenii str. P1785 FJ9997
GQ082931.1 gg_id:385877 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ082
EU293154.1 gg_id:241741 Empedobacter brevis str. Y7D EU293
AY521225.1 gg_id:99909 Winogradskyella eximia str. KMM 3944 AY5212
DQ530465.1 gg_id:161743 Winogradskyella sp. str. gap-f-41 DQ530
DQ073103.1 gg_id:152380 Psychroserpens sp. str. TW-JL-49 DQ073
AY771730.1 gg_id:143056 Winogradskyella thalassocola S4-6 AY7717
DQ356490.1 gg_id:147248 Winogradskyella sp. str. BC1 DQ356
EU195943.1 gg_id:244700 Winogradskyella sp. str. P101 EU1959
AY771731.1 gg_id:143045 Winogradskyella thalassocola S4-7 AY7717
FJ919968.1 gg_id:556977 Winogradskyella sp. str. A73 FJ9199
AY771720.1 gg_id:141948 Winogradskyella thalassocola S3-5 AY7717
AY521224.1 gg_id:99754 Winodgradskyella epiphytica str. KMM 3906 AY5212
AY521223.1 gg_id:99602 Winogradskyella thalassicola str. KMM 3907 AY5212
FJ196009.1 gg_id:315572 Winogradskyella sp. str. NF1-23 FJ1960

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DQ357769.1 gg_id:145482 Psychroserpens sp. MAC17 Mac17 DQ357
AB438962.1 gg_id:360101 Winogradskyella sp. str. R60 (=KMM 3968) AB438
AB255367.1 gg_id:223113 Galbibacter mesophilus str. Mok-17 AB255
DQ097522.1 gg_id:133522 Venteria marina str. En5 DQ097
FJ230837.1 gg_id:325922 Joostella sp. AD3 str. AN4 FJ2308
AB121976.1 gg_id:102893 Zobellia russellii str. KMM 3677 AB121
DQ066625.1 gg_id:150547 Symbiosis and Insect Ancient Symbiont Sap-Feeding Insects Phylum Bacteroidetes U DQ066
EU646081.1 gg_id:552008 symbiont EU646
DQ679965.1 gg_id:162099 Mycoplasma sp. str. B2 DQ679
EU646047.1 gg_id:572398 symbiont EU646
EU646066.1 gg_id:544736 symbiont EU646
DQ066640.1 gg_id:144003 Symbiosis and Insect Ancient Symbiont Sap-Feeding Insects Phylum Bacteroidetes U DQ066
EU646080.1 gg_id:571511 symbiont EU646
EU646049.1 gg_id:560878 symbiont EU646
DQ133563.1 gg_id:149599 Preliminary survey insects (Hemiptera:Coccoidea) scale insect clone DQ133
DQ133559.1 gg_id:147524 Preliminary survey insects (Hemiptera:Coccoidea) scale insect clone DQ133
AY922215.1 gg_id:114215 whalefall clone 131697 AY922
AM990892.1 gg_id:279587 Balneola sp. MOLA 118 AM990
DQ015824.1 gg_id:140368 Antarctic lake water clone ELB19-188 DQ015
DQ015773.1 gg_id:139513 Antarctic lake water clone ELB25-086 DQ015
GQ243712.1 gg_id:554668 consortia immobilizing nitrifying bioreactors designed penaeid and non-penaeid larv GQ243
EU735656.1 gg_id:330672 archaeal structures oil contaminated and soils China pristine soil Jidong Oilfield clone EU735
EU735648.1 gg_id:343612 archaeal structures oil contaminated and soils China pristine soil Jidong Oilfield clone EU735
FJ152978.1 gg_id:352504 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX4C FJ1529
EU328034.1 gg_id:278678 dynamics during bioremediation crude oil contaminated moderate saline soil clone B EU328
FJ152887.1 gg_id:304760 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX4C FJ1528
GQ263633.1 gg_id:560384 Structure Simulated Level Waste Site simulated level waste site clone FW3_192C GQ263
AF449784.1 gg_id:80582 CFB group clone ML615J-21 AF449
EF632720.1 gg_id:237373 Unique microbial contrasting aquatic altitude Andean Altiplano (northern Chile) wate EF6327
GQ263696.1 gg_id:587073 Structure Simulated Level Waste Site simulated level waste site clone FW3_98C GQ263
GQ263661.1 gg_id:592463 Structure Simulated Level Waste Site simulated level waste site clone FW3_49C GQ263
EU723156.1 gg_id:327281 actinobacterium str. kmd_222 EU723
AM237313.1 gg_id:150813 Cytophaga arvensicola str. T2 AM237
AM237311.1 gg_id:153828 Cytophaga arvensicola str. DSM 3695 AM237
AB264798.1 gg_id:164755 Chitinophaga ginsengisegetis str. M1-09 AB264
AB278570.1 gg_id:182778 Chitinophaga sp. str. KP01 AB278
EU133718.1 gg_id:252642 tallgrass prarie soil clone FFCH13611 EU133
EU714260.1 gg_id:328242 Chitinophaga sp. str. JS16-4 EU714
AY238335.1 gg_id:82843 Flexibacter sp. str. MDA2495 AY2383
EU714259.1 gg_id:347504 Chitinophaga sp. str. JS13-10 EU714
AB078067.1 gg_id:58620 Flexibacter sancti str. IFO 16033 AB078

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DQ298787.1 gg_id:141868 Effect Nutrient Periodicity upon Microbial Dynamics exposed 14-day nutrient flux DQ298
AF181568.1 gg_id:71851 Flexibacter cf. sancti 1 AF1815
DQ062743.1 gg_id:134254 Chitinophaga sp. str. CC-SG1B DQ062
FM865977.1 gg_id:573131 Chitinophaga sp. str. CS5-B1 FM865
DQ378248.1 gg_id:154761 oil-polluted soil clone M28_Pitesti DQ378
AB267477.1 gg_id:162563 Flavosolibacter ginsengiterrae str. Gsoil 643 AB2674
AY921684.1 gg_id:113437 farm soil clone AKYH1027 AY9216
DQ378235.1 gg_id:152427 oil-polluted soil clone M15_Pitesti DQ378
GQ116342.1 gg_id:434729 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw691f12 GQ116
AY493956.1 gg_id:136598 Fingerprinting aggregates soil clone 1417 AY4939
FJ657758.1 gg_id:532743 Metalworking Fluids and Aerosols Metallurgy Plant metalworking aerosol clone Winte FJ6577
AY211072.1 gg_id:81764 anaerobic VC-degrading enrichment clone VC10 bacterium AY2110
AB485756.1 gg_id:578831 Stratified medicinal leech Hirudo verbana bladder clone 1B-NIA AB4857
FJ457040.1 gg_id:573552 Niabella sp. str. CCBAU 05354 FJ4570
DQ457019.1 gg_id:156950 Niablella koreensis str. R2A15-11 DQ457
EU133632.1 gg_id:250223 tallgrass prarie soil clone FFCH2679 EU1336
AM085477.1 gg_id:140614 microbial subsurface west Pacific warm pool deep sea sediment clone E26 AM085
EU881188.1 gg_id:353494 Karst region natural restoration land soil clone KNR200711-019 EU8811
EU133640.1 gg_id:246952 tallgrass prarie soil clone FFCH4809 EU1336
EU917053.1 gg_id:351981 Niastella sp. str. RHYL-67 EU9170
DQ244076.1 gg_id:141748 Niastella jeongjuensis str. GR20-13 DQ244
AJ583191.1 gg_id:94468 radioactive site ground water clone S15B-MN17 AJ5831
EF516765.1 gg_id:222536 grassland soil clone FCPO489 EF5167
AB267478.1 gg_id:172843 Terribacter koreensis str. Gsoil 664 AB2674
DQ365993.1 gg_id:155441 Dominant soils Marble Point and Wright Valley Victoria Land Antarctica soil clone J3! DQ365
DQ365999.1 gg_id:154794 Dominant soils Marble Point and Wright Valley Victoria Land Antarctica soil clone BP DQ365
FJ485120.1 gg_id:558937 microbial autonomous rover world's deepest phreatic sinkhole water column El Zacat FJ4851
AF449772.1 gg_id:80757 CFB group clone ML310M-18 AF4497
AB464942.2 gg_id:338020 Altitudinal changes flora on Gulkana Glacier Alaska analyzed sequencing and -cycle c AB4649
EU104177.1 gg_id:323582 Evidence Comamonadaceae determinants settling performance activated sludge clo EU1041
AB286623.1 gg_id:208838 Reducing production and domination comamonadaceae reducing oxygen supply was AB2866
AB286615.1 gg_id:205961 Reducing production and domination comamonadaceae reducing oxygen supply was AB2866
AJ007870.1 gg_id:2554 cytophagales clone LD1 AJ0078
EU104150.1 gg_id:342905 Evidence Comamonadaceae determinants settling performance activated sludge clo EU1041
AF507866.1 gg_id:55727 Mono Lake at depth 17.5 m station 6 July 2000 clone ML617.5J-33 AF5078
CU466754.1 gg_id:327821 Evry wastewater treatment plant anoxic basin clone CU4667
GQ347704.1 gg_id:533454 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ347
FJ592611.1 gg_id:554348 Fumarole-supported islands biodiversity within hyperarid -elevation landscape on Pu FJ5926
GQ264422.1 gg_id:511320 Structure Simulated Level Waste Site simulated level waste site clone WW3_110 GQ264
AY921733.1 gg_id:113386 farm soil clone AKYG1020 AY9217

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EU861847.1 gg_id:343941 effects chronic fertilization on alpine tundra microbial implications carbon and nitrog EU861
GQ396989.1 gg_id:554086 Functional unvegetated perhumid recently-deglaciated soils do not correlate shifts s GQ396
GU208213.1 gg_id:538684 Study on Sediment Dongping Lake sediment clone 1T1-11 GU208
AB504919.1 gg_id:558029 structure microorganisms reddish-brown iron-rich snow clone oze05B16 AB504
EF516017.1 gg_id:222507 grassland soil clone FCPN444 EF516
DQ298006.1 gg_id:142330 Microbial hydrocarbon contaminated soil clone UA2 DQ298
DQ450747.1 gg_id:161257 Microbial Alpine Tundra Wet Meadow Soil: Chloroflexi Cold Water-Saturated satura DQ450
EF516344.1 gg_id:220513 grassland soil clone FCPS474 EF5163
AB240473.1 gg_id:142837 microbial structure rhizosphere biofilm Sapporo root-tip (0 40 mm) Phragmites Sosei AB240
EF520597.1 gg_id:233334 structure lakes: what controls ? acid-impacted lake clone ADK-RXe02-22 EF5205
FM201192.1 gg_id:551880 and distinct induced biofilm fouling operated under conditions laboratory-scale men FM201
GQ396857.1 gg_id:509873 Functional unvegetated perhumid recently-deglaciated soils do not correlate shifts s GQ396
DQ450743.1 gg_id:160651 Microbial Alpine Tundra Wet Meadow Soil: Chloroflexi Cold Water-Saturated satura DQ450
DQ501312.1 gg_id:180406 Seasonal dynamics free-living and particle- four lakes northeastern Germany freshw DQ501
AY218618.1 gg_id:81845 penguin droppings sediments clone KD3-81 AY218
GQ043454.1 gg_id:417385 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw97 GQ043
EU133660.1 gg_id:244018 tallgrass prarie soil clone FFCH5150 EU133
EF516340.1 gg_id:225059 grassland soil clone FCPP437 EF5163
EF018461.1 gg_id:204934 aspen rhizosphere clone Amb_16S_1087 EF0184
DQ191824.1 gg_id:140407 Microbial and geochemical heterogeneity 3 km deep South Africa fractured metaba DQ191
GU295962.1 gg_id:540458 Niastella sp. str. JCN-23 GU295
EU015106.1 gg_id:250277 Investigation estrogen-degrading bioreactors membrane bioreactor suspension and EU015
FJ479493.1 gg_id:547060 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4794
AJ295528.1 gg_id:42289 rape rhizosphere clone wr0086 AJ2955
EU861890.1 gg_id:354903 effects chronic fertilization on alpine tundra microbial implications carbon and cyclin EU861
AF529321.1 gg_id:61843 PCE-contaminated site clone CLi112 AF5293
EF516406.1 gg_id:225926 grassland soil clone FCPS640 EF5164
EF516138.1 gg_id:218051 grassland soil clone FCPP411 EF5161
EF018806.1 gg_id:204470 aspen rhizosphere clone Amb_16S_1276 EF0188
DQ640728.1 gg_id:234598 Biodiversity and microbial full-scale enhanced biological phosphorus removal plant a DQ640
AF314428.1 gg_id:41664 aerobic phosphorus-removal ecosystem clone PHOS-HE19 AF3144
AF368190.1 gg_id:58374 non-EBPR sludge clone SBRT303 AF3681
AY211071.1 gg_id:82223 anaerobic VC-degrading enrichment clone VC5 bacterium AY211
AJ295463.1 gg_id:39882 rape rhizosphere clone wr0002 AJ2954
EF018581.1 gg_id:209422 aspen rhizosphere clone Amb_16S_850 EF0185
AM990456.1 gg_id:278060 Solibium sp. str. I-28 AM990
DQ404887.1 gg_id:155209 contaminated sediment clone 654959 DQ404
AB286400.1 gg_id:216923 Reducing production and domination comamonadaceae reducing oxygen supply was AB286
FJ479490.1 gg_id:553534 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4794

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EU133736.1 gg_id:235802 tallgrass prarie soil clone FFCH8654 EU133
AB269814.1 gg_id:206019 shal eutorophic Japan freshwater lake AB269
CU922785.1 gg_id:545292 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU922
AY302126.1 gg_id:109652 sludge dentrifying reactor fed with methanol clone DSBR-B064 AY302
AJ575723.1 gg_id:96745 lake water clone SW56 AJ5757
AY948032.1 gg_id:142590 Synchrony and seasonality two temperate rivers USA: Massachusetts Parker River cl AY948
FJ710768.1 gg_id:580914 Abundance and microbial long-term operated anammox biofilm reactors initiated ino FJ7107
EF019920.1 gg_id:209940 aspen rhizosphere clone Elev_16S_1292 EF0199
GQ263562.1 gg_id:566521 Structure Simulated Level Waste Site simulated level waste site clone FW3_114C GQ263
AJ575722.1 gg_id:98865 lake water clone SW36 AJ5757
AY792295.1 gg_id:119875 Humic Lake clone CrystalBog2KE10 AY792
FJ478810.1 gg_id:576653 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4788
DQ640666.1 gg_id:234394 full-scale EBPR sludge clone Skagenf91 DQ640
GQ472392.1 gg_id:541215 Microbial Dongping Lake lake sediment clone 4D4-6 GQ472
GQ115645.1 gg_id:396424 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw689a0 GQ115
FJ478596.1 gg_id:548715 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4785
EU104030.1 gg_id:345271 Evidence Comamonadaceae determinants settling performance activated sludge clo EU104
DQ984541.1 gg_id:236776 Mt. Nan-Jen soil clone IFD_11 DQ984
AM930283.1 gg_id:535708 gradual cooling stage mass and its spatial composting clone SMG23 AM930
EF688340.1 gg_id:250093 soil clone F3-31 EF6883
GQ263274.1 gg_id:570643 Structure Simulated Level Waste Site simulated level waste site clone FW1_a2 GQ263
DQ297996.1 gg_id:143484 Microbial hydrocarbon contaminated soil clone UD10 DQ297
AB286466.1 gg_id:216092 Reducing production and domination comamonadaceae reducing oxygen supply was AB286
GQ339899.1 gg_id:540472 Niastella sp. str. Gsoil 221 GQ339
GQ263497.1 gg_id:578914 Structure Simulated Level Waste Site simulated level waste site clone FW2_191B GQ263
DQ378273.1 gg_id:154846 oil-polluted soil clone M60_Pitesti DQ378
EU644185.1 gg_id:282480 and Samoylov Island Lena active layer -centred polygon near surface horizon; Rim_T EU644
GQ263856.1 gg_id:581218 Structure Simulated Level Waste Site simulated level waste site clone WC2_10 GQ263
GU359109.1 gg_id:521439 rhizosphere soil peanut clone 2G87 GU359
AY218661.1 gg_id:82316 penguin droppings sediments clone KD9-169 AY218
EF025264.1 gg_id:190531 Examination microbial ecology avian vivo bromodeoxyuridine intestine clone B5_F26 EF0252
DQ413096.1 gg_id:153532 Microbial -dependent and Approaches Anaerobic/Aerobic SBR Reactor EBPR sludge DQ413
AB286634.1 gg_id:207342 Reducing production and domination comamonadaceae reducing oxygen supply was AB286
AB177144.1 gg_id:129332 seafloor methane hydrate clone ODP1230B11.15 AB177
EU133734.1 gg_id:255322 tallgrass prarie soil clone FFCH7779 EU133
FM866271.1 gg_id:362648 Microbial several mining wastes Bulgaria uranium mill tailings clone BuhC-1 FM866
EF516931.1 gg_id:217839 grassland soil clone FCPN422 EF5169

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EU571161.1 gg_id:270708 eubacterium sp. str. 11-14 EU5711
FJ439877.1 gg_id:511214 Investigation estrogen-degrading bioreactors membrane bioreactor biofilm clone M3 FJ4398
GQ402737.1 gg_id:510619 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
EF188431.1 gg_id:348170 Microbial Altamira Cave clone 245 EF1884
AJ318106.1 gg_id:52540 Waste-gas biofilter clone Blai2 AJ3181
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DQ378256.1 gg_id:151174 oil-polluted soil clone M39_Pitesti DQ378
GQ113676.1 gg_id:464363 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ113
EF516578.1 gg_id:223554 grassland soil clone FCPP516 EF5165
FJ536911.1 gg_id:550393 Linking performance microbiology biofilters treating dimethyl sulphide presence and FJ5369
EU104318.1 gg_id:324205 Evidence Comamonadaceae determinants settling performance activated sludge clo EU1043
GQ396884.1 gg_id:541963 Functional unvegetated perhumid recently-deglaciated soils do not correlate shifts s GQ396
GQ488016.1 gg_id:543592 Microbial metal soil polluted heavy metals clone V8-189 GQ488
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EF019363.1 gg_id:213634 aspen rhizosphere clone Elev_16S_585 EF0193
FJ716020.1 gg_id:557323 Diet- gut microbiota Lumbricus rubellus fingerprinting technique and cloning intestina FJ7160
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EU362136.1 gg_id:317483 and Mesquite Flats Site Death Valley dune sand clone 7 EU3621
EU644197.1 gg_id:280545 and Samoylov Island Lena active layer -centred polygon near surface horizon; Rim_T EU6441
EF019397.1 gg_id:211598 aspen rhizosphere clone Elev_16S_630 EF0193
EU305589.1 gg_id:255546 Short-term effect organic matter on nitrite oxidation performance structure nitrite-o EU3055
AY493955.1 gg_id:136597 Fingerprinting aggregates soil clone 435 AY4939
EU133639.1 gg_id:241705 tallgrass prarie soil clone FFCH1448 EU1336
EF032765.1 gg_id:193234 cyanobacterial mat in lava cave clone HAVOmat81 EF0327
FJ466261.1 gg_id:567628 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea FJ4662
EF516161.1 gg_id:219059 grassland soil clone FCPT501 EF5161
EU881309.1 gg_id:320742 (maize-sweet cropping field) Karst region maize-sweet potato cropland soil clone KM EU8813
AJ290042.1 gg_id:40073 Germany: Lake Fuchskuhle south basin clone FukuS59 FukuS59 AJ2900
FJ612209.1 gg_id:582864 and Biogeochemistry Dongping Lake Ecosystems lake water clone DP7.3.7 FJ6122
FM253591.1 gg_id:321965 Rock gold mine unusually microbial biofilm clone C11-1 FM253
EF516225.1 gg_id:225377 grassland soil clone FCPU633 EF5162
EU244015.1 gg_id:359585 16SrRNA probes river Leine sediment clone sls1309 EU2440
AF255635.1 gg_id:47339 EBPR sludge clone Ebpr1 AF2556
AJ888562.1 gg_id:113307 lake sediment clone TH451 AJ8885
EF522294.1 gg_id:221611 Endolithic Microbial Ecosystems Rocky Mountain endolithic sandstone clone FQSS07 EF5222
EU861946.1 gg_id:328230 effects chronic fertilization on alpine tundra microbial implications carbon and cyclin EU8619

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GQ113817.1 gg_id:445860 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw(GQ113
AY177767.1 gg_id:78422 surface soil clone AY1777
EU509144.1 gg_id:273018 cecal contents Mus musculus strain C57BL/6J; MD7 clone MD7_aap44g05 EU5091
FN396945.1 gg_id:557824 integrative isotopic approach study degradation mixed Mixed (US3-M) enriched grou FN3969
AJ581604.1 gg_id:93798 soil near uranium mill tailings clone KCM-B-27 AJ5816
AY302124.1 gg_id:110665 sludge dentrifying reactor fed with methanol clone DSBR-B032 AY3021
EF688336.1 gg_id:242284 soil clone F1-133 EF6883
AY945889.1 gg_id:145905 Thauera and Azoarcus functionally important genera denitrifying quinoline-removal r AY9458
AJ318177.1 gg_id:47356 Waste-gas biofilter clone BIsi8 AJ3181
EF019792.1 gg_id:203786 aspen rhizosphere clone Elev_16S_978 EF0197
EU283359.1 gg_id:246204 consecutively aerated submerged treating domestic wastewater activated sludge m(EU2833
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EF174291.1 gg_id:199043 direct activated sludge last compost maturation stage clone J60-814 EF1742
EU133682.1 gg_id:236693 tallgrass prarie soil clone FFCH600 EU1336
FJ793188.1 gg_id:528336 Archaea and Hot Spring Thailand Tao Dam hot spring clone TDB87 FJ7931
AY945881.1 gg_id:146138 Thauera and Azoarcus functionally important genera denitrifying quinoline-removal r AY9458
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FM200897.1 gg_id:560204 and distinct induced biofilm fouling operated under conditions laboratory-scale men FM200
FJ592637.1 gg_id:563390 Fumarole-supported islands biodiversity within hyperarid -elevation landscape on Pu FJ5926
EU978818.1 gg_id:534067 and metabolic potential metagenome glacier ice clone glb330c EU9788
AY326513.1 gg_id:136594 Amazon soil clone 6-1 AY3265
EU639180.1 gg_id:329287 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU6391
EU283384.1 gg_id:245356 consecutively aerated submerged treating domestic wastewater activated sludge m(EU2833
AY124340.1 gg_id:55504 identification and Eukarya inhabiting Antarctic glacial cryoconite hole AY1243
EF516915.1 gg_id:222635 grassland soil clone FCPP496 EF5169
EF516498.1 gg_id:225398 grassland soil clone FCPT752 EF5164
AB179522.1 gg_id:105552 sedimentary rock clone MIZ31 AB1795
AY752128.1 gg_id:101380 lake water clone S10.17 AY7521
EU335290.1 gg_id:241123 Changes microbial metabolic and along hydrogeochemically variable profile unsatura EU3352
EF516686.1 gg_id:219534 grassland soil clone FCPP584 EF5166
AY796040.1 gg_id:108759 gold mine bore hole clone 47mm40 AY7960
EF492929.1 gg_id:254256 Iron-manganese Nodule and Its Surrounding Soil soil around iron-manganese nodule EF4929
EU133676.1 gg_id:258047 tallgrass prarie soil clone FFCH5267 EU1336
EU431809.1 gg_id:552192 Troglobitic (Cansiliella) on specialized feeding apparatus calcium carbonate (moonmi EU4318
AY792299.1 gg_id:122683 Humic Lake clone CrystalBog022A2 AY7922
DQ228370.1 gg_id:142482 microbial compositions two subglacial possible role microbes chemical weathering p DQ228
EU803695.1 gg_id:341876 It's all ranking aquatic Lake Gatun clone 5C231300 EU8036
GQ221080.1 gg_id:578107 consortia immobilizing nitrifying bioreactors designed penaeid non-penaeid larval re GQ221
EU881217.1 gg_id:344260 Karst region natural restoration land soil clone KNR200711-210 EU8812

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EU283357.1 gg_id:254735 consecutively aerated submerged treating domestic wastewater activated sludge m EU2833
GQ263619.1 gg_id:540149 Structure Simulated Level Waste Site simulated level waste site clone FW3_175C GQ263
FJ386545.1 gg_id:360124 vaccination sludge backf pumping house Xilang municipal wastewater treatment plar FJ3865
FJ439829.1 gg_id:558682 Investigation estrogen-degrading bioreactors membrane bioreactor biofilm clone M2 FJ4398
AY792298.1 gg_id:123927 Humic Lake clone CrystalBog022H6 AY7922
DQ404910.1 gg_id:152725 contaminated sediment clone 661186 DQ404
AJ577141.1 gg_id:93224 Algoriphagus antarcticus str. LMG 21980 AJ5771
AJ577267.1 gg_id:93561 Algoriphagus antarcticus str. LMG 21482 AJ5772
U85891.1 gg_id:2611 Algoriphagus ratkowskyi str. IC025 U8589
AY771735.1 gg_id:144618 Algoriphagus ratkowskyi S5-5 AY7717
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EU703453.1 gg_id:450855 lakes on Eastern Tin Plateau freshwater lake altitude 4219 masl clone XZXXH9 EU7034
GQ340168.1 gg_id:585358 Prokaryotic Marathonas Reservoir Greece water column clone K07-34-BAC GQ340
AY699794.1 gg_id:100794 Algoriphagus yeomjeoni str. MSS-160 AY6997
EF392675.1 gg_id:211176 Algoriphagus vanfongensis str. KMM 6241 EF3926
FJ986206.1 gg_id:399883 Algoriphagus sp. str. HMC4223 FJ9862
EF219025.1 gg_id:266307 structure and significance Rhizobiales biofouling biofilms on reverse osmosis membra EF2190
DQ178979.1 gg_id:139018 Algoriphagus dokdonensis str. DS-44 DQ178
AY835923.1 gg_id:110855 Algoriphagus locisalis str. MSS-171 AY8359
AY264839.1 gg_id:85985 Hongiella halophila str. IMSNU 14013 JC2051 AY2648
AY264840.1 gg_id:82949 Hongiella ornithinivorans str. IMSNU 14014 JC2052 AY2648
DQ365899.1 gg_id:156351 Algoriphagus sp. str. RE3 DQ365
GQ396828.1 gg_id:537859 Functional unvegetated perhumid recently-deglaciated soils do not correlate shifts s GQ396
GQ009408.1 gg_id:500257 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw77 GQ009
FJ196000.1 gg_id:346430 Algoriphagus sp. str. ZS3-3 FJ1960
EU800233.1 gg_id:342719 It's all ranking aquatic Delaware Bay NJ clone 2C228256 EU8002
EU880511.1 gg_id:330914 Cyclobacterium sp. str. P81 EU8805
AY133105.1 gg_id:59894 TCE-contaminated site clone ccspost2184 AY1331
EF488486.1 gg_id:221747 Hongiella hitoincola str. 7-UAH EF4884
AJ717393.1 gg_id:110611 Chimaereicella alkaliphila str. AC74 AJ7173
EU283530.1 gg_id:279331 Model Early Earth Harbors Deeply Divergent Divisions Anderson Lake clone A507 EU2835
AJ697698.1 gg_id:99104 mesotrophic lake clone SF21 AJ6976
EU161637.1 gg_id:239326 Hongiella aquaeductus str. T4 EU1616
AJ244689.1 gg_id:71214 Cyclobacterium sp. str. V4.MS.32 = MM_2749 AJ2446
GU072591.1 gg_id:556145 Algoriphagus sp. str. LYX05 GU072
GQ340091.1 gg_id:569230 Prokaryotic Marathonas Reservoir Greece water column clone A07-64-BAC GQ340
AY771733.1 gg_id:144558 Algoriphagus antarcticus S4-9 AY7717
AJ744861.1 gg_id:104934 Aquiflexum balticum str. BA160 AJ7448
EU703272.1 gg_id:590303 taxon richness -altitude lakes eastern tin plateau predominance Bacteroidetes and S EU7032

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EU283503.1 gg_id:278764 Model Early Earth Harbors Deeply Divergent Divisions Anderson Lake clone A1488 EU283
AJ564643.1 gg_id:90126 Belliella baltica str. BA134 AJ5646
EU685336.1 gg_id:291455 Belliella sp. str. CC-SAL-25 EU685
AY533665.1 gg_id:105344 Cyclobacterium marinum str. DSM 745 AY5336
AY960985.1 gg_id:115015 Cyclobacterium amurskyensis str. KMM 6143 AY9609
EU419941.1 gg_id:269319 Cyclobacterium linum str. RW54 EU4199
DQ534063.1 gg_id:160672 Cyclobacterium linum str. HY9 DQ534
AM406795.1 gg_id:183122 Echinicola vietnamensis KMM 6221 AM406
DQ645421.1 gg_id:159952 Echinicola vietnamensis str. KMM 6221 DQ645
FJ152973.1 gg_id:327267 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX4CI FJ1529
FJ152601.1 gg_id:318195 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX1A_ FJ1526
FM991866.1 gg_id:553854 Belliella sp. str. LW7 FM991
FJ671714.1 gg_id:521536 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6717
AY533663.1 gg_id:105029 Hongiella marincola str. SW-2 AY5336
FJ674389.1 gg_id:514663 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6743
DQ112663.1 gg_id:130535 Rhodinella ikkaensis str. GCM70 DQ112
GU112990.2 gg_id:591576 Rhodonellum psychrophilum str. 4-5-25 GU112
AY849869.1 gg_id:110577 Microscilla sp. str. MY04 AY8498
FN554611.1 gg_id:541109 Flammeovirga aprica str. HG4 FN5546
FN377813.1 gg_id:549152 Flammeovirga sp. aga24 MB-Aga24 FN3778
AB251933.1 gg_id:178196 Flammeovirga bosoensis str. YS10 AB2519
AB078077.1 gg_id:58611 Flexithrix dorotheae str. IFO 15987 AB0780
AB078073.1 gg_id:58615 Flexibacter tractuosus str. IFO 16035 AB0780
EU328009.1 gg_id:278936 dynamics during bioremediation crude oil contaminated moderate saline soil clone B EU3280
AB433335.1 gg_id:315738 Fulvivirga kasyanovii AB4333
AB260929.1 gg_id:178637 Persicobacter diffluens str. NBRC 15940 AB2609
AB265183.1 gg_id:176970 Flexibacter sp. str. 37GB AB2651
AB444610.1 gg_id:341062 Rapidithrix sp. str. TISTR 1768 AB4446
AB265184.1 gg_id:175211 Flexibacter sp. str. 58GB AB2651
AB265186.1 gg_id:183407 Flexibacter sp. str. SH1.3.1 AB2651
EU697080.1 gg_id:293250 Roseivirga sp. str. F8 EU6970
AJ310654.1 gg_id:106339 Sporocytophaga myxococcoides str. DSM 11118T AJ3106
FJ372724.1 gg_id:357873 Sporocytophaga sp. str. 4v FJ3727
Y08958.1 gg_id:2630 Thermonema rossianum str. AG3-1 Y08958
U10877.1 gg_id:17215 Riemerella anatipestifer str. ATCC 11845 U10877
AB539957.1 gg_id:518608 Evidence syntrophic acetate oxidation coupled hydrogenotrophic methanogenesis -t AB5399
EU639239.1 gg_id:331320 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU6392
AB274511.1 gg_id:214740 packed-bed reactor clone CFB-22 AB2745
AF018199.1 gg_id:2632 hot spring clone env.OPS17 AF0181
CU918589.1 gg_id:568907 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU9185

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EF092232.1 gg_id:275754 Persistent Axinella corrugata Flexibacteraceae clone B2706_D5 EF0922
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FJ612161.1 gg_id:553065 and Biogeochemistry Dongping Lake Ecosystems lake water clone DP3.4.24 FJ6121
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EU050910.1 gg_id:252466 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_01_32 EU0509
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FJ205242.1 gg_id:540371 Prokaryotic deep-sea region East Lau Spreading Centre inactive hydrothermal field se FJ2052
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EU236347.1 gg_id:287889 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg91A5 EU2363
GQ261768.1 gg_id:512679 shifts taxa and response localized organic loading deep sea sediment whale falls clo GQ261

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EU617868.1 gg_id:323057 Seasonal variation microbial Yel Sea sediment clone A13S-92 EU617
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GU118216.1 gg_id:555186 Threatened Corals Provide Microbial Habitats clone Dstr_F06 GU118
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EU362130.1 gg_id:356181 and Mesquite Flats Site Death Valley dune sand clone 1 EU362
CP000383.1 gg_id:169083 Cytophaga hutchinsonii str. ATCC 33406 CP000
AB240469.1 gg_id:141044 microbial structure rhizosphere biofilm Sapporo root-tip (0 40 mm) Phragmites Sosei AB240
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FM877553.1 gg_id:356940 Microbial several mining wastes Bulgaria uranium mill tailings clone BuhD-239 FM877
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DQ499313.1 gg_id:159655 acidic cave snottite biofilm clone CV74 DQ499
AB286643.1 gg_id:208463 Reducing production and domination comamonadaceae reducing oxygen supply was AB286
GQ264428.1 gg_id:512079 Structure Simulated Level Waste Site simulated level waste site clone WW3_12 GQ264
AY921971.1 gg_id:112979 farm soil clone AKYG1686 AY921
EU644183.1 gg_id:284666 and Samoylov Island Lena active layer -centred polygon near surface horizon; Rim_T EU644
FN396950.1 gg_id:546606 integrative isotopic approach study degradation mixed Mixed (US3-M) enriched grou FN396
FM209126.1 gg_id:569376 Dynamics during identified and SSU libraries pilot-scale bioremediation process hydr FM209
EU015107.1 gg_id:247988 Investigation estrogen-degrading bioreactors membrane bioreactor suspension and EU015
CU924663.1 gg_id:552677 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU924
EF516777.1 gg_id:219799 grassland soil clone FCPO734 EF5167
EU335282.1 gg_id:239396 Changes microbial metabolic and along hydrogeochemically variable profile unsatura EU335
FJ529937.1 gg_id:563166 Initial ammonia- and nitrite-oxidizing compromises successful nitritation counter-diffu FJ5299
AB199572.1 gg_id:111136 river water Japan clone RVW-05 AB199
FJ479173.1 gg_id:509032 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4791
FJ516813.1 gg_id:534971 semiarid 'Tablas de Daimiel National Park' wetland (Central Spain) unravelled biofilm FJ5168
EU133703.1 gg_id:242737 tallgrass prarie soil clone FFCH11302 EU133
EU104264.1 gg_id:351446 Evidence Comamonadaceae determinants settling performance activated sludge clo EU104
AY887012.1 gg_id:114481 fresh water clone 1.9.7 AY887
FJ478744.1 gg_id:510426 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4787
GQ021719.1 gg_id:487948 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ021

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AM934889.1 gg_id:544136 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM934
AY493953.1 gg_id:136478 Fingerprinting aggregates soil clone 453 AY4939
FJ710659.1 gg_id:578102 Abundance and microbial long-term operated anammox biofilm reactors initiated ino FJ7106
EU133655.1 gg_id:247445 tallgrass prarie soil clone FFCH599 EU1336
FJ478788.1 gg_id:541511 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4787
AF137029.1 gg_id:2595 Dyadobacter fermentens str. NS114 AF1370
FN421581.1 gg_id:588757 proteogenomics physiology phyllosphere Arabidopsis thaliana clone 1_B12 FN4215
DQ335125.1 gg_id:145990 Dyadobacter sp. str. A54 DQ335
EU344946.1 gg_id:273380 Hepialus gonggaensis guts equalized library larval gut clone Hg5-36 EU3449
GQ389175.1 gg_id:510721 quality deterioration drinking system during serious red water outbreak clone D45 GQ389
FJ719038.1 gg_id:530554 Protozoan grazers alter metabolically active aquifer aquifier sediments clone p03_B0! FJ7190
AY904352.2 gg_id:112685 Tyrosinophaga indica str. GPTSA100-15 AY9043
AF502211.1 gg_id:59352 EBPR sludge lab scale clone HP1A92 AF5022
AB245370.1 gg_id:146568 Kaistomonas ginsengisoli str. Gsoil 085 AB2453
FN547417.1 gg_id:539293 Flectobacillus sp. str. WG3 FN5474
DQ112352.1 gg_id:130977 Flectobacillus sp. str. CL-GP79 DQ112
AB078051.1 gg_id:58637 Flexibacter flexilis str. IFO 16025 AB0780
AB464937.2 gg_id:350565 Altitudinal changes flora on Gulkana Glacier Alaska analyzed sequencing and -cycle c AB4649
EF639389.1 gg_id:235307 Hymenobacter sp. str. BSw20462 EF6393
DQ130048.1 gg_id:137870 microbial biota normal forearm human skin clone PR8 DQ130
GQ097346.1 gg_id:426219 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw453h0: GQ097
EF127614.1 gg_id:207271 Fossil Genes and Microbes Entombed Oldest Ice on Earth ice clone DLE129 EF1276
EF423328.1 gg_id:212044 Hymenobacter sp. str. 1018 EF4233
AF408306.1 gg_id:23691 Hymenobacter group clone KL-94-1-15 AF4083
GQ097378.1 gg_id:408445 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw454c04 GQ097
AF408278.1 gg_id:46108 Taxeobacter sp. clone KL-2-4-3 AF4082
GQ097291.1 gg_id:377316 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw453b1: GQ097
GQ131579.1 gg_id:434806 Hymenobacter sp. str. BZ33r GQ131
EF516581.1 gg_id:219318 grassland soil clone FCPN403 EF5165
AB251884.1 gg_id:151061 Hymenobacter sp. str. PB17 AB2518
GQ097358.1 gg_id:383555 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw454a0: GQ097
Y18837.1 gg_id:2605 Taxeobacter sp. str. Txc1 Y18837
AF408300.1 gg_id:47791 Hymenobacter group clone KL-2-4-4 AF4083
EU370958.1 gg_id:270190 Hymenobacter sp. str. Dae14 EU3709
FJ979849.1 gg_id:418749 Hymenobacter sp. str. tsz19 FJ9798
AM697178.1 gg_id:224467 sequencing libraries indoor dust clone BF0001C019 AM697
Y18836.1 gg_id:2604 Taxeobacter gelupurpurascens str. Txg1 Y18836
GQ097743.1 gg_id:377016 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw456b0: GQ097
DQ365992.1 gg_id:150955 Hymenobacter sp. 21/4 DQ365
Y18835.1 gg_id:2574 Taxeobacter ocellatus str. Myx2105 Y18835
EF127605.1 gg_id:209617 Fossil Genes and Microbes Entombed Oldest Ice on Earth ice clone DLE022 EF1276

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FJ202421.1 gg_id:304538 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2024
FJ005077.1 gg_id:306350 Pontibacter sp. str. RCML-11 FJ0050
AM049256.1 gg_id:132838 Sedimentibacter rubrus str. SRC-1 AM049
DQ672723.1 gg_id:161173 Chinabacter akesu str. zy-4 DQ672
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GU339183.1 gg_id:548681 Pontibacter sp. str. HMD3125 GU339
FJ903178.1 gg_id:567490 Pontibacter sp. str. HMC6020 FJ9031
FM209327.1 gg_id:567720 Microbial Negev desert s sand soil clone 1031 FM209
DQ416803.1 gg_id:265113 Delineation Chromate-Resistant and Clones Cr(VI) Contaminated Sediments landfill : DQ416
AF227830.1 gg_id:42709 str. 47077 AF2278
DQ298339.1 gg_id:153137 studies on and nifH Lasiurus sindicus Sewan grass Thar Desert Rajasthan India rhizos DQ298
EF688348.1 gg_id:247967 soil clone F4-32 EF6883
DQ365989.1 gg_id:154323 Dominant soils Marble Point and Wright Valley Victoria Land Antarctica soil clone J3! DQ365
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DQ676366.1 gg_id:223870 Archaeal and plankton freshwater pond suboxic freshwater-pond sediment clone M DQ676
AB249681.1 gg_id:153026 Runella sp. str. P.slu-06 AB2496
GQ022810.1 gg_id:486859 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu3 GQ022
DQ847443.1 gg_id:161920 human forearm skin clone GL2-106 DQ847
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AM000023.1 gg_id:146467 Spirosoma linguale str. LMG 10896 AM000
AF445698.1 gg_id:40101 travertine hot spring clone SM1G04 AF4456
EF451726.2 gg_id:259377 Spirosoma sp. str. RODSPM10 EF4517
AY792302.1 gg_id:127534 Temporal Variation and Humic Lake clone CrystalBog1D6 AY7923
EU925903.1 gg_id:309050 sediments sediment station DBS1 northern Bering Sea clone 129H24 EU9259
EF520590.1 gg_id:231977 structure lakes: what controls ? acid-impacted lake clone ADK-BTh02-48 EF5205
FJ592603.1 gg_id:549972 Fumarole-supported islands biodiversity within hyperarid -elevation landscape on Pu FJ5926
EU283380.1 gg_id:242384 consecutively aerated submerged treating domestic wastewater activated sludge m EU2833
EF516898.1 gg_id:219243 grassland soil clone FCPS427 EF5168
EU133692.1 gg_id:254714 tallgrass prarie soil clone FFCH7240 EU1336
AY218622.1 gg_id:81939 penguin droppings sediments clone KD3-93 AY2186
EU431819.1 gg_id:543813 Troglobitic (Cansiliella) on specialized feeding apparatus calcium carbonate (moonmi EU4318
AF233294.1 gg_id:51029 Tuber borchii symbiont b-10RA AF2332
CU466728.1 gg_id:328392 Evry wastewater treatment plant anoxic basin clone CU466
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EF516038.1 gg_id:222673 grassland soil clone FCPT641 EF5160
AF097805.1 gg_id:2488 activated sludge clone 49511 AF0978
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AM991273.1 gg_id:279186 Microbial groundwater and their potential use biomonitoring karst spring water clo AM991
EU133767.1 gg_id:244639 tallgrass prarie soil clone FFCH4913 EU1337
AF534435.1 gg_id:83335 Toolik Lake main station at 3 m depth clone TLM11/TLMdgge04 AF5344
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FJ612274.1 gg_id:513523 and Biogeochemistry Dongping Lake Ecosystems lake water clone DP7.4.20 FJ6122
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AM279196.1 gg_id:169294 Cytophaga-Flavobacterium-Bacteroides coastal North Sea marine water clone NorS AM279
EU091557.2 gg_id:330775 clones IRDE (IW) Western Ghats region India water clone IWENVB11 EU0915
DQ071076.1 gg_id:133154 marine surface water clone PB1.33 DQ071
GU444059.1 gg_id:516417 Effects amendments on fertility and microbial structure cucumber Cucumis sativus L GU444
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EF636834.1 gg_id:277776 Metagenomic and Namib desert sand clone 6 EF6368
EU289479.1 gg_id:245429 metagenomic approach biosynthesis ansamycin endophytes or symbionts enriched s EU2894
AB078072.1 gg_id:58616 Flexibacter tractuosus str. IFO 15989 AB0780
AJ290033.1 gg_id:20151 Austria: Lake Gossenkoellesee clone GKS2-216 GKS2-216 AJ2900
EU010168.1 gg_id:239504 Biogeography Singapore seawaters seawater clone B49 EU0101
AB078079.1 gg_id:58609 Microscilla furvescens str. IFO 15994 AB0780
AJ535729.1 gg_id:77393 Arcicella aquatica str. NO-502 AJ5357
AB078056.1 gg_id:58632 Flexibacter litoralis str. IFO 15988 AB0780
DQ917821.1 gg_id:221302 Microbial profiles bleached and wild-type Muricea elongata Microscilla clone BME34 DQ917
AJ746140.1 gg_id:112775 Arcicella sp. MG83 AJ7461
AB078059.1 gg_id:58628 Flexibacter polymorphus str. IFO 16703 AB0780
FJ667554.1 gg_id:555655 algae-lysing clone -13 FJ6675

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DQ990929.2 gg_id:175203 Microbial Rock Varnish Yungay Atacama Desert Chile rock varnish clone AYRV1-015 DQ990
AM259891.1 gg_id:210600 Spatial sponge- Mediterranean Tethya aurantia sponge cortex clone TAA-5-25 AM259
GQ350621.1 gg_id:555379 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ350
AY167829.1 gg_id:77550 Taxeobacter sp. str. SAFR-033 AY1678
EF635010.1 gg_id:244833 Rudanella aurantiaca str. 5715S-11 EF6350
EU703303.1 gg_id:444025 lakes on Eastern Tin Plateau polysaline lake altitude 3204 masl clone XZQH98 EU7033
AB078065.1 gg_id:58624 Flexibacter ruber str. IFO 16677 AB0780
FN421864.1 gg_id:590649 proteogenomics physiology phyllosphere clover clone 2_D07 FN4218
EU004198.2 gg_id:257862 Rhodocytophaga aerolata str. 5416T-29 EU0041
EF683048.1 gg_id:249391 Eastern Mediterranean atmosphere clone F27_4H_FL EF6830
EU722650.1 gg_id:352793 Microbial athalassohaline Tirez lagoon (Spain) sediment clone SB74 EU7226
DQ346479.1 gg_id:155601 during composting libraries compost clone 2B07 DQ346
AM000022.1 gg_id:150422 Larkinella insperata str. LMG 22510 AM000
AB078063.1 gg_id:58625 Flexibacter roseolus str. IFO 16707 AB0780
AY854022.2 gg_id:115032 Leadbetterella byssophila str. 4M15 AY8540
GQ020313.1 gg_id:489354 Topographical and Temporal Human Skin Microbiome skin glabella clone nbu267e04 GQ020
DQ981405.1 gg_id:188216 entrapped Puruogangri ice core clone PIC-D5 DQ981
AF445730.1 gg_id:35334 CFB group clone SM2F08 AF4457
AY168735.2 gg_id:135189 Oxidizing Biofilms: Cultivation Approaches and Rates Arsenite Oxidation arsenite-oxi AY1687
AB078054.1 gg_id:58634 Flexibacter flexilis subsp. pelliculosus str. IFO 16028 subsp. AB0780
AM746475.1 gg_id:252171 Ekhidna lutea str. BiosLi/39 AM746
EU236411.1 gg_id:288687 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg92E12 EU2364
FJ203195.1 gg_id:340708 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c FJ2031
AB078082.1 gg_id:58606 Microscilla sericea str. IFO 16561 AB0780
GQ421846.1 gg_id:549650 Adhaeribacter sp. str. 6515J-31 GQ421
AY907776.1 gg_id:136881 identification picoplankton contrasting waters Arabian Sea water clone A712037 AY9077
AB015263.1 gg_id:2577 deepest cold-seep area Japan Trench clone JTB248 sp. AB0152
DQ395524.1 gg_id:154918 deep-sea octacoral clone ctg_CGOCA57 DQ395
EU804292.1 gg_id:324075 It's all ranking aquatic 250 miles Panama City clone 6C232194 EU8042
EF016479.1 gg_id:181596 Near real-time autonomous detection marine on coastal mooring Monterey Bay Calif EF0164
EU804351.1 gg_id:320907 It's all ranking aquatic 250 miles Panama City clone 6C232257 EU8043
EF573031.1 gg_id:233619 Coco's Island site 23 marine clone S23_1130 EF5730
EU404040.1 gg_id:320521 Microbial septic tank effluent and soil biozone infiltrative surface clean water clone (EU4040
AB078048.1 gg_id:55293 Flexibacter elegans str. IFO 15055 AB0780
DQ395539.1 gg_id:153017 deep-sea octacoral clone ctg_CGOCA43 DQ395
EU005886.1 gg_id:274173 Major activity inside and outside natural iron-fertilized phytoplankton bloom 3 micro EU0058
GQ349744.1 gg_id:546322 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ349
AF217497.1 gg_id:29905 Rhodothermus marinus str. PRQ-55 AF2174
EU635948.1 gg_id:279426 Microbiology geochemistry great boiling and mud springs sediment hot spring; temp EU6359
CU467270.1 gg_id:319903 Prokaryotic Tunisian saltern Saltern solar multipond clone CU467

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AM981339.1 gg_id:274210 Microbial processed Mediterranean seawater based on salt crystal Tunisian solar sa AM981
EF459716.1 gg_id:218096 Prokaryotic Hypersaline Inland Turkey Tuz Lake (hypersaline) clone 3-55B EF4597
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CU467372.1 gg_id:337266 Prokaryotic Tunisian saltern Saltern solar multipond clone CU467
FN393464.1 gg_id:558759 prokaryotic sediments two Tunisian multipond sediment solar saltern clone 188ZA01 FN3934
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FN393524.1 gg_id:550621 prokaryotic sediments two Tunisian multipond sediment solar saltern clone SFD1D0 FN3935
EU869386.1 gg_id:317840 Microbial hypersaline soil Sidi Ameur Salt Lake Algerian Sahara clone ARDBACSS36 EU8693
FN393497.1 gg_id:575327 prokaryotic sediments two Tunisian multipond sediment solar saltern clone SFD1H1 FN3934
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CU467363.1 gg_id:314160 Prokaryotic Tunisian saltern Saltern solar multipond clone CU467
AM981385.1 gg_id:273261 Microbial processed Mediterranean seawater based on salt crystal Tunisian solar sa AM981
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CU467353.1 gg_id:347711 Prokaryotic Tunisian saltern Saltern solar multipond clone CU467
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GU447292.1 gg_id:532169 Salisaeta longa str. BX104 GU447
EF106234.1 gg_id:201362 microbial two endoevaporitic salt crusts evaporitic crust Guerrero Negro Baja clone 3 EF1062
EU050888.1 gg_id:235984 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_01_23 EU0508
FJ745114.1 gg_id:564902 Transporter genes expressed coastal response dissolved organic carbon surface wate FJ7451
GU118662.1 gg_id:577399 Threatened Corals Provide Microbial Habitats clone Mfav_C15 GU118
FJ905760.1 gg_id:570489 s Tonga-Kermadec iron oxide sediments Volcano 1 Tonga Arc clone V1F167b FJ9057
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EF648151.1 gg_id:257002 dynamics during produced water treatment aerobic activated sludge clone XJ103 EF6481
AF407678.1 gg_id:60618 Great Artesian Basin clone Y30 AF4076
GQ108731.1 gg_id:437088 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw692h0 GQ108
GU118538.1 gg_id:586741 Threatened Corals Provide Microbial Habitats clone Mfav_I11 GU118
EU592405.1 gg_id:536800 Seasonal changes Salton Sea hypersaline water clone SSW6AP EU5924
DQ889917.1 gg_id:172643 natural product producing octocoral Erythropodium caribaeorum Cytophaga clone E DQ889
AJ347046.1 gg_id:60166 sponge clone TK44 AJ3470
EU133663.1 gg_id:249217 tallgrass prarie soil clone FFCH12849 EU1336
GU056052.1 gg_id:592121 Biologic Techniques Applied Microbial Prospecting China: Ban 876 Gas Oil Field Bein GU056
AB015543.1 gg_id:2649 deep-sea sediment clone BD2-15 AB0155
DQ070835.1 gg_id:148406 Prokaryotic Structures Seafloor Basalts Varying Age East Pacific Rise and Ridge basal DQ070
AM997702.1 gg_id:571736 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A AM997
AY493957.1 gg_id:136516 Fingerprinting aggregates soil clone 9 AY4939
FN545882.2 gg_id:588351 un 2 Rupi basin Bulgaria hot spring clone S2R-130 FN5458

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EU488070.1 gg_id:574540 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU488
AB250561.1 gg_id:161044 and ecology Grotta Azzurra Palinuro Cape (Salerno Italy) microbial mat clone #2-11 AB250
DQ890437.1 gg_id:164768 phylotypes Pestarella tyrrhena (Decapoda: Thalassinidea) abdominal setal tuft clone DQ890
DQ395043.1 gg_id:153143 harbor sediment clone VHS-B5-77 DQ395
AB245934.1 gg_id:186116 Aureispira marina str. 62 (= IAM 15390 = TISTR 1728) AB245
AY907809.1 gg_id:136805 identification picoplankton contrasting waters Arabian Sea water clone A714026 AY907
AY527408.1 gg_id:101416 Saprospira grandis str. ATCC 23116 AY527
EU050913.1 gg_id:255567 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_08_95 EU050
AB088636.1 gg_id:63062 Saprospira grandis str. ATCC23116 AB088
FJ905677.1 gg_id:574719 s Tonga-Kermadec iron oxide chimney-like structure on Volcano 19 Tonga Arc clone V FJ9056
AY527409.1 gg_id:101586 Saprospira sp. str. CNJ451 AY527
AB058899.1 gg_id:35418 Saprospira sp. str. SS90-1 AB058
EF574193.1 gg_id:241532 site S25 near Coco's Island marine clone S25_537 EF5741
AY527410.1 gg_id:105211 Saprospira sp. str. CNJ640 AY527
AJ786333.1 gg_id:114960 Lake Taihu freshwater clone MS-Taihu1-L AJ7863
AY863078.1 gg_id:111774 wastewater treatment pool clone SXAU021 AY863
EU703324.1 gg_id:380678 lakes on Eastern Tin Plateau polysaline lake altitude 3204 masl clone XZQH240 EU703
EU703352.1 gg_id:411990 lakes on Eastern Tin Plateau freshwater lake altitude 4298 masl clone XZTSH74 EU703
EU703430.1 gg_id:406875 lakes on Eastern Tin Plateau freshwater lake altitude 4219 masl clone XZXXH67 EU703
EU703317.1 gg_id:447962 lakes on Eastern Tin Plateau polysaline lake altitude 3204 masl clone XZQH163 EU703
AJ786339.1 gg_id:115067 Lake Loosdrecht freshwater clone MS-Loos1-L AJ7863
AJ786335.1 gg_id:115006 Dunedin: artificial pond freshwater clone MS-NZ1-L AJ7863
EU703341.1 gg_id:439336 lakes on Eastern Tin Plateau freshwater lake altitude 4298 masl clone XZTSH25 EU703
EU703382.1 gg_id:436730 lakes on Eastern Tin Plateau freshwater lake altitude 4219 masl clone XZXXH171 EU703
EU703380.1 gg_id:440437 lakes on Eastern Tin Plateau freshwater lake altitude 4298 masl clone XZTSH82 EU703
FJ612203.1 gg_id:574154 and Biogeochemistry Dongping Lake Ecosystems lake water clone DP3.5.58 FJ6122
EU703204.1 gg_id:538387 taxon richness -altitude lakes eastern tin plateau predominance Bacteroidetes and S EU703
FJ612189.1 gg_id:557078 and Biogeochemistry Dongping Lake Ecosystems lake water clone DP3.5.22 FJ6121
EU703376.1 gg_id:378092 lakes on Eastern Tin Plateau freshwater lake altitude 4298 masl clone XZTSH97 EU703
FJ612298.1 gg_id:556107 and Biogeochemistry Dongping Lake Ecosystems lake water clone DP7.5.37 FJ6122
AJ786331.1 gg_id:114980 Lake Tanganjika freshwater clone MS-Tang1-L AJ7863
EU703161.1 gg_id:549226 taxon richness -altitude lakes eastern tin plateau predominance Bacteroidetes and S EU703
FJ612411.1 gg_id:554700 and Biogeochemistry Dongping Lake Ecosystems lake water clone DP10.4.26 FJ6124
EF520596.1 gg_id:228517 structure lakes: what controls ? acid-impacted lake clone ADK-MOe02-10 EF5205
AJ290034.1 gg_id:73931 Austria: Lake Gossenkoellesee clone GKS2-217 GKS2-217 AJ2900
AY168729.2 gg_id:76801 arsenite-oxidizing biofilm clone Hot Creek 49 AY168
AJ784892.1 gg_id:115129 Haliscomenobacter hydrossis str. DSM 1100 = ATCC 27775 AJ7848
NR_028693.1 gg_id:556906 Lewinella cohaerens str. II-2; ATCC 23123 NR_02
GQ441283.1 gg_id:584899 and dynamic mat present vs. active nitrogen-fixing microorganisms marine microbia GQ441
GQ441322.1 gg_id:584859 and dynamic mat present vs. active nitrogen-fixing microorganisms marine microbia GQ441
AB301614.1 gg_id:223475 Lewinella cohaerens str. NBRC 102661 AB301

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AM295255.1 gg_id:251371 Lewinella nigricans str. ATCC 23147 AM295
EU371935.1 gg_id:259026 Lewinella persicus EU371
EF554367.1 gg_id:219002 Lewinella antarctica str. IMCC3223 EF5543
NR_028695.1 gg_id:583989 Lewinella nigricans str. SS-2; ATCC 23147 NR_02
AB301494.1 gg_id:236361 Lewinella lutea str. FYK2402M69 (= NBRC 102634 = NCI AB301
GU061593.1 gg_id:586573 and function microbial mesoscale eddy perturbations South China Sea clone CE2-5m GU061
EF092259.1 gg_id:274109 Persistent identical Axinella corrugata on 27-Jun-2002 clone MB255_F10 EF0922
AF445681.1 gg_id:33230 travertine hot spring clone SM1E03 AF4456
AB301495.1 gg_id:255544 Lewinella marina str. MKG-38 (= NBRC 102633 = NCIMB 1 AB301
AM286229.1 gg_id:256191 Lewinella agarilytica str. SST-19 AM286
EU236397.1 gg_id:295985 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg92C6 EU2363
EU925862.1 gg_id:307334 sediments sediment station DBS1 northern Bering Sea clone 063F26 EU9258
FJ517043.1 gg_id:568024 semiarid 'Tablas de Daimiel National Park' wetland (Central Spain) unravelled water c FJ5170
EU246289.1 gg_id:243481 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-P6-D05 EU2462
EU245106.1 gg_id:244430 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-H2-B08 EU2451
FJ230926.1 gg_id:310337 under Level Antibiotic Selection Pressures river water clone F23 FJ2309
EU246805.1 gg_id:240609 polyphasic description Pocillopora meandrina Palmyra Atoll Calcinus obscurus abdon EU2468
EU245082.1 gg_id:245355 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-H1-F08 EU2450
DQ270634.1 gg_id:144512 hydrothermal carbonate chimney clone LC1408B-77 DQ270
GQ261756.1 gg_id:570841 shifts taxa and response localized organic loading deep sea sediment whale falls clo GQ261
FJ535046.1 gg_id:542634 Enhancement protein conversion volatile fatty acids accumulation during addition: ef FJ5350
CU466734.1 gg_id:336473 Evry wastewater treatment plant anoxic basin clone CU466
DQ232756.1 gg_id:194491 Identity abundance and ecophysiology filamentous Cytophaga-Flavobacterium spec DQ232
DQ330422.1 gg_id:159332 Guerrero Negro hypersaline microbial mat clone 01D1q40 DQ330
DQ640668.1 gg_id:228176 Biodiversity and microbial full-scale enhanced biological phosphorus removal plant a DQ640
EU283383.1 gg_id:253723 consecutively aerated submerged treating domestic wastewater activated sludge m EU2833
AM040132.1 gg_id:150023 sandy sediments clone Sylt 36 AM040
EU177704.1 gg_id:274126 Identification and ecophysiological epiphytic protein-hydrolyzing saprospiraceae ('Ca EU177
EU246830.1 gg_id:245374 polyphasic description Pocillopora meandrina Palmyra Atoll Calcinus obscurus abdon EU2468
CU923649.1 gg_id:557079 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU923
DQ330419.1 gg_id:159352 Guerrero Negro hypersaline microbial mat clone 01D1q39 DQ330
DQ856550.1 gg_id:246616 intestinal microflora Chinese mitten crab (Eriocheir sinensis) clone C3H DQ856
EF020003.1 gg_id:204415 aspen rhizosphere clone Elev_16S_1393 EF0200
AB476221.1 gg_id:568287 Compositional and functional transition epibiotic microbial hydrothermal vent galath AB4762
EU431829.1 gg_id:538448 Troglobitic (Cansiliella) on specialized feeding apparatus calcium carbonate (moonmi EU4318
DQ640679.1 gg_id:232231 full-scale EBPR sludge clone Skagenf44 DQ640
EU101259.1 gg_id:244393 Sulfide/oxygen supply ratio predicts outcome competition among sulfur-oxidizing wa EU1012
DQ330510.1 gg_id:159469 Guerrero Negro hypersaline microbial mat clone 072DZ68 DQ330
DQ269109.1 gg_id:200498 marine macro-alga surface clone DPC179 DQ269
DQ640691.1 gg_id:233992 full-scale EBPR sludge clone Skagenf54 DQ640
EU177700.1 gg_id:271904 Identification and ecophysiological epiphytic protein-hydrolyzing saprospiraceae ('Ca EU177

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EU246294.1 gg_id:242491 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-P6-E02 EU2462
DQ640669.1 gg_id:228572 Biodiversity and microbial full-scale enhanced biological phosphorus removal plant a DQ640
GU230422.1 gg_id:590902 Multilevel approach along Rio de la Plata-South Atlantic Ocean coastal sediment clo GU230
DQ640739.1 gg_id:228243 full-scale EBPR sludge clone Skagen114 DQ640
EU246796.1 gg_id:249508 polyphasic description Pocillopora meandrina Palmyra Atoll Calcinus obscurus abdon EU2467
DQ269043.1 gg_id:191119 marine macro-alga surface clone UA18 DQ269
DQ270658.1 gg_id:142556 hydrothermal carbonate chimney clone LC1446B-1 DQ270
EU919769.1 gg_id:314728 Kongsfjorden western Spitsbergen Svalbard ocean water clone b29 EU9197
L10944.1 gg_id:2555 marine snow clone agg32 L10944
EU925904.1 gg_id:316764 sediments sediment station DBS1 northern Bering Sea clone 130H27 EU9259
AJ704707.1 gg_id:109301 marine sediment clone HMMVBeg-23 AJ7047
FJ517715.1 gg_id:538346 Disturbing epithelial homeostasis metazoan Hydra leads drastic changes microbiota e FJ5177
EU265797.1 gg_id:268688 epibiotic assemblage recently described Yeti Kiwa hirsuta (Kiwidae) surface crab hyc EU2657
AB476272.1 gg_id:573306 Compositional and functional transition epibiotic microbial hydrothermal vent galath AB4762
DQ640718.1 gg_id:232619 full-scale EBPR sludge clone Skagen118 DQ640
AY921686.1 gg_id:112888 farm soil clone AKYH1028 AY9216
CU466747.1 gg_id:314086 Evry wastewater treatment plant anoxic basin clone CU4667
EU104094.1 gg_id:303752 Evidence Comamonadaceae determinants settling performance activated sludge clo EU1040
CU466750.1 gg_id:334860 Evry wastewater treatment plant anoxic basin clone CU4667
AB286458.1 gg_id:215105 Reducing production and domination comamonadaceae reducing oxygen supply was AB2864
AF314434.1 gg_id:34106 aerobic phosphorus-removal ecosystem clone PHOS-HE79 AF3144
EU104080.1 gg_id:329138 Evidence Comamonadaceae determinants settling performance activated sludge clo EU1040
EF471455.1 gg_id:262076 Fast Screening and Estuarine Operon Libraries whole surface water Chesapeake Bay (EF4714
DQ640703.1 gg_id:230258 Biodiversity and microbial full-scale enhanced biological phosphorus removal plant a DQ640
AJ318154.1 gg_id:52545 Waste-gas biofilter clone BIjiii32 AJ3181
AM259876.1 gg_id:211973 Spatial sponge- Mediterranean Tethya aurantia sponge cortex clone TAA-10-77 AM259
AY302114.1 gg_id:109536 sludge dentrifying reactor fed with methanol clone DSBR-B007 AY3021
EU283492.1 gg_id:278585 Model Early Earth Harbors Deeply Divergent Divisions Anderson Lake clone A1877 EU2834
EU245985.1 gg_id:256252 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-P1-B03 EU2459
CU466727.1 gg_id:325671 Evry wastewater treatment plant anoxic basin clone CU4667
DQ295906.1 gg_id:146854 Cohn's Crenothrix filamentous oxidizer unusual methane monooxygenase physical e DQ295
AB058902.1 gg_id:29244 Saprospira sp. str. SS95-4 AB0589
EF523466.1 gg_id:263176 Identification and ecophysiological epiphytic protein-hydrolyzing saprospiraceae ('Ca EF5234
EU340156.1 gg_id:252788 on Aquatic Macrophytes Geothermally Active Area Sedge Bay Yellowstone Lake WY : EU3401
DQ640672.1 gg_id:234415 full-scale EBPR sludge clone Skagenf45 DQ640
AB058901.1 gg_id:30366 Saprospira sp. str. SS92-11 AB0589
AF087087.1 gg_id:2534 activated sludge clone MK09 AF0870
EU246157.1 gg_id:246729 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-P4-E02 EU2461
AF314431.1 gg_id:35871 aerobic phosphorus-removal ecosystem clone PHOS-HE35 AF3144
EU925914.1 gg_id:340563 sediments sediment station DBS1 northern Bering Sea clone 149H54 EU9259

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EU374049.1 gg_id:270239 southern Cretan margin (eastern Mediterranean Sea) canyon and slope sediment clc EU374
AY929064.1 gg_id:112991 Saprospira sp. str. PdY3 AY929
EU245092.1 gg_id:246699 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-H1-H06 EU245
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AB267714.1 gg_id:169934 Pocheonia terrae str. Jip 13 AB267
GQ263282.1 gg_id:510706 Structure Simulated Level Waste Site simulated level waste site clone FW1_a28 GQ263
GQ263443.1 gg_id:510710 Structure Simulated Level Waste Site simulated level waste site clone FW2_12B GQ263
FJ754321.1 gg_id:574254 Parapedobacter sp. str. 4M40 FJ7543
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EU169155.1 gg_id:240279 Pedobacter cryoconitis str. B52 EU169
AJ438174.1 gg_id:29206 Pedobacter piscium str. DSM 11725T AJ4381
AM491368.1 gg_id:208050 Pedobacter duraquae str. WB2.1-25 AM491
AJ318151.1 gg_id:44075 Waste-gas biofilter clone BIji46 AJ3181
AB255102.1 gg_id:163090 corroded concrete clone SC-85 AB255
DQ298770.1 gg_id:142463 Effect Nutrient Periodicity upon Microbial Dynamics exposed 7-day nutrient flux DQ298
FN421509.1 gg_id:585420 proteogenomics physiology phyllosphere Arabidopsis thaliana clone 12_F02 FN421
EU057838.1 gg_id:237550 Pedobacter sp. CH30-5 EU057
AM237384.1 gg_id:154889 Pedobacter cryoconitis OS-119 AM237
EU030686.1 gg_id:336897 Pedobacter nyackensis str. NWG-II14 EU030
GQ389204.1 gg_id:570755 quality deterioration drinking system during serious red water outbreak clone D78 GQ389
GU377107.1 gg_id:529048 Flavobacterium sp. str. sptzw17 GU377
AF385531.1 gg_id:70559 swab advanced noma lesion clone Av100 AF385
FJ230892.1 gg_id:303672 under Level Antibiotic Selection Pressures river water clone F1 FJ2308
AM491370.1 gg_id:210212 Pedobacter metabolipauper str. WB2.3-71 AM491
FJ979862.1 gg_id:465948 Sphingobacterium sp. str. tsz34 FJ9798
NR_028977.1 gg_id:565000 Pedobacter africanus str. K 1/K2; DSM 12126 NR_02
GQ263646.1 gg_id:562141 Structure Simulated Level Waste Site simulated level waste site clone FW3_33C GQ263
EU652337.1 gg_id:282928 Pedobacter sp. str. JC2491 EU652
FN421692.1 gg_id:535873 proteogenomics physiology phyllosphere soybean clone 3_E10 FN421
AB245371.1 gg_id:148944 Pedobacter ginsengisoli str. Gsoil 104 AB245
GQ009735.1 gg_id:499930 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw77 GQ009
EF459523.1 gg_id:207247 Pedobacter sp. KFC-76 EF4595
EU652336.1 gg_id:284420 Pedobacter sp. str. JC2490 EU652
AY571816.1 gg_id:106242 Sphingobacterium sp. 44/35 AY5718
EF154114.1 gg_id:196903 SAR increases fitness Arabidopsis thaliana response natural pathogens leaf clone ME EF1541
AJ438172.1 gg_id:52839 Pedobacter heparinus str. DSM 2366T AJ4381

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EU538991.1 gg_id:283118 profile human microbiota antecubital fossa (inner elbow) skin clone nbt98a10 EU538
AB485750.1 gg_id:582642 Stratified medicinal leech Hirudo verbana bladder clone 1B-SPH AB485
DQ172992.2 gg_id:152752 Pedobacter sp. str. TSBY-22 DQ172
AM411066.1 gg_id:175904 Sphingobacterium faecium str. Z18zhy AM411
FJ950587.1 gg_id:410685 Sphingobacterium faecium str. c121 FJ9505
AM411995.1 gg_id:192089 Sphingobacterium sp. Z15zhy AM411
AY635870.1 gg_id:99322 Sphingobacterium sp. str. BM-9_2 AY6358
EU918344.1 gg_id:341269 Sphingobacterium sp. str. PM2-P1-29 EU918
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FJ194520.1 gg_id:341712 Sphingobacterium mizutaii str. LCD51 FJ1945
AM286268.1 gg_id:168576 Flavobacterium mizutaii Ch1 AM286
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EU536959.1 gg_id:280639 profile human microbiota antecubital fossa (inner elbow) skin clone nbt217f07 EU5369
EU834268.1 gg_id:344005 Sphingobacterium siyangense str. DS48 EU8342
EU240953.1 gg_id:276940 Sphingobacterium multivorum str. DW-7 EU2409
AB100739.1 gg_id:79519 Sphingobacterium multivorum str. IAM15026 AB100
EU240954.1 gg_id:268061 Sphingobacterium multivorum str. DW-1 EU2409
FJ894578.1 gg_id:552745 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B2E; ear pu FJ8945
EU306339.1 gg_id:240379 Sphingobacterium sp. str. Y15B EU3063
GQ016359.1 gg_id:493307 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ016
GQ016564.1 gg_id:493101 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ016
AJ459411.1 gg_id:66760 Sphingobacterium spiritivorum str. DSM 2582 AJ4594
DQ984207.1 gg_id:239331 Sphingobacterium sp. str. VA-15b DQ984
AJ438177.1 gg_id:26308 Sphingobacterium thalpophilum str. DSM 11723T AJ4381
GQ339910.1 gg_id:570493 Sphingobacterium sp. str. IBFC2009 GQ339
EU373423.1 gg_id:263070 Sphingobacterium siyangensis str. YRL14 EU3734
EF122436.1 gg_id:178057 Sphingobacterium compostus str. 4M24 EF1224
FJ156081.1 gg_id:348866 Sphingobacterium sp. str. MOL-1 FJ1560
EU046272.1 gg_id:239018 Sphingobacterium siyangensis str. SY1 EU0462
AY856847.1 gg_id:109982 Sphingobacterium sp. str. 62 AY8568

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EU344912.1 gg_id:270982 Hepialus gonggaensis guts equalized library larval gut clone Hg5-02 EU344
EU464820.1 gg_id:291453 Hartmann's mountain zebra feces clone AFZEB_aaj71d10 EU464
FJ816788.1 gg_id:560815 Sphingobacterium shayense str. HS39 FJ8167
AB249372.1 gg_id:155740 Sphingobacterium daejeonense str. TR6-04 AB249
EU595360.1 gg_id:277106 Sphingobacterium sp. str. 35 EU595
GU353117.1 gg_id:576006 Sphingobacterium sp. str. CH14 GU353
GQ058131.1 gg_id:410722 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ058
EU465049.1 gg_id:291433 African elephant feces clone AFYEL_aaj67c03 EU465
EU464925.1 gg_id:302702 African elephant feces clone AFYEL_aaj65c07 EU464
DQ168834.1 gg_id:138761 Fermentative biohydrogen production heated anaerobic sludge clone J16 DQ168
FJ859899.1 gg_id:442126 Sphingobacterium sp. str. XH4 FJ8598
AY838458.1 gg_id:109338 fruiting body Pleurotus eryngii clone PE02 AY8384
GQ988781.1 gg_id:573731 Sphingobacterium sp. str. LQY-18 GQ988
DQ824722.1 gg_id:183740 human fecal clone RL185_aaj72c06 DQ824
AB078046.1 gg_id:56235 Flexibacter canadensis str. IFO 15130 AB078
GQ263715.1 gg_id:543870 Structure Simulated Level Waste Site simulated level waste site clone WC1_a30 GQ263
DQ450752.1 gg_id:160802 Microbial Alpine Tundra Wet Meadow Soil: Chloroflexi Cold Water-Saturated satura DQ450
FN400860.1 gg_id:550032 Mucilaginibacter sp. str. FT2.2 FN400
GQ263411.1 gg_id:540688 Structure Simulated Level Waste Site simulated level waste site clone FW2_03B GQ263
GQ396878.1 gg_id:575305 Functional unvegetated perhumid recently-deglaciated soils do not correlate shifts GQ396
AF170741.1 gg_id:2485 Cytophagales str. QSSC5-1 AF1707
AJ295641.1 gg_id:50974 uranium mill tailing clone KF-Gitt2-34 AJ2956
EU861966.1 gg_id:347195 effects chronic fertilization on alpine tundra microbial implications carbon and cyclin EU861
AM490402.1 gg_id:205748 Mucilaginibacter paludis str. TPT56 AM490
GQ009469.1 gg_id:500195 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw77 GQ009
AB267717.1 gg_id:163173 Sphingoterrabacterium daejeonensis str. Jip10 AB267
GQ263331.1 gg_id:568750 Structure Simulated Level Waste Site simulated level waste site clone FW1_a85 GQ263
EF151805.1 gg_id:184347 Parapedobacter soli str. DCY14 EF1518
AM936258.1 gg_id:564970 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM936
EU133724.1 gg_id:236952 tallgrass prarie soil clone FFCH1521 EU133
EF516352.1 gg_id:223975 grassland soil clone FCPN446 EF5163
DQ421387.1 gg_id:154665 Olivibacter itius str. AW-6 DQ421
AF409002.1 gg_id:106893 Sphingobacteriaceae str. Ellin160 AF409
GQ129977.1 gg_id:405895 Genetic inventory 'JPL-SAF' during MSL mission spacecraft assembly clean room floc GQ129
EU196345.1 gg_id:238897 Ginsengisolibacter sp. NP11 EU196
EF516964.1 gg_id:223783 grassland soil clone FCPN666 EF5169
AY509377.1 gg_id:99619 freshwater clone LiUU-3-212 AY5093
AF492000.1 gg_id:68384 Sphingobacterium sp. str. HC-6155 AF492
FJ466361.1 gg_id:534367 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea FJ4663
EU802122.1 gg_id:341582 It's all ranking aquatic Chesapeake Bay MD clone 3C003531 EU802
AB330392.1 gg_id:243196 Pedobacter mucosus str. SCK AB330

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g__Candidatus Amoebophilus
g__Candidatus Amoebophilus
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s__unclassified	74022
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