FJ367190.1 gg_id:367962 feces adult twins and mothers; TS28 clone TS28_a04e12
FJ678613.1 gg_id:531345 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
AY916353.1 gg_id:114378 human stool clone D051
EU381774.1 gg_id:265197 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase
FJ832322.1 gg_id:558715 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P1Q301_19C03
EU463631.1 gg_id:303133 domesticated horse feces clone horsej_aai90a12
FJ440078.1 gg_id:567506 Megamonas hypermegale colonization correlates Campylobacter jejuni exclusion pou
FJ682646.1 gg_id:513042 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU844825.1 gg_id:327546 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
EU871410.1 gg_id:324570 Genetic Bovine (Bos taurus) Rumen Thailand clone CF378
DQ456306.1 gg_id:158491 pre-adolescent turkey cecum clone CFT211G6
EU381733.1 gg_id:265925 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid
DQ353915.1 gg_id:146314 Fecal Wild Gorilla (Gorilla beringei) wild gorilla feces clone Z32
EU843681.1 gg_id:325563 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
EU844239.1 gg_id:327857 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
AF001742.1 gg_id:15698 rumen clone RF9
GQ451225.1 gg_id:545091 Fecal Yunnan snub-nosed monkey feces clone J128
AM277561.2 gg_id:229533 fecal microbiota irritable bowel syndrome patients significantly that healthy subject
GU303762.1 gg_id:580081 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c
EU622737.1 gg_id:279179 -feed administered sub-therapeutic chlorotetracycline alters structure and but not a
AY916186.1 gg_id:114444 human ascending colon biopsy clone LW88
EU344299.1 gg_id:271356 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad
FJ833479.1 gg_id:591398 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J1Q201_78F10
EU871378.1 gg_id:304971 Genetic Bovine (Bos taurus) Rumen Thailand clone CF203
EF406725.1 gg_id:211308 mouse colon clone infected_14days-B9
EU842453.1 gg_id:316729 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi
AY986020.1 gg_id:127092 human stool clone D332
EU764308.1 gg_id:341905 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1
FJ172880.1 gg_id:352691 Qinghai Yak Ruminal and Fungi China rumen clone RB-2D1
EU844758.1 gg_id:347587 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
GU476604.1 gg_id:522127 microbial biogas fermentation enrichment clone BBMC-4
GU208279.1 gg_id:537538 Study on Sediment Dongping Lake sediment clone 6F1-3
EU358689.1 gg_id:325820 structure archaeal denaturing gel electrophoresis and sequencing mesophilic biogas
GQ458248.1 gg_id:513979 Microbial structure co-digestion anaerobic bioreactors treating cassava pulp and pig
AB192099.1 gg_id:143019 termite gut homogenate clone M1NP1-24
AB192110.1 gg_id:144845 termite gut homogenate clone M1PT4-30
AB255930.1 gg_id:164433 Localization Cell Morphologies Members Candidate TG3 and Subphylum Phylum Fibr
EF454354.2 gg_id:220027 termite hindgut clone 290cost002-P3L-1996
EF454970.2 gg_id:227321 termite hindgut clone 290cost002-P3L-828
AB243293.1 gg_id:149384 acetone-preserved termite gut clone M2PB4a-088
FJ202893.1 gg_id:317953 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k

FJ367190.1	367962	3457.2	4153.7	4588.2	2558.0	3203.3	3189.9
FJ678613.1	531345	3749.4	3188.5	3332.9	5185.7	3254.4	2475.7
AY916353.1	114378	250.0	326.2	346.2	279.9	144.6	165.6
EU381774.1	265197	6346.6	6389.4	5433.8	7910.6	5787.7	4819.1
FJ832322.1	558715	4608.8	6282.6	1792.9	3227.6	3253.3	2797.0
EU463631.1	303133	222.4	461.1	349.1	167.2	181.3	228.5
FJ440078.1	567506	2119.6	3207.6	5300.4	1871.6	1569.5	2444.1
FJ682646.1	513042	811.0	296.3	327.7	358.2	276.5	162.0
EU844825.1	327546	9225.7	8107.6	8877.2	10854.6	6831.5	8763.7
EU871410.1	324570	7833.4	7277.7	8183.6	6137.0	10540.1	10189.5
DQ456306.1	158491	25.7	41.0	58.2	66.3	74.2	31.5
EU381733.1	265925	928.9	869.6	2569.3	530.2	369.3	545.0
DQ353915.1	146314	248.1	448.1	756.1	389.7	134.6	256.4
EU843681.1	325563	2609.5	3212.1	4462.0	3487.5	3475.9	4605.9
EU844239.1	327857	2674.0	3254.4	2106.5	2837.7	2032.3	2371.5
AF001742.1	15698	185.8	229.9	555.6	437.0	137.2	139.3
GQ451225.1	545091	6232.6	6144.5	4722.8	5972.0	11569.2	13216.1
AM277561.2	229533	143.3	230.3	268.7	405.0	89.1	168.9
GU303762.1	580081	3905.5	1760.5	2078.1	3389.3	280.0	521.5
EU622737.1	279179	3664.2	5850.0	4287.2	2776.6	5971.4	7781.5
AY916186.1	114444	2409.3	3868.3	3974.6	3466.3	3345.0	3488.5
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EU871378.1	304971	3695.4	4835.7	3002.0	3414.2	5101.6	7871.1
EF406725.1	211308	6063.4	6080.9	7439.4	4166.9	4903.8	5496.5
EU842453.1	316729	5075.4	6351.1	6184.0	3712.3	8921.0	8975.8
AY986020.1	127092	1783.4	817.1	1106.9	935.1	939.9	953.7
EU764308.1	341905	773.3	1094.0	1902.8	1168.8	1077.2	1300.2
FJ172880.1	352691	1885.7	2952.8	3029.6	1427.9	4208.7	4498.5
EU844758.1	347587	306.6	340.1	336.4	600.8	380.5	197.7
GU476604.1	522127	4860.2	4219.9	2838.1	3266.2	2334.5	1161.6
GU208279.1	537538	7128.7	6013.4	5655.2	9003.2	6155.6	5243.6
EU358689.1	325820	2194.9	2085.2	3287.3	3143.5	3221.8	2425.0
GQ458248.1	513979	6803.7	7671.4	9456.2	4548.8	2369.9	3515.6
AB192099.1	143019	135.6	475.6	308.6	203.2	550.2	357.4
AB192110.1	144845	11221.9	11308.8	13412.7	11381.2	10900.3	9303.6
AB255930.1	164433	12042.6	12566.9	8440.2	13716.6	18150.7	16196.3
EF454354.2	220027	5817.4	3974.6	5308.3	9372.1	4352.5	4762.2
EF454970.2	227321	5321.8	6504.3	8596.2	8826.9	11434.5	13356.8
AB243293.1	149384	3588.9	4450.1	4422.9	6385.2	7799.9	6138.4
FJ202893.1	317953	1860.3	2582.8	3070.9	1729.1	1435.7	1922.6

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k__Bacteria	k__Bacteria	p__Thermi	c__Deinococci
k__Bacteria	k__Bacteria	p__Thermi	c__Deinococci
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g__sfA
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s__Deinococcus maricopensis	53012
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GQ348358.1 gg_id:560472 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
AY876379.1 gg_id:111757 Deinococcus deserti str. VCD117
AJ585983.1 gg_id:97958 Deinococcus sp. str. AA752
AJ585981.1 gg_id:97107 Deinococcus sp. str. AA692
NZ_AAHE01000002.1 gg_id:131883 Deinococcus geothermalis str. DSM 11300
AAHE01000005.1 gg_id:134272 Deinococcus geothermalis str. DSM 11300
AY743256.1 gg_id:138843 Deinococcus hohokamensis str. KR-40
AY743275.1 gg_id:138931 Deinococcus maricopensis str. KR-1
AB264133.1 gg_id:171820 Deinococcus sp. str. TDMA-21
AY743280.1 gg_id:138834 Deinococcus papagonensis str. KR-241
AE000513.1 gg_id:146329 Deinococcus radiodurans str. R1
AY743284.1 gg_id:138790 Deinococcus sonorensis str. KR-90
GQ043868.1 gg_id:461798 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw97
EF141348.1 gg_id:247857 Deinococcus peraridilitoris str. KR-200
AY743267.1 gg_id:139200 Deinococcus apachensis str. KR-32
AM988777.1 gg_id:568744 Deinococcus sp. str. K4.1
AF385541.1 gg_id:136570 Prevalent species and phylotypes advanced noma lesions Deinococcus oral clone CB(
DQ532354.2 gg_id:168505 Geographical Variation Microbial Burden and Spacecraft Assembly Kennedy Space C
EU834252.1 gg_id:347125 Deinococcus aquaticus str. DS27
DQ883809.1 gg_id:163551 Deinococcus cellulolytica str. 5516J-15
NR_026403.1 gg_id:562641 Deinococcus radiopugnans str. ATCC 19172
EU029127.1 gg_id:238409 Deinococcus sp. str. 2A2
EF635408.1 gg_id:285250 Deinococcus alpinitundrae str. ME-04-04-52
GQ357648.1 gg_id:546802 Deinococcus sp. str. YIM 75723
GQ441240.1 gg_id:556010 and dynamic mat present vs. active nitrogen-fixing microorganisms marine microbia
EU029130.1 gg_id:250755 Deinococcus sp. str. 3A5
AB374383.1 gg_id:271722 sequences Weissenstein (white rock) / few millimeters be surface rock called 'Weiss
M21413.1 gg_id:1418 Deinococcus radiodurans
EU626561.1 gg_id:282134 Deinococcus xinjiangensis str. X-82
DQ022077.1 gg_id:136712 Truepera radiovictrix str. TU-8
EU622978.1 gg_id:279041 Deinococcus sp. str. 5516T-9
EU427464.1 gg_id:264010 Deinococcus sp. str. I-0
GQ058151.1 gg_id:406491 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
AY743279.1 gg_id:138901 Deinococcus yavapaiensis str. KR-236
EU362143.1 gg_id:332198 and Mesquite Flats Site Death Valley dune sand clone 14
EF522236.1 gg_id:219134 Endolithic Microbial Ecosystems Rocky Mountain endolithic sandstone clone FQSS01
GQ058104.1 gg_id:395808 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
AM283039.1 gg_id:159842 Deinococcus sp. str. Han23
GQ072152.1 gg_id:389682 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw192g11
AM292065.1 gg_id:249433 Deinococcus radiodurans zf-69-II
GQ130053.1 gg_id:435637 Genetic inventory 'JPL-SAF' during MSL mission spacecraft assembly clean room floc

GQ348358.1	560472	8272.9	8017.8	5494.5	6725.1	5306.9	3702.6
AY876379.1	111757	6303.9	7018.4	7865.4	7263.1	3769.7	4564.6
AJ585983.1	97958	7807.7	9594.9	8386.5	7197.2	7880.2	11087.8
AJ585981.1	97107	8912.7	10125.9	7085.4	7895.6	13726.2	11782.3
NZ_AAHE01000002.1	131883	46.0	55.3	36.1	73.4	60.5	46.5
AAHE01000005.1	134272	1572.3	1105.6	794.8	1590.9	1148.7	868.8
AY743256.1	138843	3706.3	4329.3	3635.6	3179.8	3902.7	4352.1
AY743275.1	138931	7527.1	8054.6	11254.0	8855.6	5576.2	7211.2
AB264133.1	171820	7190.2	7021.8	7122.3	6819.1	8798.0	8481.1
AY743280.1	138834	1353.8	1947.3	490.7	370.6	253.9	515.0
AE000513.1	146329	12888.9	13249.2	16420.2	12667.7	15975.7	13380.3
AY743284.1	138790	1798.3	3472.8	3021.9	2286.4	1503.7	1921.5
GQ043868.1	461798	88.5	108.1	155.7	117.4	77.8	124.3
EF141348.1	247857	773.4	1696.5	4518.2	1060.4	2137.5	859.9
AY743267.1	139200	16.3	25.2	29.7	37.3	58.4	23.5
AM988777.1	568744	9006.9	7556.8	9307.2	10837.6	7439.3	7233.4
AF385541.1	136570	1547.6	697.3	399.7	673.9	114.3	172.2
DQ532354.2	168505	680.1	651.8	1419.4	509.0	1027.4	936.3
EU834252.1	347125	9318.3	7854.0	6267.4	8096.8	7754.1	9124.5
DQ883809.1	163551	24.6	24.3	22.3	52.5	63.4	29.1
NR_026403.1	562641	19596.8	18583.6	9984.0	13119.0	13902.8	12435.3
EU029127.1	238409	10096.7	8068.7	7091.1	7676.2	7185.8	7229.2
EF635408.1	285250	2955.5	3800.5	6208.1	5092.3	5996.3	4194.9
GQ357648.1	546802	5771.4	2399.9	4629.6	2764.5	2279.1	2438.4
GQ441240.1	556010	10075.4	8870.2	13354.1	9517.3	13009.5	11555.3
EU029130.1	250755	5057.6	4741.5	3303.7	2756.4	1263.2	2271.5
AB374383.1	271722	3463.5	4466.8	6008.5	805.7	8217.9	3209.6
M21413.1	1418	13144.9	11630.5	12164.8	13653.7	12217.0	11391.9
EU626561.1	282134	2484.0	1704.6	1323.3	2932.2	1585.2	1334.2
DQ022077.1	136712	40.2	56.2	42.4	81.2	99.1	52.1
EU622978.1	279041	6419.7	6474.0	5683.2	5910.1	5515.5	6650.4
EU427464.1	264010	5463.7	4271.0	4067.3	4330.4	972.8	1483.3
GQ058151.1	406491	539.9	234.4	297.9	776.1	140.6	199.5
AY743279.1	138901	1786.7	1204.0	563.0	263.2	640.4	439.9
EU362143.1	332198	4536.7	5789.2	4722.7	5622.6	5478.9	5627.7
EF522236.1	219134	9317.8	9102.7	8583.2	8471.9	7189.7	7970.3
GQ058104.1	395808	4211.8	4452.7	4356.2	4402.0	5232.5	4786.8
AM283039.1	159842	86.8	60.8	47.8	73.0	120.4	92.2
GQ072152.1	389682	12513.1	15114.5	16108.5	11920.8	13863.6	13653.6
AM292065.1	249433	7962.7	6635.2	7969.3	8031.9	8232.3	8383.7
GQ130053.1	435637	23.7	53.2	33.8	48.5	97.9	43.3

k__Bacteria	k__Bacteria	p__Thermi	c__Deinococci
k__Bacteria	k__Bacteria	p__Thermi	c__Deinococci
k__Bacteria	k__Bacteria	p__Thermi	c__Deinococci
k__Bacteria	k__Bacteria	p__Thermi	c__Deinococci
k__Bacteria	k__Bacteria	p__Thermi	c__Deinococci
k__Bacteria	k__Bacteria	p__Thermi	c__Deinococci
k__Bacteria	k__Bacteria	p__Thermi	c__Deinococci
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k__Bacteria	k__Bacteria	p__Thermi	c__Deinococci

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g__Oceanithermus
g__Thermus
g__Thermus

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s__Meiothermus ruber	53375
s__Meiothermus ruber	53594
s__Meiothermus silvanus	53576
s__Meiothermus taiwanensis	53475
s__Meiothermus taiwanensis	53897
s__Meiothermus timidus	53008
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s__Thermus antranikianii	53629
s__Thermus igniterrae	53760

DQ336980.1 gg_id:146805 subsurface water clone EV818CFSSAHH23
DQ130032.1 gg_id:138316 microbial biota normal forearm human skin clone GL109
DQ847439.1 gg_id:170011 human forearm skin clone GL2-41
DQ366016.1 gg_id:152980 Dominant soils Marble Point and Wright Valley Victoria Land Antarctica soil clone 21
EU622979.1 gg_id:279558 Deinococcus sp. str. 5516T-11
AB473897.1 gg_id:568788 sequences endolithic and archaea Weissenstein (white rock) / Albula pass few millim
DQ883808.1 gg_id:169628 Deinococcus aeria str. 5516J-6
GQ130015.1 gg_id:405062 Genetic inventory 'JPL-SAF' during MSL mission spacecraft assembly clean room floc
FJ444684.1 gg_id:562787 Cotton Rhizosphere cotton rhizosphere clone 2y-56
FJ176238.1 gg_id:307654 Deinococcus sp. str. ZLM-202
GQ026439.1 gg_id:453803 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
EU029134.1 gg_id:250725 Deinococcus sp. str. 5A5
AM940971.1 gg_id:263628 Deinococcus aquatilis str. CCUG 53370
AJ585985.1 gg_id:95404 Deinococcus sp. str. AA69
GQ052823.1 gg_id:377731 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw:
DQ223543.2 gg_id:171337 Deinococcus sp. X2
FM872722.1 gg_id:365101 occupant source house floor dust clone FB01A10
AY743278.1 gg_id:139150 Deinococcus pimensis str. KR-242
AY250871.1 gg_id:86556 lichen-dominated Antarctic cryptoendolithic community clone FBP266 bacterium
GU214174.1 gg_id:593108 and biota slimes Canadian paper mills slime mill taken wet section around papermal
DQ366015.1 gg_id:153959 Dominant soils Marble Point and Wright Valley Victoria Land Antarctica soil clone J3
DQ130037.1 gg_id:137532 microbial biota normal forearm human skin clone GR66
GQ023518.1 gg_id:486153 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu319e11
DQ683348.1 gg_id:172621 Deinococcus piscis str. 3ax
NR_026421.1 gg_id:555743 Meiothermus cerbereus str. GY-1
DQ916146.1 gg_id:167558 Meiothermus rosaceus str. WQBGR2-3
NR_027614.1 gg_id:543137 Meiothermus ruber 1279 str. DSM 1279; ATCC 35948
AJ871173.1 gg_id:114851 Meiothermus ruber str. SPS-242
X84211.1 gg_id:1405 Meiothermus silvanus str. V1-R2
AF418002.1 gg_id:20802 Meiothermus taiwanensis str. WR-220
AF418001.1 gg_id:26209 Meiothermus taiwanensis str. WR-30
AJ871171.1 gg_id:114643 Meiothermus timidus str. RQ-12
DQ899883.1 gg_id:238702 structure receiving long-term augmentations chromium contaminated wastes landfi
NR_026244.1 gg_id:540285 Meiothermus chliarophilus str. ALT-8; ATCC 700543; BCRC 17113
AJ871172.1 gg_id:114775 Meiothermus ruber str. SPS-241
L37521.1 gg_id:1398 Thermus sp str. ac-2
FN178497.1 gg_id:573829 Meiothermus sp. str. CAL-12
EU249978.1 gg_id:239060 Polyphasic description Pocillopora mucus secreted Pacillopora meandrina coral color
AB107956.1 gg_id:85579 Oceanithermus desulfurans str. St55B
Y18412.1 gg_id:35343 Thermus antranikianii str. HE-5
NR_026501.1 gg_id:533728 Thermus igniterrae str. RF-4; DSM 12459

DQ336980.1	146805	153.7	554.3	84.9	137.1	93.0	125.5
DQ130032.1	138316	1823.9	1655.3	1228.3	708.0	603.2	678.3
DQ847439.1	170011	10147.1	10563.2	10662.5	10640.8	6290.6	6011.9
DQ366016.1	152980	7723.0	7046.5	10150.4	8010.0	11741.5	8124.3
EU622979.1	279558	3226.7	2663.2	2392.7	3935.9	1176.3	1778.3
AB473897.1	568788	99.0	90.6	53.0	115.3	105.5	79.5
DQ883808.1	169628	5410.2	4234.9	4748.3	4976.1	2580.8	3660.6
GQ130015.1	405062	6597.4	7706.8	3841.1	6557.7	8907.4	6147.7
FJ444684.1	562787	2031.3	1151.8	1252.5	1069.0	436.6	594.4
FJ176238.1	307654	5492.8	10059.1	5936.4	4080.0	4801.7	5977.6
GQ026439.1	453803	10077.3	10602.7	10605.3	9967.6	10666.8	10635.9
EU029134.1	250725	1478.7	2643.7	2608.6	755.7	954.0	1043.1
AM940971.1	263628	5759.3	5243.4	5297.6	5964.1	4666.1	5467.2
AJ585985.1	95404	8195.8	7900.2	6323.6	7479.0	6258.5	8053.1
GQ052823.1	377731	7643.3	9353.9	5918.2	7348.8	9953.8	10705.3
DQ223543.2	171337	3059.1	4022.9	4928.0	3499.9	1968.1	2769.7
FM872722.1	365101	5482.0	7886.5	6262.7	7413.3	6092.1	6633.0
AY743278.1	139150	34.8	70.3	51.9	92.3	77.7	39.4
AY250871.1	86556	7102.5	8654.1	7562.5	7712.2	10904.1	12469.8
GU214174.1	593108	2588.9	4101.8	2095.1	960.1	677.0	1483.5
DQ366015.1	153959	6578.4	6747.2	7567.4	6056.8	5628.7	5078.6
DQ130037.1	137532	10794.3	10700.3	12373.4	10066.0	12033.6	11103.8
GQ023518.1	486153	1405.7	1645.7	2969.1	1914.7	370.7	1261.1
DQ683348.1	172621	13702.3	15949.0	13449.8	13386.8	18587.2	15379.0
NR_026421.1	555743	1841.9	1530.7	2069.8	1545.6	1179.3	1386.3
DQ916146.1	167558	1446.5	2168.3	3274.0	1568.1	2505.5	2450.1
NR_027614.1	543137	2015.4	2848.6	3215.2	2039.6	3744.2	3248.1
AJ871173.1	114851	8626.4	9122.3	9897.5	7501.9	10219.4	9653.7
X84211.1	1405	430.9	397.5	981.8	430.5	285.7	344.8
AF418002.1	20802	7535.3	8375.8	7150.7	6949.6	9239.5	9417.9
AF418001.1	26209	1549.6	2032.1	2679.4	1782.6	2506.1	3059.4
AJ871171.1	114643	395.5	676.0	1455.2	615.0	526.2	904.4
DQ899883.1	238702	2313.1	2332.9	3699.8	3069.7	1874.9	2225.4
NR_026244.1	540285	87.5	103.7	96.5	102.7	117.1	96.6
AJ871172.1	114775	1875.6	2852.8	3661.5	2038.5	3748.1	2817.9
L37521.1	1398	1991.7	1424.8	2079.7	1646.8	1179.0	1492.4
FN178497.1	573829	7871.6	8387.1	14939.8	7789.2	10605.2	8695.3
EU249978.1	239060	771.7	1021.3	792.3	1042.0	953.5	1155.8
AB107956.1	85579	51.6	58.0	71.0	95.0	58.9	27.2
Y18412.1	35343	16.5	27.4	48.7	54.2	49.5	30.7
NR_026501.1	533728	1403.1	1192.1	2039.6	2497.3	835.2	698.5

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EU214609.1 gg_id:323841 Thermus thermophilus yb60g
EU616794.1 gg_id:273039 Thermus thermophilus str. WG
AY557603.1 gg_id:105041 Thermus yunnanensis
NR_025901.1 gg_id:535809 Thermus filiformis str. Wai33; ATCC 43280
Y18409.1 gg_id:30085 Thermus brockianus str. 15038T
Y18416.1 gg_id:45920 Thermus oshimai str. SPS-17T
AF018197.1 gg_id:1324 temperature clone env.OPS 15
L09663.1 gg_id:1345 Thermus aquaticus
AF331969.1 gg_id:41572 Thermus rehai str. RH99-02
FJ638543.1 gg_id:511615 Temperature dependent succession sulfate reducing muddy southwestern Taiwan hc
GU233838.1 gg_id:537430 effects temperature pH salinity and sinter growth rate on microbial Icelandic waters
AY861866.1 gg_id:112463 Obsidian Pool prime community clone OPPB146
AF020205.1 gg_id:1335 Thermus scotoductus str. SA-01
EU701067.3 gg_id:290466 Thermus sp. str. K-39
Y18408.1 gg_id:47782 Thermus igniterrae str. GE-2
EU924248.1 gg_id:326104 Microbiology and geochemistry Little Hot Creek hot spring sediment temperature 8C
AB071811.1 gg_id:24092 Thermus kawarayuensis str. KW11
EU753248.1 gg_id:352672 Thermus sp. str. PRI-2268
AY028380.1 gg_id:67904 Thermus sp. str. C4
AF521188.1 gg_id:63588 Thermus sp. str. RH-1514
L77877.1 gg_id:106875 Thermothrix thiopara
L37522.1 gg_id:1357 Thermus sp str. ac-7
AF255591.1 gg_id:17962 Thermus sp. str. SRI-248
Y18410.1 gg_id:26144 Thermus scotoductus str. ITI-252T
AJ507298.1 gg_id:60062 Vulcanithermus mediatlanticus str. TR
DQ832056.1 gg_id:165232 Geochemical Controls on Microbial Rainbow and Springs Yellowstone National Park
DQ832059.1 gg_id:165655 Geochemical Controls on Microbial Rainbow and Springs Yellowstone National Park
NR_028639.1 gg_id:540517 Marinithermus hydrothermalis str. T1; JCM 11576
DQ832060.1 gg_id:173448 Geochemical Controls on Microbial Rainbow and Springs Yellowstone National Park
DQ924664.1 gg_id:177658 Microbial Norris Geyser Basin Yellowstone National Park Cistern Hot Spring clone BV
DQ924670.1 gg_id:189281 Microbial Norris Geyser Basin Yellowstone National Park Cistern Hot Spring clone BV
EU435435.1 gg_id:273276 Thermodesulfatator sp. str. AT1325
AJ969460.1 gg_id:157635 Microbial black smoker s Mid Atlantic Ridge ecological implications rock fragments ch
AY280428.1 gg_id:102075 exterior deep-sea hydrothermal vent sulfide chimney Juan de Fuca Ridge Pacific Oce
AB282756.1 gg_id:230931 Thermosulfidobacterium lithotrophicum str. ABI70S6 (= JCM13301 = DSM 17441
EU635930.1 gg_id:279109 Microbiology geochemistry great boiling and mud springs sediment hot spring; temp
EF077228.1 gg_id:253157 Anaerobic oxidation short-chain hydrocarbons marine sulphate-reducing Guaymas Ba
AM712345.1 gg_id:247140 detection and ly microbial Brothers Seamount Kermadec Arc New Zealand biofilm h
NR_025146.1 gg_id:570497 Thermodesulfobacterium hydrogeniphilum str. SL6; DSM 14290
FJ638609.1 gg_id:537018 Temperature dependent succession sulfate reducing muddy southwestern Taiwan hc
AF419676.1 gg_id:25647 Guaymas Basin hydrothermal sediment clone a2b002

EU214609.1	323841	4709.4	5175.5	3267.2	3526.6	5802.5	6092.5
EU616794.1	273039	1113.7	1452.4	1489.4	1075.4	2661.7	2042.2
AY557603.1	105041	2382.3	2319.7	2922.2	2853.7	2375.5	1649.5
NR_025901.1	535809	665.4	1355.2	468.7	591.4	2186.3	1528.6
Y18409.1	30085	149.8	351.6	207.0	159.7	113.6	222.9
Y18416.1	45920	51.8	117.8	236.8	116.4	178.4	148.6
AF018197.1	1324	337.8	1240.1	1619.9	1064.2	210.9	1396.5
L09663.1	1345	4867.6	6434.0	4868.6	5136.6	4862.2	5207.9
AF331969.1	41572	125.4	143.2	536.1	75.3	148.5	74.9
FJ638543.1	511615	41.0	47.3	81.4	57.5	45.4	39.4
GU233838.1	537430	4121.8	3164.4	2654.2	2392.7	2149.6	2187.8
AY861866.1	112463	6589.3	8168.4	7717.7	6992.4	8458.1	7122.0
AF020205.1	1335	113.7	174.4	412.7	84.9	214.2	175.8
EU701067.3	290466	198.9	157.9	337.7	164.7	152.1	69.3
Y18408.1	47782	1357.5	918.3	1590.2	2629.9	786.4	928.5
EU924248.1	326104	4432.2	4817.9	4346.8	5897.5	3547.2	5041.1
AB071811.1	24092	1729.6	2339.6	2908.8	2410.9	3796.2	2372.0
EU753248.1	352672	2334.3	3218.4	2668.5	1575.2	923.8	1981.6
AY028380.1	67904	33.9	67.5	66.4	92.9	83.4	51.4
AF521188.1	63588	336.2	997.8	869.0	318.9	384.4	1522.1
L77877.1	106875	3819.9	2538.5	714.1	1912.3	611.8	981.2
L37522.1	1357	187.4	323.5	880.2	310.3	108.4	265.6
AF255591.1	17962	5201.1	6615.8	6412.3	3142.3	4245.4	3282.7
Y18410.1	26144	34.8	36.4	32.3	66.0	62.2	35.2
AJ507298.1	60062	385.6	134.2	471.8	643.5	673.5	541.2
DQ832056.1	165232	3059.6	2190.3	3896.0	2507.9	3947.9	3527.8
DQ832059.1	165655	859.4	757.8	1068.6	695.9	610.8	1015.6
NR_028639.1	540517	103.4	118.7	103.7	76.8	93.0	72.4
DQ832060.1	173448	4875.8	5586.8	2521.9	4464.7	6584.6	4936.3
DQ924664.1	177658	1469.6	963.3	413.3	100.4	128.4	153.4
DQ924670.1	189281	318.9	36.7	32.2	88.0	73.2	29.1
EU435435.1	273276	25.5	31.2	16.8	48.0	61.3	24.6
AJ969460.1	157635	55.8	144.9	87.5	91.1	135.9	78.5
AY280428.1	102075	45.8	45.6	41.4	66.9	71.3	65.2
AB282756.1	230931	6982.0	8441.9	10526.9	7382.2	4287.1	7853.3
EU635930.1	279109	10986.3	13544.8	14360.1	9667.7	5087.9	8890.7
EF077228.1	253157	5498.9	6360.5	5226.4	4395.0	4017.6	3747.0
AM712345.1	247140	10732.8	11419.0	9753.2	8899.8	10009.6	12015.3
NR_025146.1	570497	3653.3	3589.8	5090.8	1588.7	909.4	1659.6
FJ638609.1	537018	97.1	154.1	109.6	87.0	169.6	202.0
AF419676.1	25647	8679.2	10742.4	3502.3	9034.4	10854.4	9116.9

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CU924090.1 gg_id:565047 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
Z49117.1 gg_id:1227 Fervidobacterium gondwanense
EU851047.2 gg_id:325520 Fervidobacterium sp. str. 1445t
AF509468.1 gg_id:66261 Geotoga aestuarianus str. T3B
EU245202.1 gg_id:245616 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-H4-A11
DQ080153.1 gg_id:128210 sediment clone BFA-T46
DQ080178.1 gg_id:128351 sediment clone A2
DQ080154.1 gg_id:133990 sediment clone BFA-K27
CP001634.1 gg_id:422862 Kosmotoga olearia str. TBF 19.5.1
CU918298.1 gg_id:557400 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
EU542473.1 gg_id:258468 Effects chemical structure concentration on pathways microbial during dechlorinatio
FJ901103.1 gg_id:540611 Polymorphism microbial reservoirs water cut stage oil field clone Z-49
AB530678.1 gg_id:539611 Kosmotoga sp. str. S304
AJ431250.1 gg_id:107334 Thermotogales str. Dex60-136
AJ250439.1 gg_id:1220 Marinitoga camini MV1075
FM253687.1 gg_id:341893 Marinitoga sp. str. MC3
AJ431249.1 gg_id:79381 Thermotogales str. Dex60-32
DQ834030.1 gg_id:167691 Geochemical Controls on Microbial Rainbow and Springs Yellowstone National Park
CP000879.1 gg_id:256420 Petrotoga mobilis str. SJ95
EU999020.1 gg_id:321922 Predominance Methanolobus and Methanoculleus spp. Archaeal Saline Gas Field Fo
GQ385331.1 gg_id:575997 Petrotoga sp. str. AR80
NR_029058.1 gg_id:590603 Petrotoga mexicana str. Met-12; DSM 14811; CIP 107371
EU878330.1 gg_id:550151 Investigation factors influencing production large-scale municipal biogas plant therm
EU639044.1 gg_id:325788 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n
EU639299.1 gg_id:338480 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n
EU639355.1 gg_id:316749 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n
AB274516.1 gg_id:210440 packed-bed reactor clone CFB-27
EU638581.1 gg_id:326331 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n
EU639024.1 gg_id:337040 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n
EU639041.1 gg_id:315077 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n
EU639078.1 gg_id:306674 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n
EU639209.1 gg_id:338914 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n
EU639173.1 gg_id:335791 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n
EU639281.1 gg_id:336042 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n
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CP000716.1 gg_id:243559 Thermosipho melanesiensis str. BI429
AJ272022.2 gg_id:40837 Thermosipho geolei str. DSM 13256
AF491334.1 gg_id:83498 Thermosipho ferriphilus str. GB21
AJ577471.1 gg_id:90392 Thermosipho atlanticus str. DV1140
AB024932.1 gg_id:1231 Thermosipho japonicus str. IHB1

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CU924090.1	565047	43.2	47.6	35.3	80.3	87.1	47.5
Z49117.1	1227	72.2	126.0	293.2	80.9	111.5	136.4
EU851047.2	325520	119.0	258.5	611.4	121.0	118.1	223.3
AF509468.1	66261	2700.1	4281.7	3879.1	2632.8	1834.7	1930.8
EU245202.1	245616	2766.0	4181.0	1574.8	1980.8	2148.1	1532.8
DQ080153.1	128210	1202.3	1338.2	2234.4	673.2	587.5	285.1
DQ080178.1	128351	4222.0	3058.9	4870.3	2908.0	4678.8	5733.1
DQ080154.1	133990	9627.6	5056.2	9350.8	6695.4	5006.8	6843.2
CP001634.1	422862	596.6	338.8	767.2	972.7	1065.5	993.0
CU918298.1	557400	5366.8	5394.2	4809.9	3596.7	3323.0	4067.2
EU542473.1	258468	15.6	100.7	703.2	73.3	250.8	462.5
FJ901103.1	540611	2774.6	2092.6	1362.8	264.5	942.3	365.9
AB530678.1	539611	6304.5	7190.0	5212.1	5086.8	3435.5	4039.7
AJ431250.1	107334	21.7	22.9	31.6	48.1	59.9	26.6
AJ250439.1	1220	177.9	328.5	105.3	61.6	108.3	133.5
FM253687.1	341893	7784.8	9725.9	6603.3	6472.0	6069.9	6117.7
AJ431249.1	79381	7294.0	7369.2	7891.1	8095.7	5068.3	4447.6
DQ834030.1	167691	28.1	46.6	64.9	71.9	72.6	42.8
CP000879.1	256420	3236.5	3857.6	2714.8	3345.9	5269.5	4902.2
EU999020.1	321922	110.6	206.2	360.0	102.3	79.8	49.5
GQ385331.1	575997	1288.3	1706.3	1670.8	692.1	2081.7	2047.4
NR_029058.1	590603	353.0	527.4	1749.6	372.2	769.5	674.0
EU878330.1	550151	5069.6	6200.1	3399.6	1735.5	2502.8	1900.9
EU639044.1	325788	10871.2	13790.5	10345.0	7978.7	12336.0	11520.2
EU639299.1	338480	3110.4	4886.0	3586.4	3599.8	1957.4	1898.0
EU639355.1	316749	2823.8	4311.3	4264.3	2377.6	208.5	888.7
AB274516.1	210440	7417.2	10903.4	2331.2	3497.7	1223.8	2695.1
EU638581.1	326331	4035.9	5227.6	2187.5	3880.9	433.0	894.7
EU639024.1	337040	6323.1	7816.4	4152.3	4745.9	5677.1	5424.6
EU639041.1	315077	3163.8	3766.9	4228.8	1813.5	829.7	1031.9
EU639078.1	306674	8658.2	8035.3	8464.6	5600.6	4972.0	6042.8
EU639209.1	338914	19723.0	19279.9	19012.9	12866.8	13674.5	11988.5
EU639173.1	335791	5025.9	6213.7	3342.8	2299.7	2131.9	1569.0
EU639281.1	336042	8361.7	9040.0	6079.5	5119.5	5353.8	4498.6
NC_011653.1	471469	262.0	659.8	1427.5	1463.0	182.6	213.8
CP000716.1	243559	49.9	69.8	85.2	78.1	90.6	64.5
AJ272022.2	40837	1639.8	2445.0	4957.2	954.9	439.7	867.6
AF491334.1	83498	965.7	1112.9	2552.7	1244.1	2156.5	2473.2
AJ577471.1	90392	1972.5	2397.0	3395.3	1826.6	649.6	762.6
AB024932.1	1231	108.7	140.7	671.3	178.9	116.2	139.0

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U22664.1 gg_id:1233 "Thermotoga subterranea"
AB039768.1 gg_id:41353 Thermotoga neapolitana str. DSM 4359
AJ401020.1 gg_id:32773 Thermotoga neapolitana str. LA10
AAWB01000011.1 gg_id:187003 Thermotoga petrophila str. RKU-1
EU924246.1 gg_id:303956 Microbiology and geochemistry Little Hot Creek hot spring sediment temperature 8C
AJ401017.1 gg_id:72408 Thermotoga maritima str. SL7
AY526506.1 gg_id:136778 Microbial thermophilic anaerobic sludge methanol-fed lab scale bioreactor clone H8
AJ401021.1 gg_id:24284 Thermotoga maritima str. FJSS3-B.1
AJ401016.1 gg_id:35101 Thermotoga neapolitana str. NES
AJ431248.1 gg_id:79590 Thermotogales str. BHI80-139
FN429790.1 gg_id:588200 Biogeochemistry -activity cold seep Larsen B area western Weddell Sea Antarctica m
DQ676372.1 gg_id:226370 Archaeal sediment and plankton freshwater pond suboxic freshwater-pond clone M
DQ676349.1 gg_id:225336 Archaeal sediment and plankton freshwater pond suboxic freshwater-pond clone M
AF268992.1 gg_id:32172 obtained sequencing batch reactor and sequenced Paul Burrell clone SBRH58
GQ402738.1 gg_id:592512 Accessing microbial biodiversity and metabolic potential tropical -based approach p
CU921813.1 gg_id:556480 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
EF530679.1 gg_id:225631 Extremely acidic pendulous biofilms Frasassi cave system Italy microbial biofilm clone
AF507714.1 gg_id:65675 forest soil clone S1198
AY261809.1 gg_id:82807 UASB reactor granular sludge clone PD-UASB-12
AJ387898.1 gg_id:50582 TCB-dechlorinating consortium? clone C1-3
AJ009448.1 gg_id:10538 chlorobenzene-degrading consortium clone SJA-4
U81641.2 gg_id:10536 anaerobic sludge clone vadinBA07
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DQ811945.1 gg_id:164866 mangrove soil clone MSB-4E11
GQ101240.1 gg_id:417532 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw49
GQ402806.1 gg_id:513096 Accessing microbial biodiversity and metabolic potential tropical -based approach p
AY661981.1 gg_id:137499 uranium-contaminated groundwater clone 300I-B02
DQ404590.1 gg_id:156555 contaminated sediment clone 656034
GU208307.1 gg_id:586450 Study on Sediment Dongping Lake sediment clone Ftt4-19
DQ499213.1 gg_id:159549 acidic cave snottite biofilm clone DSJB30
EU037998.1 gg_id:247518 Episodic subaerial speleogenesis controlled mineralogy microbial colonization and cc
EF516771.1 gg_id:226009 grassland soil clone FCPN632
EU135363.1 gg_id:242950 tallgrass prarie soil clone FFCH1293
AY043958.1 gg_id:61307 forest soil clone NMW3.210WL
GQ402802.1 gg_id:576700 Accessing microbial biodiversity and metabolic potential tropical -based approach p
EU386052.1 gg_id:259809 Biogeographical and microbes sediments on subseafloor sediment South China Sea c

GQ292553.1	588111	1536.0	1565.5	1969.0	298.5	710.0	578.4
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AJ401020.1	32773	2350.0	3201.6	3298.3	2540.5	3883.7	3624.1
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AJ401016.1	35101	1959.6	2474.6	3811.7	2649.1	3492.3	3121.8
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AF507714.1	65675	24.9	41.6	676.4	173.4	85.6	19.6
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AJ387898.1	50582	6927.4	7793.2	7112.7	5036.5	7538.3	5475.4
AJ009448.1	10538	16586.3	14770.3	15360.5	12105.4	15875.9	12160.5
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EU038004.1	238619	8377.9	8759.8	11357.4	10228.0	10553.4	7114.7
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DQ499222.1	159620	31.4	34.9	29.1	66.4	920.5	16.7
EF020241.1	212070	440.2	619.8	1370.4	498.8	106.7	218.9
DQ811945.1	164866	23.7	50.9	77.4	89.9	70.2	40.8
GQ101240.1	417532	5252.3	5816.8	6046.1	5441.1	4894.6	4739.8
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AY661981.1	137499	279.7	477.2	2184.3	641.8	363.6	411.1
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DQ499213.1	159549	43.4	97.9	814.2	164.9	366.3	86.6
EU037998.1	247518	2215.5	1399.0	5223.3	1849.8	1092.9	1919.6
EF516771.1	226009	85.7	121.3	493.1	95.7	69.4	58.7
EU135363.1	242950	5486.3	5321.4	4538.9	7267.6	3827.6	7098.0
AY043958.1	61307	283.6	684.8	2632.5	548.2	133.7	318.9
GQ402802.1	576700	6918.1	6798.0	6378.7	4039.7	4498.4	4418.9
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AB257652.1 gg_id:260396 Microbial few millimeters be surface dolomite rock 'Val Piora' Alps 1965 meters abov
AY945884.1 gg_id:148869 Thauera and Azoarcus functionally important genera denitrifying quinoline-removal r
FJ466109.1 gg_id:571249 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea
FJ542881.1 gg_id:528972 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone A
GU172187.1 gg_id:555087 Microbial Eucalyptus plantation soil clone DSM-R15
DQ395404.1 gg_id:154700 deep-sea octacoral clone ctg_BRRAA28
EU385703.1 gg_id:272615 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S
FJ478536.1 gg_id:576754 species richness estimates obtained nearly and simulated pyrosequencing-generated
EU332802.1 gg_id:366100 FACS assist identification TFO present aerobic enhanced biological phosphorus remo
DQ811946.1 gg_id:162674 mangrove soil clone MSB-5E11
EU038006.1 gg_id:239453 Episodic subaerial speleogenesis controlled mineralogy microbial colonization and cc
X97099.1 gg_id:10543 peat bog clone TM6
DQ070831.1 gg_id:146798 Prokaryotic Structures Seafloor Basalts Varying Age East Pacific Rise and Ridge basal
DQ394954.1 gg_id:153947 harbor sediment clone VHS-B3-63
EF019831.1 gg_id:212739 aspen rhizosphere clone Elev_16S_1183
DQ404638.1 gg_id:152373 contaminated sediment clone 654967
FM209162.1 gg_id:546081 Dynamics during identified and SSU libraries pilot-scale bioremediation process hydr
EU135398.1 gg_id:257656 tallgrass prarie soil clone FFCH4275
AM935187.1 gg_id:557742 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
AY345503.1 gg_id:91512 Lake Waiau sediment clone W4-B20
AY571850.1 gg_id:107654 hydrocarbon-contaminated soil clone 342B
EU861950.1 gg_id:316001 effects chronic fertilization on alpine tundra microbial implications carbon and cyclin
GQ396865.1 gg_id:532665 Functional unvegetated perhumid recently-deglaciated soils do not correlate shifts s
AF507687.1 gg_id:111978 forest soil clone C129
EU135387.1 gg_id:248392 tallgrass prarie soil clone FFCH16289
EU104333.1 gg_id:321742 Evidence Comamonadaceae determinants settling performance activated sludge clo
DQ906081.1 gg_id:223958 nickel resistance genes metagenome Tinto River rhizosphere clone ERF-G10
AM991156.1 gg_id:279572 Microbial groundwater and their potential use biomonitoring karst spring water clo
GU444063.1 gg_id:520918 Effects amendments on fertility and microbial structure cucumber Cucumis sativus L
AF507688.1 gg_id:65695 forest soil clone C1105
FJ542918.1 gg_id:515209 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone A
EU703288.1 gg_id:566066 taxon richness -altitude lakes eastern tin plateau predominance Bacteroidetes and S
EF688335.1 gg_id:238281 soil clone F1-127
GU444078.1 gg_id:518809 Effects amendments on fertility and microbial structure cucumber Cucumis sativus L
DQ640696.1 gg_id:234110 full-scale EBPR sludge clone Skagenf80
DQ451478.1 gg_id:156885 forest soil clone FAC39
DQ404603.1 gg_id:153216 contaminated sediment clone 656047
AJ318136.1 gg_id:26128 Waste-gas biofilter clone BIgi18
DQ404740.1 gg_id:154332 contaminated sediment clone 655080
EU381500.1 gg_id:275085 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid
EU381884.1 gg_id:258263 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase

AB257652.1	260396	2870.2	3260.1	9895.7	3655.9	6483.0	2675.9
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FJ542881.1	528972	10498.0	10521.8	12045.2	9533.6	15067.7	11657.5
GU172187.1	555087	3460.2	2945.0	6348.0	4658.0	8441.2	4021.2
DQ395404.1	154700	4331.9	5047.9	9402.8	4780.6	7636.5	6195.0
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FJ478536.1	576754	1916.3	3115.3	6413.7	2706.0	4623.6	2383.0
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DQ394954.1	153947	5104.5	3891.0	5600.9	4797.6	1307.8	1774.3
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FM209162.1	546081	2266.9	1947.6	5848.1	2134.2	1558.1	3219.6
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AM935187.1	557742	10789.6	12342.0	14902.0	11201.8	13018.9	12226.5
AY345503.1	91512	35.5	63.2	246.4	98.2	63.2	25.9
AY571850.1	107654	55.0	72.6	213.6	93.6	78.7	47.3
EU861950.1	316001	970.7	734.7	3831.5	970.2	806.2	518.8
GQ396865.1	532665	1999.1	1313.7	5187.1	3988.1	506.2	1456.5
AF507687.1	111978	74.4	182.4	1831.7	364.8	86.5	63.5
EU135387.1	248392	1571.3	1222.2	3361.0	1353.7	936.7	2492.6
EU104333.1	321742	1641.7	1380.6	4783.2	1855.9	2168.8	2527.1
DQ906081.1	223958	36.0	102.0	1086.5	166.4	108.5	43.3
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AF507688.1	65695	67.2	162.7	500.4	101.4	79.5	62.8
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EF688335.1	238281	3963.4	3376.9	5696.8	4224.5	2450.8	2717.9
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DQ640696.1	234110	614.8	573.2	4855.2	2948.4	968.4	2672.1
DQ451478.1	156885	47.1	72.0	86.7	80.5	71.9	41.1
DQ404603.1	153216	937.4	1888.5	3687.3	1865.4	3323.4	3345.1
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DQ404740.1	154332	721.6	2049.9	3249.9	3143.2	3874.4	7311.9
EU381500.1	275085	5098.8	4296.8	7847.7	6683.7	6224.5	6389.2
EU381884.1	258263	93.1	145.6	1441.6	327.8	184.4	444.8

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AF385506.1 gg_id:39443 tongue dorsa clone CW040
EU475226.1 gg_id:290144 bonobo feces clone BNO_aaa02b03
FJ881207.1 gg_id:397321 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet;
DQ815554.1 gg_id:169081 mouse cecum clone aab42f07
AM932658.1 gg_id:573677 microbiota Toll-like receptor 2 deficient mice exhibits lineage specific modifications
DQ815839.1 gg_id:169901 mouse cecum clone aab23a06
AF432141.1 gg_id:17020 oral clone FR058
EU431764.1 gg_id:575675 Troglobitic (Cansiliella) on specialized feeding apparatus calcium carbonate (moonmi
EU431761.1 gg_id:552692 Troglobitic (Cansiliella) on specialized feeding apparatus calcium carbonate (moonmi
DQ309369.1 gg_id:149506 high salinity effluent treatment plant clone HKT135
GQ035442.1 gg_id:450572 Topographical and Temporal Human Skin Microbiome skin back clone nbu372b12c1
AJ318200.1 gg_id:34261 Waste-gas biofilter clone BIxi1
AY005446.1 gg_id:72347 oral cavity clone BE109
GQ057266.1 gg_id:377444 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
AF507686.1 gg_id:65697 arid soil clone C026
DQ378246.1 gg_id:151868 oil-polluted soil clone M26_Pitesti
AJ583163.1 gg_id:95008 radioactive site ground water clone S15B-MN121
GQ009422.1 gg_id:500243 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw77
EU431832.1 gg_id:564738 Troglobitic (Cansiliella) on specialized feeding apparatus calcium carbonate (moonmi
AF513102.1 gg_id:65419 activated sludge foam clone 71
DQ640707.1 gg_id:235238 full-scale EBPR sludge clone Skagenf9
DQ521555.1 gg_id:197766 Antarctic lake ice cover clone ANTLV9_C10
GU451214.1 gg_id:519665 adult gut male clone A6H6M10
EU244101.1 gg_id:360054 16SrRNA probes river Leine sediment clone sl1394
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AY005448.1 gg_id:21239 oral cavity clone BS003
CU919840.1 gg_id:555590 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
GQ009402.1 gg_id:500262 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw77
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EU104285.1 gg_id:338215 Evidence Comamonadaceae determinants settling performance activated sludge clo
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GQ115439.1 gg_id:434423 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw685f06
AY571500.1 gg_id:114578 termite gut clone RsaM67
DQ666092.1 gg_id:165179 human vaginal epithelium clone Y2
FJ470446.1 gg_id:537729 Chinese human cavities healthy oral cavity clone A_D_01_89
EU979068.1 gg_id:340964 Effects intercropping Rhizobium inoculation on microbial biomass and rhizosphere b
CU917574.1 gg_id:569517 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
CU924524.1 gg_id:571106 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
EU861856.1 gg_id:341554 effects chronic fertilization on alpine tundra microbial implications carbon and nitrog
AF352537.1 gg_id:16693 hot spring clone BH81

AF385506.1	39443	212.8	299.3	2221.6	374.7	286.6	675.6
EU475226.1	290144	3363.9	3750.9	7805.9	3168.2	2154.2	2396.4
FJ881207.1	397321	3686.7	4005.0	5992.3	2717.2	1658.0	2783.5
DQ815554.1	169081	16.8	27.5	60.1	60.4	54.8	33.3
AM932658.1	573677	20.9	71.2	787.4	81.6	96.9	36.3
DQ815839.1	169901	23.7	27.6	40.5	60.0	63.5	32.3
AF432141.1	17020	710.5	674.3	1254.8	161.3	169.1	299.8
EU431764.1	575675	9809.4	8602.0	6889.7	4522.3	8715.6	9406.2
EU431761.1	552692	2609.2	2591.1	8266.4	2646.8	1748.7	3971.3
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AJ318200.1	34261	47.5	98.8	1156.1	114.2	71.8	212.8
AY005446.1	72347	38.9	57.4	203.8	72.0	81.8	151.1
GQ057266.1	377444	3130.2	3458.0	4433.8	3337.0	3727.4	4585.3
AF507686.1	65697	141.7	171.6	435.7	244.3	117.5	110.8
DQ378246.1	151868	3229.1	4064.1	2999.9	2323.2	4064.7	3813.3
AJ583163.1	95008	322.5	326.4	1428.5	4358.3	399.6	181.3
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DQ666092.1	165179	42.7	67.3	48.6	71.6	131.1	40.5
FJ470446.1	537729	51.7	71.0	317.2	104.0	212.5	58.7
EU979068.1	340964	7936.7	8134.6	18013.9	9874.2	10129.0	8987.1
CU917574.1	569517	3152.0	4683.8	4209.6	3948.9	4366.7	3052.6
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AF352537.1	16693	1096.4	1721.1	1083.4	1977.1	3405.6	2491.4

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EU134434.1 gg_id:254851 tallgrass prarie soil clone FFCH11147
EU043224.1 gg_id:239967 uncultivated soil clone BJ-169
EU386046.1 gg_id:265422 Biogeographical and microbes sediments on subseafloor sediment South China Sea c
AF015925.1 gg_id:13724 hot spring clone OctSpA1-106
AF419683.1 gg_id:112352 Guaymas Basin hydrothermal sediment clone CS_B017
EU385715.1 gg_id:267027 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S
GQ502666.1 gg_id:576499 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf9-
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DQ451528.1 gg_id:156660 forest soil clone FAC89
GQ340316.1 gg_id:550625 Prokaryotic Marathonas Reservoir Greece water column clone K08-115-BAC
FJ466437.1 gg_id:536133 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea
EF520638.1 gg_id:230312 structure lakes: what controls ? acid-impacted lake clone ADK-SGe02-31
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FM866301.1 gg_id:357272 Microbial several mining wastes Bulgaria uranium mill tailings clone BuhC-182
AY661974.1 gg_id:136998 uranium-contaminated groundwater clone 300G-H06
AM162467.1 gg_id:156120 and situ identification acidic sphagnum peat bog clone B36
EU800822.1 gg_id:350772 It's all ranking aquatic Delaware Bay NJ clone 2C229041
EF516172.1 gg_id:231447 grassland soil clone FCPT606
AY297806.1 gg_id:89313 archaeological wood clone? pACH90
FJ769447.1 gg_id:553713 Changes Methanogenic Microbial After Sludge Pre-treatment full-scale municipal ana
AB240503.1 gg_id:144089 microbial structure rhizosphere biofilm Sapporo root-base (80 160 mm) Phragmites
GQ339177.1 gg_id:526112 Comprehensive Investigation on Iron Cycling Freshwater Seep ing Microscopy Cultiv
AB369167.1 gg_id:237121 Microbiological Assessment Circulation Mud Fluids During First Operation Drilling De
AJ575730.1 gg_id:96609 lake water clone SW59
GQ264061.1 gg_id:566392 Structure Simulated Level Waste Site simulated level waste site clone WC3_16
AB369179.1 gg_id:245910 Microbiological Assessment Circulation Mud Fluids During First Operation Drilling De
GQ502665.1 gg_id:542290 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf9-
AY820718.1 gg_id:109053 drilling fluid clone CCSD_DF2030_B14
DQ833492.1 gg_id:167091 detected analyses depth sediment Guanting Reservoir clone 35-54
AY587231.1 gg_id:106739 termite gut clone

AB077817.1	27351	6541.3	5271.5	5448.4	6591.7	3148.1	4427.3
EU134434.1	254851	7271.0	8211.7	7232.3	6421.8	5362.8	4161.4
EU043224.1	239967	7777.4	9835.7	10334.2	6640.8	7404.6	6810.1
EU386046.1	265422	5328.0	7672.6	8276.3	5309.0	4018.2	5045.3
AF015925.1	13724	1590.7	1891.4	529.2	468.0	353.6	354.3
AF419683.1	112352	455.4	783.0	8410.8	1211.5	153.5	216.8
EU385715.1	267027	5149.1	7460.5	5559.4	5726.7	8488.0	7558.6
GQ502666.1	576499	12429.9	13260.0	9616.6	7467.9	9664.7	10236.5
EU680463.1	285033	3464.3	6802.1	12383.4	3113.4	1148.4	4181.7
DQ451528.1	156660	25.7	30.4	114.1	55.7	63.4	25.5
GQ340316.1	550625	8092.0	7825.5	2061.3	3177.1	1940.0	1751.2
FJ466437.1	536133	9847.4	13008.6	8498.4	3355.5	2915.5	3073.7
EF520638.1	230312	788.9	800.7	1737.3	216.4	229.1	195.7
NC_010794.1	295454	1704.6	1943.7	3021.9	712.7	477.9	553.9
EU419170.1	260358	21.1	59.7	63.3	60.6	74.8	45.3
EU419167.1	274373	15168.5	15152.3	12858.2	9234.1	9063.1	9296.6
EU419166.1	266894	8132.6	11039.4	7799.1	7536.4	10828.2	9591.1
FJ638587.1	511517	23498.3	21213.7	22938.4	16723.9	19502.5	17774.1
AJ229235.1	1561	7088.8	7582.9	7832.7	5102.5	3128.6	4872.7
X99391.1	1558	2488.3	3644.2	5192.9	1317.1	1590.2	1049.8
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AM162468.1	153174	1500.1	2051.6	3612.6	1473.7	1540.5	1431.2
AY922067.1	114313	2519.1	3097.9	2844.2	946.3	667.6	756.4
FJ478682.1	567922	2388.9	2133.4	6464.7	742.7	1078.7	728.9
FM866301.1	357272	521.5	1010.1	3123.6	480.4	966.2	1832.2
AY661974.1	136998	330.9	177.5	2330.3	326.7	362.8	485.0
AM162467.1	156120	2247.2	2099.8	2347.6	753.9	1159.5	1151.5
EU800822.1	350772	2017.4	3292.1	3580.7	2529.0	3131.2	1591.6
EF516172.1	231447	4413.8	7286.3	6323.0	1237.7	1593.8	1047.2
AY297806.1	89313	2134.4	3439.5	8772.5	1306.7	1908.0	1406.8
FJ769447.1	553713	5288.1	4916.4	8000.7	7905.0	4800.2	7535.8
AB240503.1	144089	245.1	259.4	1005.2	135.4	383.3	118.4
GQ339177.1	526112	586.1	658.7	5614.8	703.0	1110.3	791.9
AB369167.1	237121	184.8	605.0	1595.4	222.8	115.9	218.9
AJ575730.1	96609	31.9	48.1	452.1	84.7	64.3	66.2
GQ264061.1	566392	3755.7	4643.0	6925.6	3737.8	3020.3	4667.5
AB369179.1	245910	2240.9	2773.2	6628.7	2196.6	1529.0	1646.6
GQ502665.1	542290	1377.1	2290.9	3798.7	1260.8	3143.8	1645.7
AY820718.1	109053	55.7	52.5	254.8	99.4	76.2	48.2
DQ833492.1	167091	60.9	49.5	1148.9	113.7	318.8	130.2
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FJ169213.1 gg_id:327499 microbial and polyketide biosynthetic potential palmerolide-producing tunicate Synoi
FJ444768.1 gg_id:587631 Cotton Rhizosphere cotton rhizosphere clone 4y-121
AJ633978.1 gg_id:114788 host's accessory nidamental gland clone I1ANG45
EU015115.1 gg_id:253831 Investigation estrogen-degrading bioreactors membrane bioreactor suspension and
AB286360.1 gg_id:216828 Reducing production and domination comamonadaceae reducing oxygen supply was
AB062814.1 gg_id:18774 termite gut homogenate clone BCf3-05
EU135529.1 gg_id:246267 tallgrass prarie soil clone FFCH9358
AY622244.1 gg_id:107299 subsurface soil clone B-I12
DQ097276.1 gg_id:160664 Encapsulating and growing '' Majority mucus coral Fungia granulosa clone RS.Sph.0C
AB299563.1 gg_id:247779 Motility Symbiont Termite Gut Flagellate Caduceia versatilis Member 'Synergistes' G
DQ539046.1 gg_id:161645 Puniceibacter vermicola str. IMCC1545
AB299565.1 gg_id:241161 Motility Symbiont Termite Gut Flagellate Caduceia versatilis Member 'Synergistes' G
GQ502667.1 gg_id:578464 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf9-
EU803670.1 gg_id:338096 It's all ranking aquatic Lake Gatun clone 5C231275
DQ302114.1 gg_id:153206 Rubromonas marinus gen. sp. nov. first marine representative subdivision one Verru
FM242275.1 gg_id:341545 sequences sediment clone 13bis T0h-oil
GQ347889.1 gg_id:585626 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
U81738.2 gg_id:1556 anaerobic digestor clone vadinHA64
AY695840.1 gg_id:105129 Opitutus sp. str. SA-9
FM242391.1 gg_id:310512 sequences sediment clone 89 T12d-oil
EF574171.1 gg_id:235121 site S25 near Coco's Island marine clone S25_515
AJ240909.1 gg_id:74031 marine clone CHAB-II-49
EU617885.1 gg_id:332206 Seasonal variation microbial Yel Sea sediment clone D13S-153
FJ202864.1 gg_id:353683 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k
AB198611.1 gg_id:135899 termite gut fluid and protists fraction clone RsC01-040
EU283474.1 gg_id:278788 Model Early Earth Harbors Deeply Divergent Divisions Anderson Lake clone A210
AB299566.1 gg_id:256775 Motility Symbiont Termite Gut Flagellate Caduceia versatilis Member 'Synergistes' G
AB073978.1 gg_id:41135 Fucophilus fucoidanolyticus str. SI-1234
EU328081.1 gg_id:278462 dynamics during bioremediation crude oil contaminated moderate saline soil clone Y
FJ745063.1 gg_id:545467 Transporter genes expressed coastal response dissolved organic carbon surface wate
GQ984310.1 gg_id:588321 surface water Northern Bering Sea clone DBS1a9
AB192188.1 gg_id:143442 termite gut homogenate clone RsTz-69
FJ516822.1 gg_id:513750 semiarid 'Tablas de Daimiel National Park' wetland (Central Spain) unravelled biofilm
AF075271.2 gg_id:9675 Alterococcus agarolyticus str. ADT3; CCRC17102
FJ717327.1 gg_id:535151 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United Kingc
FJ717277.1 gg_id:511489 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United Kingc
FJ717325.1 gg_id:510475 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United Kingc
AY114312.1 gg_id:72268 anoxic marine sediment clone LD1-PA15
AB189371.1 gg_id:114335 cold seep sediment clone JT75-134
AF449255.1 gg_id:61856 vent worm clone R76-B128

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FJ169213.1	327499	1852.7	1852.8	3915.0	2580.2	1152.1	1847.2
FJ444768.1	587631	4068.0	3685.8	5403.8	3477.2	5957.5	4751.3
AJ633978.1	114788	117.5	168.1	216.6	107.3	105.5	96.6
EU015115.1	253831	10535.8	12127.4	14519.1	8883.5	12129.2	11220.4
AB286360.1	216828	989.6	2225.5	7118.9	759.4	788.7	1760.3
AB062814.1	18774	25.9	70.2	34.2	56.2	69.7	27.2
EU135529.1	246267	25.5	49.2	366.4	89.9	141.6	53.2
AY622244.1	107299	11129.4	11615.1	9076.4	9182.6	10884.4	8894.4
DQ097276.1	160664	54.1	97.0	341.7	102.7	140.1	91.4
AB299563.1	247779	1371.2	1384.3	3910.5	2818.8	1600.8	1307.7
DQ539046.1	161645	649.5	921.6	1366.2	2193.0	1230.1	216.9
AB299565.1	241161	4930.8	6139.8	5509.3	6193.2	8437.3	7580.9
GQ502667.1	578464	6568.6	7405.4	5799.0	5202.8	4158.7	4463.7
EU803670.1	338096	822.7	805.7	718.1	5180.0	256.1	332.5
DQ302114.1	153206	97.2	69.1	176.5	679.8	78.0	50.5
FM242275.1	341545	495.7	613.8	1378.7	494.7	508.6	494.9
GQ347889.1	585626	2971.6	3834.6	5860.9	2581.8	2145.4	3472.0
U81738.2	1556	528.6	282.0	1137.9	356.2	643.3	793.1
AY695840.1	105129	73.6	99.1	161.0	96.3	103.9	75.9
FM242391.1	310512	3623.2	5449.9	5442.0	6146.1	1422.8	1444.3
EF574171.1	235121	2098.6	1233.0	3233.6	3310.2	1240.4	2472.0
AJ240909.1	74031	190.2	194.0	1282.7	397.9	64.3	44.9
EU617885.1	332206	12711.7	13069.6	15815.9	13407.2	11890.4	11252.8
FJ202864.1	353683	16.4	36.2	26.9	52.8	68.3	40.3
AB198611.1	135899	552.9	289.2	1926.4	1067.2	368.3	171.4
EU283474.1	278788	6941.3	8822.9	6912.3	7349.2	8338.6	6084.3
AB299566.1	256775	7908.9	9869.4	9799.7	5234.5	5863.9	5949.5
AB073978.1	41135	36.2	51.5	125.2	79.9	70.5	41.5
EU328081.1	278462	2123.7	3325.9	3888.1	1362.3	2222.8	1090.4
FJ745063.1	545467	54.5	105.3	101.7	76.0	1585.9	165.5
GQ984310.1	588321	10242.3	9128.1	3013.1	4784.3	4765.3	3235.4
AB192188.1	143442	4201.2	6230.1	5860.4	4553.5	3158.6	3079.0
FJ516822.1	513750	4063.1	5487.0	5782.2	5301.6	5270.2	5955.9
AF075271.2	9675	138.4	222.5	566.1	150.0	127.5	123.0
FJ717327.1	535151	6509.1	6607.8	5673.8	3347.6	4136.6	3032.2
FJ717277.1	511489	9447.5	7943.4	6451.4	5926.6	3661.2	3632.1
FJ717325.1	510475	6230.3	5414.9	6609.1	5189.8	2697.8	3169.8
AY114312.1	72268	95.4	206.1	274.3	132.2	83.5	40.9
AB189371.1	114335	50.4	65.5	124.0	150.8	63.3	43.5
AF449255.1	61856	9913.0	10131.1	6457.5	6671.1	5659.9	5319.0

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FJ717312.1 gg_id:547597 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United Kingc
FJ717308.1 gg_id:535176 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United Kingc
AF449257.1 gg_id:61853 Riftia pachyptila's tube clone R76-B18
EU287160.1 gg_id:240419 Pacific arctic surface sediment clone P13-67
FJ717273.1 gg_id:510216 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United Kingc
FJ717296.1 gg_id:510340 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United Kingc
FJ717311.1 gg_id:572386 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United Kingc
FJ717270.1 gg_id:568860 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United Kingc
FM165269.1 gg_id:564018 seep chitineous tube vestimentiferan tubeworm Lamellibrachia sp. cold seeps clone
FJ717291.1 gg_id:548455 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United Kingc
EU804364.1 gg_id:341372 It's all ranking aquatic 250 miles Panama City clone 6C232274
DQ513023.1 gg_id:160321 Microbial life fluids ridge flank crustal fluid clone FS142-12B-02
AY222315.1 gg_id:113883 host hindgut caecum clone Ver 1
EF520620.1 gg_id:232855 structure lakes: what controls ? acid-impacted lake clone ADK-BTh02-31
AJ575731.1 gg_id:97376 lake water clone NE06
EU703279.1 gg_id:554393 taxon richness -altitude lakes eastern tin plateau predominance Bacteroidetes and S
EF520637.1 gg_id:231528 structure lakes: what controls ? acid-impacted lake clone ADK-HDh02-03
AY752089.1 gg_id:99083 lake water clone P38.12
FJ543046.1 gg_id:519253 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone B
FJ543079.1 gg_id:527379 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone B
AJ863245.1 gg_id:127649 poplar tree microcosm, bulk soil, flooded clone 21BSF50
EF516165.1 gg_id:221896 grassland soil clone FCPP479
FJ612408.1 gg_id:535790 and Biogeochemistry Dongping Lake Ecosystems lake water clone DP10.4.22
AY792308.1 gg_id:123679 Humic Lake clone CrystalBog1B6
AB369162.1 gg_id:256945 Microbiological Assessment Circulation Mud Fluids During First Operation Drilling De
AY388649.1 gg_id:108024 Chthoniobacter flavus
DQ450786.1 gg_id:160871 Microbial Alpine Tundra Wet Meadow Soil: Chloroflexi Cold Water-Saturated saturat
EF516096.1 gg_id:224503 grassland soil clone FCPT710
EF515981.1 gg_id:220364 grassland soil clone FCPT465
EF516968.1 gg_id:223379 grassland soil clone FCPS729
FJ822655.1 gg_id:588551 and metagenomic Verrucomicrobia former agricultural grassland soil rhizosphere clor
AY960766.1 gg_id:115027 Detection and Cultivation Soil Verrucomicrobia Ellin503
EU135441.1 gg_id:251499 tallgrass prarie soil clone FFCH5517
AB486453.1 gg_id:588961 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC
AB374368.1 gg_id:270180 sequences Weissenstein (white rock) / few millimeters be surface rock called 'Weiss
GQ402701.1 gg_id:541789 Accessing microbial biodiversity and metabolic potential tropical -based approach pe
EF516529.1 gg_id:221334 grassland soil clone FCPN729
FJ822636.1 gg_id:535268 and metagenomic Verrucomicrobia former agricultural grassland soil rhizosphere clor
GQ397058.1 gg_id:538238 Functional unvegetated perhumid recently-deglaciated soils do not correlate shifts s
FM877557.1 gg_id:358664 Microbial several mining wastes Bulgaria uranium mill tailings clone BuhD-321
AY960770.1 gg_id:114998 Detection and Cultivation Soil Verrucomicrobia Ellin507

FJ717312.1	547597	13212.5	11635.4	15360.2	9308.7	10721.9	10115.1
FJ717308.1	535176	9861.2	11066.3	7046.3	9319.1	10707.9	10587.5
AF449257.1	61853	4947.1	5076.9	4616.2	2600.0	3490.6	3398.4
EU287160.1	240419	2822.6	2711.5	2979.3	4247.0	3284.1	3403.7
FJ717273.1	510216	9339.5	9961.2	8445.6	7855.3	12357.5	11823.6
FJ717296.1	510340	6685.0	6807.0	6552.0	3471.5	4124.7	3359.8
FJ717311.1	572386	2961.7	2617.2	1573.3	2636.9	443.5	484.6
FJ717270.1	568860	11828.5	10007.1	11657.8	7908.1	7053.6	7057.8
FM165269.1	564018	2919.5	3496.1	4033.4	1607.6	1807.6	1578.0
FJ717291.1	548455	13704.3	13932.7	13850.6	13088.0	10861.7	11743.9
EU804364.1	341372	388.4	200.6	385.3	206.9	252.6	60.0
DQ513023.1	160321	2206.0	3205.9	4560.4	2215.0	2816.3	2901.7
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EF520620.1	232855	94.6	180.3	1361.2	226.0	140.7	146.1
AJ575731.1	97376	4585.8	4207.6	3263.1	566.7	1107.4	947.9
EU703279.1	554393	6403.2	6811.7	11108.1	5594.5	2727.4	4145.2
EF520637.1	231528	3161.0	5978.8	4026.7	786.2	348.3	454.5
AY752089.1	99083	2766.0	9174.4	271.6	57.1	57.2	17.1
FJ543046.1	519253	4670.2	6015.6	2717.1	4317.8	4115.6	2999.8
FJ543079.1	527379	7239.7	10024.3	7259.0	4849.4	4235.9	5363.5
AJ863245.1	127649	205.8	435.4	572.6	157.3	313.8	281.5
EF516165.1	221896	6649.9	8000.9	4701.1	813.3	1020.6	1288.9
FJ612408.1	535790	324.6	1126.5	90.2	107.4	69.3	44.9
AY792308.1	123679	3725.4	5790.3	5726.5	2749.6	598.4	1159.9
AB369162.1	256945	13644.8	18559.3	14091.1	8166.1	6163.9	8005.5
AY388649.1	108024	825.0	1590.9	817.6	478.0	85.7	129.5
DQ450786.1	160871	766.7	1423.5	494.1	532.7	732.9	516.5
EF516096.1	224503	669.8	717.4	339.3	292.7	307.8	562.3
EF515981.1	220364	524.1	1160.1	1110.9	257.5	92.6	118.7
EF516968.1	223379	151.3	647.0	252.1	227.7	67.5	57.7
FJ822655.1	588551	3471.9	3743.7	4199.4	1603.9	887.9	754.6
AY960766.1	115027	248.0	370.5	132.9	122.0	64.7	50.1
EU135441.1	251499	2279.0	7925.4	3652.9	744.8	1376.2	333.0
AB486453.1	588961	560.4	1569.3	1404.5	547.7	121.5	118.0
AB374368.1	270180	1716.8	3475.5	2524.0	1072.8	316.3	776.2
GQ402701.1	541789	2627.9	3307.7	3808.9	2325.5	646.1	1025.9
EF516529.1	221334	841.9	1536.4	2032.4	441.1	782.2	454.2
FJ822636.1	535268	844.6	2250.8	3612.2	996.9	240.5	466.1
GQ397058.1	538238	5958.2	6498.6	8828.6	6883.4	4702.7	6870.0
FM877557.1	358664	4603.5	4379.6	2136.8	2935.9	2563.9	1139.5
AY960770.1	114998	4663.1	7133.8	4142.8	3737.5	3805.1	1946.0

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AY960764.1 gg_id:114899 Detection and Cultivation Soil Verrucomicrobia Ellin501
EU131041.1 gg_id:236458 alkaline China coal mine soil clone SIP CM42
EU644180.1 gg_id:286072 and Samoylov Island Lena active layer -centred polygon near surface horizon; Rim_T
EF018510.1 gg_id:214306 aspen rhizosphere clone Amb_16S_1148
EF018524.1 gg_id:207125 aspen rhizosphere clone Amb_16S_784
GQ264267.1 gg_id:511817 Structure Simulated Level Waste Site simulated level waste site clone WW1_b71
FJ822653.1 gg_id:554650 and metagenomic Verrucomicrobia former agricultural grassland soil rhizosphere clor
DQ228393.1 gg_id:142335 microbial compositions two subglacial possible role microbes chemical weathering p
EU135556.1 gg_id:249859 tallgrass prarie soil clone FFCH4930
AY212589.1 gg_id:104784 water 10 m downstream manure clone 139ds10
FM253596.1 gg_id:325609 Rock gold mine unusually microbial biofilm clone D07-1
AY960769.1 gg_id:115085 Detection and Cultivation Soil Verrucomicrobia Ellin506
EU881176.1 gg_id:354713 Karst region natural restoration land soil clone KNR200711-119
AY395330.1 gg_id:100320 pasture soil clone EB1011
AY326520.1 gg_id:136989 Amazon soil clone 28-1
AY218772.1 gg_id:82424 penguin droppings sediments clone KD6-84
AY395325.1 gg_id:104976 pasture soil clone EB1006
EF018259.1 gg_id:213922 aspen rhizosphere clone Amb_16S_615
EF516966.1 gg_id:223148 grassland soil clone FCPS574
EF494340.1 gg_id:222682 Nunnock River granitic landscape clone NR.1.035
EF516048.1 gg_id:222701 grassland soil clone FCPS405
FJ592654.1 gg_id:557191 Fumarole-supported islands biodiversity within hyperarid -elevation landscape on Pu
Y07576.1 gg_id:1624 grassland soil clone DA101
DQ298012.1 gg_id:143982 Microbial hydrocarbon contaminated soil clone UA4
EU881274.1 gg_id:335630 (long-term grazing and burned annual) Karst region serious disturbance field soil clor
EF018412.1 gg_id:213519 aspen rhizosphere clone Amb_16S_1028
EU861826.1 gg_id:320598 effects chronic fertilization on alpine tundra microbial implications carbon and nitrog
EU881282.1 gg_id:320201 (long-term grazing and burned annual) Karst region serious disturbance field soil clor
EF494343.1 gg_id:227202 Nunnock River granitic landscape clone NR.1.076
DQ404689.1 gg_id:154629 contaminated sediment clone 655902
FJ822650.1 gg_id:582528 and metagenomic Verrucomicrobia former agricultural grassland rhizosphere soil clor
EF019688.1 gg_id:214739 aspen rhizosphere clone Elev_16S_849
EF516045.1 gg_id:217322 grassland soil clone FCPN578
DQ395984.1 gg_id:155782 deep-sea octacoral clone ctg_CGOGA62
EF019129.1 gg_id:212017 aspen rhizosphere clone Amb_16S_1762
EF516305.1 gg_id:225899 grassland soil clone FCPN716
EU335341.1 gg_id:241683 Changes microbial metabolic and along hydrogeochemically variable profile unsatura
EF019121.1 gg_id:206632 aspen rhizosphere clone Amb_16S_1750
FM877556.1 gg_id:359072 Microbial several mining wastes Bulgaria uranium mill tailings clone BuhD-107
EF018766.1 gg_id:206493 aspen rhizosphere clone Amb_16S_1227
EF516889.1 gg_id:220177 grassland soil clone FCPO660

AY960764.1	114899	207.9	538.0	594.2	228.3	58.2	107.4
EU131041.1	236458	151.8	433.7	660.7	191.3	61.2	34.8
EU644180.1	286072	1996.0	5871.0	3719.6	740.8	2019.2	358.5
EF018510.1	214306	384.5	1313.4	2048.6	417.9	93.1	175.5
EF018524.1	207125	997.7	3395.4	1061.2	726.5	149.2	319.2
GQ264267.1	511817	6385.4	8325.7	9996.8	3843.3	1753.0	2390.5
FJ822653.1	554650	1254.5	2049.1	1548.5	740.0	507.5	573.0
DQ228393.1	142335	24.4	60.2	28.8	59.5	52.8	15.5
EU135556.1	249859	3763.7	6262.3	6236.4	2402.6	2478.2	1613.3
AY212589.1	104784	7421.4	10525.6	8460.8	6164.7	7849.0	7262.9
FM253596.1	325609	1462.1	3156.9	1601.6	838.5	1787.1	448.1
AY960769.1	115085	3040.6	2226.8	1733.0	757.5	373.3	154.1
EU881176.1	354713	2358.7	3563.3	4166.0	1986.8	1084.1	1522.0
AY395330.1	100320	17126.9	17476.7	8473.1	14733.2	17810.3	15505.6
AY326520.1	136989	27.1	46.9	33.6	53.5	126.5	43.7
AY218772.1	82424	142.1	128.0	55.1	67.4	75.3	37.9
AY395325.1	104976	19.8	47.2	25.2	62.9	69.6	40.0
EF018259.1	213922	4140.8	5040.2	2104.0	2898.4	4772.5	3785.2
EF516966.1	223148	292.3	185.7	55.8	61.3	81.7	41.3
EF494340.1	222682	3319.5	4893.4	4315.7	855.7	2569.1	2440.8
EF516048.1	222701	2935.6	1838.5	932.5	297.2	110.5	351.7
FJ592654.1	557191	10754.9	9139.1	5306.4	6252.1	6373.6	6767.3
Y07576.1	1624	11825.9	12715.7	10925.2	10934.7	12555.9	12594.1
DQ298012.1	143982	3322.4	5648.6	3415.2	1866.6	1874.2	3269.9
EU881274.1	335630	8862.2	8714.5	3975.8	4630.6	3968.0	3098.6
EF018412.1	213519	3405.3	8472.5	4700.6	945.5	1148.9	1856.5
EU861826.1	320598	23.2	19.7	21.5	49.0	37.0	28.8
EU881282.1	320201	1497.4	2534.1	3979.6	681.0	707.2	1290.4
EF494343.1	227202	1265.2	2971.3	905.9	194.2	97.8	166.5
DQ404689.1	154629	9467.6	11535.6	9837.8	7334.3	7253.3	9263.1
FJ822650.1	582528	18.9	33.0	42.0	49.0	52.9	33.7
EF019688.1	214739	78.9	159.0	507.9	160.3	82.4	84.9
EF516045.1	217322	204.9	599.9	732.5	137.3	119.6	131.2
DQ395984.1	155782	1087.6	1299.2	2898.9	1174.3	1693.9	2412.5
EF019129.1	212017	32.0	29.9	19.4	59.6	73.7	24.1
EF516305.1	225899	75.6	99.5	48.9	620.2	89.0	36.0
EU335341.1	241683	24.7	102.5	48.2	43.2	50.6	18.6
EF019121.1	206632	92.3	221.0	171.7	141.7	64.2	132.1
FM877556.1	359072	411.0	2323.1	116.9	47.6	90.5	38.7
EF018766.1	206493	419.9	595.8	132.8	115.4	117.9	52.6
EF516889.1	220177	2554.1	3377.8	4089.2	721.0	1413.5	1875.4

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DQ404692.1 gg_id:154883 contaminated sediment clone 655905
GU172180.1 gg_id:578268 Microbial Eucalyptus plantation soil clone DSM-R8
EF019126.1 gg_id:209352 aspen rhizosphere clone Amb_16S_1757
EF516261.1 gg_id:220494 grassland soil clone FCPO467
EF019883.1 gg_id:211980 aspen rhizosphere clone Elev_16S_1248
GQ356142.1 gg_id:594250 biomarkers ammonia oxidation activity anaerobic ammonium-oxidation (Anammox)
CU919143.1 gg_id:572340 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
CU918228.1 gg_id:549254 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
CU920760.1 gg_id:571409 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
EU773048.1 gg_id:331675 Banteng feces clone BG_aaa03d04.Contig1
EU471776.1 gg_id:294166 Asiatic elephant feces clone AE2_aaa01b10
EU771419.1 gg_id:339447 Asiatic elephant feces clone AE1_aaa02h11
EU463717.1 gg_id:297614 domesticated horse feces clone horsej_aai91e11
EU471538.1 gg_id:291474 Asiatic elephant feces clone AE1_aaa02e02
EU471740.1 gg_id:291133 Asiatic elephant feces clone AE2_aaa04d02
EU473570.1 gg_id:300038 Somali wild ass feces clone WA_aaa01g06
EU775815.1 gg_id:338441 Horse feces clone horsem_aai95h08
EU471942.1 gg_id:292730 Asiatic elephant feces clone AE3_aaa04e08
EU471839.1 gg_id:298259 Asiatic elephant feces clone AE2_aaa02c03
EU471710.1 gg_id:288899 Asiatic elephant feces clone AE2_aaa01a07
EU773126.1 gg_id:349774 Banteng feces clone BG_aaa02h07.Contig1
AB185519.1 gg_id:99547 rumen clone F23-B04
EU470381.1 gg_id:298808 Grevy's zebra feces clone GZ_aaa02b08
EU776446.1 gg_id:326916 Red Kangaroo feces clone KO2_aai18a10
EU864491.1 gg_id:327984 structures under selection pressure levels antibiotics Xiao River receiving treated oxy
AB015546.1 gg_id:203309 deep-sea sediments depths clone BD2-18
AY114334.1 gg_id:63771 anoxic marine sediment clone LD1-PB20
CU920931.1 gg_id:556915 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
GQ259319.1 gg_id:534591 Microbial activities coastal marine sediments and water column Svalbard surface se
FN396736.1 gg_id:546665 constant flux thermophilic cold seabed Arctic marine surface sediment clone s5_8_II
AY114328.1 gg_id:70013 anoxic marine sediment clone LD1-PA50
AY963317.1 gg_id:151682 structures and correlated ecological factors soils two evergreen broad-leaved forests
EU881223.1 gg_id:333383 Karst region natural restoration land soil clone KNR200711-042
EU135433.1 gg_id:257941 tallgrass prarie soil clone FFCH3955
AM162463.1 gg_id:154318 and situ identification acidic sphagnum peat bog clone B69
EU135525.1 gg_id:236593 tallgrass prarie soil clone FFCH8458
EU135455.1 gg_id:240895 tallgrass prarie soil clone FFCH1225
EF516767.1 gg_id:220193 grassland soil clone FCPT575
EU135479.1 gg_id:251458 tallgrass prarie soil clone FFCH10633
AF465651.1 gg_id:50325 thermal soil clone YNPRH34A
EU135506.1 gg_id:249781 tallgrass prarie soil clone FFCH14037

DQ404692.1	154883	486.7	1833.5	1246.2	218.7	105.6	136.5
GU172180.1	578268	18.8	29.2	25.4	36.6	48.1	39.7
EF019126.1	209352	2008.2	2177.9	400.3	183.1	187.8	172.6
EF516261.1	220494	2853.8	3244.5	3235.3	1831.7	440.5	1333.6
EF019883.1	211980	79.1	314.1	290.5	77.9	77.1	62.9
GQ356142.1	594250	1848.3	2850.9	2482.3	581.2	516.0	559.4
CU919143.1	572340	35.7	35.7	29.8	53.9	70.2	40.0
CU918228.1	549254	11613.3	12365.5	13618.0	11322.7	12071.6	13106.2
CU920760.1	571409	1351.7	2844.5	1121.9	473.9	728.6	806.7
EU773048.1	331675	1657.9	4754.2	3434.8	1181.1	1052.2	1781.8
EU471776.1	294166	2937.1	5505.8	1554.1	1814.9	1449.7	1445.3
EU771419.1	339447	5083.0	7796.8	6437.0	4598.3	4651.0	5568.6
EU463717.1	297614	3415.1	4857.3	3354.0	4268.1	1951.8	3679.1
EU471538.1	291474	6667.5	9992.1	6389.4	5200.2	4865.2	5435.1
EU471740.1	291133	2413.5	2844.1	4802.3	2276.2	1295.1	2410.7
EU473570.1	300038	3570.0	6360.7	2463.1	1876.1	1747.0	1670.5
EU775815.1	338441	3388.6	4138.8	3827.1	2962.3	4057.9	4095.2
EU471942.1	292730	2135.1	5222.4	4287.8	2139.6	2074.2	2459.3
EU471839.1	298259	4210.3	5751.4	3968.3	4698.5	6123.0	5953.3
EU471710.1	288899	693.2	965.2	1907.6	699.9	1444.8	928.9
EU773126.1	349774	1177.4	1905.2	6112.8	640.2	175.2	195.2
AB185519.1	99547	2306.2	3518.5	2240.3	498.5	250.2	545.8
EU470381.1	298808	4274.3	9444.7	11165.5	3611.6	3513.7	4603.4
EU776446.1	326916	8278.3	8784.7	8136.7	7811.8	8145.9	9410.7
EU864491.1	327984	6109.6	7085.4	7977.6	5342.6	6657.8	6481.8
AB015546.1	203309	6564.4	7965.8	7712.5	6832.0	8210.2	6973.0
AY114334.1	63771	65.9	131.4	333.4	94.7	87.4	76.6
CU920931.1	556915	480.2	1032.1	574.6	345.0	355.8	495.8
GQ259319.1	534591	3827.0	3524.1	7250.3	2572.4	1696.8	3118.4
FN396736.1	546665	281.2	842.3	2855.9	136.4	188.5	316.3
AY114328.1	70013	738.9	591.5	585.6	888.2	126.1	328.3
AY963317.1	151682	1202.3	863.9	692.9	708.1	387.8	426.0
EU881223.1	333383	433.4	392.0	2045.1	150.3	112.3	107.5
EU135433.1	257941	1606.1	2583.7	1520.9	3184.9	905.9	1582.0
AM162463.1	154318	1309.6	1536.7	644.3	1152.4	1206.3	1073.6
EU135525.1	236593	4462.5	7460.2	10484.0	3677.0	2617.9	3564.9
EU135455.1	240895	4247.3	5382.5	6419.0	1828.3	1853.2	1718.8
EF516767.1	220193	110.9	219.3	449.0	207.4	243.9	246.2
EU135479.1	251458	5864.7	6725.3	3786.3	2925.3	1371.3	1365.8
AF465651.1	50325	258.2	738.4	739.3	272.9	266.7	317.1
EU135506.1	249781	2056.3	2590.6	1652.0	1478.3	1786.7	991.6

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AY960780.1 gg_id:114975 Isolation members phylum Verrucomicrobia soil Ellin517
EF019719.1 gg_id:215142 aspen rhizosphere clone Elev_16S_885
EU644232.1 gg_id:284038 and Samoylov Island Lena active layer -centred polygon near surface horizon; Rim_T
EF516676.1 gg_id:221568 grassland soil clone FCPO598
DQ676318.1 gg_id:221692 Archaeal and plankton freshwater pond suboxic freshwater-pond sediment clone M
AY212643.1 gg_id:107428 water 20 m upstream manure clone 190up
GQ339133.1 gg_id:514963 Comprehensive Investigation on Iron Cycling Freshwater Seep ing Microscopy Cultiv
FM209351.1 gg_id:567812 Microbial Negev desert s sand soil clone 2031
AM162456.1 gg_id:155778 and situ identification acidic sphagnum peat bog clone B52
FJ625341.1 gg_id:551837 Influence lead contamination on boreal pine forest soil clone HF_NC_2
AM162459.1 gg_id:151165 and situ identification acidic sphagnum peat bog clone B129
FJ479471.1 gg_id:512910 species richness estimates obtained nearly and simulated pyrosequencing-generated
EF516574.1 gg_id:221251 grassland soil clone FCPP665
EU335294.1 gg_id:251275 Changes microbial metabolic and along hydrogeochemically variable profile unsatura
EU135503.1 gg_id:238929 tallgrass prarie soil clone FFCH13652
DQ676422.1 gg_id:220892 Archaeal and plankton freshwater pond suboxic freshwater-pond sediment clone M
EU335227.1 gg_id:248808 Changes microbial metabolic and along hydrogeochemically variable profile unsatura
FJ478628.1 gg_id:512539 species richness estimates obtained nearly and simulated pyrosequencing-generated
EU135464.1 gg_id:255118 tallgrass prarie soil clone FFCH5116
EF516222.1 gg_id:218456 grassland soil clone FCPT508
AJ617869.1 gg_id:110756 oxic-anoxic interphase flooded paddy soil clone D142114
EF516552.1 gg_id:217929 grassland soil clone FCPU600
DQ125505.1 gg_id:132722 uranium contaminated soil clone AKAU3464
FJ479069.1 gg_id:590252 species richness estimates obtained nearly and simulated pyrosequencing-generated
AJ863241.1 gg_id:126772 poplar tree microcosm bulk soil flooded clone 21BSF21
EF516075.1 gg_id:223550 grassland soil clone FCPT406
DQ450782.1 gg_id:161263 Microbial Alpine Tundra Wet Meadow Soil: Chloroflexi Cold Water-Saturated saturat
EU937949.1 gg_id:321753 Biogeochemistry Iron Oxidation Circumneutral Freshwater Habitat riparian iron oxidi
EF515942.1 gg_id:225894 grassland soil clone FCPP485
FJ468383.1 gg_id:585431 Bioaugmentation Pseudomonas sp. strain MHP41 promotes attenuation and changes
EU135478.1 gg_id:250253 tallgrass prarie soil clone FFCH10577
EU135518.1 gg_id:253183 tallgrass prarie soil clone FFCH17360
AF523995.1 gg_id:63232 coal effluent wetland clone FW4
EF612425.1 gg_id:248066 historic semiarid lead-zinc mine tailings site soil clone OS-C04
EF019315.1 gg_id:206560 aspen rhizosphere clone Elev_16S_510
AM162462.1 gg_id:155827 and situ identification acidic sphagnum peat bog clone B64
GU444057.1 gg_id:523991 Effects amendments on fertility and microbial structure cucumber Cucumis sativus L
AM162461.1 gg_id:151640 and situ identification acidic sphagnum peat bog clone B147
DQ521482.1 gg_id:186160 Antarctic lake ice cover clone ANTLV1_D01
EU135543.1 gg_id:248805 tallgrass prarie soil clone FFCH18403
EF516440.1 gg_id:219094 grassland soil clone FCPU636

AY960780.1	114975	204.5	714.3	2664.6	217.6	155.3	272.3
EF019719.1	215142	52.1	165.0	140.3	70.9	75.7	35.0
EU644232.1	284038	579.3	645.7	2051.9	464.0	391.7	358.8
EF516676.1	221568	8250.7	9874.8	7372.7	3763.1	5155.4	4550.2
DQ676318.1	221692	625.9	1519.5	1988.4	3208.6	577.6	1406.2
AY212643.1	107428	167.0	455.5	359.8	233.9	80.9	70.2
GQ339133.1	514963	3720.1	4725.2	2347.9	5045.1	7554.9	7895.1
FM209351.1	567812	3747.8	2819.4	2997.4	1093.2	969.9	1145.6
AM162456.1	155778	32.1	59.8	363.1	67.6	63.0	61.7
FJ625341.1	551837	6167.1	6072.9	6234.8	1294.1	1387.2	1688.6
AM162459.1	151165	126.5	404.6	662.1	137.4	193.4	95.0
FJ479471.1	512910	212.3	887.5	786.0	526.5	170.8	243.0
EF516574.1	221251	73.2	108.5	84.0	80.6	122.4	64.8
EU335294.1	251275	4912.9	6906.9	6571.9	3919.2	5504.1	3861.5
EU135503.1	238929	7347.1	11116.2	8878.9	3354.0	567.2	1229.4
DQ676422.1	220892	62.6	191.0	464.0	95.3	89.1	49.0
EU335227.1	248808	5136.8	7105.3	8087.5	4318.8	4200.5	5869.7
FJ478628.1	512539	7147.2	9297.8	6261.6	6519.8	8199.7	6831.6
EU135464.1	255118	1158.8	1460.8	3414.1	725.6	337.1	499.7
EF516222.1	218456	1097.6	673.0	1187.4	305.6	236.4	307.3
AJ617869.1	110756	48.3	110.7	234.5	64.6	91.1	31.3
EF516552.1	217929	78.8	171.3	102.9	106.5	496.5	222.8
DQ125505.1	132722	50.7	197.1	175.6	77.7	72.0	46.9
FJ479069.1	590252	659.3	1370.8	2689.6	237.2	120.6	125.2
AJ863241.1	126772	87.9	323.6	430.5	74.0	119.6	75.6
EF516075.1	223550	39.5	120.5	760.7	87.0	97.2	148.3
DQ450782.1	161263	111.6	253.6	1679.2	124.5	235.5	435.9
EU937949.1	321753	2144.0	4100.4	5477.5	2900.3	1509.9	1691.0
EF515942.1	225894	14956.8	15416.8	15563.3	12042.0	15813.7	15120.7
FJ468383.1	585431	1663.1	2442.4	3248.1	521.2	867.0	697.7
EU135478.1	250253	918.7	1581.0	2576.3	572.8	399.3	302.9
EU135518.1	253183	5780.0	6627.7	4655.1	3968.1	3522.2	2315.1
AF523995.1	63232	65.3	147.3	300.8	111.7	74.4	34.0
EF612425.1	248066	508.8	710.8	1176.5	191.4	127.1	128.9
EF019315.1	206560	2276.8	2600.7	1740.9	2956.6	2945.6	3007.6
AM162462.1	155827	202.2	798.5	2329.5	161.2	59.6	37.6
GU444057.1	523991	6105.2	11571.4	7045.0	5805.6	9230.0	8177.3
AM162461.1	151640	4184.8	5402.9	8493.7	3044.0	2723.2	2999.0
DQ521482.1	186160	215.0	1004.7	1301.7	231.6	447.8	205.9
EU135543.1	248805	9162.2	9017.7	7843.7	4485.7	5609.4	5610.2
EF516440.1	219094	19.5	50.5	50.9	40.7	53.6	25.1

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AY921923.1 gg_id:113303 farm soil clone AKYH1372
EU135437.1 gg_id:256933 tallgrass prarie soil clone FFCH6314
EU135514.1 gg_id:257782 tallgrass prarie soil clone FFCH15477
EF020079.1 gg_id:207326 aspen rhizosphere clone Elev_16S_1488
FJ592707.1 gg_id:543327 Fumarole-supported islands biodiversity within hyperarid -elevation landscape on Pu
EU335255.1 gg_id:241999 Changes microbial metabolic and along hydrogeochemically variable profile unsatura
EF516775.1 gg_id:218032 grassland soil clone FCPU668
GQ348914.1 gg_id:560563 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
FJ155059.1 gg_id:318309 seasonal fluctuation coastal Bohai Bay sequencing and RFLP soil clone CB
GQ348513.1 gg_id:542753 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
GQ348797.1 gg_id:535223 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
DQ302118.1 gg_id:156301 Rubromonas marinus gen. sp. nov. first marine representative subdivision one Verru
FJ628330.1 gg_id:513658 transition and zone within near-shore basin: brackish water anoxic fjord Nitinat Lake
FJ615181.1 gg_id:544538 Microbial dynamics seasonally fjord: British Columbia Saanich Inlet depth 125m anoxi
FJ615159.1 gg_id:557490 Microbial dynamics seasonally fjord: British Columbia Saanich Inlet depth 100m anoxi
DQ071110.1 gg_id:131960 marine surface water clone SJC1.38
AY028219.1 gg_id:32593 marine clone Arctic97B-4
DQ071044.1 gg_id:130139 islts and fld smplng Glf Strm Rng chlrphll mxmm cln Chl1.3
AM176893.1 gg_id:159970 Recovery mangrove sediment clone SZB49
GU061235.1 gg_id:574533 Evaluation culturing methods cultivate previously Yel Sea intertidal beach seawater
GU208329.1 gg_id:570490 Study on Sediment Dongping Lake sediment clone Se2-17
EU135454.1 gg_id:237237 tallgrass prarie soil clone FFCH12732
DQ125868.1 gg_id:131444 uranium contaminated soil clone AKAU4117
EU135432.1 gg_id:254690 tallgrass prarie soil clone FFCH13487
FJ479563.1 gg_id:579528 species richness estimates obtained nearly and simulated pyrosequencing-generated
EU135494.1 gg_id:237927 tallgrass prarie soil clone FFCH12670
EU937926.1 gg_id:337426 Biogeochemistry Iron Oxidation Circumneutral Freshwater Habitat riparian iron oxidi
AJ853567.1 gg_id:110302 landfill leachate clone GZKB73
CU917597.1 gg_id:546967 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
AF027005.1 gg_id:1572 hot spring clone OPB35
FM994912.1 gg_id:550907 springs Velingrad region Bulgaria hot spring Mizinka clone VS-21
EU104111.1 gg_id:310462 Evidence Comamonadaceae determinants settling performance activated sludge clo
DQ017913.1 gg_id:134130 upland stream clone S-Btb7_11
DQ396294.1 gg_id:153452 deep-sea octacoral clone ctg_NISA252
FJ905685.1 gg_id:535898 s Tonga-Kermadec iron oxide chimney-like structure on Volcano 19 Tonga Arc clone V
EF516930.1 gg_id:225632 grassland soil clone FCPN502
EF516856.1 gg_id:224253 grassland soil clone FCPS671
EF018903.1 gg_id:212324 aspen rhizosphere clone Amb_16S_1397
AY395425.1 gg_id:102024 pasture soil clone EB1106
FJ478519.1 gg_id:536090 species richness estimates obtained nearly and simulated pyrosequencing-generated

EF516510.1	218434	965.6	2492.8	1598.9	391.3	161.7	278.0
AY921923.1	113303	142.2	304.3	522.8	348.5	198.8	82.5
EU135437.1	256933	4144.6	2571.3	6123.4	2830.9	1161.0	1943.9
EU135514.1	257782	57.7	261.5	220.6	66.1	62.6	33.6
EF020079.1	207326	38.7	66.3	108.3	65.2	63.7	44.4
FJ592707.1	543327	4560.1	7153.7	8917.5	3075.1	963.7	1682.0
EU335255.1	241999	856.7	1430.8	1198.8	217.6	580.5	200.6
EF516775.1	218032	2407.6	4037.0	5033.7	3412.4	3672.6	2876.4
GQ348914.1	560563	5473.3	6254.0	9843.6	4945.8	6252.6	4727.1
FJ155059.1	318309	1027.6	1057.3	488.6	1576.1	736.3	525.1
GQ348513.1	542753	10301.1	11067.0	8476.5	6783.5	8288.2	6331.3
GQ348797.1	535223	11244.8	13133.7	9891.3	5995.4	4241.9	4217.3
DQ302118.1	156301	36.8	96.2	41.6	154.9	96.6	54.7
FJ628330.1	513658	3510.9	4597.5	3116.7	4038.6	1888.6	2308.0
FJ615181.1	544538	1837.0	1297.3	613.1	916.0	191.6	388.4
FJ615159.1	557490	16387.7	12193.9	6405.6	9377.6	9100.2	9263.5
DQ071110.1	131960	1090.8	764.6	531.6	622.0	188.0	230.6
AY028219.1	32593	1952.5	3178.1	5514.0	1942.9	1175.2	3240.2
DQ071044.1	130139	44.5	77.6	166.2	57.3	64.5	39.7
AM176893.1	159970	61.9	232.1	83.4	58.8	74.7	14.3
GU061235.1	574533	10727.7	13774.5	12655.3	6552.2	6053.7	7638.9
GU208329.1	570490	10613.1	8633.3	5622.0	4442.4	3987.3	4735.8
EU135454.1	237237	4600.2	4168.5	5601.1	1491.1	1385.7	1438.5
DQ125868.1	131444	342.8	696.0	3402.8	422.0	262.0	296.5
EU135432.1	254690	2142.1	2435.6	5985.9	2289.9	2453.0	2262.3
FJ479563.1	579528	8923.5	11303.9	9890.4	5320.1	2836.9	5059.0
EU135494.1	237927	3295.6	3493.0	12364.6	3507.4	2379.2	1780.9
EU937926.1	337426	4898.4	4655.5	7884.9	5425.5	2637.6	3027.8
AJ853567.1	110302	3568.5	6825.5	7085.9	1751.0	1406.3	1761.2
CU917597.1	546967	6062.9	8379.4	4604.0	4161.0	2765.4	1999.2
AF027005.1	1572	249.2	459.4	423.1	129.5	151.4	169.1
FM994912.1	550907	676.9	1182.6	2360.6	458.1	838.9	995.0
EU104111.1	310462	341.7	447.5	121.9	92.5	315.4	127.5
DQ017913.1	134130	2678.3	3930.7	1218.3	439.2	529.1	482.2
DQ396294.1	153452	6038.8	7102.2	6001.8	6230.3	4028.9	4340.8
FJ905685.1	535898	324.0	1012.8	766.1	798.0	1543.6	2585.1
EF516930.1	225632	280.7	1193.5	1059.2	641.6	187.9	509.5
EF516856.1	224253	3433.7	3565.9	3036.5	3337.8	4323.0	3894.7
EF018903.1	212324	244.7	866.5	1970.3	257.4	410.7	204.1
AY395425.1	102024	4318.9	4048.4	2882.7	2241.9	3749.7	3471.7
FJ478519.1	536090	2150.3	4534.7	3548.5	1097.0	979.6	1124.5

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AB487257.1 gg_id:549692 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNIR0
EU135434.1 gg_id:238183 tallgrass prarie soil clone FFCH7408
GQ402552.1 gg_id:593900 Accessing microbial biodiversity and metabolic potential tropical -based approach p
EF019592.1 gg_id:212455 aspen rhizosphere clone Elev_16S_1113
DQ404817.1 gg_id:151664 contaminated sediment clone 655945
DQ451523.1 gg_id:156917 forest soil clone FAC84
EU335323.1 gg_id:242989 Changes microbial metabolic and along hydrogeochemically variable profile unsatura
EF099597.1 gg_id:184418 mouse cecum clone SWPT4_aaa01f05
EU459611.1 gg_id:291051 ring-tailed lemur feces clone RT_aai09c04
EF099110.1 gg_id:192171 mouse cecum clone SWPT2_aaa02d09
CP001071.1 gg_id:278234 Akkermansia muciniphila str. ATCC BAA-835
DQ807825.1 gg_id:178569 human fecal clone RL180_aah37f08
DQ805565.1 gg_id:183323 human fecal clone RL203_aai64c10
EF400323.1 gg_id:214443 human fecal clone SJTU_E_11_61
DQ805338.1 gg_id:177459 human fecal clone RL203_aai61d02
EU508722.1 gg_id:262854 cecal contents Mus musculus strain C57BL/6J; MD4 clone MD4_aap49h09
EF099112.1 gg_id:174132 mouse cecum clone SWPT2_aaa02d11
EF604904.1 gg_id:230139 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous
AY982401.1 gg_id:125420 human sigmoid colon mucosal biopsy clone MK66
EU459638.1 gg_id:298839 ring-tailed lemur feces clone RT_aai09g05
EU763463.1 gg_id:345321 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A
EF604517.1 gg_id:234298 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous
DQ793539.1 gg_id:178086 human fecal clone RL246_aai73b07
AY977829.1 gg_id:118714 human cecum mucosal biopsy clone LF22
EU506706.1 gg_id:261175 cecal contents Mus musculus strain C57BL/6J; MD20 clone MD20_aap54h02
DQ807201.1 gg_id:185152 human fecal clone RL244_aaj47e04
DQ805485.1 gg_id:174822 human fecal clone RL203_aai63c06
DQ805597.1 gg_id:177705 human fecal clone RL203_aai64g05
EU506506.1 gg_id:274986 cecal contents Mus musculus strain C57BL/6J; MD19 clone MD19_aaa03b03
DQ805539.1 gg_id:185779 human fecal clone RL203_aai64a01
FJ365265.1 gg_id:368894 feces adult twins and mothers; TS1 clone TS1_a04g10
AJ408970.1 gg_id:31006 human colonic clone HuCA18
EU507500.1 gg_id:258589 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_2aaa04b09
FJ364958.1 gg_id:359195 feces adult twins and mothers; TS1 clone TS1_a01c01
AY986145.1 gg_id:116910 human stool clone D491
EU006397.1 gg_id:255263 Salmonella enterica serovar typhimurium exploits inflammation compete intestinal r
DQ805319.1 gg_id:195328 human fecal clone RL203_aai61b04
EU763313.1 gg_id:334717 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A
FJ365018.1 gg_id:365334 feces adult twins and mothers; TS1 clone TS1_a01h05
DQ803989.1 gg_id:181549 human fecal clone RL200_aai60g06
DQ805473.1 gg_id:197876 human fecal clone RL203_aai63b03

AB487257.1	549692	6048.6	4810.3	2616.4	2401.3	1699.7	1197.0
EU135434.1	238183	5600.7	4530.1	4029.5	6486.9	1073.7	2270.0
GQ402552.1	593900	5713.3	8569.1	7085.9	4168.3	5034.2	3861.4
EF019592.1	212455	4372.0	4313.5	2875.7	5398.1	6271.1	6188.5
DQ404817.1	151664	65.2	130.4	102.7	90.2	115.0	60.1
DQ451523.1	156917	1614.5	1723.9	1659.1	2073.2	1977.6	2152.4
EU335323.1	242989	1798.7	770.6	689.6	105.0	104.0	136.0
EF099597.1	184418	19943.4	19507.9	12934.8	14312.7	17101.8	14649.4
EU459611.1	291051	19587.9	17837.5	12616.3	11484.7	11948.6	9613.8
EF099110.1	192171	11676.5	11217.9	6518.3	8204.2	7508.0	5255.9
CP001071.1	278234	6680.6	6347.8	2568.9	2243.6	1885.5	942.3
DQ807825.1	178569	8776.3	6163.3	5382.2	1828.7	1162.9	1079.6
DQ805565.1	183323	10417.4	12066.3	5286.0	6270.8	6730.7	6842.7
EF400323.1	214443	10329.0	6263.3	3231.5	1750.8	1192.4	1228.7
DQ805338.1	177459	8599.6	10072.1	2832.4	2802.2	2545.9	1432.8
EU508722.1	262854	11112.0	9222.8	5674.4	1956.2	1285.4	1049.3
EF099112.1	174132	9363.2	8259.8	4649.0	1807.4	1265.5	1120.7
EF604904.1	230139	6899.4	7273.3	2803.3	1270.0	1169.4	2364.2
AY982401.1	125420	8704.1	6356.5	4956.8	1531.7	926.1	797.4
EU459638.1	298839	9019.1	10189.2	5300.4	2449.4	2521.5	1861.0
EU763463.1	345321	9512.2	10606.4	2919.1	3850.9	3188.9	2619.7
EF604517.1	234298	4799.6	7044.6	7632.0	2461.2	2622.4	3413.1
DQ793539.1	178086	9780.5	7520.2	4626.0	1790.2	1251.9	995.4
AY977829.1	118714	8166.0	6615.7	4217.8	1816.3	1239.2	1062.9
EU506706.1	261175	9617.0	7085.6	5720.6	1580.4	1140.1	1643.2
DQ807201.1	185152	9852.8	6975.3	5801.9	2678.8	1649.4	1447.7
DQ805485.1	174822	7589.8	7500.5	3543.9	1270.2	904.9	1059.4
DQ805597.1	177705	7105.7	5629.8	3810.3	866.2	231.5	557.8
EU506506.1	274986	6899.5	5698.7	2849.0	1706.1	1234.7	944.0
DQ805539.1	185779	10011.5	9094.8	5233.7	1988.3	1228.8	1022.0
FJ365265.1	368894	9175.8	10254.8	6057.5	1628.6	1222.2	1405.7
AJ408970.1	31006	9722.0	6881.4	3389.3	1811.4	552.3	973.1
EU507500.1	258589	8047.9	6046.2	4365.4	1101.6	998.6	1134.3
FJ364958.1	359195	7531.7	6100.8	5073.0	2252.3	1901.6	1967.4
AY986145.1	116910	4136.9	5918.7	2717.5	2255.1	2332.9	1660.2
EU006397.1	255263	5685.2	4731.4	3178.7	2003.4	1656.3	1912.2
DQ805319.1	195328	7493.8	7639.8	4365.8	861.1	550.7	945.9
EU763313.1	334717	7860.0	6547.6	3320.1	1861.0	969.4	1104.4
FJ365018.1	365334	15533.6	12251.7	10576.3	4521.7	6133.6	5398.2
DQ803989.1	181549	8863.5	9184.3	5590.0	2345.8	2116.8	1546.3
DQ805473.1	197876	6917.1	6342.4	4139.7	1007.3	265.5	679.7

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s__Akkermansia muciniphila	55338
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s__Akkermansia muciniphila	55805
s__Akkermansia muciniphila	55808

EU509469.1 gg_id:263656 cecal contents Mus musculus strain C57BL/6J; MD9 clone MD9_aap58h05
DQ805273.1 gg_id:192919 human fecal clone RL249_aaj84b10
EU939409.1 gg_id:335768 Fecal wild pygmy loris feces clone WF16S_131
DQ803720.1 gg_id:179163 human fecal clone RL200_aai57e09
DQ803687.1 gg_id:177813 human fecal clone RL200_aai57b09
EU763746.1 gg_id:346624 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A4
EF099090.1 gg_id:180789 mouse cecum clone SWPT2_aaa02b02
EF099511.1 gg_id:185740 mouse cecum clone SWPT3_aaa04b11
DQ805333.1 gg_id:187220 human fecal clone RL203_aai61c08
EF099126.1 gg_id:181513 mouse cecum clone SWPT2_aaa02f08
FJ371231.1 gg_id:359222 feces adult twins and mothers; TS6 clone TS6_a02e02
FJ364037.1 gg_id:360894 feces adult twins and mothers; TS150 clone TS150_a02c03
FJ365015.1 gg_id:367987 feces adult twins and mothers; TS1 clone TS1_a01h02
EU768083.1 gg_id:340215 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C4
FJ364103.1 gg_id:366847 feces adult twins and mothers; TS150 clone TS150_a03a07
EF098492.1 gg_id:197822 mouse cecum clone SWPT15_aaa04b09
DQ805416.1 gg_id:197098 human fecal clone RL203_aai62d02
FJ371195.1 gg_id:361687 feces adult twins and mothers; TS6 clone TS6_a02a08
FJ366647.1 gg_id:361853 feces adult twins and mothers; TS27 clone TS27_a02b07
FJ363943.1 gg_id:359085 feces adult twins and mothers; TS150 clone TS150_a01b10
DQ793729.1 gg_id:185943 human fecal clone RL246_aai76c11
FJ369647.1 gg_id:366053 feces adult twins and mothers; TS51 clone TS51_a03b08
FJ369644.1 gg_id:366982 feces adult twins and mothers; TS51 clone TS51_a03b04
EF099031.1 gg_id:188922 mouse cecum clone SWPT2_aaa01c10
FJ369652.1 gg_id:365331 feces adult twins and mothers; TS51 clone TS51_a03c03
EU768211.1 gg_id:349733 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C4
FJ364059.1 gg_id:368699 feces adult twins and mothers; TS150 clone TS150_a02e04
DQ803799.1 gg_id:180056 human fecal clone RL200_aai58e09
DQ806904.1 gg_id:187104 human fecal clone RL198_aaj75b08
EU768169.1 gg_id:344643 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C4
DQ803992.1 gg_id:185431 human fecal clone RL200_aai60g09
FJ371678.1 gg_id:366631 feces adult twins and mothers; TS8 clone TS8_a01a06
FJ365028.1 gg_id:359843 feces adult twins and mothers; TS1 clone TS1_a02a04
EU506426.1 gg_id:277079 cecal contents Mus musculus strain C57BL/6J; MD19 clone MD19_aaa01e12
FJ371109.1 gg_id:358268 feces adult twins and mothers; TS6 clone TS6_a01a10
AY978065.1 gg_id:120670 human cecum mucosal biopsy clone LI24
DQ805371.1 gg_id:191984 human fecal clone RL203_aai61g09
DQ805313.1 gg_id:185545 human fecal clone RL203_aai61a06
FJ369694.1 gg_id:359376 feces adult twins and mothers; TS51 clone TS51_a03f11
FJ371129.1 gg_id:364544 feces adult twins and mothers; TS6 clone TS6_a01c08
EU509276.1 gg_id:263476 cecal contents Mus musculus strain C57BL/6J; MD8 clone MD8_aap47a09

EU509469.1	263656	8208.8	6524.4	4803.5	973.2	595.7	630.3
DQ805273.1	192919	2610.4	1704.9	1214.4	2662.7	428.4	729.6
EU939409.1	335768	4011.2	2254.7	1754.2	617.4	173.1	287.1
DQ803720.1	179163	9123.7	9058.1	6066.7	2475.7	2150.1	1652.7
DQ803687.1	177813	7248.7	5906.0	4190.8	1196.6	1014.1	1562.9
EU763746.1	346624	6386.5	5452.5	4478.7	1451.8	743.1	856.8
EF099090.1	180789	4163.7	3980.7	1054.3	626.2	352.0	518.2
EF099511.1	185740	11219.3	9457.4	7157.4	2273.7	1504.5	1301.5
DQ805333.1	187220	7536.5	7724.2	4423.8	1001.6	554.3	851.6
EF099126.1	181513	5812.0	6911.6	4768.1	4694.8	3895.1	5477.3
FJ371231.1	359222	10286.8	6943.4	5695.9	2551.4	1612.1	1346.6
FJ364037.1	360894	6774.3	5166.7	4168.9	2506.7	1645.3	1324.3
FJ365015.1	367987	10129.2	6010.7	5377.8	1825.1	1094.3	1077.8
EU768083.1	340215	7684.1	7948.9	5660.9	1984.0	1890.5	2355.9
FJ364103.1	366847	9601.1	6865.3	5948.8	2187.1	1188.0	1215.0
EF098492.1	197822	14908.5	18252.4	14726.6	12322.9	12429.7	12326.4
DQ805416.1	197098	18050.6	17478.4	12846.2	8181.2	10179.0	9387.2
FJ371195.1	361687	6093.7	8068.0	5019.1	3429.7	2630.2	2785.6
FJ366647.1	361853	9714.3	8733.0	7791.9	2889.9	1515.4	2033.4
FJ363943.1	359085	7207.2	5457.1	3679.7	3881.5	4511.6	3954.0
DQ793729.1	185943	5085.5	5039.2	3856.0	765.7	262.6	759.6
FJ369647.1	366053	6919.8	5557.3	3849.9	716.3	577.4	564.5
FJ369644.1	366982	6624.2	6509.6	3823.4	1809.9	1268.5	983.6
EF099031.1	188922	9224.8	7879.7	5163.5	1868.9	1250.2	1052.7
FJ369652.1	365331	5327.8	4702.8	3021.6	834.7	578.5	526.8
EU768211.1	349733	11539.5	11955.4	7851.2	5981.5	9540.9	8048.7
FJ364059.1	368699	10374.7	7148.4	7832.4	4443.1	4536.5	4096.0
DQ803799.1	180056	8554.8	7376.9	5954.5	1832.2	1102.7	1074.8
DQ806904.1	187104	9560.6	6536.8	5665.7	2562.1	1627.0	1384.8
EU768169.1	344643	1241.3	3071.4	199.5	1018.0	293.6	441.3
DQ803992.1	185431	10123.2	8573.7	5961.2	2348.8	2116.1	1551.1
FJ371678.1	366631	7303.2	5042.8	4716.7	1674.8	1453.1	1337.5
FJ365028.1	359843	13752.7	8317.1	7562.8	1873.3	1601.5	1290.0
EU506426.1	277079	4607.4	3546.0	1263.8	250.2	444.8	411.6
FJ371109.1	358268	11993.2	12676.2	10533.7	6808.7	5510.9	5742.1
AY978065.1	120670	9505.2	8331.2	5605.3	1887.4	1285.8	1030.0
DQ805371.1	191984	5545.1	4989.9	4065.3	681.0	289.9	738.5
DQ805313.1	185545	7106.4	6029.9	3810.5	869.4	230.2	558.7
FJ369694.1	359376	619.3	5175.0	1148.9	1380.6	1711.3	1650.4
FJ371129.1	364544	7290.7	5160.0	4464.3	2508.7	1645.4	1329.4
EU509276.1	263476	4047.1	2749.8	2229.5	3265.5	708.5	1077.4

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AY271254.1 gg_id:108381 Akkermansia muciniphila
EU763663.1 gg_id:329021 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A4
DQ803966.1 gg_id:175631 human fecal clone RL200_aai60e04
FJ365471.1 gg_id:364577 feces adult twins and mothers; TS20 clone TS20_a03c08
FJ369765.1 gg_id:360437 feces adult twins and mothers; TS51 clone TS51_a04e09
FJ365053.1 gg_id:361231 feces adult twins and mothers; TS1 clone TS1_a02c08
EU768293.1 gg_id:335652 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C4
DQ803735.1 gg_id:174931 human fecal clone RL200_aai57g05
EU763518.1 gg_id:324181 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A4
EF605150.1 gg_id:228461 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
AY977862.1 gg_id:117139 human cecum mucosal biopsy clone LF60
DQ805536.1 gg_id:187614 human fecal clone RL203_aai63h08
AY979545.1 gg_id:122434 human transverse colon mucosal biopsy clone M203
AY978016.1 gg_id:116512 human cecum mucosal biopsy clone LH55
EF099119.1 gg_id:196722 mouse cecum clone SWPT2_aaa02e11
DQ805988.1 gg_id:193357 human fecal clone RL186_aah59f01
DQ806880.1 gg_id:181550 human fecal clone RL198_aaj74f05
DQ805309.1 gg_id:190845 human fecal clone RL203_aai61a01
EU768222.1 gg_id:353694 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C4
DQ806875.1 gg_id:199020 human fecal clone RL198_aaj74e01
FJ369500.1 gg_id:359082 feces adult twins and mothers; TS51 clone TS51_a01c11
FJ365276.1 gg_id:362860 feces adult twins and mothers; TS1 clone TS1_a04h10
EU467005.1 gg_id:289470 African elephant feces clone AFEL2_aao32f01
FJ369724.1 gg_id:359380 feces adult twins and mothers; TS51 clone TS51_a04a08
DQ805402.1 gg_id:187472 human fecal clone RL203_aai62b06
FJ363939.1 gg_id:356979 feces adult twins and mothers; TS150 clone TS150_a01b06
DQ806025.1 gg_id:178761 human fecal clone RL186_aah60b02
EU763566.1 gg_id:308538 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A4
EU459757.1 gg_id:291532 ring-tailed lemur feces clone RT_aai12c06
EU763340.1 gg_id:355331 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A4
FJ371365.1 gg_id:356771 feces adult twins and mothers; TS6 clone TS6_a04b02
DQ824286.1 gg_id:194232 human fecal clone RL304_aal74a01
FJ366780.1 gg_id:361014 feces adult twins and mothers; TS27 clone TS27_a03g05
EU767349.1 gg_id:307006 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C2
AJ315481.1 gg_id:24442 isolate HuCC13 clone
DQ824346.1 gg_id:187580 human fecal clone RL304_aal74g09
EF402545.1 gg_id:216106 human fecal clone SJTU_B_09_36
DQ805361.1 gg_id:180315 human fecal clone RL203_aai61f09
EF098504.1 gg_id:179446 mouse cecum clone SWPT15_aaa04d10
EU006393.1 gg_id:253279 Salmonella enterica serovar typhimurium exploits inflammation compete intestinal r
EU470114.1 gg_id:290245 trancaspain urial feces clone TU1_aaa01e03

AY271254.1	108381	3730.6	3774.1	1141.3	1536.1	1678.9	475.6
EU763663.1	329021	8076.4	6968.6	3617.8	1663.2	935.4	979.4
DQ803966.1	175631	6983.6	5574.7	3526.1	1972.3	2422.9	1618.4
FJ365471.1	364577	8736.9	6959.4	5960.6	2181.3	1898.9	2068.0
FJ369765.1	360437	6490.0	6451.1	3206.2	1623.9	1261.4	979.7
FJ365053.1	361231	6510.7	5394.5	3871.7	3051.1	2114.6	1806.2
EU768293.1	335652	8605.8	7564.7	5850.7	1468.5	1782.9	1542.1
DQ803735.1	174931	7981.2	7358.9	5291.6	1815.5	1089.1	1026.5
EU763518.1	324181	8561.3	6845.1	4229.8	4009.3	3557.9	3822.4
EF605150.1	228461	7053.7	6059.6	3696.1	2598.5	3236.1	1614.1
AY977862.1	117139	3870.8	3411.5	3062.7	502.4	126.9	511.2
DQ805536.1	187614	10248.5	10053.5	7107.9	5921.7	8944.5	7850.1
AY979545.1	122434	4460.5	3417.9	3801.0	501.4	213.6	485.2
AY978016.1	116512	16242.1	12146.7	8585.4	6844.4	8613.6	7762.3
EF099119.1	196722	9095.2	7210.8	5076.1	1266.7	456.9	781.7
DQ805988.1	193357	8337.9	7466.4	4861.0	1522.5	1106.6	1167.9
DQ806880.1	181550	12629.4	8136.1	5656.1	3042.7	2075.8	2046.0
DQ805309.1	190845	6637.6	5682.0	2911.0	1231.6	485.5	781.7
EU768222.1	353694	7509.4	6589.3	5166.0	2330.5	2073.1	2259.8
DQ806875.1	199020	1670.6	1792.7	1172.7	984.6	324.5	403.4
FJ369500.1	359082	3159.6	5606.0	3342.0	4418.4	7342.9	5684.9
FJ365276.1	362860	6347.8	5067.9	4400.4	2890.8	1880.3	2045.1
EU467005.1	289470	6240.1	6345.5	4605.5	1572.3	1082.3	1003.7
FJ369724.1	359380	9247.7	9482.4	5472.9	8750.9	8537.7	8564.6
DQ805402.1	187472	5275.9	5843.7	3417.2	894.6	329.0	667.5
FJ363939.1	356979	7553.8	5719.0	5566.7	2275.4	1408.3	1663.7
DQ806025.1	178761	9115.8	8802.9	4894.0	1807.4	1324.8	1357.3
EU763566.1	308538	6116.2	6860.2	4168.6	1015.9	519.0	917.0
EU459757.1	291532	15689.5	11961.1	9574.7	6921.2	6441.6	5223.2
EU763340.1	355331	7075.0	7046.8	3096.0	1655.1	961.5	896.5
FJ371365.1	356771	9198.9	7431.5	5801.5	2680.8	1647.4	1448.2
DQ824286.1	194232	7270.2	7178.1	4755.5	1300.1	467.3	780.6
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EU006393.1	253279	6100.9	5860.8	3721.4	3249.3	4271.3	4079.5
EU470114.1	290245	8861.6	11254.6	4697.5	5594.1	3567.9	2737.5

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EU474283.1 gg_id:295446 western lowland gorilla feces clone GORSD_aaa01c08
EF099214.1 gg_id:199361 mouse cecum clone SWPT2_aaa04a08
FJ362945.1 gg_id:363199 feces adult twins and mothers; TS148 clone TS148_a01b02
AY982465.1 gg_id:118488 human sigmoid colon mucosal biopsy clone MM09
GQ491900.1 gg_id:546153 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
EU006398.1 gg_id:239988 Salmonella enterica serovar typhimurium exploits inflammation compete intestinal r
EF605166.1 gg_id:230601 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF099268.1 gg_id:175690 mouse cecum clone SWPT2_aaa04g11
GQ492728.1 gg_id:575407 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
DQ803889.1 gg_id:175601 human fecal clone RL200_aai59f02
DQ803798.1 gg_id:179022 human fecal clone RL200_aai58e08
EF098506.1 gg_id:198546 mouse cecum clone SWPT15_aaa04e05
EU458622.1 gg_id:299422 European rabbit feces clone RA_h03_1
DQ794836.1 gg_id:186705 human fecal clone RL240_aaj32h12
EF605168.1 gg_id:229647 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EU507410.1 gg_id:261213 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_2aaa02h04
DQ803912.1 gg_id:181118 human fecal clone RL200_aai59h02
EU459648.1 gg_id:296229 ring-tailed lemur feces clone RT_aai10a08
GQ491639.1 gg_id:577568 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
DQ793400.1 gg_id:194055 human fecal clone RL199_aaj43c05
DQ806918.1 gg_id:181978 human fecal clone RL198_aaj75d07
EU507531.1 gg_id:258255 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_2aaa04f08
EU508159.1 gg_id:264121 cecal contents Mus musculus strain C57BL/6J; MD26 clone MD26_aaa02a06
DQ793672.1 gg_id:184483 human fecal clone RL246_aai75d06
EU459667.1 gg_id:288635 ring-tailed lemur feces clone RT_aai10e08
DQ797676.1 gg_id:190478 human fecal clone RL206_aaj14e06
DQ803739.1 gg_id:174281 human fecal clone RL200_aai57g10
EU506565.1 gg_id:277003 cecal contents Mus musculus strain C57BL/6J; MD19 clone MD19_aaa04d05
GQ492737.1 gg_id:585879 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
EU506534.1 gg_id:260817 cecal contents Mus musculus strain C57BL/6J; MD19 clone MD19_aaa03e12
DQ795501.1 gg_id:182004 human fecal clone RL178_aan65b11
EU006176.1 gg_id:255048 Salmonella enterica serovar typhimurium exploits inflammation compete intestinal r
DQ806760.1 gg_id:178399 human fecal clone RL186_aao48d05
DQ803815.1 gg_id:197646 human fecal clone RL200_aai58g02
EF098337.1 gg_id:191825 mouse cecum clone SWPT15_aaa01a11
EF099264.1 gg_id:191956 mouse cecum clone SWPT2_aaa04g06
EF099136.1 gg_id:191681 mouse cecum clone SWPT2_aaa02g09
EF602830.1 gg_id:234575 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
DQ803955.1 gg_id:174718 human fecal clone RL200_aai60d02
DQ793678.1 gg_id:173820 human fecal clone RL246_aai75e04
GQ493064.1 gg_id:577245 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice

EU474283.1	295446	9444.6	8567.0	5272.7	2483.4	2102.8	1714.4
EF099214.1	199361	7022.2	7629.2	3596.6	3013.4	4128.3	3304.6
FJ362945.1	363199	8153.1	5838.9	5543.4	776.6	268.2	848.1
AY982465.1	118488	14596.7	12675.9	8709.4	10555.6	9749.1	7963.0
GQ491900.1	546153	5859.8	7700.3	3419.9	5087.0	4871.8	4408.7
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EF605166.1	230601	6739.5	5027.3	3037.8	1390.8	1556.7	1135.5
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DQ803889.1	175601	5132.0	4908.8	4073.0	852.9	388.2	563.2
DQ803798.1	179022	6348.7	5652.7	3170.7	841.1	514.4	901.5
EF098506.1	198546	4866.8	5417.4	2086.2	2506.8	1708.2	1370.3
EU458622.1	299422	2638.8	3032.5	2287.1	1141.4	2346.8	1593.7
DQ794836.1	186705	9617.6	10112.8	6189.7	4885.9	4715.5	4531.4
EF605168.1	229647	10023.4	8078.3	5161.5	2797.0	3633.6	2060.9
EU507410.1	261213	9772.8	7507.3	4286.8	1889.7	1238.8	1085.1
DQ803912.1	181118	5882.4	8426.2	10697.8	8498.1	7008.7	8141.8
EU459648.1	296229	7101.0	8406.1	6108.3	5938.7	5832.1	6005.2
GQ491639.1	577568	6313.8	7758.6	6412.9	5186.7	4660.3	4297.1
DQ793400.1	194055	3638.8	3757.9	796.7	1569.1	1213.3	656.3
DQ806918.1	181978	4524.2	3803.1	4044.1	4576.4	2424.8	3017.1
EU507531.1	258255	11129.7	10746.0	3364.7	6911.9	8569.1	7177.1
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DQ793672.1	184483	12831.9	7328.8	2409.6	357.6	150.0	445.9
EU459667.1	288635	3746.5	2110.7	1091.0	5119.5	715.8	1786.1
DQ797676.1	190478	13183.9	11897.0	7823.2	6152.6	5637.6	5288.2
DQ803739.1	174281	9613.4	8848.1	5817.6	2364.5	2631.8	2455.8
EU506565.1	277003	7807.2	5905.1	4988.2	1173.8	439.4	709.3
GQ492737.1	585879	13755.9	12678.7	7761.6	6564.4	6045.9	5442.1
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DQ795501.1	182004	2607.1	3138.1	886.6	1357.4	3265.6	2346.8
EU006176.1	255048	5423.6	4470.5	2746.4	2716.6	2156.3	1990.0
DQ806760.1	178399	11238.0	12755.2	4402.8	8099.6	9923.0	10201.3
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EF098337.1	191825	9440.5	8318.0	6129.9	1849.3	936.9	985.8
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EF099136.1	191681	8237.9	6039.1	3813.1	4655.8	3873.4	5137.5
EF602830.1	234575	8529.5	7404.5	3849.5	1627.3	2012.7	1529.7
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DQ793678.1	173820	11074.9	9569.7	6226.1	2635.6	2325.6	1723.3
GQ493064.1	577245	9442.0	9029.4	4955.3	3403.4	3746.3	3451.5

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k__Bacteria	k__Bacteria	p__Verrucomicrobia	c__Verrucomicrobiae

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DQ803951.1 gg_id:189536 human fecal clone RL200_aai60c10
EU507216.1 gg_id:270914 cecal contents Mus musculus strain C57BL/6J; MD22 clone MD22_aaa03f12
FJ367560.1 gg_id:365237 feces adult twins and mothers; TS2 clone TS2_a01a04
DQ823974.1 gg_id:179397 human fecal clone RL204_aaj57f06
GQ491465.1 gg_id:537012 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
EU506850.1 gg_id:260295 cecal contents Mus musculus strain C57BL/6J; MD21 clone MD21_aar07c08
DQ797870.1 gg_id:196376 human fecal clone RL206_aaj16g12
EU006464.1 gg_id:245541 Salmonella enterica serovar typhimurium exploits inflammation compete intestinal r
FJ367593.1 gg_id:359766 feces adult twins and mothers; TS2 clone TS2_a01d01
DQ805310.1 gg_id:177858 human fecal clone RL203_aai61a03
EF605156.1 gg_id:227800 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF603774.1 gg_id:233386 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF099020.1 gg_id:180596 mouse cecum clone SWPT2_aaa01b09
GQ491995.1 gg_id:584653 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
EU006396.1 gg_id:251790 Salmonella enterica serovar typhimurium exploits inflammation compete intestinal r
EU006177.1 gg_id:253234 Salmonella enterica serovar typhimurium exploits inflammation compete intestinal r
FJ371421.1 gg_id:363508 feces adult twins and mothers; TS6 clone TS6_a04g05
EU507388.1 gg_id:276012 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_2aaa02e06
EU507089.1 gg_id:266625 cecal contents Mus musculus strain C57BL/6J; MD22 clone MD22_aaa01a11
AY979494.1 gg_id:123265 human transverse colon mucosal biopsy clone M135
DQ824431.1 gg_id:176638 human fecal clone RL304_aal75h11
GQ491867.1 gg_id:579826 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
DQ803761.1 gg_id:190136 human fecal clone RL200_aai58b01
DQ793686.1 gg_id:182478 human fecal clone RL246_aai75f02
DQ803743.1 gg_id:194760 human fecal clone RL200_aai57h03
EF603613.1 gg_id:233237 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF602796.1 gg_id:232549 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
DQ803928.1 gg_id:176439 human fecal clone RL200_aai60a08
GQ492726.1 gg_id:543645 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
GQ492710.1 gg_id:533891 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
EU469988.1 gg_id:289362 trancaspain urial feces clone TU1_aaa03b07
GQ491356.1 gg_id:589626 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
DQ793673.1 gg_id:177438 human fecal clone RL246_aai75d08
GQ493744.1 gg_id:562137 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
DQ803674.1 gg_id:182771 human fecal clone RL200_aai57a07
DQ824465.1 gg_id:199450 human fecal clone RL304_aal76c12
EU451703.1 gg_id:316576 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83N
EU006404.1 gg_id:254430 Salmonella enterica serovar typhimurium exploits inflammation compete intestinal r
EF605151.1 gg_id:234253 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF603854.1 gg_id:230720 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
DQ803856.1 gg_id:179974 human fecal clone RL200_aai59b12

DQ803951.1	189536	6236.2	5933.3	4162.9	1648.6	1057.1	971.3
EU507216.1	270914	15374.3	11594.6	10438.1	6117.3	8888.1	7993.9
FJ367560.1	365237	6820.8	7487.4	4503.5	3754.9	4206.4	3875.8
DQ823974.1	179397	26.8	38.6	22.6	45.4	73.2	27.3
GQ491465.1	537012	10846.0	10948.5	8270.3	6121.7	5892.2	4463.4
EU506850.1	260295	16055.4	13706.5	8916.5	10426.0	10469.1	8793.7
DQ797870.1	196376	2915.2	3681.9	2107.5	463.6	311.4	590.7
EU006464.1	245541	9070.4	6102.7	3481.8	1779.1	1115.3	1212.8
FJ367593.1	359766	7691.0	5413.7	5915.3	563.3	152.6	369.7
DQ805310.1	177858	1874.7	2527.3	976.4	366.3	354.4	461.8
EF605156.1	227800	9782.5	7893.1	4666.4	2121.8	2769.8	1396.9
EF603774.1	233386	9151.3	8052.3	4449.9	1841.0	2689.3	1428.3
EF099020.1	180596	15066.2	13208.0	8617.4	5290.5	3809.4	3108.1
GQ491995.1	584653	7661.3	7151.8	3879.6	2428.1	3227.9	2756.7
EU006396.1	251790	12899.5	13264.8	6057.2	2968.6	2353.4	3135.7
EU006177.1	253234	13967.1	9949.5	7514.2	4635.4	5911.4	5125.6
FJ371421.1	363508	6724.4	7385.9	4429.7	2788.8	2764.5	1725.6
EU507388.1	276012	71.1	146.9	673.1	114.9	166.2	99.5
EU507089.1	266625	21420.1	12971.1	13055.1	11196.3	11060.5	8960.9
AY979494.1	123265	5703.3	6572.1	9014.9	2068.5	1058.3	2410.9
DQ824431.1	176638	5719.7	5570.7	3299.1	505.4	117.2	258.1
GQ491867.1	579826	12528.4	12933.4	8247.0	6733.1	6473.9	5938.0
DQ803761.1	190136	5510.2	7717.1	3515.4	1529.2	1090.0	1404.8
DQ793686.1	182478	5387.5	7135.5	6637.1	7206.2	12909.1	9774.9
DQ803743.1	194760	7484.5	7879.1	5211.3	1814.6	1090.5	1025.3
EF603613.1	233237	15666.3	15041.1	8696.9	7603.9	6232.3	6058.2
EF602796.1	232549	9811.6	8195.4	5151.6	2789.1	3629.1	2057.0
DQ803928.1	176439	1546.1	3001.5	897.8	1827.9	4050.0	2955.0
GQ492726.1	543645	4524.0	4282.4	1912.2	1221.3	548.2	885.6
GQ492710.1	533891	3079.0	4090.1	2115.6	1319.8	1043.0	1068.4
EU469988.1	289362	10610.5	12577.7	13850.9	5560.7	3660.2	4685.2
GQ491356.1	589626	12564.3	12908.6	7933.7	7147.4	6533.6	6056.2
DQ793673.1	177438	9899.3	8325.1	6449.9	1308.7	855.9	1206.2
GQ493744.1	562137	11341.9	11618.9	7832.1	6431.8	6079.9	5584.9
DQ803674.1	182771	94.5	88.4	87.7	88.7	86.8	51.2
DQ824465.1	199450	4385.3	3643.4	2949.8	740.2	213.1	630.1
EU451703.1	316576	16839.7	19553.1	14119.6	12455.6	17362.9	13280.4
EU006404.1	254430	5686.9	5085.9	3170.7	1885.1	1654.9	1659.3
EF605151.1	234253	7086.0	6017.1	3518.6	1957.5	3430.1	1624.2
EF603854.1	230720	7125.8	5070.5	3655.2	650.1	1058.8	911.8
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DQ795332.1 gg_id:189416 human fecal clone RL178_aah53a10
GQ493707.1 gg_id:588996 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
EU474343.1 gg_id:297296 western lowland gorilla feces clone GORSD_aaa02d12
DQ803801.1 gg_id:175615 human fecal clone RL200_aai58e11
EU508365.1 gg_id:262989 cecal contents Mus musculus strain C57BL/6J; MD27 clone MD27_aaa03h06
FJ367694.1 gg_id:364483 feces adult twins and mothers; TS2 clone TS2_a02e02
DQ797786.1 gg_id:197591 human fecal clone RL206_aaj15g12
DQ824257.1 gg_id:192313 human fecal clone RL304_aal73f01
EF605153.1 gg_id:232422 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF603066.1 gg_id:230664 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF099628.1 gg_id:184620 mouse cecum clone SWPT4_aaa02b07
EF099133.1 gg_id:198936 mouse cecum clone SWPT2_aaa02g06
EU507293.1 gg_id:262054 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_2aaa01c03
GQ493815.1 gg_id:568909 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
EU509193.1 gg_id:268293 cecal contents Mus musculus strain C57BL/6J; MD8 clone MD8_aap45f10
GQ448638.1 gg_id:544288 Microbiome neonatal calves: shedding microorganisms fecal clone calf784_6wks_gr
EU474260.1 gg_id:294287 western lowland gorilla feces clone GORSD_aaa03a03
EF604906.1 gg_id:234335 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF099038.1 gg_id:178077 mouse cecum clone SWPT2_aaa01d08
EU459692.1 gg_id:300791 ring-tailed lemur feces clone RT_aai10h12
EF603938.1 gg_id:227678 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
GQ493480.1 gg_id:540440 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
DQ824314.1 gg_id:194496 human fecal clone RL304_aal74d01
GQ491874.1 gg_id:550767 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
EU508387.1 gg_id:270147 cecal contents Mus musculus strain C57BL/6J; MD27 clone MD27_aaa04g02
EF604791.1 gg_id:232493 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
GQ492159.1 gg_id:561627 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
EU451506.1 gg_id:353432 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N
EF604911.1 gg_id:227993 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
DQ807255.1 gg_id:187988 human fecal clone RL244_aaj48b11
GQ493932.1 gg_id:570491 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
AY980944.1 gg_id:121335 human rectum mucosal biopsy clone LR95
EU474294.1 gg_id:294378 western lowland gorilla feces clone GORSD_aaa03b05
DQ824408.1 gg_id:199666 human fecal clone RL304_aal75f10
EU506595.1 gg_id:269033 cecal contents Mus musculus strain C57BL/6J; MD20 clone MD20_aap53a03
EF099070.1 gg_id:175442 mouse cecum clone SWPT2_aaa01g10
EF099675.1 gg_id:187986 mouse cecum clone SWPT4_aaa02g06
EF602794.1 gg_id:228401 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF099117.1 gg_id:180918 mouse cecum clone SWPT2_aaa02e08
GQ492323.1 gg_id:588591 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
DQ803906.1 gg_id:183355 human fecal clone RL200_aai59g07

DQ795332.1	189416	7097.3	6228.8	5037.9	1804.6	2207.2	2058.9
GQ493707.1	588996	12309.5	11889.4	8341.0	6143.9	5610.8	5275.0
EU474343.1	297296	11901.6	9273.9	7818.5	2282.4	3150.6	2624.9
DQ803801.1	175615	12156.5	10242.7	7790.9	2851.9	2357.3	1884.7
EU508365.1	262989	4050.0	3394.4	4591.7	457.4	89.0	164.1
FJ367694.1	364483	10914.5	9608.4	5713.9	2032.5	2078.6	2285.4
DQ797786.1	197591	1385.9	1307.8	1020.3	646.7	630.5	597.5
DQ824257.1	192313	4744.9	4205.0	4580.6	860.8	401.7	904.9
EF605153.1	232422	7097.8	5071.0	4058.4	1987.3	2040.7	1366.5
EF603066.1	230664	10025.8	10040.4	5489.5	3455.2	3803.2	2788.4
EF099628.1	184620	5611.2	6255.4	4045.5	6454.9	10670.9	9038.4
EF099133.1	198936	2785.5	3349.5	1147.5	2347.2	2586.6	1743.2
EU507293.1	262054	9117.7	7229.4	4653.2	1391.7	942.1	1330.9
GQ493815.1	568909	6661.6	8195.7	4204.2	5933.8	3963.6	3709.5
EU509193.1	268293	10285.1	7996.9	7710.5	2761.0	4290.0	3482.1
GQ448638.1	544288	7679.6	10074.9	4421.3	5883.3	2116.8	3117.6
EU474260.1	294287	7761.9	6750.6	5096.2	1239.5	479.7	728.9
EF604906.1	234335	2804.8	2827.6	1828.6	1222.0	1449.0	1407.8
EF099038.1	178077	2791.5	3840.6	1277.1	937.4	1100.8	1686.3
EU459692.1	300791	9658.2	8931.2	4153.8	5852.8	6570.7	7577.8
EF603938.1	227678	9781.8	7408.6	4673.3	2278.9	2767.4	1608.8
GQ493480.1	540440	5921.8	4381.9	3606.5	479.5	449.2	625.1
DQ824314.1	194496	10797.3	8672.1	6725.4	2486.1	3833.0	3545.3
GQ491874.1	550767	7870.7	9002.6	5159.9	4609.7	4695.2	4460.1
EU508387.1	270147	8957.6	7089.0	5543.5	1301.0	772.6	1038.8
EF604791.1	232493	8833.1	8813.1	4943.9	3805.1	4481.5	3973.9
GQ492159.1	561627	11224.9	11814.4	6385.2	5810.1	6366.3	5126.5
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EF604911.1	227993	6473.7	5440.5	3507.7	2090.4	2417.0	1842.3
DQ807255.1	187988	4269.3	3339.6	3222.3	1005.0	1860.0	1130.7
GQ493932.1	570491	1938.6	2402.5	2555.9	2128.2	1536.4	1671.4
AY980944.1	121335	12538.3	7120.6	3288.6	2010.3	827.7	1215.2
EU474294.1	294378	8182.5	6794.4	3079.0	1059.5	690.7	990.5
DQ824408.1	199666	9398.6	8772.0	5184.7	1874.3	1668.0	1281.9
EU506595.1	269033	2902.2	3130.7	1810.3	2504.3	2520.3	2613.2
EF099070.1	175442	9969.5	7935.6	5594.0	1882.9	1278.8	1028.5
EF099675.1	187986	8127.4	6907.5	2626.7	2876.3	4052.2	3564.7
EF602794.1	228401	13712.2	13252.4	7746.9	6038.8	7514.9	5565.4
EF099117.1	180918	12498.5	13264.1	9072.8	3388.1	2279.3	2860.7
GQ492323.1	588591	6258.3	5286.2	3499.8	2427.7	757.4	1019.0
DQ803906.1	183355	10511.5	9120.5	7490.7	2941.4	2085.5	1891.4

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EU474311.1 gg_id:295992 western lowland gorilla feces clone GORSD_aaa04a06
EF099272.1 gg_id:196113 mouse cecum clone SWPT2_aaa04h05
GQ493776.1 gg_id:555563 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
EU509172.1 gg_id:269922 cecal contents Mus musculus strain C57BL/6J; MD8 clone MD8_aap45d02
GQ491371.1 gg_id:546571 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
EF602896.1 gg_id:234636 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF603614.1 gg_id:231947 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF602832.1 gg_id:227688 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF605159.1 gg_id:232648 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EU507757.1 gg_id:262819 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_aaa04c08
EU453217.1 gg_id:340374 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N
DQ793746.1 gg_id:183820 human fecal clone RL246_aai76f06
GQ493424.1 gg_id:594106 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
EU506859.1 gg_id:275140 cecal contents Mus musculus strain C57BL/6J; MD21 clone MD21_aar07d09
DQ302110.1 gg_id:153007 Rubromonas marinus gen. sp. nov. first marine representative subdivision one Verru
AF513965.1 gg_id:62479 Verrucomicrobia clone LA1-B30N
EF632724.1 gg_id:239291 Unique microbial contrasting aquatic altitude Andean Altiplano (northern Chile) wate
AB252090.1 gg_id:155636 entrapped Puruogangri ice core clone PIC-D19
DQ015833.1 gg_id:140683 Antarctic lake water clone ELB19-212
AJ318188.1 gg_id:46876 Waste-gas biofilter clone BItii14
GU208316.1 gg_id:546058 Study on Sediment Dongping Lake sediment clone Ser1-21
AB154319.1 gg_id:105709 freshwater clone S9JA-40
FJ437947.1 gg_id:509859 Benthic okenone production Fayetteville New York Green Lake surface sediments 16.
DQ396121.1 gg_id:154817 deep-sea octacoral clone ctg_NISA122
AY770729.1 gg_id:111348 Verrucomicrobia sea urchin Paracentrotus lividus clone PlS48
FJ715972.1 gg_id:558186 Diet- gut microbiota Lumbricus rubellus fingerprinting technique and cloning intestina
FJ437966.1 gg_id:511993 Benthic okenone production Fayetteville New York Green Lake surface sediments 16.
FJ825946.1 gg_id:556103 Succession during spring Sea filtered surface sea water period diatom bloom Yel Sea;
GQ850550.1 gg_id:586112 surface water northern Bering Sea clone u82
EU682496.1 gg_id:517793 Four Primer Sets Detecting Anammox s estuary sediment Mai Po Nature Reserve clo
GU061933.1 gg_id:570181 and function microbial mesoscale eddy perturbations South China Sea clone S-5m-9
NR_026024.1 gg_id:564314 Prosthecobacter fusiformis str. FC4; ATCC 25309
U60012.1 gg_id:1588 Prosthecobacter dejongeii
U60013.1 gg_id:1593 Prosthecobacter vanneervenii str. FC2
EU104166.1 gg_id:319751 Evidence Comamonadaceae determinants settling performance activated sludge clo
FJ612153.1 gg_id:585360 and Biogeochemistry Dongping Lake Ecosystems lake water clone DP3.2.74
EU580493.1 gg_id:556878 Benthic diatoms Constance: functional interactions regarding growth and EPS-secret
AY922120.1 gg_id:113378 farm soil clone AKYH1486
AB305640.1 gg_id:248402 Prosthecobacter sp. str. HAQ-1
EF516716.1 gg_id:225469 grassland soil clone FCPT546
AB297805.1 gg_id:246659 Rubritalea spongiae str. YM21-132

EU474311.1	295992	2093.1	4873.7	3224.1	2150.3	789.1	1027.8
EF099272.1	196113	1928.1	892.1	723.4	1538.3	597.3	1069.4
GQ493776.1	555563	4388.6	4372.0	1574.3	1048.3	869.3	918.6
EU509172.1	269922	6289.6	7168.0	10680.2	4993.4	907.9	2341.1
GQ491371.1	546571	2861.1	1949.2	2334.4	1262.2	301.6	518.9
EF602896.1	234636	9346.9	9525.8	5953.5	3077.8	5040.0	4464.4
EF603614.1	231947	11954.9	8725.8	4552.7	1947.3	2152.6	1650.5
EF602832.1	227688	7004.8	5239.8	3532.6	2168.6	2427.1	1729.7
EF605159.1	232648	11053.1	11126.8	6168.1	5318.1	6304.7	4903.9
EU507757.1	262819	10276.8	8171.5	6267.5	1515.6	1382.0	1300.0
EU453217.1	340374	3158.3	3370.0	2071.6	1333.8	170.6	555.6
DQ793746.1	183820	8331.9	7870.2	5276.3	3826.1	2656.5	2664.1
GQ493424.1	594106	8778.1	10348.1	6682.7	5354.7	5563.0	4963.5
EU506859.1	275140	21629.2	19201.7	18862.1	14838.6	19194.6	16392.6
DQ302110.1	153007	3930.0	3776.9	2088.3	1427.8	437.4	807.4
AF513965.1	62479	9999.8	8084.5	6698.6	3422.7	1900.0	2969.9
EF632724.1	239291	11225.1	9537.9	5612.3	5745.4	1846.9	3088.0
AB252090.1	155636	10576.2	7408.1	2488.5	764.8	90.2	88.5
DQ015833.1	140683	549.1	507.9	516.5	54.0	54.8	92.8
AJ318188.1	46876	3524.5	2234.9	819.4	201.7	99.4	75.2
GU208316.1	546058	78.2	232.8	58.3	114.1	312.0	134.6
AB154319.1	105709	24274.3	15095.9	1880.9	1597.8	607.7	1038.0
FJ437947.1	509859	8229.3	5983.1	5109.2	504.2	1212.3	1044.4
DQ396121.1	154817	449.4	197.6	77.4	148.0	168.7	52.4
AY770729.1	111348	10510.8	8284.6	5685.7	2667.5	645.9	851.2
FJ715972.1	558186	11034.9	7626.1	6534.5	1427.3	206.3	494.9
FJ437966.1	511993	20697.7	17102.9	10852.2	4793.5	2452.5	4007.1
FJ825946.1	556103	4103.4	3475.5	3748.7	1503.6	2606.6	2841.3
GQ850550.1	586112	1150.0	1196.5	2360.4	661.5	2346.2	1039.0
EU682496.1	517793	7919.0	5912.2	7245.8	3733.1	4284.0	4826.9
GU061933.1	570181	2216.4	2071.1	590.6	238.2	285.3	408.6
NR_026024.1	564314	9304.5	15489.9	10474.2	4729.0	4783.6	5260.6
U60012.1	1588	615.7	2323.0	177.7	139.8	525.7	219.3
U60013.1	1593	2413.5	2064.8	1393.0	504.0	1770.9	976.8
EU104166.1	319751	2084.8	3276.5	3621.3	801.5	550.1	666.6
FJ612153.1	585360	4945.7	7403.7	2059.5	1771.5	1544.4	1508.2
EU580493.1	556878	4256.1	5148.8	3326.6	2427.3	1866.7	1326.4
AY922120.1	113378	5420.2	6606.6	4989.1	2139.2	6339.7	4016.3
AB305640.1	248402	3460.7	3688.8	3773.5	1310.7	1800.8	2152.9
EF516716.1	225469	214.4	269.5	200.6	119.0	477.9	473.3
AB297805.1	246659	5524.6	4247.4	3799.5	1456.1	626.8	1180.3

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FJ202109.1 gg_id:344975 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k
AF454310.2 gg_id:63827 Mono lake clone ML316M-1
AM040118.1 gg_id:149984 sandy sediments clone Sylt 22
AJ401121.1 gg_id:39097 Elbe river clone DEV055
EU491625.1 gg_id:258236 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39
EU050932.1 gg_id:238891 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_02_56
FJ437955.1 gg_id:549407 Benthic okenone production Fayetteville New York Green Lake surface sediments 16.
FJ543052.1 gg_id:523568 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone B
FJ437954.1 gg_id:565073 Benthic okenone production Fayetteville New York Green Lake surface sediments 16.
DQ300578.1 gg_id:146066 microbial ocean's interior amplicon single fosmid library pool 10m depth HOT statior
AY344427.1 gg_id:91270 Lake Kauhako 30 m clone K2-30-31
EU236414.1 gg_id:290527 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg92F4
DQ071119.1 gg_id:134657 marine surface water clone SJC3.21
FJ205365.1 gg_id:549372 Prokaryotic deep-sea hydrothermal region East Lau Spreading Centre deep marine se
DQ395400.1 gg_id:155518 deep-sea octacoral clone ctg_BRRAA57
GQ350683.1 gg_id:562414 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
EU491679.1 gg_id:269422 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39
FJ542863.1 gg_id:522575 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone A
AM997555.1 gg_id:562351 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A
AJ441222.1 gg_id:55975 hydrothermal vent polychaete mucous clone P. palm C 85
DQ499289.1 gg_id:159582 acidic cave snottite biofilm clone CV35
X90515.1 gg_id:1596 Verrucomicrobium spinosum
FJ872374.1 gg_id:591617 and metagenomic Verrucomicrobia former agricultural grassland soil rhizosphere clor
AJ441243.1 gg_id:57441 hydrothermal vent polychaete mucous clone P. palm A 54
GQ167324.1 gg_id:585845 Microbial Life -13C Brine Ice-Sealed Antarctic ice-entrained brine 16.5 m Lake Vida c
FJ623333.1 gg_id:510359 Efficient polyhydroxyalkanoates production waste-activated submitted process seque
FJ543001.1 gg_id:526403 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone B
AB240273.1 gg_id:142471 microbial structure rhizosphere Phragmites bulk soil reed bed reactor laboratory clor
GQ259220.1 gg_id:552165 Microbial activities coastal marine sediments and column Svalbard deep water clone
EU135492.1 gg_id:255112 tallgrass prarie soil clone FFCH1244
FJ543027.1 gg_id:525506 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone B
AF234714.1 gg_id:23971 sludge clone A38
GQ452903.1 gg_id:544574 Biodiversity planktonic bottom water Northern Bering Sea clone b31
EU050940.1 gg_id:240964 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_04_25
EU236322.1 gg_id:293293 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg5a1A9
GQ259291.1 gg_id:560235 Microbial activities coastal marine sediments and water column Svalbard deep sedir
AJ401116.1 gg_id:48886 Elbe river clone DEV035
EU245399.1 gg_id:253042 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M1-B1:
AM259830.1 gg_id:211686 Spatial sponge- Mediterranean Tethya aurantium sponge endosome clone TAI-2-28
DQ513026.1 gg_id:161217 Microbial life fluids ridge flank crustal fluid clone FS142-18B-02

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AF454310.2	63827	195.2	223.0	516.2	253.6	83.8	46.1
AM040118.1	149984	60.7	122.2	98.5	77.8	63.1	34.1
AJ401121.1	39097	1504.2	1294.5	447.5	818.8	1150.6	930.9
EU491625.1	258236	6825.3	9832.1	12639.4	7037.5	7962.9	10129.7
EU050932.1	238891	3062.3	2943.2	7241.0	3585.9	2665.2	4325.6
FJ437955.1	549407	5736.8	5901.3	7325.5	6187.2	4646.9	6035.9
FJ543052.1	523568	4323.8	5116.3	2408.8	813.4	1151.7	945.3
FJ437954.1	565073	2739.2	2989.7	1231.7	1068.3	490.5	872.3
DQ300578.1	146066	564.5	439.8	178.5	104.0	98.0	84.8
AY344427.1	91270	8102.3	7755.5	6192.5	7176.5	3286.2	4211.9
EU236414.1	290527	13833.9	13184.3	11625.9	4494.8	7741.9	6674.4
DQ071119.1	134657	1768.1	1255.5	1142.2	979.9	218.6	487.1
FJ205365.1	549372	4929.6	4665.3	936.0	241.9	174.9	256.4
DQ395400.1	155518	3525.3	1579.6	1292.2	2362.3	717.2	731.2
GQ350683.1	562414	1073.6	590.6	257.3	60.6	73.8	59.6
EU491679.1	269422	13224.4	15101.2	12387.4	11085.3	13232.1	14051.8
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AM997555.1	562351	7862.3	7411.3	7294.4	2895.2	2651.4	2495.8
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DQ499289.1	159582	23.3	31.8	28.9	41.6	60.0	22.8
X90515.1	1596	76.2	96.4	59.2	73.8	118.0	135.8
FJ872374.1	591617	16678.1	14711.4	19730.9	14758.6	9388.4	13690.9
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FJ543001.1	526403	7022.8	7739.4	5374.7	2513.5	3744.0	3909.6
AB240273.1	142471	5345.9	4939.2	1982.8	1518.1	685.0	1419.9
GQ259220.1	552165	5474.8	4019.9	5334.4	1890.1	1924.7	1815.0
EU135492.1	255112	2992.6	2253.2	1873.7	272.4	1247.6	938.1
FJ543027.1	525506	13879.6	16356.7	12318.2	10070.2	14130.1	13111.5
AF234714.1	23971	638.0	217.2	143.4	993.0	239.9	468.1
GQ452903.1	544574	8598.0	6630.8	6520.0	3631.8	2441.1	2069.6
EU050940.1	240964	8968.5	8640.8	5146.4	3620.1	2605.4	4429.1
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GQ259291.1	560235	16983.5	14720.3	10799.1	13230.3	5305.1	7014.3
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EU662468.1 gg_id:564160 Productivity- Chemolithoautotrophically Based Sulfidic Karst Systems microbial mat s
AB179534.1 gg_id:102039 sedimentary rock clone MIZ43
GU454934.1 gg_id:519950 Understanding short-chain fatty acids accumulation enhanced alkaline digestion: kir
AB353310.1 gg_id:235366 Rubritalea sp. str. YM29-052
DQ395559.1 gg_id:154124 deep-sea octacoral clone ctg_CGOCA10
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EU491715.1 gg_id:264509 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39
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FJ203597.1 gg_id:346553 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h
DQ329657.1 gg_id:159169 Guerrero Negro hypersaline microbial mat clone 02D2Z31
EF683078.1 gg_id:256408 Eastern Mediterranean atmosphere clone F13_3F_FL
AB300129.1 gg_id:223836 Wide ancient microbial DNAs Quaternary sediments holocene mud sediment clone K
EU385928.1 gg_id:261272 Stratified microbes sediments Core MD05-2902 subseafloor sediment South China S
AY592662.1 gg_id:100607 deep-sea mud volcano clone Napoli-2B-40; BC07-2B-40
FJ228319.1 gg_id:352371 sulfate-reducing enriched during bioremediation experiment sediments (Brandenburg
DQ660867.1 gg_id:256422 DongChuan copper pyrites PRC determined acid mine drainage (AMD) clone DC-II-1
GU205283.1 gg_id:518048 unusual Microbial Venezuelan Tepui (Orthoquartzite) Cave: Dominance Chloroflexal
GQ402706.1 gg_id:575107 Accessing microbial biodiversity and metabolic potential tropical -based approach p
AY326529.1 gg_id:136276 Amazon soil clone 271-2
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FJ625369.1 gg_id:509179 Influence lead contamination on boreal pine forest soil clone HF_NC_30
AY963380.1 gg_id:155824 structures and correlated ecological factors soils two evergreen broad-leaved forests
FJ228289.1 gg_id:318438 sulfate-reducing enriched during bioremediation experiment sediments (Brandenburg
AY425789.1 gg_id:101372 volcanic deposit 1959 clone 1959-5
FJ466032.1 gg_id:535993 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea
FJ202176.1 gg_id:329801 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k
AY328768.1 gg_id:90217 drinking water system simulator clone DSSD70
FJ230920.1 gg_id:308650 under Level Antibiotic Selection Pressures river water clone F46
GQ009527.1 gg_id:500138 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw77
FJ437978.1 gg_id:513669 Benthic okenone production Fayetteville New York Green Lake surface sediments 16.
GU444060.1 gg_id:517876 Effects amendments on fertility and microbial structure cucumber Cucumis sativus L
EU475339.1 gg_id:299049 rock hyrax feces clone RHSD_aaa03d09
GU174155.1 gg_id:594307 Microbial Bactrian camel estimated rumen clone XJC95
EU475271.1 gg_id:295252 rock hyrax feces clone RHSD_aaa02g09
EU385881.1 gg_id:269023 Stratified microbes sediments Core MD05-2902 subseafloor sediment South China S

FJ623345.1	537149	16858.0	20079.2	20562.4	10553.3	7912.5	10876.0
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EU386111.1 gg_id:275107 Biogeographical and microbes sediments on subseafloor sediment South China Sea c
AJ009463.1 gg_id:12396 chlorobenzene-degrading consortium clone SJA-43
EF515388.1 gg_id:224753 Electricigen Enrichment MFC upf microbial fuel cell anode clone 23g04
EU385810.1 gg_id:276009 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S
EU385957.1 gg_id:261806 Stratified microbes sediments Core MD05-2902 subseafloor sediment South China S
EU491440.1 gg_id:267092 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X4 clone
EU491860.1 gg_id:264692 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39
EU734965.1 gg_id:332707 assemblages sediment station DBSE Northern Bering Sea clone 059D21
GU119378.1 gg_id:556653 Threatened Corals Provide Microbial Habitats reef water clone Reef_E10
DQ499326.1 gg_id:159595 acidic cave snottite biofilm clone CV106
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GQ850584.1 gg_id:565629 bottom water northern Bering Sea clone d148
EF687368.1 gg_id:286220 Biogeochemistry iron- and sulfur-precipitating microbial mats (Nile Mediterranean) s
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EF632751.1 gg_id:252204 Unique microbial contrasting aquatic altitude Andean Altiplano (northern Chile) fresh
DQ067004.1 gg_id:131610 Lake Washington sediment clone pLW-70
AF286036.1 gg_id:33594 mercury and PCB contaminated saltmarsh sediment clone LCP-67
GQ433939.1 gg_id:567951 Subseafloor ocean crust microbial observatories: (F-through Osmo Colonization Syst
FJ905749.1 gg_id:511928 s Tonga-Kermadec iron oxide sediments Volcano 1 Tonga Arc clone V1F127b
GQ246340.1 gg_id:547431 Temporal and spatial China North Yel Sea sediments clone Cm1-3
EF687180.1 gg_id:281078 Biogeochemistry iron- and sulfur-precipitating microbial mats (Nile Mediterranean) ir
EU925882.1 gg_id:348335 sediments sediment station DBS1 northern Bering Sea clone 088G2
EF687393.1 gg_id:279693 Biogeochemistry iron- and sulfur-precipitating microbial mats (Nile Mediterranean) s
EF602490.1 gg_id:229278 metabolic phylum Planctomycetes anaerobic sulfide and sulfur-rich spring (Zodletone
EU925892.1 gg_id:324346 sediments sediment station DBS1 northern Bering Sea clone 106G50
AY114311.1 gg_id:63800 anoxic marine sediment clone LD1-PA13
AM086134.1 gg_id:148962 Abundance and archaea mesotrophic Lake Kinneret lake profundal sediment clone
DQ067002.1 gg_id:130730 Lake Washington sediment clone pLW-100
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EU592418.1 gg_id:572696 Seasonal changes Salton Sea hypersaline sediment clone SSS7N
FJ712411.1 gg_id:529621 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) K
DQ811955.1 gg_id:164821 mangrove soil clone MSB-5B4
EU385788.1 gg_id:259376 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S
GQ246450.1 gg_id:586441 Temporal and spatial China North Yel Sea sediments clone Ld1-55
EU385764.1 gg_id:266329 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S
GQ348493.1 gg_id:590821 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
AB177136.1 gg_id:131965 seafloor methane hydrate clone ODP1230B10.05
DQ330720.1 gg_id:159127 Guerrero Negro hypersaline microbial mat clone 08D2Z74
DQ004678.1 gg_id:158922 Microbial Reduce Methane Efflux Mud Volcano Sediments Gulf Cadiz marine hydroc
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o__Sediment-1	f__PRR-10
o__Sediment-1	f__PRR-10
o__Sediment-1	f__PRR-10
o__Sediment-1	f__PRR-10
o__Sediment-1	f__PRR-10
o__Sediment-1	f__PRR-10
o__Sediment-1	f__PRR-10
o__Sediment-1	f__PRR-10
o__Sediment-1	f__unclassified
o__Sediment-1	f__unclassified
o__Sediment-1	f__unclassified
o__Sediment-1	f__unclassified
o__Sediment-1	f__unclassified
o__Sediment-1	f__unclassified
o__Sediment-1	f__unclassified
o__SSS58A	f__unclassified
o__SSS58A	f__unclassified
o__SSS58A	f__unclassified
o__SSS58A	f__unclassified
o__SSS58A	f__unclassified
o__SSS58A	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
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o__wb1_H11	f__unclassified

g__sfC
g__sfD
g__sfA
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g__sfE
g__sfA

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s__unclassified	57817
s__unclassified	58569
s__unclassified	58036
s__unclassified	58814
s__unclassified	58757
s__unclassified	58839
s__unclassified	57786

EU385954.1 gg_id:274093 Stratified microbes sediments Core MD05-2902 subseafloor sediment South China S
EU385924.1 gg_id:259885 Stratified microbes sediments Core MD05-2902 subseafloor sediment South China S
AY114332.1 gg_id:63773 anoxic marine sediment clone LD1-PB19
FJ716267.1 gg_id:563562 Chlorobi dominate shal chemocline Bahamas Sawmill Sink column 10.3 m water dept
FJ712501.1 gg_id:526723 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) K
AM745159.1 gg_id:290797 Impact oil er hydrocarbons on microbial and activity Gulf Mexico cold seep marine s
DQ067003.1 gg_id:131050 Lake Washington sediment clone pLW-69
GQ500696.1 gg_id:556217 Surveys Biofilms and Sediments Mammoth Cave Karst Aquifers Charon's Cascade sa
EU528261.1 gg_id:281647 Seasonal Dynamics Mudflat Mouth Major Kentucky Lake Reservoir Tributary sedime
AJ854267.1 gg_id:211083 Impact flooding on (Populus sp.) trees poplar tree microcosm bulk soil unflooded clor
AJ582051.1 gg_id:94268 soil near uranium mill tailings clone JG36-GS-103
AJ390482.1 gg_id:22777 soil clone PRR-12
FJ479218.1 gg_id:570966 species richness estimates obtained nearly and simulated pyrosequencing-generated
EU135569.1 gg_id:240877 tallgrass prarie soil clone FFCH3040
FJ479480.1 gg_id:540938 species richness estimates obtained nearly and simulated pyrosequencing-generated
EF032778.1 gg_id:185827 cyanobacterial mat in lava cave clone HAVOmat06
FJ478598.1 gg_id:553028 species richness estimates obtained nearly and simulated pyrosequencing-generated
AM991194.1 gg_id:277712 Microbial groundwater and their potential use biomonitoring karst spring water clo
AJ863228.1 gg_id:125819 poplar tree microcosm bulk soil flooded clone 21BSF64
AJ390458.1 gg_id:28793 soil clone PBS-III-30
EU135567.1 gg_id:242108 tallgrass prarie soil clone FFCH1818
EU135572.1 gg_id:243244 tallgrass prarie soil clone FFCH12488
AY921903.1 gg_id:113334 farm soil clone AKYG868
FJ479290.1 gg_id:585878 species richness estimates obtained nearly and simulated pyrosequencing-generated
EU135568.1 gg_id:254604 tallgrass prarie soil clone FFCH18316
AF280852.1 gg_id:45661 bioreactor clone mle1-16
FJ712468.1 gg_id:525404 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) K
FN396645.1 gg_id:541341 constant flux thermophilic cold seabed Arctic marine surface sediment clone s5_0_I
FJ484438.1 gg_id:567353 microbial autonomous rover world's deepest phreatic sinkhole wall biomat El Zacator
EF999394.1 gg_id:247500 Vertical and Methanotrophs Estuarine Sediments Pearl River Estuary sediments 50cn
EF602491.1 gg_id:228206 metabolic phylum Planctomycetes anaerobic sulfide and sulfur-rich spring (Zodletone
DQ521801.1 gg_id:161669 Anaerobic Methane Oxidizing ANME-1b Archaea Hypersaline Sediments Gulf Mexic
AY114325.1 gg_id:63782 anoxic marine sediment clone LD1-PA39
FJ485054.1 gg_id:555839 microbial autonomous rover world's deepest phreatic sinkhole biomat El Zacaton 114
EU491142.1 gg_id:260737 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak
DQ289929.2 gg_id:172911 Microbial Carbon and Nitrogen Cycling Sediments South Atlantic Bight Permeable Sh
FJ485078.1 gg_id:562684 microbial autonomous rover world's deepest phreatic sinkhole biomat El Zacaton 114
FJ902124.1 gg_id:552555 phreatic limestone sinkholes northeastern Mexico orange biomat 8m deep cenote Ca
EF602497.1 gg_id:231901 metabolic phylum Planctomycetes anaerobic sulfide and sulfur-rich spring (Zodletone
EU135574.1 gg_id:248536 tallgrass prarie soil clone FFCH4663
AF317770.1 gg_id:136806 Nullarbor cave clone wb1_H11

EU385954.1	274093	6828.6	7810.2	10739.0	8082.4	10995.0	9353.1
EU385924.1	259885	258.2	596.7	2761.9	1507.7	442.1	1617.3
AY114332.1	63773	37.5	59.8	68.5	88.2	111.0	88.9
FJ716267.1	563562	6458.8	4829.9	4500.7	5029.2	2804.8	3703.8
FJ712501.1	526723	8313.6	13600.5	17305.1	7317.5	10432.7	13235.2
AM745159.1	290797	6181.7	7367.5	3646.0	3811.4	955.7	1324.1
DQ067003.1	131050	135.9	350.9	894.8	173.5	465.8	924.0
GQ500696.1	556217	1416.0	1579.4	2619.9	1108.8	1438.1	1344.5
EU528261.1	281647	10538.4	11939.7	10706.0	7330.5	11111.5	8946.9
AJ854267.1	211083	20.0	53.5	175.5	97.0	75.8	25.5
AJ582051.1	94268	206.2	391.0	1019.4	266.6	171.0	323.2
AJ390482.1	22777	979.3	1596.0	3510.5	403.1	1063.3	1272.9
FJ479218.1	570966	6074.5	6005.8	3260.9	2590.4	4860.8	2786.6
EU135569.1	240877	1745.9	3085.9	7748.3	2299.1	3455.3	4424.8
FJ479480.1	540938	1586.0	3740.7	4400.5	2329.6	2938.1	4294.1
EF032778.1	185827	71.1	254.7	631.2	236.1	134.7	116.0
FJ478598.1	553028	4401.7	8385.6	2489.0	3981.4	1515.7	1567.2
AM991194.1	277712	5640.7	6399.7	5712.6	5316.8	6381.4	7144.5
AJ863228.1	125819	793.0	3180.8	2570.7	701.3	1461.1	1049.8
AJ390458.1	28793	6083.4	7568.7	4726.3	3269.2	7256.3	5474.9
EU135567.1	242108	9367.9	10582.5	8632.1	8080.8	8860.8	8772.7
EU135572.1	243244	4904.8	3768.5	5008.5	1323.3	2091.9	1732.6
AY921903.1	113334	6296.5	8910.4	9785.5	5209.9	11229.6	9476.2
FJ479290.1	585878	1095.0	991.0	3043.0	1996.5	1805.2	1533.3
EU135568.1	254604	161.8	300.1	442.3	406.3	348.6	546.5
AF280852.1	45661	4653.2	4756.0	1926.4	6025.5	2836.5	3729.0
FJ712468.1	525404	4776.6	4359.2	4441.7	6975.0	5452.6	5284.5
FN396645.1	541341	3491.6	2811.6	2702.3	3235.8	463.1	1504.7
FJ484438.1	567353	6469.3	9129.6	8656.2	7944.2	10758.3	10864.0
EF999394.1	247500	2374.0	2292.1	5294.8	1324.7	402.3	481.6
EF602491.1	228206	442.8	182.0	202.3	293.1	105.2	112.3
DQ521801.1	161669	79.4	230.7	302.8	105.3	101.7	98.6
AY114325.1	63782	75.6	192.1	747.9	105.5	77.4	95.9
FJ485054.1	555839	11280.3	13234.8	13281.5	9255.8	12710.2	9605.8
EU491142.1	260737	8118.9	11538.0	6829.1	8787.4	9531.8	6968.1
DQ289929.2	172911	132.3	234.9	261.7	115.9	162.3	291.7
FJ485078.1	562684	4084.7	5013.8	8110.0	3445.2	8827.6	9925.3
FJ902124.1	552555	4521.6	4564.7	3238.4	2840.8	3857.0	3940.7
EF602497.1	231901	179.5	821.3	582.2	155.9	176.8	235.4
EU135574.1	248536	3039.2	5772.0	4567.2	1555.8	3577.2	3884.4
AF317770.1	136806	47.0	91.6	141.5	84.6	90.5	73.7

k__Bacteria	k__Bacteria	p__WS3	c__PRR-12
k__Bacteria	k__Bacteria	p__WS3	c__PRR-12
k__Bacteria	k__Bacteria	p__WS6	c__SC72
k__Bacteria	k__Bacteria	p__WS6	c__SC72
k__Bacteria	k__Bacteria	p__WS6	c__SC72
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k__Bacteria	k__Bacteria	p__WS6	c__unclassified
k__Bacteria	k__Bacteria	p__ZB2	c__unclassified
k__Bacteria	k__Bacteria	p__ZB2	c__unclassified
k__Bacteria	k__Bacteria	p__ZB2	c__unclassified
k__Bacteria	k__Bacteria	p__ZB2	c__unclassified
k__Bacteria	k__Bacteria	p__ZB2	c__unclassified
k__Bacteria	k__Bacteria	p__ZB3	c__Rs-J96
k__Bacteria	k__Bacteria	p__ZB3	c__Rs-J96
k__Bacteria	k__Bacteria	p__ZB3	c__Rs-J96
k__Bacteria	k__Bacteria	p__ZB3	c__Rs-J96
k__Bacteria	k__Bacteria	p__ZB3	c__Rs-J96
k__Bacteria	k__Bacteria	p__ZB3	c__Rs-J96
k__Bacteria	k__Bacteria	p__ZB3	c__unclassified
k__Bacteria	k__Bacteria	p__ZB3	c__unclassified
k__Bacteria	k__Bacteria	p__ZB3	c__unclassified
k__Bacteria	k__Bacteria	p__ZB3	c__unclassified

*OTU intensities in samples with sufficient DNA and PCR product normalized to total ar

o__wb1_H11	f__unclassified
o__wb1_H11	f__unclassified
o__unclassified	f__unclassified
o__WCHB1-15	f__unclassified
o__WCHB1-15	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified

ray intensity

g__sfA
g__sfA
g__sfA
g__sfA
g__sfB
g__sfA
g__sfA
g__sfA
g__sfA
g__sfB
g__sfB
g__sfC
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfB
g__sfC

s__unclassified	57975
s__unclassified	58023
s__unclassified	75085
s__unclassified	75110
s__unclassified	75271
s__unclassified	75446
s__unclassified	75732
s__unclassified	74617
s__unclassified	75567
s__unclassified	74979
s__unclassified	75009
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s__unclassified	50981
s__unclassified	51060
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EU652628.1 gg_id:279399 Seasonal variation microbial Yel Sea sediment clone A8S-81
GU208350.1 gg_id:580844 Study on Sediment Dongping Lake sediment clone Td3-9
GQ347695.1 gg_id:534156 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
EU721779.1 gg_id:550488 microbial production water Alaskan mesothermic petroleum reservoir two methods
GU112185.1 gg_id:590013 library biogas slurry anaerobic fermentation pig manure clone 180
DQ329651.1 gg_id:200370 Guerrero Negro hypersaline microbial mat clone 062DZ75
DQ329650.1 gg_id:201943 Guerrero Negro hypersaline microbial mat clone 062DZ40
FJ719034.1 gg_id:529088 Protozoan grazers alter metabolically active aquifer aquifier sediments clone p03_A0
EF516850.1 gg_id:218322 grassland soil clone FCPS649
AY532578.1 gg_id:106562 uranium-contaminated aquifer clone 1013-28-CG38
EF516449.1 gg_id:225148 grassland soil clone FCPT678
AY850299.1 gg_id:135358 depending on what microbial treatment present soil clone c1
AB089068.1 gg_id:78071 termite gut homogenate clone Rs-J96
EF454817.2 gg_id:218493 termite hindgut clone 290cost002-P3L-449
EF454921.2 gg_id:225715 termite hindgut clone 290cost002-P3L-678
AB192117.1 gg_id:141608 termite gut homogenate clone M2PT2-63
EF454187.2 gg_id:217932 termite hindgut clone 290cost002-P3L-1771
AB188635.1 gg_id:113660 termite gut homogenate clone Pl-P1-21
GQ340261.1 gg_id:572828 Prokaryotic Marathonas Reservoir Greece water column clone A08-131-BAC
DQ520188.1 gg_id:161631 shal China sequences hypertrophic freshwater lake clone ML-9-34.2
DQ300591.1 gg_id:146168 microbial ocean's interior amplicon single fosmid library pool 130m depth HOT static
GQ350069.1 gg_id:588419 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich

EU652628.1	279399	8224.8	12770.8	11429.9	6325.5	10848.3	10664.5
GU208350.1	580844	7273.5	8610.0	7163.1	6356.3	4910.9	7116.1
GQ347695.1	534156	3253.9	3591.5	6401.1	3660.4	4781.5	5048.9
EU721779.1	550488	1754.5	1374.5	1025.5	1506.4	508.6	510.9
GU112185.1	590013	116.6	151.6	896.4	110.1	96.0	104.9
DQ329651.1	200370	7694.4	5508.2	7924.4	7033.7	6600.9	6799.1
DQ329650.1	201943	1997.5	2732.9	8097.9	3146.5	5168.7	6613.2
FJ719034.1	529088	4716.0	3688.5	13120.7	8116.6	612.9	1970.0
EF516850.1	218322	686.0	1297.1	12652.8	2098.7	933.3	810.7
AY532578.1	106562	1971.4	2761.8	7587.8	2288.2	423.7	1783.5
EF516449.1	225148	2781.9	3884.9	8228.4	4426.2	2664.9	3972.3
AY850299.1	135358	165.4	224.7	5922.7	1454.4	226.6	295.0
AB089068.1	78071	4183.8	4232.9	4047.0	4556.4	809.4	1375.0
EF454817.2	218493	12810.8	12474.4	8889.9	9571.6	3559.2	5814.1
EF454921.2	225715	10354.5	10438.4	8197.2	9820.4	8966.0	8348.2
AB192117.1	141608	2060.9	1757.5	2552.8	2956.8	800.6	1213.7
EF454187.2	217932	7636.0	7943.2	9540.6	5041.8	1359.3	4009.2
AB188635.1	113660	10614.7	10613.7	11413.2	8672.1	5445.5	6009.7
GQ340261.1	572828	6270.1	7763.9	6511.1	4298.8	6728.0	6867.2
DQ520188.1	161631	532.6	443.6	540.5	240.3	117.1	203.4
DQ300591.1	146168	4966.3	5557.2	2097.8	3617.8	3414.1	4155.1
GQ350069.1	588419	1967.0	1064.6	3655.7	2376.2	991.4	1372.7