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AM113778.1 gg_id:140432 Lactobacillus graminis str. DSM 20719 AM113
NR_024885.1 gg_id:538781 Paralactobacillus selangorensis str. LMG 17710 NR_02
GQ131183.1 gg_id:426143 Lactobacillus reuteri str. IMAU70067; HS1302 GQ131
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GU125459.1 gg_id:569558 Lactobacillus alimentarius str. IMAU80037 GU125
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EU456468.1 gg_id:322647 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75N EU456
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L23507.1 gg_id:15143 Lactobacillus reuteri L23507
AB362735.1 gg_id:247913 Lactobacillus pentosus str. NRIC 1732 AB362
AY690834.1 gg_id:123663 Lactobacillus nantesii str. Lp33 AY690
EU454131.1 gg_id:316490 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83N EU454
EU456036.1 gg_id:319309 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N EU456
EU456289.1 gg_id:316723 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU456
EU455211.1 gg_id:326968 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU455
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EU457691.1 gg_id:318641 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU457
AM905388.1 gg_id:268188 Lactobacillus fabifermentans str. LMG 24284 AM905
GQ030571.1 gg_id:428757 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw880a05c GQ030
EU508681.1 gg_id:270597 cecal contents Mus musculus strain C57BL/6J; MD4 clone MD4_aap49d02 EU508
EU509957.1 gg_id:261239 cecal contents Mus musculus strain C57BL/6J; WD11 clone WD11_aak24c10 EU509
EU776728.1 gg_id:333200 Lion feces clone LI2_aae49c06 EU776
EF536364.1 gg_id:219489 Lactobacillus casei str. Zhang EF536
EU450898.1 gg_id:344695 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75N EU450

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EU508703.1 gg_id:259236 cecal contents Mus musculus strain C57BL/6J; MD4 clone MD4_aap49f06 EU508
AB362982.1 gg_id:247174 Lactobacillus plantarum str. LQ80 AB362
EU453721.1 gg_id:316608 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83N EU453
E17066.1 gg_id:36168 Lactobacillus sp E17066
EU474925.1 gg_id:299491 red river hog feces clone RRH_aaa04e04 EU474
FJ861112.1 gg_id:554107 Lactobacillus plantarum str. KLDS 1.0628 FJ8611
DQ057436.1 gg_id:133363 str. ii1204 DQ057
AB290830.1 gg_id:514694 Lactobacillus equicursoris str. DI70 AB290
AB362657.1 gg_id:245705 Lactobacillus pentosus str. NRIC 0390 AB362
EU509821.1 gg_id:274002 cecal contents Mus musculus strain C57BL/6J; WD11 clone WD11_aak21f01 EU509
DQ815684.1 gg_id:169512 mouse cecum clone aab44g09 DQ815
EU452068.1 gg_id:332130 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N EU452
EF097607.1 gg_id:189318 mouse cecum clone SWPT20_aaa01b09 EF0976
EU451715.1 gg_id:342038 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83N EU451
GQ275139.1 gg_id:590798 gut symbionts are tightly linked herbivory ants extract single ant clone #163 GQ275
EU507448.1 gg_id:275991 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_2aaa03d04 EU507
EU456851.1 gg_id:306115 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75N EU456
AM697058.1 gg_id:226751 sequencing libraries indoor dust clone BF0002B008 AM697
EU465427.1 gg_id:300717 lion feces clone LI3_aah77b08 EU465
EU451859.1 gg_id:328253 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K79S EU451
EU507501.1 gg_id:259734 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_2aaa04b10 EU507
EU381121.1 gg_id:267051 Lactobacillus reuteri str. ls4 EU381

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AL935261.1 gg_id:80366 Lactobacillus plantarum str. WCFS1 AL9352
FM177140.1 gg_id:338585 Lactobacillus casei str. BL23 FM177
EF098024.1 gg_id:182758 mouse cecum clone SWPT12_aaa04c03 EF0980
EU507563.1 gg_id:267604 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_aaa01b05 EU5075
EU455156.1 gg_id:339840 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU4551
DQ239695.1 gg_id:141655 Lactobacillus plantarum str. L2 DQ239
AB470237.1 gg_id:363520 Lactobacillus sakei str. S2 AB4702
EU460915.1 gg_id:296432 short-beaked echidna feces clone ECH_aai40d09 EU4609
EF097172.1 gg_id:182972 mouse cecum clone SWPT18_aaa02d10 EF0971
EF097176.1 gg_id:190167 mouse cecum clone SWPT18_aaa02e05 EF0971
EU454503.1 gg_id:326900 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU4545
EU510255.1 gg_id:266771 cecal contents Mus musculus strain C57BL/6J; WD3 clone WD3_aak03f06 EU5102
AY204897.1 gg_id:81036 Lactobacillus sakei str. HNSL5c AY2048
EU455625.1 gg_id:315788 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N EU4556
EU451160.1 gg_id:335029 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N EU4511
EF412985.1 gg_id:208876 Lactobacillus gallinarum str. I26 EF4129
EU507280.1 gg_id:272684 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_2aaa01a06 EU5072
FJ405227.1 gg_id:359669 Lactobacillus casei str. ZJ3 FJ4052
AB368904.1 gg_id:282265 Lactobacillus plantarum str. T8-7 AB3689
AF308146.1 gg_id:72717 Lactobacillus thermotolerans str. G 12 AF3081
EU474952.1 gg_id:299475 red river hog feces clone RRH_aaa04g03 EU4749
EU508709.1 gg_id:264123 cecal contents Mus musculus strain C57BL/6J; MD4 clone MD4_aap49g05 EU5087
AB362741.1 gg_id:249746 Lactobacillus pentosus str. NRIC 1753 AB3627
AY735404.1 gg_id:108108 Lactobacillus plantarum str. LP1 AY7354
GQ131182.1 gg_id:376168 Lactobacillus reuteri str. IMAU70066; HS1301 GQ131
DQ015426.1 gg_id:130724 mouse cecum clone M3_h10 DQ015
AB368903.1 gg_id:282170 Lactobacillus plantarum str. T4-5 AB3689
EU074828.1 gg_id:243630 Lactobacillus plantarum str. TC41 EU0748
AB162131.1 gg_id:106519 Lactobacillus nagelii str. NRIC 0559 AB1621
EU457936.1 gg_id:323012 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N EU4579
DQ399353.1 gg_id:154984 Lactobacillus paracasei str. SFCB2-4 DQ399
EU453809.1 gg_id:318211 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU4538
GQ461596.1 gg_id:593464 Lactobacillus plantarum str. K25 GQ461
EU457051.1 gg_id:317830 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU4570
EU451427.1 gg_id:354114 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU4514
GQ156407.1 gg_id:537937 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
EU456062.1 gg_id:308210 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N EU4560
AB362731.1 gg_id:255682 Lactobacillus sakei str. NRIC 1609 AB3627
GU177634.1 gg_id:578809 Lactobacillus casei str. C-1 GU177
EU474892.1 gg_id:287698 red river hog feces clone RRH_aaa04e08 EU4748

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EU453930.1 gg_id:328325 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75 EU453
EU453867.1 gg_id:313722 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75 EU453
EU457601.1 gg_id:337406 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H74 EU457
EU455334.1 gg_id:317894 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU455
NR_029084.1 gg_id:576663 Lactobacillus gastricus str. Kx156A7; LMG 22113T; DSM 16045T NR_02
AB362607.1 gg_id:244469 Lactobacillus sakei str. NRIC 0126 AB362
EU510005.1 gg_id:274605 cecal contents Mus musculus strain C57BL/6J; WD1 clone WD1_aaf15e11 EU510
GU369759.1 gg_id:524305 Lactobacillus plantarum str. YM-4-5 GU369
EU452893.1 gg_id:303591 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU452
GQ155548.1 gg_id:512953 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
AB362667.1 gg_id:258139 Lactobacillus pentosus str. NRIC 0403 AB362
GQ231436.1 gg_id:588182 Lactobacillus reuteri str. DSPV 002C GQ231
GU299083.1 gg_id:534440 Lactobacillus casei str. NQ2-2 GU299
DQ815681.1 gg_id:166336 mouse cecum clone aab44g06 DQ815
AJ965487.1 gg_id:126988 Lactobacillus arizonensis str. DSM 13273 AJ9654
AB239468.1 gg_id:141834 Lactobacillus casei str. CP1-13 AB239
EU457018.1 gg_id:330111 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77 EU457
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GQ155587.1 gg_id:513479 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EF096038.1 gg_id:187066 mouse cecum clone lean2_aaa02e07 EF0960
AB303848.1 gg_id:257805 Monitoring Pickling Bed Fermented Rice Bran Which Dominated S-Growing Lactobac AB3038
EU439433.1 gg_id:267700 Lactobacillus plantarum str. 1L48P35 EU439
EF097557.1 gg_id:196803 mouse cecum clone SWPT19_aaa04c12 EF0975
DQ815682.1 gg_id:167719 mouse cecum clone aab44g07 DQ815
DQ015553.1 gg_id:135934 mouse cecum clone M3_e03_2 DQ015
EU460783.1 gg_id:296454 short-beaked echidna feces clone ECH_aai37h09 EU460
EU454204.1 gg_id:347044 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74 EU454
FJ678780.1 gg_id:521424 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6787
EU465367.1 gg_id:302089 lion feces clone LI3_aah76b05 EU465
AB332024.2 gg_id:246232 Lactobacillus nodaensis str. IZ4B AB332
EU526816.1 gg_id:276202 Lactobacillus plantarum str. Z6 EU526
GQ900606.1 gg_id:550314 Lactobacillus plantarum str. F34 GQ900
EU505359.1 gg_id:276978 cecal contents Mus musculus strain C57BL/6J; myd4 clone myd4_aaa03b09 EU505
GQ131153.1 gg_id:385174 Lactobacillus casei str. IMAU70037; BM10307 GQ131
AJ242968.1 gg_id:15128 Lactobacillus gallinarum str. ATCC 33199 AJ2429

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EU161635.1 gg_id:239571 Lactobacillus murinus str. LR EU1616
GU191837.1 gg_id:581162 Lactobacillus reuteri str. BR11 GU191
AB303841.1 gg_id:236486 Lactobacillus acetotolerans str. JCM 3825 AB3038
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EU504504.1 gg_id:276180 cecal contents Mus musculus strain C57BL/6J; myd1 clone myd1_aaa01e09 EU5045
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EU331307.1 gg_id:244766 Pediococcus damnosus str. Bpe233 EU3313
AB258357.1 gg_id:158048 Pediococcus siamensis MCH3-2 AB2583
GU125433.1 gg_id:560139 Pediococcus ethanolidurans str. IMAU80011 GU125
AJ271383.1 gg_id:19307 Pediococcus inopinatus str. DSM 20285 AJ2713
EU331259.1 gg_id:239673 Pediococcus parvulus str. Bpe301 EU3312
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AB018215.1 gg_id:15152 Pediococcus pentosaceus str. LS 5 AB0182
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EU483113.1 gg_id:265290 Pediococcus pentosaceus str. MY-800 EU4831
EU878171.1 gg_id:328309 Pediococcus pentosaceus str. SH 740 EU8781
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FJ378890.1 gg_id:359769 Pediococcus pentosaceus str. B-38 FJ3788
AJ621555.1 gg_id:113414 Pediococcus claussenii str. DSM 14800 AJ6215
FJ405228.1 gg_id:366574 Pediococcus claussenii str. ZJ5 FJ4052
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AM279764.2 gg_id:161185 Lactobacillus plantarum 7.8.2 AM279

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EU460868.1 gg_id:296482 short-beaked echidna feces clone ECH_aai39f03 EU460
AB240455.1 gg_id:145715 Lactobacillus halophilus str. KG34 AB240
EU460734.1 gg_id:303093 short-beaked echidna feces clone ECH_aai37b12 EU460
EU460924.1 gg_id:300991 short-beaked echidna feces clone ECH_aai40e11 EU460
EU626008.1 gg_id:277639 Lactobacillus coryniformis str. KLDS 1.0723 EU626
EU460820.1 gg_id:297646 short-beaked echidna feces clone ECH_aai38g03 EU460
AF360737.1 gg_id:67685 Leuconostoc fructosum str. DSM 20349 AF360
DQ837629.1 gg_id:163654 structures honeybee intestines and their response insecticidal proteins gut clone HB DQ837
AY169967.1 gg_id:101369 Leuconostoc pseudoficulneum str. LC51 AY169
AM157423.1 gg_id:141780 Leuconostoc citreum mother C3 AM157
AM157430.1 gg_id:143322 Leuconostoc citreum mother C4 AM157
GQ392137.1 gg_id:553432 Leuconostoc citreum str. CJGN34 GQ392
FJ040200.1 gg_id:535439 Leuconostoc citreum str. C16 FJ0402
EU074846.1 gg_id:245787 Leuconostoc citreum str. TM319 EU074
AM157444.1 gg_id:141773 Leuconostoc citreum mother V4 AM157
AM600682.1 gg_id:226092 Leuconostoc holzapfelii str. LMG 23990 = BFE 700 AM600
AY929286.1 gg_id:113747 Leuconostoc fallax str. BFE 6749 AY929
EU074837.1 gg_id:240308 Leuconostoc mesenteroides str. CM160 EU074
GQ351321.1 gg_id:533637 Leuconostoc mesenteroides str. OR2P-2 GQ351
EU074843.1 gg_id:249310 Leuconostoc mesenteroides str. AC318 EU074
FJ040199.1 gg_id:550853 Leuconostoc mesenteroides str. C12 FJ0401
GQ915096.1 gg_id:539665 Leuconostoc mesenteroides str. AaD8 GQ915
FJ215674.1 gg_id:312330 Leuconostoc mesenteroides str. IMAU60052 FJ2156
EU074838.1 gg_id:238676 Leuconostoc mesenteroides str. PC216 EU074
EU074836.1 gg_id:252222 Leuconostoc mesenteroides str. CM135 EU074
EU074841.1 gg_id:247929 Leuconostoc mesenteroides str. CC317 EU074
EU177638.1 gg_id:341233 Leuconostoc mesenteroides str. ANN12 EU177
EU074839.1 gg_id:248008 Leuconostoc mesenteroides str. PM249 EU074
AF515228.1 gg_id:64385 Leuconostoc pseudomesenteroides str. RO1 AF515
EU177631.1 gg_id:337944 Leuconostoc pseudomesenteroides str. NS28 EU177
EU074840.1 gg_id:253688 Leuconostoc mesenteroides str. PM141 EU074
EU177632.1 gg_id:345546 Leuconostoc pseudomesenteroides str. NS33 EU177
FJ015056.1 gg_id:315407 Leuconostoc pseudomesenteroides str. FL6 FJ0150
EU337117.1 gg_id:546379 Leuconostoc pseudomesenteroides str. MC EU337
EF121354.2 gg_id:249922 Leuconostoc citreum str. GJ7 EF1213
EU574896.1 gg_id:267454 Leuconostoc mesenteroides str. NRRL B-1355 EU574
FJ749310.1 gg_id:547101 Leuconostoc lactis str. IMAU40034; QH4-6-2 FJ7493
FJ480207.1 gg_id:592022 Leuconostoc mesenteroides str. WCP907 FJ4802
AB362723.1 gg_id:238348 Leuconostoc citreum str. NRIC 1581 AB362
AB362719.1 gg_id:244448 Leuconostoc garlicum str. NRIC 1577 AB362
AB470239.1 gg_id:365285 Leuconostoc gelidum str. GD AB470

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AM940225.1 gg_id:349734 Leuconostoc palmae str. TMW 2.694 AM940
AB362720.1 gg_id:252701 Leuconostoc garlicum str. NRIC 1578 AB3627
AF111948.1 gg_id:15110 Leuconostoc citreum str. ATCC49370; KCTC3526 AF1119
AB362722.1 gg_id:256844 Leuconostoc garlicum str. NRIC 1580 AB3627
EU463822.1 gg_id:290159 Seba's short-tailed bat feces clone bat_aaj05d07 EU4638
AY165007.4 gg_id:75964 Leuconostoc citreum str. CY2 AY1650
AB022921.1 gg_id:24935 Leuconostoc gelidum str. NRIC 1778 AB0229
AB362682.1 gg_id:246692 Leuconostoc mesenteroides str. NRIC 0587 AB3626
AB470240.1 gg_id:363305 Leuconostoc gasicomitatum str. GC AB4702
AB054806.1 gg_id:43827 Oenococcus oeni str. 95 St.Mer-2-4 AB0548
CP000411.1 gg_id:175948 Oenococcus oeni str. PSU-1 CP0004
FM878590.1 gg_id:571983 Oenococcus oeni str. LA126 FM878
AB221475.1 gg_id:159865 Oenococcus kitaharae str. NRIC 0645 AB2214
GU138518.1 gg_id:568005 Weissella confusa str. LSBM3-1 GU138
AB022926.1 gg_id:45087 Weissella halotolerans str. NRIC 1627 AB0229
EU465515.1 gg_id:292431 lion feces clone LI3_aah78f11 EU4655
AB022922.1 gg_id:43687 Weissella kandleri str. NRIC 1628 AB0229
AM157446.1 gg_id:144619 Weissella confusa mother V4 AM157
EU855224.1 gg_id:352468 Weissella paramesenteroides str. CTSPL5 EU8552
FJ193714.1 gg_id:346360 Genetic inventory 'KSC-Astrotek' spacecraft assembly clean room during DAWN missi FJ1937
AM157435.1 gg_id:142903 Weissella cibaria mother C4 AM157
AB015642.1 gg_id:15084 Weissella hellenica str. DS-12 AB0156
EU439435.2 gg_id:560064 Weissella sp. str. 2L24P13 EU4394
AM882997.1 gg_id:241383 Weissella ghanensis str. LMG 24286 AM882
EU177641.1 gg_id:320990 Weissella paramesenteroides str. NS74 EU1776
EU869290.1 gg_id:331921 Weissella sp. str. JZ-1L EU8692
DQ294962.1 gg_id:143027 Weissella cibaria str. Uga57 DQ294
EU074829.1 gg_id:251397 Weissella cibaria str. BC48 EU0748
DQ294964.1 gg_id:142786 Weissella cibaria str. Uga69 DQ294
AF477495.1 gg_id:23573 Weissella confusa str. PL9001 AF4774
AF477498.1 gg_id:36439 Lactobacillus fermentum str. PL9005 AF4774
AF312874.1 gg_id:22775 Weissella cibaria str. CHJ3 AF3128
FJ429974.1 gg_id:565622 Weissella confusa str. C3-7 FJ4299
GU369772.1 gg_id:530233 Weissella confusa str. JS-7-1 GU369
FJ263453.1 gg_id:366705 Weissella confusa str. XW1 FJ2634
AB257595.1 gg_id:158275 Weissella salipiscis str. FS55-1 AB2575
X95981.1 gg_id:15090 Weissella hellenica str. NCFB 2973 X95981
FJ654456.1 gg_id:537058 Weissella hellenica str. 138 FJ6544
FJ654465.1 gg_id:511014 Weissella hellenica str. 1507 FJ6544
DQ883229.1 gg_id:163888 Weissella koreensis str. 405 DQ883
EU180607.1 gg_id:335281 Weissella soli str. NS26 EU1806

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AB023236.1 gg_id:33970 Weissella viridescens str. NRIC 1536 AB023
EU775634.1 gg_id:315664 Hedgehog feces clone HH_d06 EU775
EU777721.1 gg_id:330069 Polar bear feces clone PB1_aai28f10 EU777
EU460570.1 gg_id:298506 polar bear feces clone PB2_aai22g09 EU460
EU460926.1 gg_id:299075 short-beaked echidna feces clone ECH_aai40f04 EU460
EU791208.1 gg_id:455671 Enteric Defensins are Essential Regulators Intestinal Microbial Ecology MMP7++ mou EU791
AB018211.1 gg_id:42931 Lactococcus garvieae str. E 1 AB018
EU460718.1 gg_id:302924 polar bear feces clone PB2_aai24h07 EU460
EU467542.1 gg_id:296207 southern three-banded armadillo feces clone arma_f03 EU467
EU775705.1 gg_id:333803 Hedgehog feces clone HH_aai36e07 EU775
EU460397.1 gg_id:302882 polar bear feces clone PB1_aai28a07 EU460
AF283499.1 gg_id:45250 Lactococcus garvieae AF283
EU775674.1 gg_id:336969 Hedgehog feces clone HH_d10 EU775
EU460462.1 gg_id:293407 polar bear feces clone PB2_aai21b11 EU460
EU458153.1 gg_id:297489 North American black bear feces clone BB2_f02 EU458
AB244446.1 gg_id:257338 Lactococcus garvieae str. An10-2 AB244
EU460864.1 gg_id:292600 short-beaked echidna feces clone ECH_aai39e07 EU460
DQ223877.1 gg_id:173259 Lactococcus sp. str. RT5 DQ223
DQ223876.1 gg_id:167936 Lactococcus lactis str. RT4 DQ223
AM490366.1 gg_id:203331 Lactococcus lactis str. C22 AM490
AM157445.1 gg_id:141784 Lactococcus lactis mother V4 AM157
AJ488176.1 gg_id:66046 Lactococcus lactis str. 04 AJ488
AY348313.1 gg_id:93048 Lactococcus lactis str. Akira2 AY348
AM157424.1 gg_id:141720 Lactococcus lactis mother C3 AM157
EU203156.1 gg_id:251182 Lactococcus lactis str. WH11-1 EU203
GQ337889.1 gg_id:594031 Lactococcus lactis str. KLDS4.0352 GQ337
AY762104.1 gg_id:108349 Lactococcus sp. str. MKRL19 AY762
AJ133479.1 gg_id:69992 Lactococcus sp. TmLO5 AJ1334
EU073957.2 gg_id:240865 Lactococcus sp. Da-18 EU073
AB234513.1 gg_id:150304 termite gut homogenate clone MgMjW-44 AB234
AJ439543.2 gg_id:110020 Lactovum miscens str. anNAG3 AJ4395
DQ856510.1 gg_id:253776 intestinal microflora Chinese mitten crab (Eriocheir sinensis) clone C1N DQ856
AB089063.1 gg_id:78015 termite gut homogenate clone Rs-C68 sp. AB089
DQ343754.1 gg_id:146404 Lactococcus piscium str. CCUG 32732 DQ343
EF204369.1 gg_id:201186 Lactococcus sp. G23 EF2043
EU460490.1 gg_id:294254 polar bear feces clone PB2_aai21f02 EU460
AB089061.2 gg_id:78223 termite gut homogenate clone Rs-B70 AB089
AY571411.1 gg_id:114538 termite gut clone RsaM9 AY5714
EF694029.1 gg_id:256029 Lactococcus plantarum str. DSM 20686 EF6940
GQ502570.1 gg_id:555286 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf4- GQ502
AM944736.1 gg_id:270649 Enterococcus sp. str. UNK1 AM944

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EU689104.1 gg_id:564529 Lactococcus sp. str. YM05290 EU689
NZ_AAJO01000148.1 gg_id:140424 Streptococcus agalactiae str. 18RS21 NZ_AA
AAJO01000006.1 gg_id:139711 Streptococcus agalactiae str. 18RS21 AAJO0
EU473184.1 gg_id:300948 giant panda feces clone GP_1aaa04g12 EU473
AB002519.1 gg_id:15456 Streptococcus alactolyticus str. ATCC 43492 AB002
EU473340.1 gg_id:289833 giant panda feces clone GP_1aaa04h11 EU473
AB355611.1 gg_id:240886 Streptococcus anginosus str. IMU103 AB355
AY691534.1 gg_id:107288 Streptococcus anginosus str. ChDC YA1 AY691
AY986761.1 gg_id:115190 Streptococcus anginosus str. ChDC YA2 AY986
EU075058.1 gg_id:239570 Streptococcus canis str. 3-35MP EU075
FJ557869.1 gg_id:525128 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5578
FJ557854.1 gg_id:527756 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5578
AB182324.1 gg_id:169991 Streptococcus orisuis str. NUM 1001 AB182
AJ853835.1 gg_id:108737 Streptococcus cristatus str. PD01A5 AJ8538
AY281090.1 gg_id:90588 Streptococcus cristatus str. ATCC 49999 AY281
AB008313.1 gg_id:15567 Streptococcus cristatus str. NCTC12479 AB008
NR_029015.1 gg_id:589575 Streptococcus devriesei str. CCUG 47156 NR_02
DQ303185.1 gg_id:167230 Streptococcus didelphis str. ATCC 700828 DQ303
AF176107.1 gg_id:15363 Streptococcus didelphis str. 95-3349-1 AF176
AY942561.1 gg_id:133561 Streptococcus downei str. ChDC YD1 AY9425
AY942564.1 gg_id:137388 Streptococcus downei str. ChDC YD4 AY9425
EF405993.1 gg_id:219796 Streptococcus subsp. equi str. Bd 5895/99 EF4059
AB002516.1 gg_id:15355 Streptococcus equi subsp. zooepidemicus str. ATCC 43079 AB002
AB002515.1 gg_id:15354 Streptococcus subsp. equi str. ATCC 33398 NCTC 9682 AB002
AJ420197.1 gg_id:39498 Streptococcus ferus str. 8S1 AJ4201
U87827.1 gg_id:15564 aortic heart valve patient with endocarditis clone v2 U8782
AJ427479.1 gg_id:36023 Streptococcus gordonii str. DL1 AJ4274
AB355602.1 gg_id:243837 Streptococcus gordonii str. NUK38 AB355
AB002518.1 gg_id:15428 Streptococcus hyointestinalis str. ATCC 49169 DSM 20770 AB002
DQ462420.1 gg_id:203615 Streptococcus icataluri LS0706-05 DQ462
GQ050656.1 gg_id:398932 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu488f1 GQ050
GQ115486.1 gg_id:393307 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw686c07 GQ115
EU156759.1 gg_id:331335 Streptococcus infantis str. CCUG 39817 EU156
AB008315.1 gg_id:15551 Streptococcus infantis str. GTC849 AB008
GQ077246.1 gg_id:395569 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw115 GQ077
EU620580.1 gg_id:279591 Streptococcus iniae str. CMS003 EU620
EU467794.1 gg_id:287876 North American black bear feces clone BB1_b04 EU467
AB002482.1 gg_id:15458 Streptococcus bovis str.ATCC 33317 AB002
AJ297214.1 gg_id:30971 Streptococcus luteciae str. NEM 760 AJ2972
EU461863.1 gg_id:299806 white-faced saki feces clone Saki_aaj62e05 EU461
EU467738.1 gg_id:295347 North American black bear feces clone BB1_a07 EU467

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

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

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s__Streptococcus salivarius	44274

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D38483.1 gg_id:15561 Streptococcus gordonii str. NCTC7865 D3848
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AY053482.1 gg_id:17851 gas hydrate clone AT425_EubB10 AY053
AY281076.1 gg_id:88205 Streptococcus mitis str. ATCC 15914 AY281
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GQ088993.1 gg_id:454354 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw3 GQ088
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GQ000464.1 gg_id:469029 Topographical and Temporal Human Skin Microbiome skin palm clone nbu103h07c1 GQ000
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GQ074369.1 gg_id:392384 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw162b GQ074
GQ026868.1 gg_id:426596 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ026
GQ074391.1 gg_id:392084 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw162c GQ074
NC_011375.1 gg_id:314875 Streptococcus pyogenes NZ131 str. NZ131; ATCC BAA-1633 NC_01
CP000829.1 gg_id:319062 Streptococcus pyogenes NZ131 str. NZ131; ATCC BAA-1633 CP000
AM157451.1 gg_id:143051 Streptococcus salivarius mother V5 AM157

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GQ032967.1 gg_id:401843 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ032
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GQ076850.1 gg_id:445671 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw1154 GQ076
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GQ019319.1 gg_id:490350 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor GQ019
GQ041356.1 gg_id:452091 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ041
FJ154805.1 gg_id:545804 Streptococcus vestibularis str. CCRI 17387 FJ1548
GQ076777.1 gg_id:376055 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw1153 GQ076
GQ073340.1 gg_id:405098 Topographical and Temporal Human Skin Microbiome skin palm clone nbw207h04c1 GQ073
EF463056.1 gg_id:219466 Streptococcus salivarius str. RKA2 EF463C
GQ073226.1 gg_id:417324 Topographical and Temporal Human Skin Microbiome skin palm clone nbw206e07c1 GQ073
GQ076892.1 gg_id:379619 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw1154 GQ076
EF463059.1 gg_id:224298 Streptococcus salivarius str. RKA5 EF463C
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GQ073204.1 gg_id:424160 Topographical and Temporal Human Skin Microbiome skin palm clone nbw206c08c1 GQ073
GQ073389.1 gg_id:452062 Topographical and Temporal Human Skin Microbiome skin palm clone nbw208e03c1 GQ073
GQ032174.1 gg_id:418733 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw9 GQ032
GQ073349.1 gg_id:468290 Topographical and Temporal Human Skin Microbiome skin palm clone nbw208a01c1 GQ073
GQ057898.1 gg_id:393890 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw1 GQ057
GQ027365.1 gg_id:396642 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw9 GQ027
GQ007920.1 gg_id:501744 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw1 GQ007
AM157419.1 gg_id:141989 Streptococcus salivarius mother C3 AM157
GQ032472.1 gg_id:384506 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw9 GQ032
GQ019505.1 gg_id:490163 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu190g GQ019
GQ073065.1 gg_id:378696 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw204f09c GQ073
GQ088234.1 gg_id:440158 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw1 GQ088
GQ076935.1 gg_id:386247 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw1155 GQ076
DQ801238.1 gg_id:190678 human fecal clone RL116_aaf02c02 DQ801
GQ073241.1 gg_id:451593 Topographical and Temporal Human Skin Microbiome skin palm clone nbw206g03c1 GQ073
GQ019428.1 gg_id:490239 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu189h GQ019
GQ073128.1 gg_id:374338 Topographical and Temporal Human Skin Microbiome skin palm clone nbw205d10c1 GQ073
GQ073291.1 gg_id:376264 Topographical and Temporal Human Skin Microbiome skin palm clone nbw207c12c1 GQ073
GQ057595.1 gg_id:413021 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ057
FJ154803.1 gg_id:549813 Streptococcus salivarius str. CCUG 7215 FJ1548
GQ041484.1 gg_id:426958 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ041
FJ363912.1 gg_id:358274 feces adult twins and mothers; TS14 clone TS14_a04g10 FJ3639
GQ019436.1 gg_id:490234 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu190a GQ019

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GQ027302.1 gg_id:380914 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw! GQ027
FJ365649.1 gg_id:367692 feces adult twins and mothers; TS21 clone TS21_a01d05 FJ3656
GQ995676.1 gg_id:548391 Streptococcus sanguinis str. Hanzhong-A2 GQ995
CP000387.1 gg_id:210400 Streptococcus sanguinis str. SK36 CP000
AB002524.1 gg_id:38234 Streptococcus sanguinis str. ATCC 10556 AB002
U87828.1 gg_id:15570 aortic heart valve patient with endocarditis clone v3 U8782
U87829.1 gg_id:15571 aortic heart valve patient with endocarditis clone v5 U8782
NC_009009.1 gg_id:205756 Streptococcus sanguinis str. SK36 NC_00
NR_028833.1 gg_id:593803 Streptococcus sinensis str. HKU4; DSM 14990 NR_02
AY691533.1 gg_id:107142 Streptococcus sobrinus str. ChDC YS1 AY691
DQ677799.1 gg_id:170824 Streptococcus sobrinus str. ChDC YS13; 40125 DQ677
DQ677794.1 gg_id:167103 Streptococcus sobrinus str. ChDC YS206; PD1017 DQ677
AJ871181.1 gg_id:110876 Streptococcus sp. 1040-02B AJ8711
AF009484.1 gg_id:15515 Streptococcus suis str. 22083 AF009
DQ113766.1 gg_id:136603 dog jejunum clone J5-01 DQ113
GQ101022.1 gg_id:380857 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw48 GQ101
GQ007632.1 gg_id:502032 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ007
X68418.1 gg_id:15434 Streptococcus thermophilus str. DSM 20617 X6841
GQ104143.1 gg_id:374288 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw563g1 GQ104
GQ058136.1 gg_id:376543 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ058
GQ155489.1 gg_id:577395 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ033163.1 gg_id:406397 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ033
GQ101185.1 gg_id:408208 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw49 GQ101
GQ031863.1 gg_id:372703 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ031
GQ021918.1 gg_id:487750 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ021
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GQ052795.1 gg_id:404186 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ052
GQ057721.1 gg_id:447223 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ057
GQ031888.1 gg_id:374845 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ031
GQ045675.1 gg_id:449085 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw! GQ045
GQ052810.1 gg_id:451499 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ052
FJ363751.1 gg_id:357648 feces adult twins and mothers; TS14 clone TS14_a02h07 FJ3637
DQ327131.1 gg_id:148345 Metagenomic gut microbiome healthy human stool clone E649 DQ327
DQ176426.1 gg_id:139353 Streptococcus thermophilus DQ176
GU195648.1 gg_id:578630 Streptococcus thermophilus str. M4 GU195
GQ058082.1 gg_id:392901 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ058
GQ069727.1 gg_id:406513 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ069
NC_008532.1 gg_id:197884 Streptococcus thermophilus str. LMD-9 NC_00
GQ052788.1 gg_id:423913 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ052

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

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EU156788.1 gg_id:349229 Streptococcus pseudopneumoniae str. CCUG 50870 EU156
EU458191.1 gg_id:288025 North American black bear feces clone BB2_d10_1 EU458
AJ871184.1 gg_id:110043 Streptococcus sp. 1606-02B AJ8711
GQ156276.1 gg_id:511755 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
EU458233.1 gg_id:300876 North American black bear feces clone BB2_c02_2 EU458
EU463426.1 gg_id:295495 domesticated horse feces clone horsem_aai93f11 EU463
GQ072611.1 gg_id:398533 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw19 GQ072
GQ069087.1 gg_id:426030 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ069
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EU461988.1 gg_id:300951 white-faced saki feces clone Saki_aaj64h04 EU461
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GQ072785.1 gg_id:440026 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw201b07 GQ072
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AY525794.1 gg_id:111799 Streptococcus pneumoniae str. VN_O27 AY525
EU461851.1 gg_id:289861 white-faced saki feces clone Saki_aaj62c04 EU461
EU458245.1 gg_id:288170 North American black bear feces clone BB2_f04_2 EU458
EU467179.1 gg_id:297263 white-faced saki feces clone Saki_b01 EU467
GQ105172.1 gg_id:446697 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ105
GQ110037.1 gg_id:465867 Topographical and Temporal Human Skin Microbiome skin back clone nbw658a08c1 GQ110
EU458137.1 gg_id:299774 North American black bear feces clone BB2_c11 EU458
GQ032551.1 gg_id:392746 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ032
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FJ154804.1 gg_id:561563 Streptococcus salivarius str. K12 FJ1548

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EU467758.1 gg_id:291579 North American black bear feces clone BB1_d10 EU4677
EU458258.1 gg_id:299395 North American black bear feces clone BB2_h04_1 EU4582
GQ086143.1 gg_id:389175 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ086
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FJ679590.1 gg_id:525580 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6795
EU483251.1 gg_id:265868 Streptococcus sp. str. 24180-02 EU4832
EU467842.1 gg_id:291050 North American black bear feces clone BB1_c02 EU4678
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FJ558046.1 gg_id:525966 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5580
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EU461911.1 gg_id:303202 white-faced saki feces clone Saki_aaj63e11 EU4619

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EU467774.1 gg_id:302237 North American black bear feces clone BB1_f09 EU467
FJ673292.1 gg_id:520118 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6732
EU458129.1 gg_id:299791 North American black bear feces clone BB2_c01 EU458
EU775692.1 gg_id:343045 Hedgehog feces clone HH_d11 EU775
EU461849.1 gg_id:294466 white-faced saki feces clone Saki_aaj62b10 EU461
EU467158.1 gg_id:297683 white-faced saki feces clone Saki_c09 EU467
EU458133.1 gg_id:302604 North American black bear feces clone BB2_c05 EU458
GQ058671.1 gg_id:465504 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbu58 GQ058
EU458141.1 gg_id:294837 North American black bear feces clone BB2_d06 EU458
EU461875.1 gg_id:291824 white-faced saki feces clone Saki_aaj62g04 EU461
EU461834.1 gg_id:301274 white-faced saki feces clone Saki_aaj61h04 EU461
FJ680001.1 gg_id:521890 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6800
AB038371.1 gg_id:42006 Streptococcus sp. str. PSH2 AB038
AY525792.1 gg_id:111812 Streptococcus pneumoniae str. SI_P7 AY525
EU458282.1 gg_id:295664 North American black bear feces clone BB2_d02_2 EU458
GQ081650.1 gg_id:437407 Topographical and Temporal Human Skin Microbiome skin back clone nbw1197g04c GQ081
EU458172.1 gg_id:289129 North American black bear feces clone BB2_h11 EU458
AJ608938.1 gg_id:107158 Streptococcus pneumoniae str. 101 AJ6089
FJ823146.1 gg_id:548508 Streptococcus infantis str. ToTI FJ8231
EU458250.1 gg_id:288235 North American black bear feces clone BB2_g02_2 EU458
EU461821.1 gg_id:288580 white-faced saki feces clone Saki_aaj61f03 EU461
EU774846.1 gg_id:304567 Short-beaked Echidna feces clone ECH_aai39a01 EU774
GQ073297.1 gg_id:451731 Topographical and Temporal Human Skin Microbiome skin palm clone nbw207d08c GQ073
EU467802.1 gg_id:299936 North American black bear feces clone BB1_d04_1 EU467
FJ679627.1 gg_id:522003 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6796
EU458256.1 gg_id:295491 North American black bear feces clone BB2_h01_1 EU458
AM774229.1 gg_id:256872 Streptococcus sp. str. 1355-03 AM774
EU461915.1 gg_id:300834 white-faced saki feces clone Saki_aaj63f06 EU461
EU461938.1 gg_id:295646 white-faced saki feces clone Saki_aaj64b02 EU461
EU458276.1 gg_id:294389 North American black bear feces clone BB2_c06_2 EU458
GQ101337.1 gg_id:461282 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw493h GQ101
EU467854.1 gg_id:293702 North American black bear feces clone BB1_d12_2 EU467
EU458163.1 gg_id:288669 North American black bear feces clone BB2_g05 EU458
EU779414.1 gg_id:333660 Grevy's Zebra feces clone GZ_aaa01g10 EU779
GQ154714.1 gg_id:578309 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
FJ675847.1 gg_id:518137 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6758
EU458305.1 gg_id:290994 North American black bear feces clone BB2_g04_2 EU458
GQ057676.1 gg_id:414752 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ057
AY976601.1 gg_id:124166 human cecum mucosal biopsy clone K155 AY976

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FJ675711.1 gg_id:529778 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6757
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EU467772.1 gg_id:295379 North American black bear feces clone BB1_f07 EU467
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EU467768.1 gg_id:291502 North American black bear feces clone BB1_e12 EU467
GQ016664.1 gg_id:493003 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw824b0 GQ016
GQ022888.1 gg_id:486781 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu3 GQ022
GU470907.1 gg_id:549026 Streptococcus mitis bv. 2 str. F0392 GU470
EU458155.1 gg_id:287652 North American black bear feces clone BB2_f04 EU458
EU458251.1 gg_id:293413 North American black bear feces clone BB2_g04_1 EU458
GU045386.1 gg_id:558644 Streptococcus oralis str. DSMZ 20395 GU045
GQ072839.1 gg_id:408605 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw201g11c GQ072
FJ679770.1 gg_id:524800 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6797
EU458207.1 gg_id:301617 North American black bear feces clone BB2_g02_1 EU458
FJ673446.1 gg_id:527638 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6734
GQ112397.1 gg_id:449675 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ112
FJ558181.1 gg_id:526804 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5581
FJ678184.1 gg_id:527125 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6781
EU461987.1 gg_id:297081 white-faced saki feces clone Saki_aaj64h03 EU461
AY485604.1 gg_id:102076 Streptococcus australis str. ATCC 700641 AY485
EU458221.1 gg_id:292142 North American black bear feces clone BB2_a07_1 EU458
EU458291.1 gg_id:302636 North American black bear feces clone BB2_e02_3 EU458
EU473431.1 gg_id:301627 giant panda feces clone GP_1aaa02c05 EU473
EU467885.1 gg_id:293888 North American black bear feces clone BB1_c08_3 EU467
FJ684898.1 gg_id:518374 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6848
FJ558211.1 gg_id:525410 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5582
FJ678668.1 gg_id:523145 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6786
GQ116366.1 gg_id:403611 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw692b0 GQ116
EU458192.1 gg_id:302661 North American black bear feces clone BB2_d12 EU458
GQ032269.1 gg_id:391176 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ032
GQ038600.1 gg_id:432587 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu4 GQ038
GQ032521.1 gg_id:396059 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ032

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FJ662826.1 gg_id:551205 Streptococcus pyogenes str. Sp4 FJ6628
EU460892.1 gg_id:302391 short-beaked echidna feces clone ECH_aai40b02 EU460
EU467908.1 gg_id:292450 North American black bear feces clone BB1_g03_1 EU467
GQ068224.1 gg_id:458497 Topographical and Temporal Human Skin Microbiome skin alar crease clone nbw148 GQ068
EU458149.1 gg_id:289551 North American black bear feces clone BB2_e07 EU458
GQ076119.1 gg_id:372054 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ076
EU458116.1 gg_id:296356 North American black bear feces clone BB2_a05 EU458
GQ013235.1 gg_id:496431 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ013
GQ073338.1 gg_id:418360 Topographical and Temporal Human Skin Microbiome skin palm clone nbw207h02c GQ073
GQ057439.1 gg_id:371684 Topographical and Temporal Human Skin Microbiome skin interdigital web space clo GQ057
NC_003485.1 gg_id:129068 Streptococcus pyogenes str. MGAS8232 NC_00
EU535969.1 gg_id:281999 profile human microbiota antecubital fossa (inner elbow) skin clone nbt06g07 EU535
FJ676264.1 gg_id:525392 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6762
EF509615.1 gg_id:225348 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aerug EF5096
GQ101509.1 gg_id:465878 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw495h GQ101
EU467763.1 gg_id:294288 North American black bear feces clone BB1_e06 EU467
EU461902.1 gg_id:295919 white-faced saki feces clone Saki_aaj63d11 EU461
EU156782.1 gg_id:350039 Streptococcus pneumoniae str. CCRI-15796 EU156
FJ678537.1 gg_id:526366 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6785
EU461866.1 gg_id:298094 white-faced saki feces clone Saki_aaj62e09 EU461
EU458187.1 gg_id:302971 North American black bear feces clone BB2_c08_1 EU458
GQ074067.1 gg_id:404983 Topographical and Temporal Human Skin Microbiome skin interdigital web space clo GQ074
EU458210.1 gg_id:292277 North American black bear feces clone BB2_g09_1 EU458
EU458286.1 gg_id:295358 North American black bear feces clone BB2_d06_1 EU458
GQ028155.1 gg_id:406593 Topographical and Temporal Human Skin Microbiome skin interdigital web space clo GQ028
GQ018843.1 gg_id:490825 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu191d GQ018
EU458252.1 gg_id:296907 North American black bear feces clone BB2_g05_1 EU458
GQ018860.1 gg_id:490807 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu191f GQ018
EU458292.1 gg_id:302364 North American black bear feces clone BB2_e03_1 EU458
GQ010556.1 gg_id:499109 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ010
FJ679324.1 gg_id:509856 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6793
EU774903.1 gg_id:319192 Short-beaked Echidna feces clone ECH_aai38d02 EU774
GQ000869.1 gg_id:469434 Topographical and Temporal Human Skin Microbiome skin interdigital web space clo GQ000
EU461949.1 gg_id:297276 white-faced saki feces clone Saki_aaj64c03 EU461
EU467748.1 gg_id:289224 North American black bear feces clone BB1_c07 EU467
AM157421.1 gg_id:141768 Streptococcus parasanguinis mother C3 AM157
GQ058009.1 gg_id:449776 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ058
EU458304.1 gg_id:297241 North American black bear feces clone BB2_f10_2 EU458
FJ894952.1 gg_id:555959 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota BME; ear p FJ8949
EU471452.1 gg_id:295151 spectacled bear feces clone SB_2aaa01f05 EU471

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EU473378.1 gg_id:303070 giant panda feces clone GP_1aaa03e07 EU473
EU660341.1 gg_id:293142 Streptococcus pyogenes str. Sp30 EU660
GQ060712.1 gg_id:431280 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw04e07 GQ060
EU467898.1 gg_id:291675 North American black bear feces clone BB1_e07_1 EU467
EU460848.1 gg_id:288152 short-beaked echidna feces clone ECH_aai39c04 EU460
AB002510.1 gg_id:15413 Streptococcus dysgalactiae V24 AB002
GU045379.1 gg_id:578793 Streptococcus oralis str. KCOM 1401 GU045
EU458169.1 gg_id:288654 North American black bear feces clone BB2_h04 EU458
EU774892.1 gg_id:353416 Short-beaked Echidna feces clone ECH_aai38e06 EU774
AF184974.1 gg_id:42170 Streptococcus australis str. AI1; ATCC 700641 AF184
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GQ156288.1 gg_id:582512 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
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EU467891.1 gg_id:290897 North American black bear feces clone BB1_d09_2 EU467
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EU475847.1 gg_id:298266 white-faced saki feces clone Saki_g03 EU475
GQ088816.1 gg_id:422570 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ088
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AF335573.1 gg_id:33357 Streptococcus iniae str. Dan 1 AF335
EU461941.1 gg_id:297117 white-faced saki feces clone Saki_aaj64b06 EU461
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EU461957.1 gg_id:303168 white-faced saki feces clone Saki_aaj64d06 EU461
GQ003166.1 gg_id:506496 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbu19 GQ003
EU470337.1 gg_id:292055 Grevy's zebra feces clone GZ_aaa03c12 EU470
DQ148957.1 gg_id:139480 Streptococcus bovis SbH8.11 DQ148
GQ156147.1 gg_id:580333 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
GQ096744.1 gg_id:446169 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ096
EU458211.1 gg_id:300882 North American black bear feces clone BB2_g10_1 EU458
EU467816.1 gg_id:298015 North American black bear feces clone BB1_f06_1 EU467
GQ069073.1 gg_id:404627 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ069
EU156767.1 gg_id:325913 Streptococcus oligofermentans str. CCUG 48365 EU156
GQ076979.1 gg_id:425421 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw115 GQ076
EU156773.1 gg_id:342992 Streptococcus pneumoniae str. ATCC 49619 EU156
GQ101197.1 gg_id:419981 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw49 GQ101

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FJ672424.1 gg_id:519177 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface FJ6724
CU917914.1 gg_id:568929 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU917
EU458167.1 gg_id:291884 North American black bear feces clone BB2_g11 EU458
EU467806.1 gg_id:291430 North American black bear feces clone BB1_d10_1 EU467
DQ824669.1 gg_id:193137 human fecal clone RL185_aaj71d09 DQ824
GQ113281.1 gg_id:456797 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clo GQ113
EU475811.1 gg_id:295833 white-faced saki feces clone Saki_a01_1 EU475
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EU467843.1 gg_id:297229 North American black bear feces clone BB1_c04_1 EU467
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EU467830.1 gg_id:299221 North American black bear feces clone BB1_h10 EU467
DQ232533.1 gg_id:179010 Streptococcus mitis str. CIP 104996 DQ232
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GQ057669.1 gg_id:375780 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ057
AF003933.1 gg_id:15555 Streptococcus parasanguinis str. ATCC 15912 AF003
FJ673895.1 gg_id:518670 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6738
AY691525.1 gg_id:102441 Streptococcus mutans str. ChDC YM2 AY691
FJ558016.1 gg_id:517987 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5580
EU467856.1 gg_id:298009 North American black bear feces clone BB1_e05 EU467
EU458177.1 gg_id:296799 North American black bear feces clone BB2_a07 EU458

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EU467865.1 gg_id:293109 North American black bear feces clone BB1_g07_1 EU467
EU458255.1 gg_id:292733 North American black bear feces clone BB2_g11_2 EU458
AY500370.1 gg_id:104134 Streptococcus bovis Sb5 AY500
AB264619.1 gg_id:164145 Streptococcus sp. bSSV21 AB264
EU461840.1 gg_id:294868 white-faced saki feces clone Saki_aaj62a02 EU461
AY485603.1 gg_id:101921 Streptococcus infantis str. ATCC 700779 AY485
EU461967.1 gg_id:297953 white-faced saki feces clone Saki_aaj64e08 EU461
EU467779.1 gg_id:298188 North American black bear feces clone BB1_g08 EU467
AY324611.1 gg_id:90414 Streptococcus bovis str. MPR2 AY324
GQ073778.1 gg_id:391010 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor GQ073
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GQ011458.1 gg_id:498208 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw792b1: GQ011
AJ634751.1 gg_id:111084 Streptococcus marimammalium str. M54/01/1 AJ634
EU458212.1 gg_id:291889 North American black bear feces clone BB2_h01 EU458
GQ018924.1 gg_id:490744 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu192d GQ018
GQ023586.1 gg_id:486084 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu320c12 GQ023
FJ677566.1 gg_id:530906 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ677
AM183037.1 gg_id:253441 and its spatial composts compost clone SMB52 AM183
GQ072181.1 gg_id:391890 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw193b1(GQ072
EU467826.1 gg_id:301858 North American black bear feces clone BB1_h03_1 EU467
NR_027214.1 gg_id:535803 Streptococcus pseudopneumoniae str. 108; ATCC BAA-960 NR_02
EU458243.1 gg_id:296265 North American black bear feces clone BB2_f02_2 EU458
GQ155808.1 gg_id:588046 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ074087.1 gg_id:401778 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ074
FJ673496.1 gg_id:527788 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ673
GQ155734.1 gg_id:592904 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EU467871.1 gg_id:303225 North American black bear feces clone BB1_h05_2 EU467
FJ678041.1 gg_id:518979 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ678
GU045388.1 gg_id:541157 Streptococcus mitis str. KCOM 1350 GU045
AY324610.1 gg_id:89376 Streptococcus bovis str. MPR1 AY324
EU458295.1 gg_id:295303 North American black bear feces clone BB2_e07_2 EU458
EU772625.1 gg_id:349233 North American Black Bear feces clone BB1_a08_1 EU772
GQ051010.1 gg_id:373888 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ051
GQ018662.1 gg_id:491006 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu141e05 GQ018
FJ673875.1 gg_id:528552 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ673
GQ027253.1 gg_id:388019 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw! GQ027
EU772603.1 gg_id:349682 North American Black Bear feces clone BB2_c10 EU772
EU772567.1 gg_id:350483 North American Black Bear feces clone BB2_d03 EU772
EU473235.1 gg_id:296749 giant panda feces clone GP_1aaa01e12 EU473
GQ019637.1 gg_id:490031 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu205c03 GQ019
EU458213.1 gg_id:302190 North American black bear feces clone BB2_h05_1 EU458

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GU470899.1 gg_id:558469 Streptococcus cristatus str. F0329 GU470
GQ032924.1 gg_id:416414 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ032
EU458218.1 gg_id:299212 North American black bear feces clone BB2_a03_2 EU458
GQ027310.1 gg_id:434159 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ027
GQ006598.1 gg_id:503066 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu85d08c GQ006
GQ010315.1 gg_id:499348 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw736b1 GQ010
GQ104022.1 gg_id:456295 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw562a0 GQ104
EU458216.1 gg_id:293266 North American black bear feces clone BB2_h10 EU458
EU458302.1 gg_id:299685 North American black bear feces clone BB2_f07_1 EU458
EU475848.1 gg_id:293772 white-faced saki feces clone Saki_aaj62b04 EU475
EU460835.1 gg_id:288716 short-beaked echidna feces clone ECH_aai39a03 EU460
DQ294302.1 gg_id:160607 Streptococcus equi Hyena M149 DQ294
AF084832.1 gg_id:15483 Streptococcus sp. str. KN1 AF084
GQ091850.1 gg_id:416768 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ091
AM157428.1 gg_id:142502 Streptococcus mitis mother C4 AM157
FJ678391.1 gg_id:513075 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6783
GQ155781.1 gg_id:550710 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EU473460.1 gg_id:297804 Somali wild ass feces clone WA_aaa03b08 EU473
GQ030486.1 gg_id:407093 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw878h11 GQ030
EU473991.1 gg_id:299801 giant panda feces clone GP_2aaa04a03 EU473
GQ074320.1 gg_id:386466 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw161 GQ074
FJ367135.1 gg_id:361983 feces adult twins and mothers; TS28 clone TS28_a03h09 FJ3671
GQ073355.1 gg_id:434919 Topographical and Temporal Human Skin Microbiome skin palm clone nbw208a09c GQ073
EU467888.1 gg_id:294779 North American black bear feces clone BB1_c11_2 EU467
EU458114.1 gg_id:302527 North American black bear feces clone BB2_a02 EU458
FJ679191.1 gg_id:519599 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6791
GQ021841.1 gg_id:487827 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ021
AB469560.1 gg_id:359502 Streptococcus sp. str. NUM 1529 AB469
EU474107.1 gg_id:290522 giant panda feces clone GP_2aaa03a05 EU474
GQ102163.1 gg_id:457320 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw561g1 GQ102
EU467809.1 gg_id:288523 North American black bear feces clone BB1_e06_1 EU467
EU474171.1 gg_id:289475 western lowland gorilla feces clone GORSD_2aaa04h03 EU474
EU473228.1 gg_id:294997 giant panda feces clone GP_1aaa04d08 EU473
AY442818.1 gg_id:104405 Streptococcus sp. YE54 AY442
GU045389.1 gg_id:578175 Streptococcus mitis str. KCOM 1379 GU045
GU045392.1 gg_id:512763 Streptococcus mitis str. KCOM 1286 GU045
EU458209.1 gg_id:302903 North American black bear feces clone BB2_g06_1 EU458
EU458287.1 gg_id:296176 North American black bear feces clone BB2_d09_2 EU458
FJ675732.1 gg_id:509993 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6757
GQ073629.1 gg_id:413473 Topographical and Temporal Human Skin Microbiome skin interdigital web space cl GQ073

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GQ156134.1 gg_id:581022 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
EU774840.1 gg_id:319809 Short-beaked Echidna feces clone ECH_aai38g08 EU774
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EU458220.1 gg_id:291672 North American black bear feces clone BB2_a06_2 EU458
EU156779.1 gg_id:334078 Streptococcus pneumoniae str. CCRI-14734 EU156
EU461935.1 gg_id:301946 white-faced saki feces clone Saki_aaj64a07 EU461
EU289129.1 gg_id:245916 microbiome cloacal openings urogenital and anal tracts tammar wallaby Macropus e EU289
FJ893225.1 gg_id:571456 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota HM3; ear p FJ8932
FJ676607.1 gg_id:526041 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6766
GQ079517.1 gg_id:393671 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ079
EU467801.1 gg_id:297452 North American black bear feces clone BB1_d02_1 EU467
EU458173.1 gg_id:301800 North American black bear feces clone BB2_h12 EU458
AY281085.1 gg_id:90432 Streptococcus sanguinis str. ATCC 29667 AY281
EU467151.1 gg_id:298042 white-faced saki feces clone Saki_a06 EU467
EU461955.1 gg_id:301020 white-faced saki feces clone Saki_aaj64c10 EU461
FJ678419.1 gg_id:516100 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6784
GQ032429.1 gg_id:384627 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu542h04 GQ032
FJ677709.1 gg_id:519382 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6777
AJ420199.1 gg_id:27408 Streptococcus macacae str. NCTC11558 AJ4201
EU775424.1 gg_id:336695 Western lowland gorilla feces clone GORSD_2aaa04d03 EU775
EU467754.1 gg_id:299092 North American black bear feces clone BB1_d05 EU467
GQ067186.1 gg_id:394313 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ067
AB501126.1 gg_id:515853 Streptococcus ursoris str. NUM 1615 AB501
GQ019375.1 gg_id:490293 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu189c GQ019
AY273147.1 gg_id:84371 Streptococcus pyogenes AY273
EU467739.1 gg_id:287916 North American black bear feces clone BB1_a08 EU467
GQ023335.1 gg_id:486334 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu317a0 GQ023
GQ076817.1 gg_id:395887 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw1153 GQ076
GQ073289.1 gg_id:421921 Topographical and Temporal Human Skin Microbiome skin palm clone nbw207c10c1 GQ073
GQ018889.1 gg_id:490779 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu192a GQ018
AM420093.1 gg_id:240905 Noma subgingival plaque clone 302F04(oral) AM420
GQ154900.1 gg_id:557859 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
AY324612.1 gg_id:88822 Streptococcus bovis str. MPR4 AY3246
GQ040793.1 gg_id:374127 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw958g01 GQ040
DQ232536.1 gg_id:199646 Streptococcus oralis str. CIP 104985 DQ232
EU461824.1 gg_id:297884 white-faced saki feces clone Saki_aaj61f09 EU461
GQ155776.1 gg_id:585008 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EF364097.1 gg_id:226980 Streptococcus henryi str. 126 EF364
FJ682683.1 gg_id:514572 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6826

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NC_006086.1 gg_id:128611 Streptococcus pyogenes str. MGAS10394 NC_00
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GQ073111.1 gg_id:429959 Topographical and Temporal Human Skin Microbiome skin palm clone nbw205c02c1 GQ073
EU458224.1 gg_id:293705 North American black bear feces clone BB2_a12_1 EU458
EU467860.1 gg_id:296641 North American black bear feces clone BB1_f04_1 EU467
EU467199.1 gg_id:299664 white-faced saki feces clone Saki_g09 EU467
EU779062.1 gg_id:311993 Prevost's squirrel feces clone SQ_aah79h08 EU779
AF396920.1 gg_id:39742 Streptococcus bovis str. B315 AF396
GQ115601.1 gg_id:400616 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw688b1 GQ115
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EU458307.1 gg_id:289803 North American black bear feces clone BB2_h08_3 EU458
AB002522.1 gg_id:15573 Streptococcus pneumoniae str. MAFF 911410 AB002
GQ156243.1 gg_id:561883 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
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GQ021817.1 gg_id:487851 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ021
EU467781.1 gg_id:299667 North American black bear feces clone BB1_g10 EU467
GQ023571.1 gg_id:486098 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu320b09 GQ023
EU458196.1 gg_id:292217 North American black bear feces clone BB2_e11 EU458
DQ318881.1 gg_id:150451 -DGGE and sequencing piglet stomachs stomach clone SY6 DQ318
GQ095863.1 gg_id:435368 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ095
EU467163.1 gg_id:301619 white-faced saki feces clone Saki_f02 EU467
GQ102584.1 gg_id:390165 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ102
EU471514.1 gg_id:294127 spectacled bear feces clone SB_2aaa01d12 EU471
EU467165.1 gg_id:300974 white-faced saki feces clone Saki_f06 EU467
EU474059.1 gg_id:302396 giant panda feces clone GP_2aaa01c07 EU474
GQ074646.1 gg_id:464930 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw164f GQ074
AM157442.1 gg_id:142694 Streptococcus pneumoniae mother V4 AM157
GQ021904.1 gg_id:487765 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ021
EU458151.1 gg_id:291631 North American black bear feces clone BB2_e12 EU458
GQ032381.1 gg_id:399032 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu542a07 GQ032
GQ156168.1 gg_id:590723 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
EU460825.1 gg_id:295866 short-beaked echidna feces clone ECH_aai38g10 EU460
AJ307888.1 gg_id:63461 Streptococcus gallinaceus str. CCUG 42692 AJ3078
AF009507.1 gg_id:15367 Streptococcus suis str. EA1172.91 AF009
EU772622.1 gg_id:314465 North American Black Bear feces clone BB2_c10_1 EU772
EU467845.1 gg_id:287347 North American black bear feces clone BB1_c06_2 EU467
EU775569.1 gg_id:324468 Giant Panda feces clone GP_2aaa01h07 EU775
GU045397.1 gg_id:586088 Streptococcus pneumoniae str. CCARM 4033 GU045
EU473918.1 gg_id:293540 giant panda feces clone GP_2aaa04e06 EU473

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AY281079.1 gg_id:89930 Streptococcus oralis str. ATCC 9811 AY281
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DQ232534.1 gg_id:190717 Streptococcus mitis str. CIP 104997 DQ232
EU475873.1 gg_id:302995 white-faced saki feces clone Saki_aaj62f09 EU475
GQ073509.1 gg_id:431778 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ073
GQ113226.1 gg_id:461942 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor GQ113
GQ155674.1 gg_id:512915 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
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EU660342.1 gg_id:299977 Streptococcus pyogenes str. Sp32 EU660
EU461896.1 gg_id:290594 white-faced saki feces clone Saki_aaj63c10 EU461
EU458288.1 gg_id:295039 North American black bear feces clone BB2_d11 EU458
EU156784.1 gg_id:331800 Streptococcus pseudopneumoniae str. CCRI-8984 EU156
FJ679815.1 gg_id:531369 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6798
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DQ232537.1 gg_id:196966 Streptococcus oralis str. CIP 105158 DQ232
FJ674207.1 gg_id:527106 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6742
AM941160.1 gg_id:259084 Streptococcus sp. 2923-03 AM941
GQ102114.1 gg_id:374555 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw561c0! GQ102
GU045383.1 gg_id:550425 Streptococcus oralis str. KCOM 1416 GU045
NR_029052.1 gg_id:538185 Streptococcus oligofermentans str. 2-4; LMG 21535 NR_02
FJ674309.1 gg_id:509855 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6743
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GQ019723.1 gg_id:489945 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu206c09 GQ019
FJ672838.1 gg_id:515480 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6728
GQ011178.1 gg_id:498488 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ011
GQ155339.1 gg_id:546051 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EU458183.1 gg_id:296971 North American black bear feces clone BB2_b12_1 EU458
EU461976.1 gg_id:300448 white-faced saki feces clone Saki_aaj64f08 EU461
EU471475.1 gg_id:302979 spectacled bear feces clone SB_2aaa03d08 EU471
EU458160.1 gg_id:287785 North American black bear feces clone BB2_g02 EU458
GQ073238.1 gg_id:377455 Topographical and Temporal Human Skin Microbiome skin palm clone nbw206f11c1 GQ073
AB008314.1 gg_id:15560 Streptococcus peroris str. GTC848 AB008

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

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

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

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EU777768.1 gg_id:349666 Polar bear feces clone PB1_aai27f03 EU777
EU461813.1 gg_id:294792 white-faced saki feces clone Saki_aaj61e02 EU461
FJ678126.1 gg_id:520301 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6781
GQ267979.1 gg_id:563263 Surveys lactic acid yak Tibet China method fermented milk product clone IMAU 462 GQ267
GQ087792.1 gg_id:375084 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ087
EU458219.1 gg_id:291040 North American black bear feces clone BB2_a04_1 EU458
AF009508.1 gg_id:15540 Streptococcus suis str. EA1832.92 AF009
AM157420.1 gg_id:142116 Streptococcus mitis mother C3 AM157
EU289036.1 gg_id:238994 microbiome cloacal openings urogenital and anal tracts tammar wallaby Macropus e EU289
GQ018929.1 gg_id:490737 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu192d GQ018
EU461983.1 gg_id:296189 white-faced saki feces clone Saki_aaj64g06 EU461
GQ030493.1 gg_id:459696 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw879a10 GQ030
AM157441.1 gg_id:142633 Streptococcus parasanguinis mother V4 AM157
EF509782.1 gg_id:219258 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aeru EF5097
EU458152.1 gg_id:292449 North American black bear feces clone BB2_f01 EU458
EU467884.1 gg_id:299150 North American black bear feces clone BB1_c06_3 EU467
GQ018857.1 gg_id:490812 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu191f GQ018
EU458161.1 gg_id:293794 North American black bear feces clone BB2_g03 EU458
GQ060042.1 gg_id:441561 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ060
EU461878.1 gg_id:301061 white-faced saki feces clone Saki_aaj62h01 EU461
GQ074530.1 gg_id:394032 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw164c GQ074
AM157443.1 gg_id:143690 Origen y potencial probiotico microbiota de la leche materna breast milk clone 5V4 AM157
EU638618.1 gg_id:337396 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU638
EU638858.1 gg_id:316255 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU638
EU638622.1 gg_id:319590 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU638
EU638451.1 gg_id:334625 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU638
NR_025355.1 gg_id:534827 Thermicanus aegyptius str. ET-5b; DSM 12793 NR_02
GQ079892.1 gg_id:439457 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ079
EU638737.1 gg_id:333346 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU638
EU638544.1 gg_id:354384 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU638
EU638577.1 gg_id:340110 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU638
EU638576.1 gg_id:333359 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU638
EU638435.1 gg_id:336118 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU638
EU638466.1 gg_id:340259 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU638
EU638734.1 gg_id:355173 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU638
EU638336.1 gg_id:339047 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU638
EU638556.1 gg_id:303923 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU638
EU638526.1 gg_id:328129 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU638
EU638732.1 gg_id:336395 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU638
AY518549.1 gg_id:107665 Bacillus solfatarensis str. Sol1 AY518

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

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DQ815454.1 gg_id:164595 mouse cecum clone aab48f09 DQ815
GQ175436.1 gg_id:592913 Chicken intestinal microbiota modulations various feed supplementations DGGE anc GQ175
EF445143.1 gg_id:205846 rabbit cecum clone NED2A2 EF4451
AB192047.1 gg_id:142288 termite gut homogenate clone M2PT2-06 AB192
DQ015494.1 gg_id:133077 mouse cecum clone M3_g04_1 DQ015
AY426451.1 gg_id:101401 full-scale anaerobic UASB bioreactor treating paper mill wastewater clone B7 AY4264
AB234456.1 gg_id:146392 termite gut homogenate clone MgMjD-038 AB234
EF604609.1 gg_id:227821 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6046
DQ800941.1 gg_id:197539 human fecal clone RL387_aao89f10 DQ800
AB062822.1 gg_id:18245 termite gut homogenate clone BCf4-09 AB0628
EU472310.1 gg_id:291318 francois langur feces clone FL_2aaa03d08 EU4723
EF454103.1 gg_id:221121 termite hindgut clone 290cost002-P3L-1640 EF4541
FJ881172.1 gg_id:416837 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8811
AB243284.1 gg_id:148219 acetone-preserved termite gut clone M2PB4a-024 AB243
AB299541.1 gg_id:237802 Motility Symbiont Termite Gut Flagellate Caduceia versatilis Member 'Synergistes' G AB2995
DQ815908.1 gg_id:161771 mouse cecum clone aab24b02 DQ815
DQ456434.1 gg_id:157545 pre-adolescent turkey cecum clone CFT214E5 DQ456
FJ681080.1 gg_id:528434 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6810
DQ815614.1 gg_id:166791 mouse cecum clone aab43f01 DQ815
EF445166.1 gg_id:216356 rabbit cecum clone NED1H7 EF4451
FJ881210.1 gg_id:418334 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8812
EF604503.1 gg_id:232085 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6045
FJ681260.1 gg_id:525729 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6812
FJ681301.1 gg_id:511624 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6813
EF454637.1 gg_id:220301 termite hindgut clone 290cost002-P3L-2450 EF4546
EF098915.1 gg_id:197478 mouse cecum clone SWPT1_aaa03b11 EF0989
FJ367654.1 gg_id:365731 feces adult twins and mothers; TS2 clone TS2_a02a06 FJ3676
GQ422712.1 gg_id:552928 Human Oral Microbiome dental plaque clone CK059 GQ422
AF371714.1 gg_id:69942 swine intestine clone p-4154-6Wa5 AF3717
DQ456425.1 gg_id:157989 pre-adolescent turkey cecum clone CFT214F4 DQ456
EU508608.1 gg_id:276402 cecal contents Mus musculus strain C57BL/6J; MD2 clone MD2_aap36b11 EU508
AB243285.1 gg_id:149668 acetone-preserved termite gut clone M2PB4a-031 AB243
DQ815372.1 gg_id:161993 mouse cecum clone aab47b03 DQ815
EF604607.1 gg_id:234054 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6046
DQ015370.1 gg_id:135193 mouse cecum clone M3_c05 DQ015
GQ175384.1 gg_id:554511 Chicken intestinal microbiota modulations various feed supplementations DGGE anc GQ175
GQ175467.1 gg_id:585880 Chicken intestinal microbiota modulations various feed supplementations DGGE anc GQ175
AB009208.1 gg_id:16273 rumen clone RFN54 bacterium AB009
EU458602.1 gg_id:299565 European rabbit feces clone RA_c03 EU458
DQ905244.1 gg_id:172163 human fecal clone 013-e8 DQ905

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EF436324.1 gg_id:204369 library-based ruminal water buffalo (Bubalus bubalis) rumen fluid clone BRC38 EF4363
GQ897552.1 gg_id:555547 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ897
EU845633.1 gg_id:346636 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8456
AJ009493.1 gg_id:16086 anaerobic TCB-transforming consortium clone SJA-136 AJ0094
AB487703.1 gg_id:538197 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNSR0 AB4877
EF436352.1 gg_id:208802 library-based ruminal water buffalo (Bubalus bubalis) rumen fluid clone BRC66 EF4363
GU303307.1 gg_id:576911 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU303
EU474551.1 gg_id:288952 bighorn sheep feces clone BHSD_aaa03g05 EU4745
EF063613.1 gg_id:174127 Microbial ecology autotrophic denitrifying anaerobic methanogenic UASB reactor clo EF0636
AY858451.2 gg_id:110439 gastrointestinal tract zebra clone ZEBRA_12 AY8584
EF603775.1 gg_id:230542 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6037
EU842417.1 gg_id:327471 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU8424
CU925649.1 gg_id:569463 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU925
EU843209.1 gg_id:351235 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8432
EF401880.1 gg_id:217109 human fecal clone SJTU_D_15_78 EF4018
EU778048.1 gg_id:344860 Black rhinoceros feces clone RH_aaj90h01 EU7780
GU302617.1 gg_id:538833 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU302
FJ416096.1 gg_id:359349 sediments sediment station NEC5 Northern Bering Sea clone 056M55 FJ4160
AB486406.1 gg_id:549867 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC AB4864
CU924768.1 gg_id:550433 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU9247
AM278890.2 gg_id:231376 fecal microbiota irritable bowel syndrome patients significantly that healthy subject AM278
CU927708.1 gg_id:571884 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU9277
FJ517038.1 gg_id:513057 semiarid 'Tablas de Daimiel National Park' wetland (Central Spain) unravelled water c FJ5170
AF275916.1 gg_id:72230 anaerobic digester clone AA05 AF2759
AY692049.1 gg_id:99789 UASB reactor clone M77 AY6920
EU844816.1 gg_id:315276 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8448
DQ800959.1 gg_id:178394 human fecal clone RL387_aao89h10 DQ800
EU842554.1 gg_id:346151 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU8425
EU844348.1 gg_id:330515 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8443
AB062820.1 gg_id:33347 termite gut homogenate clone BCf4-07 AB0628
AY574991.1 gg_id:102360 Catabacter hongkongensis str. HKU16 AY5749
EF434372.1 gg_id:215573 human infant gastrointestinal tract microbiota stool mother babies 13 and 14 7 mont EF4343
AB486418.1 gg_id:584437 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC AB4864
EF688248.1 gg_id:317224 Detection microbial sludge anaerobic wastewater treatment system clone 6D9_cons EF6882
AY985462.1 gg_id:116947 human stool clone C418 AY9854
CU923982.1 gg_id:551149 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU9239
EU774614.1 gg_id:331966 Angola Colobus feces clone EAC_1aaa02d10 EU7746
CU927863.1 gg_id:557576 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU9278
DQ326341.1 gg_id:145236 Metagenomic gut microbiome healthy human stool clone C332 DQ326
FJ535031.1 gg_id:592702 Enhancement protein conversion volatile fatty acids accumulation during addition: ef FJ5350

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

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s__Clostridium cellulolyticum	27653

AY569285.1 gg_id:101611 pink microbial mat clone YJQ-8 AY5692
EF559033.1 gg_id:235642 Microbial functional groups solid waste digestor stable isotope probing thermophilic EF5590
AM183354.1 gg_id:169422 genetic physiological d deep-biosphere Equatorial Pacific and Peru Margin marine su AM183
X75788.1 gg_id:16108 Caloramator indicus str. IndiB4 X75788
NR_026265.1 gg_id:564401 Caloramator proteoclasticus str. Uruguayensis; DSM 10124 NR_02
AF104215.1 gg_id:16110 Caloramator coolhaasii str. Z AF1042
L09187.1 gg_id:16111 Caloramator fervidus str. RT4. B1 L09187
AF489534.1 gg_id:68459 Caloramator uzoniensis str. JW/VK-KU2 AF4895
AF181848.1 gg_id:34407 Caloramator viterbiensis str. JW/MS-VS5 AF1818
DQ676295.1 gg_id:220054 Archaeal sediment and plankton freshwater pond suboxic freshwater-pond clone M DQ676
GQ906581.1 gg_id:584933 Clostridium sp. str. SW003 GQ906
AB486915.1 gg_id:558768 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCORC AB4869
AB486702.1 gg_id:575035 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCORC AB4867
AB487603.1 gg_id:536237 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNSRC AB4876
GQ906580.1 gg_id:558972 Clostridium sp. str. SW002 GQ906
AB488197.1 gg_id:548100 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSSURC AB4881
DQ129398.1 gg_id:151986 microarray level air two cities Texas urban aerosol clone AKIW1006 DQ129
AB486298.1 gg_id:554614 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC AB4862
Y18179.1 gg_id:32182 Clostridium cylindrosporum str. DSM 605 Y18179
DQ129395.1 gg_id:138500 microarray level air two cities Texas urban aerosol clone AKIW981 DQ129
AJ431243.1 gg_id:102801 Clostridium sp. str. Dex60-61 AJ4312
FN356335.1 gg_id:590922 Prokaryotic structure sulfate reducer activity -temperature reservoirs and without ni FN3563
AJ431244.1 gg_id:79318 Clostridium sp. str. Dex60-75 AJ4312
FN356332.1 gg_id:563046 Prokaryotic structure sulfate reducer activity -temperature reservoirs and without ni FN3563
FN356242.1 gg_id:583876 Prokaryotic structure sulfate reducer activity -temperature reservoirs and without ni FN3562
AM231183.1 gg_id:151509 Clostridium acetobutylicum str. 7 MSU AM231
AB240207.1 gg_id:141357 Clostridium baratii str. T8 AB2402
AB240209.1 gg_id:142276 Clostridium baratii str. T10 AB2402
EU547723.1 gg_id:271569 Clostridium bifermentans str. SL186 EU5477
EU460327.1 gg_id:299386 polar bear feces clone PB1_aai26f05 EU4603
AB539899.1 gg_id:535555 Clostridium sp. str. C5S3 AB5398
EF589987.2 gg_id:227564 changes structure sediments Songhua River contaminated nitrobenzene -DGGE cloni EF5899
AJ506120.1 gg_id:60735 Clostridium bowmanii str. DSM 14206 AJ5061
EF063634.1 gg_id:191245 Microbial ecology autotrophic anaerobic denitrifying UASB reactor clone R1Cb41 EF0636
EF570920.1 gg_id:231269 Clostridium frigoriphilum str. 14F EF5709
AJ297443.1 gg_id:29618 Clostridium psychrophilum str. -1/C-/I AJ2974
DQ831126.1 gg_id:170961 Clostridium butyricum str. W4 DQ831
ABDT01000025.2 gg_id:262123 Clostridium butyricum str. 5521 ABDT0
AJ289705.1 gg_id:21382 Clostridium butyricum str. IBUN 125C AJ2897
AM930366.1 gg_id:541328 gradual cooling stage mass and its spatial composting clone SMR62 AM930
NC_011898.1 gg_id:471235 Clostridium cellulolyticum H10 str. H10; ATCC 35319 NC_01

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s__Clostridium cellulovorans	72712
s__Clostridium colicanis	45774
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X73438.1 gg_id:16231 Clostridium cellulovorans str. DSM 3052
FJ957870.1 gg_id:454680 Clostridium colicanis str. JPL_15
NZ_ABHE02000055.1 gg_id:559187 Clostridium difficile QCD-76w55
AY007244.1 gg_id:40074 Clostridium glycolicum str. CIN5
FJ384385.1 gg_id:359641 Clostridium glycolicum str. BG-C128
EU887819.1 gg_id:340525 Clostridium glycolicum str. SN10
L37590.1 gg_id:16126 Clostridium botulinum
AB035087.3 gg_id:22235 Clostridium novyi str. ATCC25758
EU458365.1 gg_id:288771 spotted hyena feces clone HY1_e01
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EU776124.1 gg_id:345246 Spotted hyena feces clone HY1_h10
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DQ800626.1 gg_id:185590 human fecal clone RL183_aao01c05
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EU776059.1 gg_id:306891 Spotted hyena feces clone HY1_f06
EU468383.1 gg_id:295187 lion feces clone LI2_aae49a09
EU467616.1 gg_id:297934 southern three-banded armadillo feces clone arma_g12_1
EU459388.1 gg_id:289373 cheetah feces clone CE3_aai06g06
EU776726.1 gg_id:305526 Lion feces clone LI1_c05_1
EU778549.1 gg_id:312781 Ring-tailed lemur feces clone RT_aai09b05
EU468210.1 gg_id:288094 lion feces clone LI1_f02_2
EU463367.1 gg_id:300475 bush dog feces clone bdog1_aai80b06
EU772883.1 gg_id:320308 Bush dog feces clone bdog1_aai79c02
EU458351.1 gg_id:301967 spotted hyena feces clone HY1_b05_1
EU773971.1 gg_id:322366 Cheetah feces clone CE3_aai06a11
EU465484.1 gg_id:293823 lion feces clone LI3_aah78b07
EU772860.1 gg_id:347235 Bush dog feces clone bdog1_aai77b09
EU772796.1 gg_id:355548 Bush dog feces clone bdog1_aai79e10
EU774859.1 gg_id:324938 Short-beaked Echidna feces clone ECH_aai37g08
EU772948.1 gg_id:310880 Bush dog feces clone bdog1_aai80a09
EU773973.1 gg_id:341829 Cheetah feces clone CE3_aai07f08
EU458412.1 gg_id:295090 spotted hyena feces clone HY1_g02_2

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DQ800
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EU4655
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EU4654
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EU4584

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

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EU869242.1 gg_id:336112 Clostridium sordellii str. CM-C96 EU869
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FJ375781.1 gg_id:312800 and prevalence blaTEM genes polar bear feces clone PBF_b10 FJ3757
FJ375891.1 gg_id:304496 and prevalence blaTEM genes polar bear feces clone PBF_d29 FJ3758
FJ375832.1 gg_id:337750 and prevalence blaTEM genes polar bear feces clone PBF_c14 FJ3758
FJ375879.1 gg_id:304036 and prevalence blaTEM genes polar bear feces clone PBF_d17 FJ3758
AJ310082.1 gg_id:31278 Clostridium stercorarium str. DSM 8532T AJ3100
EF030542.1 gg_id:190008 Clostridium botulinum str. G196 EF0305
NC_004557.1 gg_id:471257 Clostridium tetani E88 str. Massachusetts NC_00
AABG04000051.1 gg_id:130271 Clostridium thermocellum str. ATCC 27405 AABG0
FJ599513.1 gg_id:545541 Clostridium thermocellum str. CTL-6 FJ5995
NR_026112.1 gg_id:569919 Clostridium thermopalmarium str. BVP; ATCC 51427 NR_02
DQ887919.1 gg_id:164481 thermophilic anaerobic solid waste bioreactor clone GHB3A06 DQ887
X71856.1 gg_id:15980 Clostridium cellobioparum str. DSM 1351 X71856
AB307636.1 gg_id:271652 clay wall used Japanese traditional buildings clone B46 AB3076
EF559080.1 gg_id:218474 mesophilic anaerobic digester clone B35_F_B_A02 EF5590
AJ863357.1 gg_id:122896 poplar tree microcosm rhizosphere flooded clone 17RHF8 AJ8633
EU753611.1 gg_id:315396 modern freshwater stromatolites Ruidera Pools Natural Park Spain dry stromatolite EU753
AY959944.2 gg_id:114917 Clostridium alkalicellum str. Z-7026 AY9599
AB240379.1 gg_id:142282 microbial structure Phragmites rhizosphere biofilm reed bed reactor laboratory clon AB2403
AF280831.1 gg_id:41245 bioreactor clone tbr4-15 AF2808
AF482449.1 gg_id:77496 granular sludge clone R6b7 AF4824
AB486179.1 gg_id:577580 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC AB486
AB198481.1 gg_id:135577 termite gut wall fraction clone RsW01-052 AB1984
AB294296.1 gg_id:216349 Microbial structure deep coal seem groundwater clone YWB27 AB2942
AM982551.2 gg_id:278657 microbial and slurry pig straw spent bedding clone PIST-AGE08 AM982
EU703284.1 gg_id:538658 taxon richness -altitude lakes eastern tin plateau predominance Bacteroidetes and S EU703
AB486460.1 gg_id:574342 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC AB4864
X71852.1 gg_id:15957 Clostridium papyrosolvens str. DSM 2782 X71852
AY684073.1 gg_id:130444 methanogenic enrichment 'MRE50' clone MRE50b28 AY6840
CU918823.1 gg_id:556438 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU918
AB486564.1 gg_id:560650 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCORC AB4865
FJ502269.1 gg_id:578409 Co-occurrence denitrification and nitrogen fixation meromictic lake (Switzerland) Lak FJ5022
EU753609.1 gg_id:353886 modern freshwater stromatolites Ruidera Pools Natural Park Spain dry stromatolite EU753
AB374114.1 gg_id:245904 Effect temperature on microbial glucose-degrading methanogenic consortium under AB374
GQ921436.1 gg_id:590008 Worms hell: presence Nematoda terrestrial deep subsurface (0.9-3.6 km) fracture w GQ921
AF407388.1 gg_id:68943 MCB-contaminated groundwater-treating reactor clone RA9C1 AF4073
AB488016.1 gg_id:579868 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSSURC AB4880
L35517.1 gg_id:15955 Bacteroides cellulosolvens L35517
AJ229249.1 gg_id:15960 Clostridium sp. str. FCB90-1 AJ2292
AB240232.1 gg_id:144522 microbial structure rhizosphere Phragmites bulk soil reed bed reactor laboratory clo AB2402

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FN436024.1 gg_id:547395 Molekularbiologische Charakterisierung der bakteriellen Populationsdynamik eines t FN436
DQ125722.1 gg_id:136404 uranium contaminated soil clone AKAU3820 DQ125
DQ125755.1 gg_id:132457 uranium contaminated soil clone AKAU3868 DQ125
AB274495.1 gg_id:213313 packed-bed reactor clone CFB-6 AB274
EF586065.1 gg_id:245011 Methanol-assimilating anaerobic solid waste digester fed methanol clone M55_D21_ EF586
DQ887967.1 gg_id:161992 thermophilic anaerobic solid waste bioreactor clone TIBE03 DQ887
CR933129.1 gg_id:109994 Evry municipal wastewater treatment plant clone 013B04_B_SD_P15 CR933
DQ125655.1 gg_id:134002 uranium contaminated soil clone AKAU3717 DQ125
AF050580.1 gg_id:16001 contaminated aquifer clone WCHB1-21 AF050
GQ487969.1 gg_id:550979 Microbial metal soil polluted heavy metals clone G10-80 GQ487
EU250962.1 gg_id:360102 degraded cellulose lindane NSC-7 NFC-7 grown 50 degrees Celsius compost compose EU250
AF407399.1 gg_id:48313 MCB-contaminated groundwater-treating reactor clone RA13C2 AF407
EF205577.1 gg_id:205562 among geographically regions central Tibet geothermal spring mat clone TP20 EF2055
AJ318164.1 gg_id:16925 Waste-gas biofilter clone BIri47 AJ3181
AB011057.1 gg_id:15977 Clostridium josui str. FERM P-9684 AB011
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X71854.1 gg_id:15963 Clostridium termitidis str. DSM 5396 X71854
AB487128.1 gg_id:587360 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNIR0 AB487
AJ229248.1 gg_id:15959 Clostridium sp. str. FCB45 AJ2292
EF559108.1 gg_id:219192 mesophilic anaerobic digester clone C35_D7_H_B_G09 EF5591
AB486913.1 gg_id:572847 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCOR AB486
AY330128.1 gg_id:97132 methanogenic landfill leachate bioreactor clone AC065 AY330
GQ502575.1 gg_id:564645 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf4- GQ502
NC_011898.1 gg_id:471233 Clostridium cellulolyticum H10 str. H10; ATCC 35319 NC_01
DQ069224.1 gg_id:128200 gold mine clone SRB16 DQ069
AY642570.1 gg_id:153096 and carbonate precipitation giant microbialites ly alkaline Lake Van Turkey microbiali AY642
X71847.1 gg_id:15998 Clostridium cellulolyticum str. ATCC 35319 X71847
FM994911.1 gg_id:534331 springs Velingrad region Bulgaria hot spring Mizinka clone VS-7 FM994
AB486893.1 gg_id:532875 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCOR AB486
AB486146.1 gg_id:561133 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBAR AB486
AJ229216.1 gg_id:50120 anoxic bulk soil flooded rice microcosm clone BSV72 clone AJ2292
AB294749.1 gg_id:211979 Dechlorination biphenyl polychlorinated dibenzo-p-dioxin species genus Dehalobact AB294
GQ406191.1 gg_id:509371 Benthic submerged sinkhole ecosystems sediment clone -39-11 GQ406
AB240269.1 gg_id:142277 microbial structure rhizosphere Phragmites bulk soil reed bed reactor laboratory clo AB240
EU057605.1 gg_id:252234 Clostridium sp. str. CJT-3 EU057
EU772520.1 gg_id:306873 Hamadryas Baboon feces clone BAZ_aah92f09 EU772
AY337519.1 gg_id:91168 Clostridium sp. str. L15 AY337
EU459349.1 gg_id:288632 cheetah feces clone CE3_aai05a07 EU459
FJ672914.1 gg_id:523511 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface FJ6729

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FJ683489.1 gg_id:519525 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6834
EU473709.1 gg_id:287502 banteng feces clone BG_aaa04c08.Contig1 EU473
EU473983.1 gg_id:288648 giant panda feces clone GP_2aaa03h01 EU473
GQ458239.1 gg_id:547433 Microbial structure co-digestion anaerobic bioreactors treating cassava pulp and pig GQ458
EU467045.1 gg_id:291305 hedgehog feces clone HH_b05 EU467
EU459232.1 gg_id:288088 hedgehog feces clone HH_aai34e01 EU459
FJ674874.1 gg_id:531852 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6748
AM183095.1 gg_id:241843 and its spatial composts compost clone SMC146 AM183
EU473956.1 gg_id:301835 giant panda feces clone GP_2aaa04d05 EU473
EU473643.1 gg_id:302631 banteng feces clone BG_aaa01c06.Contig1 EU473
FJ682017.1 gg_id:512879 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6820
EU459171.1 gg_id:299102 hedgehog feces clone HH_aai33b11 EU459
EU467934.1 gg_id:299336 cheetah feces clone CE2_e04 EU467
DQ196630.2 gg_id:172362 Clostridium sp. str. BL-26 DQ196
FJ960229.1 gg_id:564094 bottlenose dolphin upper respiratory tract blowhole clone D9A4_121 FJ9602
FJ370179.1 gg_id:356848 feces adult twins and mothers; TS56 clone TS56_a01d05 FJ3701
EU775688.1 gg_id:315362 Hedgehog feces clone HH_aai33h06 EU775
GQ868440.1 gg_id:582630 Fungal and Structure Bioaerosols Pig Stable pig stable bioaerosols clone BBC518 GQ868
FJ375881.1 gg_id:328969 and prevalence blaTEM genes polar bear feces clone PBF_d19 FJ3758
FJ683394.1 gg_id:530072 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6833
DQ238608.1 gg_id:145018 Effect daidzein on piglets piglet gastrointestinal tract clone 8 DQ238
EU468026.1 gg_id:294154 cheetah feces clone CE2_d12_2 EU468
EU777813.1 gg_id:322174 Polar bear feces clone PB2_aai23a05 EU777
EU474114.1 gg_id:301771 giant panda feces clone GP_2aaa02g05 EU474
EU459181.1 gg_id:291701 hedgehog feces clone HH_aai33d07 EU459
EU475570.1 gg_id:288446 babirusa feces clone BARB_aaa03g08 EU475
DQ817233.1 gg_id:172276 mouse cecum clone aaa70d07 DQ817
AJ245413.1 gg_id:16236 Clostridium tertium str. ATCC 14573 AJ2454
EU474799.1 gg_id:292527 takin feces clone TAK_aaa01g04 EU474
DQ238613.1 gg_id:142447 Effect daidzein on piglets piglet gastrointestinal tract clone 6 DQ238
FJ670668.1 gg_id:528824 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6706
EU473968.1 gg_id:295254 giant panda feces clone GP_2aaa03d03 EU473
DQ800540.1 gg_id:199214 human fecal clone RL183_aah29d02 DQ800
GQ129976.1 gg_id:403839 Genetic inventory 'JPL-SAF' during MSL mission spacecraft assembly clean room floc GQ129
FM874206.1 gg_id:356785 occupant source house mattress dust clone MC03A02 FM874
AF371844.1 gg_id:33176 swine intestine clone p-1965-s959-5 AF371
FJ679483.1 gg_id:527748 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6794
AB332117.1 gg_id:247793 Continuous cultivation and structure thermophilc propionate-degrading microbial co AB332
EU474794.1 gg_id:293733 takin feces clone TAK_aaa03c02 EU474
AB540985.1 gg_id:572196 Eubacterium moniliforme str. JCM 9990 AB540

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X68174.1 gg_id:16213 Clostridium baratii str. ATCC27638 X68174
AM183061.1 gg_id:248563 and its spatial composts compost clone SMB82 AM183
EU464172.1 gg_id:289404 reticulated giraffe feces clone gir_aah95e03 EU464
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EU773016.1 gg_id:333228 Banteng feces clone BG_aaa01d12.Contig1 EU773
EU473216.1 gg_id:287467 giant panda feces clone GP_1aaa01d05 EU473
AB018184.1 gg_id:40062 Eubacterium multiforme str. JCM 6484 AB018
EF559177.1 gg_id:223161 mesophilic anaerobic digester clone G35_D8_H_B_B06 EF5591
EU474087.1 gg_id:295458 giant panda feces clone GP_2aaa02h06 EU474
GQ492949.1 gg_id:569263 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
FJ881333.1 gg_id:433124 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8813
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EU459334.1 gg_id:287565 hedgehog feces clone HH_aai36f05 EU459
DQ015563.1 gg_id:133360 mouse cecum clone M3_f01_1 DQ015
EU471447.1 gg_id:291025 spectacled bear feces clone SB_2aaa03f07 EU471
EU462622.1 gg_id:302041 Sumatran orangutan feces clone orang2_aai66c04 EU462
EU472577.1 gg_id:289501 Angola colobus feces clone EAC_2_aaa03a09 EU472
EU473337.1 gg_id:292010 giant panda feces clone GP_1aaa01h01 EU473
FJ682831.1 gg_id:530824 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6828
FM873505.1 gg_id:359728 occupant source house floor dust clone FD04G02 FM873
GQ007726.1 gg_id:501938 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ007
FJ681425.1 gg_id:525936 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6814
EU473883.1 gg_id:301102 giant panda feces clone GP_2aaa04c03 EU473
EU762963.1 gg_id:329216 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU762
DQ793454.1 gg_id:187953 human fecal clone RL199_aaj43h11 DQ793
EU460613.1 gg_id:295137 polar bear feces clone PB2_aai23d09 EU460
EU473225.1 gg_id:288164 giant panda feces clone GP_1aaa01d11 EU473
EU763600.1 gg_id:340717 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU763
FJ683685.1 gg_id:531765 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6836
EU474080.1 gg_id:290462 giant panda feces clone GP_2aaa03d09 EU474
DQ325781.1 gg_id:149036 Metagenomic gut microbiome healthy human stool clone B469 DQ325
EU473304.1 gg_id:289102 giant panda feces clone GP_1aaa04a09 EU473
FJ684155.1 gg_id:524467 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6841
FJ680008.1 gg_id:525078 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6800
EU459342.1 gg_id:293771 hedgehog feces clone HH_aai36g12 EU459
EU473952.1 gg_id:294441 giant panda feces clone GP_2aaa01e11 EU473
EU473891.1 gg_id:289769 giant panda feces clone GP_2aaa01h11 EU473
EU474127.1 gg_id:295740 giant panda feces clone GP_2aaa01b01 EU474
EU772351.1 gg_id:313142 Babirusa feces clone BARB_aaa01b09 EU772
GQ898543.1 gg_id:541594 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ898

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EU475622.1 gg_id:301597 babirusa feces clone BARB_aaa03f01 EU475
FJ681136.1 gg_id:512574 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6811
DQ801475.1 gg_id:193154 human fecal clone RL388_aao96a07 DQ801
X77842.1 gg_id:16234 Clostridium sardiniense str. DSM 599 X77842
GQ458227.1 gg_id:512965 Microbial structure co-digestion anaerobic bioreactors treating cassava pulp and pig GQ458
DQ808504.1 gg_id:182358 human fecal clone RL239_aaj09d12 DQ808
EU460604.1 gg_id:290233 polar bear feces clone PB2_aai23c07 EU460
EU774647.1 gg_id:324893 Angola Colobus feces clone EAC_1aaa02a10 EU774
FJ683095.1 gg_id:514947 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6830
GQ249583.1 gg_id:509782 Microbial anaerobic sediments Bay Cadiz (Spain) marine sediment: 12-14 cm layer cl GQ249
EU473255.1 gg_id:290901 giant panda feces clone GP_1aaa01f11 EU473
DQ817220.1 gg_id:169629 mouse cecum clone aaa70b08 DQ817
GQ359970.1 gg_id:582866 Microbial intestinal contents and mucus yel catfish (Pelteobagrus fulvidraco) intestir GQ359
FJ682482.1 gg_id:524162 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6824
EU473352.1 gg_id:287684 giant panda feces clone GP_1aaa02h03 EU473
AB018185.1 gg_id:31869 Eubacterium nitritogenes str. JCM 6485 AB018
DQ796773.1 gg_id:182452 human fecal clone RL179_aao54c09 DQ796
EU772391.1 gg_id:315755 Hamadryas Baboon feces clone BAZ_e03 EU772
EU869238.1 gg_id:306622 Clostridium sp. str. CM-C81 EU869
DQ129391.1 gg_id:138056 microarray level air two cities Texas urban aerosol clone AKIW654 DQ129
EU777055.1 gg_id:348224 Okapi feces clone OK2_b02_1 EU777
DQ815970.1 gg_id:164332 mouse cecum clone aaa85a09 DQ815
FJ678772.1 gg_id:525918 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6787
DQ800727.1 gg_id:190296 human fecal clone RL183_aao02f08 DQ800
EU473932.1 gg_id:301964 giant panda feces clone GP_2aaa03b11 EU473
EU459282.1 gg_id:290241 hedgehog feces clone HH_aai35e07 EU459
GU293208.1 gg_id:538968 Microbial contents and mucus yel catfish (Pelteobagrus fulvidraco) stomach content GU293
EU474817.1 gg_id:297379 takin feces clone TAK_aaa02d10 EU474
DQ815984.1 gg_id:171437 mouse cecum clone aaa85c02 DQ815
EU474090.1 gg_id:295920 giant panda feces clone GP_2aaa01c04 EU474
FJ678171.1 gg_id:518018 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6781
EU761992.1 gg_id:333674 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1 EU761
NR_026149.1 gg_id:534306 Clostridium quinii str. DSM 6736 NR_02
GQ492067.1 gg_id:574003 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
EU473929.1 gg_id:288858 giant panda feces clone GP_2aaa01h06 EU473
DQ807486.1 gg_id:180069 human fecal clone RL307_aam07b11 DQ807
EU777067.1 gg_id:338591 Okapi feces clone OK2_d10 EU777
FM873847.1 gg_id:359116 occupant source house mattress dust clone MB01G06 FM873
EU779088.1 gg_id:317926 Takin feces clone TAK_aaa02h01 EU779
FJ679435.1 gg_id:517527 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6794
FJ685390.1 gg_id:512217 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6853

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AB020189.1 gg_id:34846 Clostridium beijerinckii str. JCM 7844 AB0201
X77843.1 gg_id:16243 Clostridium caliptrosporum str. DSM 5905 X77843
NR_026013.1 gg_id:565322 Clostridium chauvoei str. 2585; ATCC 10092 NR_02
EU474076.1 gg_id:287515 giant panda feces clone GP_2aaa03a12 EU474
EU777692.1 gg_id:307341 Polar bear feces clone PB2_aai22c01 EU777
DQ796807.1 gg_id:184442 human fecal clone RL179_aao54g10 DQ796
FJ673626.1 gg_id:529116 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6736
DQ817225.1 gg_id:168712 mouse cecum clone aaa70c01 DQ817
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EU473278.1 gg_id:289356 giant panda feces clone GP_1aaa04e09 EU473
FJ681715.1 gg_id:529490 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6817
FJ679026.1 gg_id:514689 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6790
DQ808581.1 gg_id:195664 human fecal clone RL239_aaj10d07 DQ808
EU777219.1 gg_id:319567 Okapi feces clone OK2_b04 EU777
EU473193.1 gg_id:290998 giant panda feces clone GP_1aaa01f06 EU473
EU473368.1 gg_id:287591 giant panda feces clone GP_1aaa01h05 EU473
EU777716.1 gg_id:338956 Polar bear feces clone PB1_aai28h01 EU777
AM183092.1 gg_id:252144 and its spatial composts compost clone SMC120 AM183
EU459246.1 gg_id:289622 hedgehog feces clone HH_aai34f09 EU459
AM998793.1 gg_id:283776 Clostridium saccharobutylicum str. Ox29 AM998
CP001056.1 gg_id:286203 Clostridium botulinum B str. Eklund 17B CP001
DQ326262.1 gg_id:150131 Metagenomic gut microbiome healthy human stool clone C203 DQ326
EU473286.1 gg_id:289372 giant panda feces clone GP_1aaa03c01 EU473
EU473395.1 gg_id:298080 giant panda feces clone GP_1aaa01d09 EU473
DQ810116.1 gg_id:196719 human fecal clone RL184_aao68c04 DQ810
FJ678592.1 gg_id:519790 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6785
DQ808820.1 gg_id:194032 human fecal clone RL243_aai85f11 DQ808
FJ680093.1 gg_id:515102 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6800
DQ793612.1 gg_id:197786 human fecal clone RL246_aai74d08 DQ793
EU775619.1 gg_id:330962 Hedgehog feces clone HH_aai35b03 EU775
X68175.1 gg_id:16232 Clostridium baratii str. ATCC43756 X68175
X97432.1 gg_id:16227 Clostridium vincentii X97432
FJ682951.1 gg_id:526262 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6829
GU060306.1 gg_id:564332 Clostridium saccharobutylicum str. BS2 GU060
FJ880242.1 gg_id:429210 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8802
FJ685096.1 gg_id:514508 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6850
AY133085.1 gg_id:59906 TCE-contaminated site clone ccslm2120 AY133
EU473145.1 gg_id:295777 giant panda feces clone GP_1aaa01b06 EU473
DQ326540.1 gg_id:147920 Metagenomic gut microbiome healthy human stool clone C693 DQ326
FJ683485.1 gg_id:522966 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6834

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EU474123.1 gg_id:295402 giant panda feces clone GP_2aaa03d05 EU474
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GQ868434.1 gg_id:558476 Fungal and Structure Bioaerosols Pig Stable pig stable bioaerosols clone BBC512 GQ868
FJ684781.1 gg_id:524895 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6847
DQ196631.1 gg_id:166896 Clostridium sp. str. BL-24 DQ196
AJ420008.1 gg_id:76200 Clostridium colicanis str. DSM 13634 AJ420
DQ808612.1 gg_id:196359 human fecal clone RL239_aaj10h09 DQ808
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EU460605.1 gg_id:296166 polar bear feces clone PB2_aai23c08 EU460
AM183065.1 gg_id:237935 and its spatial composts compost clone SMB112 AM183
FJ681311.1 gg_id:530465 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6813
EU473935.1 gg_id:291622 giant panda feces clone GP_2aaa04g05 EU473
FM873828.1 gg_id:361822 occupant source house mattress dust clone MB01D07 FM873
DQ800217.1 gg_id:191808 human fecal clone RL303_aal69g05 DQ800
DQ800538.1 gg_id:184824 human fecal clone RL183_aah29c10 DQ800
EU474813.1 gg_id:297938 takin feces clone TAK_aaa04g11 EU474
EU773874.1 gg_id:326918 Cheetah feces clone CE3_aai05f04 EU773
FJ960326.1 gg_id:571221 bottlenose dolphin upper respiratory tract blowhole clone D9A4_224 FJ9603
EU470820.1 gg_id:295850 red panda feces clone RP_2aaa01e02 EU470
DQ015110.1 gg_id:130878 mouse cecum clone M2_e05_1 DQ015
FJ680768.1 gg_id:511288 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6807
AJ810554.1 gg_id:104410 superficial sediments clone AJ8105
EU475686.1 gg_id:303104 babirusa feces clone BARB_aaa03c12 EU475
EU459347.1 gg_id:296403 hedgehog feces clone HH_aai36h12 EU459
EU766580.1 gg_id:348914 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU766
EU468766.1 gg_id:298784 okapi feces clone OK3_c11_1 EU468
GQ867474.1 gg_id:582379 and prevalence blaTEM genes Arctic seals colon content clone CSG45 GQ867
EU460716.1 gg_id:299954 polar bear feces clone PB2_aai24h05 EU460
AB198536.1 gg_id:135311 termite gut wall fraction clone RsW02-061 AB198
FJ375811.1 gg_id:332200 and prevalence blaTEM genes polar bear feces clone PBF_b42 FJ3758

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GQ491217.1 gg_id:553388 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
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DQ796870.1 gg_id:184692 human fecal clone RL179_aao55f12 DQ796
EU472395.1 gg_id:288493 Angola colobus feces clone EAC_1aaa01b08 EU472
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EU459194.1 gg_id:295462 hedgehog feces clone HH_aai33f07 EU459
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EU528192.1 gg_id:287156 Seasonal Dynamics Mudflat Mouth Major Kentucky Lake Reservoir Tributary sedime EU528
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AB075771.1 gg_id:46716 Clostridium sordellii str. ATCC 9714 AB075
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FJ366569.1 gg_id:368997 feces adult twins and mothers; TS27 clone TS27_a01c06 FJ3665
GQ458231.1 gg_id:594005 Microbial structure co-digestion anaerobic bioreactors treating cassava pulp and pig GQ458
FJ978707.1 gg_id:384411 feces clone CL_F_403 FJ9787
EU775276.1 gg_id:308502 Reticulated giraffe feces clone gir_aah94h12 EU775
FJ673530.1 gg_id:528464 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6735
EU468826.1 gg_id:291183 okapi feces clone OK3_c04_1 EU468
DQ445857.1 gg_id:156623 Clostridium sp. C01-2409 DQ445
DQ810015.1 gg_id:185149 human fecal clone RL184_aao67a12 DQ810
EU460560.1 gg_id:299990 polar bear feces clone PB2_aai22f08 EU460
EU775664.1 gg_id:337083 Hedgehog feces clone HH_aai35f05 EU775
FJ366714.1 gg_id:357630 feces adult twins and mothers; TS27 clone TS27_a03a04 FJ3667
EF682951.1 gg_id:247473 Eastern Mediterranean atmosphere clone F13_9D_FL EF6829
GQ868388.1 gg_id:541925 Fungal and Structure Bioaerosols Pig Stable pig stable bioaerosols clone BBC65 GQ868
FJ366695.1 gg_id:369406 feces adult twins and mothers; TS27 clone TS27_a02g04 FJ3666
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FJ375874.1 gg_id:316634 and prevalence blaTEM genes polar bear feces clone PBF_d11 FJ3758
EU459287.1 gg_id:288071 hedgehog feces clone HH_aai35f07 EU459
EU475638.1 gg_id:295162 babirusa feces clone BARB_aaa02d07 EU475
EU763479.1 gg_id:349439 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A4 EU763
FJ375912.1 gg_id:306812 and prevalence blaTEM genes polar bear feces clone PBM_a4 FJ3759
DQ798320.1 gg_id:179306 human fecal clone RL181_aah40f08 DQ798

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EU475100.1 gg_id:290125 visayam warty pig feces clone VWP_aaa01h04 EU4751
FJ678801.1 gg_id:514611 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6788
FJ366693.1 gg_id:366425 feces adult twins and mothers; TS27 clone TS27_a02g02 FJ3666
EU475586.1 gg_id:292078 babirusa feces clone BARB_aaa03g02 EU4755
EU773916.1 gg_id:332962 Cheetah feces clone CE3_aai05g07 EU7739
FJ681620.1 gg_id:511228 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6816
EU460520.1 gg_id:290323 polar bear feces clone PB2_aai22a08 EU4605
GQ359984.1 gg_id:577153 Microbial intestinal contents and mucus yel catfish (Pelteobagrus fulvidraco) intestir GQ359
DQ799856.1 gg_id:193066 human fecal clone RL247_aaj21a04 DQ799
FJ366818.1 gg_id:365641 feces adult twins and mothers; TS27 clone TS27_a04c03 FJ3668
EU560842.1 gg_id:534075 Assessment genetic Apriona germari (Hope) larvae normalization techniques intestir EU5608
AM697422.1 gg_id:218452 sequencing libraries indoor dust clone BF0001D037 AM697
EU468628.1 gg_id:291564 okapi feces clone OK2_f08 EU4686
AM982558.1 gg_id:279235 microbial and slurry pig saw dust spent bedding clone PISD-AIH04 AM982
FJ375835.1 gg_id:348777 and prevalence blaTEM genes polar bear feces clone PBF_c17 FJ3758
EU465318.1 gg_id:299076 lion feces clone LI3_aah75b10 EU4653
AJ810555.1 gg_id:104561 superficial sediments clone AJ8105
GQ868411.1 gg_id:561998 Fungal and Structure Bioaerosols Pig Stable pig stable bioaerosols clone BBC812 GQ868
FJ363465.1 gg_id:362524 feces adult twins and mothers; TS149 clone TS149_a03e09 FJ3634
DQ113746.2 gg_id:136804 dog duodenum clone D1-17 DQ113
GQ492355.1 gg_id:547714 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
FJ680320.1 gg_id:526583 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6803
EU475618.1 gg_id:298176 babirusa feces clone BARB_aaa01b01 EU4756
EU475575.1 gg_id:293486 babirusa feces clone BARB_aaa02f04 EU4755
FJ679600.1 gg_id:516687 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6796
EU462544.1 gg_id:295449 Sumatran orangutan feces clone orang1_aai56g06 EU4625
FJ673752.1 gg_id:526864 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6737

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AJ409003.1 gg_id:21834 human colonic clone HuCB31 AJ409
FJ975999.1 gg_id:586027 Human gut microbiome adopts alternative state bowel transplantation ileum effluent FJ9759
EU475604.1 gg_id:288181 babirusa feces clone BARB_aaa02d12 EU475
EF644506.1 gg_id:255177 Structure and performance microbial involved reductive dechlorination 1122-tetrach EF6445
AB218295.1 gg_id:147444 Fecal microbial (dugong dugon) determined genes Dugong feces clone dgA-7 AB218
EU828373.1 gg_id:562096 Microbial effects changeover without CO2 sparging two-stage biological and methan EU828
EU236399.1 gg_id:295330 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg92C10 EU236
DQ126679.1 gg_id:138256 Clostridium dongmakense str. HY-45-18; IMSNU 40129; KCTC 5147 DQ126
L37589.1 gg_id:16150 Clostridium botulinum B str. B3 L37589
AJ810553.1 gg_id:104248 superficial sediments clone AJ8105
NR_028898.1 gg_id:594284 Clostridium acidisoli str. CK74; DSM 12555 NR_02
EU535463.1 gg_id:281510 profile human microbiota antecubital fossa (inner elbow) skin clone nbt25f11 EU535
NZ_ABDQ01000035.1 gg_id:263445 Clostridium botulinum C str. Eklund NZ_AB
EU468033.1 gg_id:291999 cheetah feces clone CE2_f03_2 EU468
GU227151.1 gg_id:574341 Clostridium tyrobutyricum str. B6-2 GU227
AB186864.1 gg_id:104466 polychlorinated dioxin dechlorinating microcosm clone TSAF01 AB186
AB486908.1 gg_id:541432 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCOR AB486
AB081585.1 gg_id:71518 Clostridiaceae str. A4d AB081
NZ_ABDQ01000017.1 gg_id:264222 Clostridium botulinum C str. Eklund NZ_AB
AY742899.1 gg_id:106253 Clostridium crotonatovorans str. R6B AY742
AJ229185.1 gg_id:36004 anoxic bulk soil flooded rice microcosm clone BSV20 clone AJ2291
AB486626.1 gg_id:566529 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCOR AB486
EU474720.1 gg_id:297378 takin feces clone TAK_aaa03e09 EU474
GU476608.1 gg_id:525790 microbial biogas fermentation enrichment clone BBMC-8 GU476
AJ222546.1 gg_id:16199 Anaerobacter polyendosporus AJ2225
AB486197.1 gg_id:563918 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBAR AB486
AY395437.1 gg_id:107326 pasture soil clone EB1118 AY3954
L08062.1 gg_id:16144 Clostridium tyrobutyricum str. NIZO 51 L08062
AB487095.1 gg_id:589921 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNIR AB487
EU467918.1 gg_id:298719 cheetah feces clone CE2_a09 EU467
AB509218.1 gg_id:543607 Microbial reservior produced water oil reservoir clone HNB-13 AB509
AJ427628.1 gg_id:64232 Clostridium scatologenes str. FP AJ4276
NR_029250.1 gg_id:591228 Clostridium proteolyticum str. CG; DSM 3090 NR_02
AB470964.1 gg_id:535657 Clostridium sp. str. r13 AB470
AB470961.1 gg_id:571639 Clostridium sp. str. r53 AB470
EU536517.1 gg_id:279856 profile human microbiota antecubital fossa (inner elbow) skin clone nbt215c07 EU536
DQ129397.1 gg_id:137941 microarray level air two cities Texas urban aerosol clone AKIW662 DQ129
EU467972.1 gg_id:297029 cheetah feces clone CE2_c12_1 EU467
EF088329.1 gg_id:177051 Clostridium hveragerdense str. AK14 EF0883
AB264078.1 gg_id:190766 Fecal microbial (dugong dugon) determined genes Dugong feces clone dgD-151 AB264
AY167950.1 gg_id:75821 Isolation and identification hyper-ammonia producing swine storage pits manure AY167

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AB470965.1 gg_id:533504 Clostridium sp. str. r22 AB470
AY858804.1 gg_id:137989 Clostridium lundensis str. DSM 17049 AY858
AY581269.1 gg_id:114950 Clostridium sp. str. HY-34-8 AY581
L37585.1 gg_id:16148 Clostridium botulinum type A L37585
AY548785.1 gg_id:104893 Clostridium sp. str. PPf35E10 AY548
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AB487685.1 gg_id:550171 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNSRO AB487
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AB218294.1 gg_id:146143 Fecal microbial (dugong dugon) determined genes Dugong feces clone dgA-121 AB218
GQ503831.1 gg_id:588312 Taptapani hot water spring clone tpsrb003 GQ503
EU307088.1 gg_id:257735 Changes microbial metabolic and along hydrogeochemically variable profile unsatura EU307
AF092548.1 gg_id:16239 Clostridium gasigenes str. DSM 12272 AF092
EF197795.1 gg_id:192526 Clostridium tepidiprofundum str. SG508 EF197
AF317650.1 gg_id:31985 Clostridium thiosulfatireducens str. Lup21 AF317
NR_029246.1 gg_id:578922 Clostridium collagenovorans str. SG; DSM 3089 NR_02
AB488292.1 gg_id:591402 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSSURO AB488
FJ269106.1 gg_id:308659 dissimilatory ferric iron reducers arsenic contaminated Hunan south China paddy soil FJ2691
GQ461617.1 gg_id:581078 Coupling -ITS Clone Libraries and Automated Intergenic Spacer Microbial TCE Bioren GQ461
AB487999.1 gg_id:563768 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSSURO AB487
GU118536.1 gg_id:574100 Threatened Corals Provide Microbial Habitats clone Mfav_O15 GU118
AB218319.1 gg_id:148431 Fecal microbial (dugong dugon) determined genes Dugong feces clone dgB-84 AB218
FJ384387.1 gg_id:368281 Clostridium sp. str. BG-C131 FJ3843
AB486212.1 gg_id:554530 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC AB486
AB479046.1 gg_id:571847 SSU sequences Alps Cadagno di Fuori submerged biofilm mats montane wetland ma AB479
DQ129267.1 gg_id:137771 microarray level air two cities Texas urban aerosol clone AKIW1140 DQ129
FJ167457.1 gg_id:310070 microbiology granular sludge under autotrophic mixotrophic and heterotrophic denit FJ1674
EU376532.1 gg_id:275993 Clostridium sp. str. SL149 EU376
AB486270.1 gg_id:586263 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC AB486
EU540396.1 gg_id:280295 profile human microbiota antecubital fossa (inner elbow) skin clone nbt114d04 EU540
EF515406.1 gg_id:224769 Electricigen Enrichment MFC upf microbial fuel cell anode clone 24a07 EF5154
AB488015.1 gg_id:587690 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSSURO AB488

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AB487443.1 gg_id:551963 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNIR0 AB4874
AB486434.1 gg_id:587168 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC AB4864
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AB237714.1 gg_id:139836 microorganisms deep subsurface groundwater sedimentary rock milieu clone HDBW AB2377
AY548784.1 gg_id:104736 Clostridium sp. str. PPf35E8 AY5487
FJ455907.1 gg_id:513952 Variations archaeal and sulfate-methane transition zone continental margin sedimen FJ4559
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EU470933.1 gg_id:297215 red panda feces clone RP_2aaa02d08 EU4709
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EU467216.1 gg_id:296163 black-handed spider monkey feces clone SPIM_c12 EU4672
EU469939.1 gg_id:293118 western lowland gorilla feces clone GOR_aag74h05 EU4699
EU471395.1 gg_id:295548 spectacled bear feces clone SB_2aaa01f09 EU4713

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EU471394.1 gg_id:302208 spectacled bear feces clone SB_2aaa02c08
EU775362.1 gg_id:304758 Western lowland gorilla feces clone GOR_aag74d03
EU777443.1 gg_id:322847 Sumatran orangutan feces clone orang1_aai53a11
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EU778647.1 gg_id:349573 Spectacled bear feces clone SB_2aaa03d12
EU773056.1 gg_id:336187 Banteng feces clone BG_aaa03e12.Contig1
EU470735.1 gg_id:292631 red panda feces clone RP_2aaa01a07
EU778503.1 gg_id:316285 Red Panda feces clone RP_2aaa04c01
EU462430.1 gg_id:296507 Sumatran orangutan feces clone orang1_aai54d09
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EU777615.1 gg_id:325073 Sumatran orangutan feces clone orang1_aai55g02
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EU470843.1 gg_id:292525 red panda feces clone RP_2aaa02c06
EU467479.1 gg_id:289409 Sumatran orangutan feces clone orang1_f07_1
EU778399.1 gg_id:312733 Red Panda feces clone RP_2aaa02h11
EU469758.1 gg_id:293303 flying fox feces clone FF_d05
EU470773.1 gg_id:302078 red panda feces clone RP_2aaa04h10
EU467437.1 gg_id:292461 Sumatran orangutan feces clone orang1_b03
EU471327.1 gg_id:300582 spectacled bear feces clone SB_2aaa01b12
EU774131.1 gg_id:344202 Chimpanzee feces clone CHIMP12_h06
EU773439.1 gg_id:332920 Black lemur feces clone BKLE_e08_1
EU471402.1 gg_id:300228 spectacled bear feces clone SB_2aaa04h09
EU470984.1 gg_id:295643 red panda feces clone RP_2aaa01a08
EU467293.1 gg_id:288118 hamadryas baboon feces clone BAZ_f08
EU776880.1 gg_id:352379 Mongoose lemur feces clone ML_aaj26c04
EU471517.1 gg_id:290669 spectacled bear feces clone SB_2aaa01h09
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AF373919.2 gg_id:28874 Tindallia californiensis str. APO
AJ271456.1 gg_id:71603 Clostridium alcaliphilum B8NS1-

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EU775653.1 gg_id:356516 Hedgehog feces clone HH_aai34d11 EU775
EU467043.1 gg_id:288286 hedgehog feces clone HH_a10_1 EU467
AF458779.1 gg_id:67640 Clostridium caminithermale str. DVird3 AF458
EU573106.1 gg_id:279224 and Dependent Microbial Oil Reservoir North Sea Ekofisk oil field Norwegian sector c EU573
AB294306.1 gg_id:216573 Microbial structure deep coal seem groundwater clone YWB37 AB294
AF507894.1 gg_id:62667 Mono Lake at depth 23m station 6 July 2000 clone ML623J-36 AF507
EU443727.1 gg_id:442217 Thermotalea metallivorans str. B2-1 EU443
DQ234642.1 gg_id:141863 subsurface water clone DR546BH1103001SAD18 DQ234
Y16716.1 gg_id:43181 Natronincola histidinovorans str. Z-7940T (DSM 11416) Y16716
DQ206418.1 gg_id:140290 microbial mediates arsenate reduction soda lake water clone ML-S-1 DQ206
DQ643978.1 gg_id:170026 Geosporobacter subterrenus str. VNs68 DQ643
DQ234901.1 gg_id:141051 Tindallia texcocoense str. IMP-300 DQ234
AJ271453.1 gg_id:19154 Clostridium elmenteitii E2SE1-B AJ2714
AY464940.1 gg_id:104179 Caldanaerocella colombiensis str. P4.4 AY464
GQ848202.1 gg_id:582632 and Archaeal Xiarinur Soda Lake Water-sediment Interface water-sediment interfac GQ848
FM178809.1 gg_id:337073 Monitoring abundance and expression 'dehalococcoides' species chloroethene-redu FM178
AF407695.1 gg_id:60603 Great Artesian Basin clone R82 AF407
EU458270.1 gg_id:288703 North American black bear feces clone BB2_b06_2 EU458
EU775654.1 gg_id:310410 Hedgehog feces clone HH_aai36a02 EU775
AF069742.1 gg_id:16220 Clostridium frigidicarnis str. SPL77A AF069
EF420221.1 gg_id:208357 Mature fine processing harbour methanogenic oil sands tailings pond clone 12-10F EF4202
EU775663.1 gg_id:311928 Hedgehog feces clone HH_aai33c11 EU775
EF614838.1 gg_id:227851 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o EF6148
EU471505.1 gg_id:300929 spectacled bear feces clone SB_2aaa01c11 EU471
DQ015091.1 gg_id:133265 mouse cecum clone M2_c01 DQ015
X77676.1 gg_id:16200 Clostridium algidicarnis str. NCFB 2931 X77676
EU470498.1 gg_id:290076 red panda feces clone RP_1aaa01f09 EU470
EU775623.1 gg_id:321747 Hedgehog feces clone HH_d12 EU775
EU458271.1 gg_id:298041 North American black bear feces clone BB2_b07_3 EU458
EF687331.1 gg_id:282549 Biogeochemistry iron- and sulfur-precipitating microbial mats (Nile Mediterranean) s EF6873
EU470672.1 gg_id:295461 red panda feces clone RP_1aaa04f06 EU470
EU471456.1 gg_id:288039 spectacled bear feces clone SB_2aaa01f07 EU471
AJ229222.1 gg_id:31072 anoxic bulk soil flooded rice microcosm clone BSV78 clone AJ2292
EU458119.1 gg_id:296563 North American black bear feces clone BB2_a10 EU458
EU776900.1 gg_id:306522 Mongoose lemur feces clone ML_aae89h03 EU776
EU459248.1 gg_id:295190 hedgehog feces clone HH_aai34g01 EU459
FJ671124.1 gg_id:519851 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6711
EF174499.1 gg_id:180489 Clostridium sp. str. R6T EF1744
AB487300.1 gg_id:555862 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNIR0 AB487
EU471302.1 gg_id:289222 red panda feces clone RP_3aaa03a04 EU471

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EU334518.1 gg_id:268609 Hexahydro-135-trinitro-135-triazine (RDX) mediated microbial shift under sulfate-rec EU3345
AB487835.1 gg_id:573564 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNSR0 AB4878
EU459314.1 gg_id:302597 hedgehog feces clone HH_aai36b12 EU4593
EU791182.1 gg_id:583383 Enteric defensins are essential regulators intestinal microbial ecology MMP7++ mou: EU7911
EU467034.1 gg_id:297538 hedgehog feces clone HH_b12 EU4670
EU459211.1 gg_id:290495 hedgehog feces clone HH_aai34a09 EU4592
DQ113757.1 gg_id:133349 dog duodenum clone D1-79 DQ113
EU471060.1 gg_id:295623 red panda feces clone RP_3aaa03e04 EU4710
GU370097.1 gg_id:530236 Clostridium sp. str. P530(2) GU370
FJ671035.1 gg_id:530294 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6710
AB487325.1 gg_id:570714 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNIR0 AB4873
EU471294.1 gg_id:298559 red panda feces clone RP_3aaa02e09 EU4712
EU471296.1 gg_id:295884 red panda feces clone RP_3aaa01b07 EU4712
GU370092.1 gg_id:531462 Clostridium sp. str. P410(2) GU370
AM179918.1 gg_id:147513 Identification microflora (Oncorhynchus mykiss) rainbow trout intestine clone G15-: AM179
DQ378249.1 gg_id:155706 oil-polluted soil clone M29_Pitesti DQ378
AJ229181.1 gg_id:49771 unidentified eubacterium clone BSV07 AJ2291
EF614827.1 gg_id:228319 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o EF6148
AY188850.1 gg_id:100886 Clostridium sp. str. C4/1 AY1888
X80834.1 gg_id:16195 long segmented filamentous organism X80834
EU471048.1 gg_id:298484 red panda feces clone RP_3aaa04c09 EU4710
FJ672742.1 gg_id:515811 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6727
EU458241.1 gg_id:302475 North American black bear feces clone BB2_e07_1 EU4582
EU470690.1 gg_id:300663 red panda feces clone RP_1aaa01a07 EU4706
EU471212.1 gg_id:301163 red panda feces clone RP_3aaa03e11 EU4712
DQ339713.1 gg_id:207741 assessment complex microbial degrading long chain fatty acids (LCFA) methanogeni DQ339
AB486591.1 gg_id:535624 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCOR0 AB4865
EU459196.1 gg_id:299207 hedgehog feces clone HH_aai33f09 EU4591
EF512134.1 gg_id:275472 Clostridium bovipellis str. B30 EF5121
AB487343.1 gg_id:586332 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNIR0 AB4873
FJ675375.1 gg_id:524340 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6753
EU459197.1 gg_id:303389 hedgehog feces clone HH_aai33f10 EU4591
EU471292.1 gg_id:293132 red panda feces clone RP_3aaa04d12 EU4712
EU470539.1 gg_id:296716 red panda feces clone RP_1aaa02d04 EU4705
AB487691.1 gg_id:541232 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNSR0 AB4876
FJ670764.1 gg_id:514451 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6707
EF614891.1 gg_id:230025 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o EF6148
EF614886.1 gg_id:232991 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o EF6148
EU471288.1 gg_id:288145 red panda feces clone RP_3aaa04h03 EU4712
EU458168.1 gg_id:294391 North American black bear feces clone BB2_h02 EU4581
GQ014753.1 gg_id:494913 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw763g GQ014

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k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

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AM183108.1 gg_id:239292 and its spatial composts compost clone SMC65 AM183
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GQ075849.1 gg_id:415537 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1 GQ075

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GQ080759.1 gg_id:410475 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1 GQ080
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GQ089736.1 gg_id:461914 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw3 GQ089
GQ042145.1 gg_id:455500 Topographical and Temporal Human Skin Microbiome skin alar crease clone nbw93e GQ042
GQ081175.1 gg_id:462037 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1 GQ081

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EF586060.1 gg_id:241189 Methanol-assimilating anaerobic solid waste digester fed methanol clone M55_D21_ EF586
EU369163.1 gg_id:314592 libraries oyster shell clone MBFOS-04 EU369
AF550609.1 gg_id:84656 Peptostreptococcaceae bacterium 19gly3 AF550
EF586042.1 gg_id:246996 Methanol-assimilating anaerobic solid waste digester fed methanol clone M55_D15_ EF586
AB109772.2 gg_id:87971 Finegoldia magna str. ATCC 29328 AB109
NZ_ACHM01000169.1 gg_id:470400 Finegoldia magna str. ATCC 53516 NZ_AC
NC_010376.1 gg_id:471282 Finegoldia magna str. ATCC 29328 NC_01
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NR_029237.1 gg_id:590651 Helcococcus kunzii str. 22; NCFB 2900 NR_02
EU931445.1 gg_id:523124 examined methods chronic venous leg ulcer clone CONR27 EU931
AB542081.1 gg_id:541571 Helcococcus ovis str. H10-Yamagata-990517 AB542
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FJ671232.1 gg_id:524188 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6712
DQ532264.1 gg_id:162924 Geographical Variation Microbial Burden and Spacecraft Assembly Johnson Space Ce DQ532
FJ959755.1 gg_id:537785 bottlenose dolphin upper respiratory tract blowhole clone D8A8_086 FJ9597
FJ671016.1 gg_id:512501 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6710
FJ959635.1 gg_id:570400 bottlenose dolphin upper respiratory tract blowhole clone D896_235 FJ9596

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FJ672944.1 gg_id:527947 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6729
FJ672144.1 gg_id:515690 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6721
FJ959504.1 gg_id:586313 bottlenose dolphin upper respiratory tract blowhole clone D896_088 FJ9595
FJ670651.1 gg_id:523741 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6706
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FJ960159.1 gg_id:590557 bottlenose dolphin upper respiratory tract blowhole clone D9A4_045 FJ9601
FJ675329.1 gg_id:512373 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6753
FJ674777.1 gg_id:529441 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6747
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FJ960145.1 gg_id:556060 bottlenose dolphin upper respiratory tract blowhole clone D9A4_031 FJ9601
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AM176532.1 gg_id:181489 Peptostreptococcus micros gpac134 AM176
AY349390.1 gg_id:92862 human oral cavity clone FJ023 AY3493
AF542231.1 gg_id:83408 Peptostreptococcus micros str. ATCC 33270 AF5422
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FJ577254.2 gg_id:567933 Peptoniphilus sp. 'Oral Taxon 386' str. F0131 FJ5772
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FJ557799.1 gg_id:524282 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5577
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GQ101711.1 gg_id:392255 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw498d03c GQ101
AY153431.1 gg_id:86504 Peptoniphilus indolicus str. CCUG 46591 AY1534
GQ014236.1 gg_id:495429 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw760e GQ014
GQ087341.1 gg_id:448805 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw GQ087
AB538435.1 gg_id:583324 Peptoniphilus sp. str. JCM 8143 AB5384
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GQ043038.1 gg_id:405497 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1012d GQ043
GQ046233.1 gg_id:430948 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw GQ046
GQ014651.1 gg_id:495015 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw762c GQ014
GQ004003.1 gg_id:505659 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu67d0 GQ004
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GQ070679.1 gg_id:456602 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw GQ070
GQ076958.1 gg_id:415523 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw1155 GQ076
FJ557959.1 gg_id:521795 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5579
GQ003957.1 gg_id:505704 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu66g0 GQ003
EU526289.1 gg_id:269603 Peptoniphilus sp. str. WAL 1768N EU5262
GQ016450.1 gg_id:493216 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ016
GQ031247.1 gg_id:464237 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor GQ031
AF481225.1 gg_id:68341 Peptostreptococcus sp. str. E3_32 AF4812

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Y07840.1 gg_id:14275 Peptoniphilus ivorii str. DSM 10022; SBH093 Y07840
EU289040.1 gg_id:249152 microbiome cloacal openings urogenital and anal tracts tammar wallaby Macropus e EU289
X90471.1 gg_id:14281 Peptostreptococcus sp str. 9succ1 X90471
FJ671194.1 gg_id:521628 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6711
AY167967.1 gg_id:75475 Isolation and identification hyper-ammonia producing swine storage pits manure AY1679
FJ675039.1 gg_id:528981 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6750
CU919308.1 gg_id:540944 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU919
AY754832.1 gg_id:108707 Hudson river sediment clone Z35 AY7548
FJ674316.1 gg_id:518267 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6743
FJ825558.1 gg_id:535477 Microbial during start-up mesophilic biogas plant clone 45_BS4_8 FJ8255
FJ675649.1 gg_id:529080 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6756
DQ168650.1 gg_id:157172 sediment-free PCB-dechlorinating enrichment culture clone JN18_A14_H DQ168
FJ671648.1 gg_id:528290 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6716
NR_025498.1 gg_id:569679 Sedimentibacter saalensis str. ZF2; DSM 13558 NR_02
FJ674650.1 gg_id:513014 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6746
EF059533.1 gg_id:221904 Sedimentibacter sp. JN18_V27_I EF0595
CU927625.1 gg_id:567949 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU927
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AF427155.1 gg_id:34493 Clostridium sp. LTR1 AF4271
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AB294744.1 gg_id:207626 Dechlorination biphenyl polychlorinated dibenzo-p-dioxin species genus Dehalobacte AB2947
AY353956.1 gg_id:103341 Soehngenia saccharolytica str. BOR-Y AY3539
NR_025151.1 gg_id:553089 Sporanaerobacter acetigenes str. Lup33; DSM 13106 NR_02
GQ461820.1 gg_id:585584 Tissierella sp. str. LBN 299 GQ461
AB175360.1 gg_id:102260 mesophilic anaerobic BSA digester clone BSA1B-06 AB1753
AB332034.1 gg_id:312984 Tepidimicrobium sp. str. HUT8119 AB3320
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AB436741.1 gg_id:284303 Clostridium sp. str. AAN13 AB4367
AF280824.1 gg_id:72660 bioreactor clone tbr1-9 AF2808
GQ461826.1 gg_id:587283 Tepidimicrobium ferriphilum str. DSM 16624 GQ461
X80833.1 gg_id:14261 Tissierella praeacuta str. ATCC 25539 X80833
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FJ675493.1 gg_id:517458 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6754
DQ378266.2 gg_id:151594 oil-polluted soil clone M50_Pitesti DQ378
FJ825564.1 gg_id:561089 Microbial during start-up mesophilic biogas plant clone 62_BS5_26 FJ8255
AM500851.1 gg_id:560842 proof spatial heterogeneity hot composting clone F132 AM500
EU887816.1 gg_id:321681 Tissierella praeacuta str. SN5 EU8878
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GQ461818.1 gg_id:579451 Tissierella sp. str. LBN 291 GQ461

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DQ532342.1 gg_id:172183 Geographical Variation Microbial Burden and Spacecraft Assembly Kennedy Space C DQ532
GQ004946.1 gg_id:504716 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu65b0 GQ004
GQ026805.1 gg_id:447236 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ026
GQ029521.1 gg_id:436394 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw862e05 GQ029
GU455219.1 gg_id:515391 Understanding short-chain fatty acids accumulation enhanced alkaline digestion: kir GU455
DQ887969.1 gg_id:164133 thermophilic anaerobic solid waste bioreactor clone TIBG06 DQ887
AY169425.1 gg_id:81585 Finegoldia magna AY1694
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EF586050.1 gg_id:240034 Methanol-assimilating anaerobic solid waste digester fed methanol clone M55_D15_ EF5860
GQ015365.1 gg_id:494301 Topographical and Temporal Human Skin Microbiome skin palm clone nbw767e08c1 GQ015
GQ079937.1 gg_id:406655 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ079
GQ016716.1 gg_id:492950 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw824g0 GQ016
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FM873737.1 gg_id:364028 occupant source house mattress dust clone MA03H02 FM873
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FJ672003.1 gg_id:527552 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6720
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FM873179.1 gg_id:367696 occupant source house floor dust clone FC02H05 FM873
EF559008.1 gg_id:256589 Microbial functional groups solid waste digestor stable isotope probing thermophilic EF5590
GU455217.1 gg_id:514459 Understanding short-chain fatty acids accumulation enhanced alkaline digestion: kir GU455
FJ674852.1 gg_id:522075 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6748
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EU289126.1 gg_id:236687 microbiome cloacal openings urogenital and anal tracts tammar wallaby Macropus e EU2891
FJ672085.1 gg_id:524642 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6720
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GQ009384.1 gg_id:500281 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ009
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AM500842.1 gg_id:561616 proof spatial heterogeneity hot composting clone F68 AM500
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GQ033406.1 gg_id:464209 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ033
EU407217.1 gg_id:259078 household biogas digester clone GW-34 EU407
AF016691.1 gg_id:14132 Acidaminobacter hydrogenoformans str. glu 65 AF0166
EU591652.1 gg_id:275236 Microbial Ecology Focused-Pulsed Electric Field Sludge Pretreatment Methanogenic EU5916
EU517558.1 gg_id:267846 methanogenic microbial consortia mature oil sands tailings clone 22-7A EU5175
AF491333.1 gg_id:85424 Fusibacter sp. str. SA1 AF4913

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AB243990.1 gg_id:245248 Methods Investigate Microbial Niigata oil well clone Niigata-22 AB243
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GU208315.1 gg_id:584294 Study on Sediment Dongping Lake sediment clone Sef3-12 GU208
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GQ054198.1 gg_id:422335 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1099g GQ054
GQ014246.1 gg_id:495420 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw760f GQ014
EF562251.1 gg_id:241088 Subsurface microbial deep-granitic-fracture water colorado Henderson Molybdenum EF5622
GQ014194.1 gg_id:495473 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw760a GQ014
GQ054010.1 gg_id:426893 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1097e GQ054
EF419415.1 gg_id:213421 Substantial alterations cutaneous biota psoriatic lesions human skin clone 6PN20 EF4194
GQ009336.1 gg_id:500329 Topographical and Temporal Human Skin Microbiome skin interdigital web space cl GQ009
AJ005636.1 gg_id:14151 Eubacterium minutum str. ATCC 700079 AJ0056
AJ006963.1 gg_id:14160 Eubacterium sulci str. ATCC 35585 AJ0069
GQ502514.1 gg_id:552342 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf4- GQ502
FJ880553.1 gg_id:426130 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8805
EF099448.1 gg_id:178412 mouse cecum clone SWPT3_aaa03d03 EF0994
DQ793597.1 gg_id:191389 human fecal clone RL246_aai74b05 DQ793
EU844897.1 gg_id:344416 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
GU303039.1 gg_id:576991 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU303
EU842953.1 gg_id:332719 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU842
FJ880679.1 gg_id:420891 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8806
FJ879943.1 gg_id:380842 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8799
EU773171.1 gg_id:324364 BigHorn sheep feces clone BH1_aao26e07 EU773
GU304138.1 gg_id:583497 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU304
GU304385.1 gg_id:553278 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU304
U13041.1 gg_id:14155 Eubacterium nodatum str. ATCC 33099 U1304
GQ458236.1 gg_id:579985 Microbial structure co-digestion anaerobic bioreactors treating cassava pulp and pig GQ458
EU842678.1 gg_id:340989 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
FJ687606.2 gg_id:552238 Eubacterium sp. str. WAL 14571 FJ6876
AF044945.1 gg_id:14152 Eubacterium sp. str. C2 AF044
EF099332.1 gg_id:181305 mouse cecum clone SWPT3_aaa01h03 EF0993
EU452756.1 gg_id:318652 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83 EU452
EU469216.1 gg_id:294038 Speke's gazelle feces clone SP3_c03_2 EU469
AB034093.1 gg_id:39613 rumen clone 4C3d-12 AB034
FJ879878.1 gg_id:409369 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8798
GU304486.1 gg_id:592803 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU304

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FJ983009.1 gg_id:451218 Aspects Oral Microbiome root canal clone FJ9830
EU777969.1 gg_id:342539 Black rhinoceros feces clone RH_aaj90f11 EU777
Z36296.1 gg_id:14163 Mogibacterium timidum str. ATCC 33093 Z36296
AB037875.1 gg_id:46159 Mogibacterium neglectum str. ATCC 700924 (=P9a-h) AB0378
AF371681.1 gg_id:36226 swine intestine clone p-3263-42A2 AF3716
EU794083.1 gg_id:304402 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_E28 EU7940
FJ680355.1 gg_id:525024 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6803
DQ797373.1 gg_id:189641 human fecal clone RL248_aai98e08 DQ797
EU771238.1 gg_id:309179 Asiatic elephant feces clone AE1_aaa03b04 EU771
GU303467.1 gg_id:588896 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU303
EU234217.1 gg_id:239736 river and un techniques downstream Wang Yang River receiving penicillin G producti EU2342
EU457038.1 gg_id:342368 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU4570
GU304097.1 gg_id:584897 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU304
GQ014713.1 gg_id:494953 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw763c GQ014
FJ833233.1 gg_id:508773 Microbial Ecology Crop Folivorous Hoatzin crop contents clone A3Q202_47G06 FJ8332
GU303409.1 gg_id:583010 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU303
EU842915.1 gg_id:335229 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU8429
EU470097.1 gg_id:289968 trancaspain urial feces clone TU1_aaa01h04 EU4700
AY858404.3 gg_id:112328 gastrointestinal tract Grant's gazelle clone GRANT32 AY8584
EU469300.1 gg_id:301283 Speke's gazelle feces clone SP3_f08_3 EU4693
EU462515.1 gg_id:302242 Sumatran orangutan feces clone orang1_aai56b09 EU4625
EU468647.1 gg_id:295362 okapi feces clone OK2_d11_1 EU4686
DQ353910.1 gg_id:150089 Fecal Wild Gorilla (Gorilla beringei) wild gorilla feces clone Z23 DQ353
GU303120.1 gg_id:580364 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU303
DQ325886.1 gg_id:148168 Metagenomic gut microbiome healthy human stool clone B691 DQ325
GU304081.1 gg_id:577079 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU304
EU234134.1 gg_id:236437 receiving river and un techniques anaerobic process WWTP treating penicillin G prod EU2341
EU776276.1 gg_id:319547 Red Kangaroo feces clone KO1_aai42d10 EU7762
DQ325813.1 gg_id:147447 Metagenomic gut microbiome healthy human stool clone B543 DQ325
EU344320.1 gg_id:276794 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU3443
GU304446.1 gg_id:586769 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU304
GU302749.1 gg_id:589680 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU302
DQ801393.1 gg_id:196828 human fecal clone RL388_aao94h07 DQ801
EU463611.1 gg_id:288422 domesticated horse feces clone horsej_aai89g02 EU4636
EU748523.1 gg_id:341085 neotropical folivorous flying bird adult hoatzin crop clone hoa61_11e08 EU7485
EU748100.1 gg_id:307485 neotropical folivorous flying bird adult hoatzin crop clone hoa2_42b01 EU7481
DQ325766.1 gg_id:147449 Metagenomic gut microbiome healthy human stool clone B444 DQ325
AF371687.1 gg_id:28381 swine intestine clone p-1032-a5 AF3716
DQ394650.1 gg_id:151714 on -Arctic peninsula Svalbard Norway determined genes and rumen isolates reindee DQ394
AY854283.1 gg_id:109624 herbivore gastrointestinal tract clone CATTLE_21 AY8542
GU303390.1 gg_id:535500 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU303

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AB218305.1 gg_id:148228 Fecal microbial (dugong dugon) determined genes Dugong feces clone dgA-3 AB2183
EU775736.1 gg_id:320853 Horse feces clone horsej_aai91a05 EU7757
DQ797955.1 gg_id:184240 human fecal clone RL302_aal93g12 DQ797
EF586058.1 gg_id:249539 Methanol-assimilating anaerobic solid waste digester fed methanol clone M55_D21_ EF5860
EU878314.1 gg_id:510808 Investigation factors influencing production large-scale municipal biogas plant therm EU8783
EF559085.1 gg_id:223604 mesophilic anaerobic digester clone B35_F_B_E05 EF5590
EU639283.1 gg_id:324728 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU6392
EU591634.1 gg_id:271468 Microbial Ecology Focused-Pulsed Electric Field Sludge Pretreatment Methanogenic : EU5916
AB274505.1 gg_id:203717 packed-bed reactor clone CFB-16 AB2745
AY684094.1 gg_id:137161 first genome data rice I methanogens combination cultivation and techniques metha AY6840
FN563391.1 gg_id:572575 Impact changing HRT OLR on prokaryotes involved biomethanizitaion and fuzzy logic FN5633
EU639029.1 gg_id:316446 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU6390
EU358732.1 gg_id:304420 structure archaeal denaturing gel electrophoresis and sequencing mesophilic biogas EU3587
EF603619.1 gg_id:229057 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6036
X86690.1 gg_id:13929 Dehalobacterium formicoaceticum str. DMC X86690
AB486500.1 gg_id:568326 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC AB4865
EF603618.1 gg_id:230762 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6036
AM943569.1 gg_id:258502 Microbial dolomite formation Lagoa Vermelha Brazil carbonaceous sediments hyper AM943
EU259468.1 gg_id:238635 Rumen yak (Bos grunniens) sequences rumen fluid clone YRC92 EU2594
EU469050.1 gg_id:296184 Speke's gazelle feces clone SP2_e04_3 EU4690
AY426448.1 gg_id:106335 full-scale anaerobic UASB bioreactor treating paper mill wastewater clone B35 AY4264
EF614786.1 gg_id:229827 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o EF6147
EF515659.1 gg_id:227372 Electricigen Enrichment MFC full-scale anaerobic bioreactor sludge treating brewery EF5156
AY991064.1 gg_id:130311 mouse cecum clone C13_I13 AY9910
FJ879326.1 gg_id:449353 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8793
EF614689.1 gg_id:231836 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o EF6146
GU303484.1 gg_id:575101 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU303
EU134643.1 gg_id:244028 tallgrass prarie soil clone FFCH13041 EU1346
EF559162.1 gg_id:221790 mesophilic anaerobic digester clone G35_D8_L_B_E01 EF5591
EU474249.1 gg_id:288109 western lowland gorilla feces clone GORSD_aaa02b06 EU4742
AY990091.1 gg_id:135305 mouse cecum clone C12_E08 AY9900
EF602919.1 gg_id:228772 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6029
CU918616.1 gg_id:545232 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU9186
DQ015163.1 gg_id:131268 mouse cecum clone M2_d06_2 DQ015
AB546238.1 gg_id:532064 Acetobacterium carbinolicum str. Mic2c03 AB5462
AB546237.1 gg_id:523930 Acetobacterium carbinolicum str. Mic2c01 AB5462
AB294288.1 gg_id:213453 Microbial structure deep coal seem groundwater clone YWB19 AB2942
FM178819.1 gg_id:354559 Monitoring abundance and expression 'dehalococcoides' species chloroethene-redu FM178
X96960.1 gg_id:14231 Acetobacterium bakii str. DSM 8239 X96960
AY185326.1 gg_id:79463 Acetobacterium sp. clone AKS48 AY1853

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AY185325.1 gg_id:79549 Acetobacterium sp. clone AKS42 AY1853
AB546245.1 gg_id:522312 Acetobacterium sp. str. Mic7c05 AB5462
AY185319.1 gg_id:79098 Acetobacterium sp. clone AKS04 AY1853
X96958.1 gg_id:14249 Acetobacterium paludosum str. DSM 8237 X96958
DQ447180.1 gg_id:156581 Coexistence homoacetogens and heterotrophic sulfate-reducing synthesis gas fed la DQ447
AF132739.1 gg_id:14234 Acetobacterium psammolithicum str. CN-E AF1327
AY185318.1 gg_id:79515 Acetobacterium sp. clone AKS02 AY1853
X96959.1 gg_id:14257 Acetobacterium fimetarium str. DSM 8238 X96959
AY185323.1 gg_id:79093 Acetobacterium sp. clone AKS29 AY1853
AJ518871.2 gg_id:104008 Anaerofustis stercorihominis str. wal 14563 AJ5188
DQ353902.1 gg_id:148988 Fecal Wild Gorilla (Gorilla beringei) wild gorilla feces clone Z4 DQ353
AB198513.1 gg_id:135410 termite gut wall fraction clone RsW01-091 AB1985
EU843431.1 gg_id:319993 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8434
FJ833673.1 gg_id:543902 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J1Q402_77E10 FJ8336
DQ353937.1 gg_id:149723 Fecal Wild Gorilla (Gorilla beringei) wild gorilla feces clone Z105 DQ353
EU462735.1 gg_id:291786 Sumatran orangutan feces clone orang2_aai68b12 EU4627
EU844993.1 gg_id:323946 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8449
AB088988.1 gg_id:77821 termite gut homogenate clone Rs-H81 bacterium AB0889
AM691886.2 gg_id:527988 Microbial level alterations overall gastrointestinal microbiota diarrhoea-predominar AM691
AB298910.1 gg_id:275347 Eubacterium limosum str. #5 AB2989
AY533381.1 gg_id:106035 Eubacterium yurii subsp. margaretiae str. ATCC 43715 AY5333
EU463292.1 gg_id:294324 naked mole-rat feces clone molerat_aai72h11 EU4632
AJ518868.1 gg_id:109633 Eubacterium sp. str. CS1 Van AJ5188
AY533382.1 gg_id:106183 Eubacterium yurii subsp. schtitka str. ATCC 43716 AY5333
AM419991.1 gg_id:247984 Noma subgingival plaque clone 102C12(oral) AM419
AB036759.1 gg_id:46867 Pseudoramibacter alactolyticus str. 23263T AB0367
EU474929.1 gg_id:296092 red river hog feces clone RRH_aaa02e07 EU4749
AF073898.1 gg_id:14253 Eubacterium aggregans str. SR12; DSM 12183 AF0738
EU845579.1 gg_id:335896 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8455
EU468268.1 gg_id:302875 domesticated horse feces clone horsej_g07 EU4682
DQ478748.1 gg_id:157142 UASB reactor treating brewery wastewater clone CLONG19 DQ478
DQ339707.1 gg_id:214750 assessment complex microbial degrading long chain fatty acids (LCFA) methanogeni DQ339
FJ672150.1 gg_id:514900 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6721
GU180172.1 gg_id:554177 Impact coplanar PCBs on microbial activity anaerobic estuarine sediments sediment GU180
AY312403.2 gg_id:89746 Alkalibacter saccharofermentans str. Z-79820 AY3124
EU843219.1 gg_id:311974 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8432
FJ672463.1 gg_id:524649 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6724
EU344196.1 gg_id:274259 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU3441
FJ672328.1 gg_id:532190 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6723

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AY554414.1 gg_id:103303 Alkalibacterium sp. 8B AY5544
CP000930.2 gg_id:262344 Heliobacterium modesticaldum Ice1 str. Ice1; ATCC 51547 CP0009
NC_010337.1 gg_id:268302 Heliobacterium modesticaldum Ice1 str. Ice1; ATCC 51547 NC_01
AB100837.1 gg_id:110646 Heliobacterium gestii str. DSM 11169 AB1008
AF249678.1 gg_id:73860 Heliobacterium sulfidophilum str. BR4 (T) AF2496
NR_028721.1 gg_id:571373 Heliorestis daurensis str. BT-H1; ATCC 700798 NR_02
NR_025932.1 gg_id:548015 Heliobacterium chlorum str. ATCC 35205 NR_02
AF028351.1 gg_id:14069 Clostridium indolis CM971 AF0283
NR_024993.1 gg_id:555445 Clostridium fimetarium str. Z-2189; DSM 9179 NR_02
DQ513077.1 gg_id:161135 Microbial life fluids ridge flank crustal fluid clone FS266-27B-03 DQ513
EF559143.1 gg_id:221028 mesophilic anaerobic digester clone G35_D8_L_B_A11 EF5591
FJ672313.1 gg_id:524287 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6723
AF275914.2 gg_id:72606 anaerobic digester clone AA02 AF2759
ABVQ01000036.1 gg_id:561391 Bacteroides pectinophilus str. ATCC 43243 ABVQ0
GQ493997.1 gg_id:594268 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
FJ369932.1 gg_id:360069 feces adult twins and mothers; TS55 clone TS55_a02d10 FJ3699
FJ978689.1 gg_id:458990 feces clone CL_F_376 FJ9786
EU463007.1 gg_id:293490 southern three-banded armadillo feces clone arma_aaj56d10 EU463
FJ678747.1 gg_id:512569 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6787
DQ804305.1 gg_id:195563 human fecal clone RL187_aan77g02 DQ804
FJ364622.1 gg_id:368535 feces adult twins and mothers; TS19 clone TS19_a01b05 FJ3646
FJ978518.1 gg_id:412390 feces clone CL_F_049 FJ9785
DQ804223.1 gg_id:183849 human fecal clone RL187_aah70e06 DQ804
EU465331.1 gg_id:290362 lion feces clone LI3_aah75d08 EU465
GQ867449.1 gg_id:578056 and prevalence blaTEM genes Arctic seals colon content clone CSG14 GQ867
EU772751.1 gg_id:318444 Bush dog feces clone bdog3_aad67f09 EU772
EU468418.1 gg_id:298896 lion feces clone LI2_aae50b09 EU468
GQ491687.1 gg_id:571472 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
EU465525.1 gg_id:288367 lion feces clone LI3_aah78h10 EU465
AY977095.1 gg_id:119459 human cecum mucosal biopsy clone K786 AY977
FJ677562.1 gg_id:532487 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6775
AY975491.1 gg_id:120281 human ascending colon mucosal biopsy clone N930 AY9754
GQ491473.1 gg_id:562403 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
FJ368564.1 gg_id:365763 feces adult twins and mothers; TS49 clone TS49_a01g11 FJ3685
EU462872.1 gg_id:291656 southern three-banded armadillo feces clone arma_aaj54c07 EU462
FJ364917.1 gg_id:369814 feces adult twins and mothers; TS19 clone TS19_a04g02 FJ3649
EU467598.1 gg_id:297131 southern three-banded armadillo feces clone arma_h05_1 EU467
FJ368665.1 gg_id:365150 feces adult twins and mothers; TS49 clone TS49_a03a07 FJ3686
EU465383.1 gg_id:287495 lion feces clone LI3_aah76d08 EU465
DQ803632.1 gg_id:179340 human fecal clone RL251_aaj88d11 DQ803
EU458570.1 gg_id:302128 spotted hyena feces clone HY2_h05_1 EU458

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EU772730.1 gg_id:304309 Bush dog feces clone bdog1_aai80c10 EU772
EU463036.1 gg_id:301318 southern three-banded armadillo feces clone arma_aaj56g11 EU463
EU467565.1 gg_id:296174 southern three-banded armadillo feces clone arma_e09 EU467
DQ456327.1 gg_id:158939 pre-adolescent turkey cecum clone CFT212A8 DQ456
AY980578.1 gg_id:115563 human rectum mucosal biopsy clone X564 AY980
DQ804061.1 gg_id:194041 human fecal clone RL187_aah67h08 DQ804
DQ804970.1 gg_id:192897 human fecal clone RL385_aao83d06 DQ804
EU465381.1 gg_id:295456 lion feces clone LI3_aah76d06 EU465
AY984413.1 gg_id:115474 human stool clone B322 AY984
FJ370721.1 gg_id:363714 feces adult twins and mothers; TS57 clone TS57_a04d11 FJ3707
EF403112.1 gg_id:205138 human fecal clone SJTU_B_15_05 EF4031
EU462960.1 gg_id:289142 southern three-banded armadillo feces clone arma_aaj55g02 EU462
EU462816.1 gg_id:301634 southern three-banded armadillo feces clone arma_aaj53e06 EU462
GQ491355.1 gg_id:585006 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
AY858537.2 gg_id:109545 gastrointestinal tract eland clone ELAND_90 AY858
EU462957.1 gg_id:287601 southern three-banded armadillo feces clone arma_aaj55f09 EU462
EU771926.1 gg_id:304393 Southern three-banded armadillo feces clone arma_aaj55d07 EU771
EU465322.1 gg_id:291815 lion feces clone LI3_aah75c06 EU465
EU462823.1 gg_id:299390 southern three-banded armadillo feces clone arma_aaj53f04 EU462
EU467568.1 gg_id:292964 southern three-banded armadillo feces clone arma_f10 EU467
EU467548.1 gg_id:301090 southern three-banded armadillo feces clone arma_h01 EU467
DQ807651.1 gg_id:192025 human fecal clone RL180_aah35e03 DQ807
EU467605.1 gg_id:288469 southern three-banded armadillo feces clone arma_c03_1 EU467
DQ804131.1 gg_id:181706 human fecal clone RL187_aah69a12 DQ804
AM276759.2 gg_id:231704 fecal microbiota irritable bowel syndrome patients significantly that healthy subject AM276
GQ491435.1 gg_id:566739 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
DQ793721.1 gg_id:194494 human fecal clone RL246_aai76b10 DQ793
EU771867.1 gg_id:311777 Southern three-banded armadillo feces clone arma_h08 EU771
DQ803436.1 gg_id:176107 human fecal clone RL251_aaj85g06 DQ803
AB534168.1 gg_id:537101 Blautia hansenii DSM 20583 str. JCM 14655 AB534
GQ492373.1 gg_id:564101 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
EU773903.1 gg_id:310173 Cheetah feces clone CE3_aai06h09 EU773
EU771961.1 gg_id:337246 Southern three-banded armadillo feces clone arma_aaj56h08 EU771
DQ804247.1 gg_id:183955 human fecal clone RL187_aah70h02 DQ804
EU772709.1 gg_id:311712 Bush dog feces clone bdog1_aai79g01 EU772
EF399220.1 gg_id:211999 human fecal clone SJTU_F_13_18 EF3992
FJ368791.1 gg_id:357004 feces adult twins and mothers; TS49 clone TS49_a04f03 FJ3687
DQ905190.1 gg_id:163706 human fecal clone 013-a11 DQ905
GQ079651.1 gg_id:433152 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1232g(GQ079
EF402578.1 gg_id:214316 human fecal clone SJTU_B_09_74 EF4025

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EU530199.1 gg_id:268713 mucosa adherent and invasive microbes profile adenoma colorectal cancer clone M1 EU5301
GQ897170.1 gg_id:564568 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ897
FJ367882.1 gg_id:360376 feces adult twins and mothers; TS2 clone TS2_a04f09 FJ3678
AY978324.1 gg_id:120310 human transverse colon mucosal biopsy clone F221 AY9783
FJ366070.1 gg_id:366070 feces adult twins and mothers; TS25 clone TS25_a02d03 FJ3660
DQ804337.1 gg_id:176335 human fecal clone RL187_aan78c04 DQ804
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FJ368690.1 gg_id:360794 feces adult twins and mothers; TS49 clone TS49_a03d02 FJ3686
FJ367559.1 gg_id:362330 feces adult twins and mothers; TS2 clone TS2_a01a03 FJ3675
EU762964.1 gg_id:330799 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A> EU7629
FJ368669.1 gg_id:366222 feces adult twins and mothers; TS49 clone TS49_a03b03 FJ3686
DQ326724.1 gg_id:146107 Metagenomic gut microbiome healthy human stool clone E179 DQ326
GQ077133.1 gg_id:436257 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1207e GQ077
X85101.1 gg_id:13989 Ruminococcus obeum X85101
EF404046.1 gg_id:206980 human fecal clone SJTU_C_03_91 EF4040
NZ_AAVO02000010.1 gg_id:254715 Ruminococcus obeum str. ATCC 29174 NZ_AA
DQ804388.1 gg_id:180845 human fecal clone RL187_aan79b02 DQ804
FJ371930.1 gg_id:363437 feces adult twins and mothers; TS8 clone TS8_a03h01 FJ3719
EF402596.1 gg_id:215785 human fecal clone SJTU_B_10_02 EF4025
FJ363590.1 gg_id:361362 feces adult twins and mothers; TS14 clone TS14_a01b02 FJ3635
FJ363622.1 gg_id:358484 feces adult twins and mothers; TS14 clone TS14_a01d10 FJ3636
FJ369679.1 gg_id:362541 feces adult twins and mothers; TS51 clone TS51_a03e08 FJ3696
AY976610.1 gg_id:122356 human cecum mucosal biopsy clone K164 AY9766
FJ368962.1 gg_id:365261 feces adult twins and mothers; TS4 clone TS4_a02f04 FJ3689
FJ364994.1 gg_id:366762 feces adult twins and mothers; TS1 clone TS1_a01f02 FJ3649
GQ897939.1 gg_id:546581 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ897
FJ363819.1 gg_id:362428 feces adult twins and mothers; TS14 clone TS14_a03g02 FJ3638
FJ366168.1 gg_id:364536 feces adult twins and mothers; TS25 clone TS25_a03e05 FJ3661
AY982558.1 gg_id:118219 human descending colon mucosal biopsy clone KW23 AY9825
EU728790.1 gg_id:346709 Ruminococcus sp. str. DJF_VR66 EU7287
FJ363623.1 gg_id:362465 feces adult twins and mothers; TS14 clone TS14_a01d11 FJ3636
FJ367436.1 gg_id:368938 feces adult twins and mothers; TS29 clone TS29_a03e06 FJ3674
FJ366601.1 gg_id:368132 feces adult twins and mothers; TS27 clone TS27_a01f03 FJ3666
FJ366452.1 gg_id:366345 feces adult twins and mothers; TS26 clone TS26_a03d10 FJ3664
FJ368714.1 gg_id:360328 feces adult twins and mothers; TS49 clone TS49_a03f04 FJ3687
AY978747.1 gg_id:118593 human transverse colon mucosal biopsy clone KU92 AY9787
DQ806775.1 gg_id:176537 human fecal clone RL186_aao48e10 DQ806
FJ363900.1 gg_id:359930 feces adult twins and mothers; TS14 clone TS14_a04f10 FJ3639
DQ807635.1 gg_id:187021 human fecal clone RL180_aah35c04 DQ807

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DQ326454.1 gg_id:146226 Metagenomic gut microbiome healthy human stool clone C529 DQ326
EU466824.1 gg_id:289535 African elephant feces clone AFEL2_aao29h11 EU466
DQ808076.1 gg_id:183267 human fecal clone RL180_aan72a03 DQ808
DQ825011.1 gg_id:198532 human fecal clone RL185_aao72c02 DQ825
DQ807333.1 gg_id:196082 human fecal clone RL307_aam05c04 DQ807
DQ808105.1 gg_id:187385 human fecal clone RL180_aan72e11 DQ808
DQ801994.1 gg_id:194896 human fecal clone RL241_aaj01e12 DQ801
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DQ808200.1 gg_id:179609 human fecal clone RL180_aao73g10 DQ808
DQ799237.1 gg_id:191132 human fecal clone RL205_aaj19e10 DQ799
DQ800722.1 gg_id:178016 human fecal clone RL183_aao02f03 DQ800
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DQ795471.1 gg_id:197050 human fecal clone RL178_aah54g05 DQ795
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DQ326114.1 gg_id:148619 Metagenomic gut microbiome healthy human stool clone BB74 DQ326
DQ802802.1 gg_id:173917 human fecal clone RL188_aan96g04 DQ802
DQ800314.1 gg_id:181003 human fecal clone RL303_aal71c11 DQ800
DQ808280.1 gg_id:193210 human fecal clone RL180_aao74g04 DQ808
DQ823693.1 gg_id:191950 human fecal clone RL250_aaj77g04 DQ823
FJ370624.1 gg_id:359520 feces adult twins and mothers; TS57 clone TS57_a03c09 FJ3706
DQ803440.1 gg_id:188945 human fecal clone RL251_aaj85g11 DQ803
DQ803485.1 gg_id:181226 human fecal clone RL251_aaj86d09 DQ803
EU460987.1 gg_id:293389 red kangaroo feces clone KO1_aai41f04 EU460
EU771800.1 gg_id:356581 African elephant feces clone AFEL2_aao29b06 EU771
DQ057459.1 gg_id:130214 str. ic1296 DQ057
DQ805983.1 gg_id:186994 human fecal clone RL186_aah59e06 DQ805
DQ797262.1 gg_id:198626 human fecal clone RL248_aai97a11 DQ797
DQ799354.1 gg_id:193868 human fecal clone RL305aal85c08 DQ799
DQ799334.1 gg_id:176070 human fecal clone RL305aal85a09 DQ799
FJ674172.1 gg_id:510818 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6741
DQ800278.1 gg_id:179866 human fecal clone RL303_aal70g01 DQ800
DQ801693.1 gg_id:183940 human fecal clone RL201_aai45e12 DQ801
DQ804358.1 gg_id:189998 human fecal clone RL187_aan78e11 DQ804
DQ801564.1 gg_id:198752 human fecal clone RL117_aae91d03 DQ801
DQ808168.1 gg_id:187796 human fecal clone RL180_aao73d11 DQ808

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FJ681567.1 gg_id:509707 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6815
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DQ794954.1 gg_id:189588 human fecal clone RL310_aam38d06 DQ794
GQ492255.1 gg_id:570706 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
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EU778183.1 gg_id:342468 feces clone RL388_aao94c02 EU778
EU766659.1 gg_id:332436 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU766
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FJ369341.1 gg_id:359787 feces adult twins and mothers; TS50 clone TS50_a03c12 FJ3693
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DQ804656.1 gg_id:199135 human fecal clone RL187_aao71a01 DQ804
DQ801910.1 gg_id:190027 human fecal clone RL201_aai48d05 DQ801
FJ370830.1 gg_id:366957 feces adult twins and mothers; TS5 clone TS5_a01g05 FJ3708
FJ368442.1 gg_id:361708 feces adult twins and mothers; TS3 clone TS3_a04d06 FJ3684
DQ327155.1 gg_id:150223 Metagenomic gut microbiome healthy human stool clone E676 DQ327
DQ808062.1 gg_id:176424 human fecal clone RL180_aan71f05 DQ808
DQ808152.1 gg_id:198845 human fecal clone RL180_aao73c07 DQ808
DQ808775.1 gg_id:188753 human fecal clone RL243_aai85b01 DQ808
FJ365594.1 gg_id:360717 feces adult twins and mothers; TS20 clone TS20_a04g01 FJ3655
FJ367376.1 gg_id:359034 feces adult twins and mothers; TS29 clone TS29_a02g04 FJ3673
FJ673633.1 gg_id:519730 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6736
EF398335.1 gg_id:209425 human fecal clone SJTU_F_01_26 EF3983
DQ824458.1 gg_id:188557 human fecal clone RL304_aal76c05 DQ824
DQ795572.1 gg_id:193771 human fecal clone RL178_aan66d07 DQ795
FJ365831.1 gg_id:363623 feces adult twins and mothers; TS21 clone TS21_a03e10 FJ3658
DQ809636.1 gg_id:179734 human fecal clone RL184_aan81h06 DQ809
EU462008.1 gg_id:296699 black-handed spider monkey feces clone SPIM_aaj33c03 EU462
FJ363818.1 gg_id:362676 feces adult twins and mothers; TS14 clone TS14_a03g01 FJ3638
DQ804899.1 gg_id:179597 human fecal clone RL385_aao82c04 DQ804
EU461755.1 gg_id:292588 mongoose lemur feces clone ML_aaj28c11 EU461
GQ046085.1 gg_id:408619 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ046
AF371545.1 gg_id:71965 swine intestine clone p-2624-9F5 AF3715
FJ368685.1 gg_id:368329 feces adult twins and mothers; TS49 clone TS49_a03c09 FJ3686
DQ805105.1 gg_id:188292 human fecal clone RL249_aaj81c09 DQ805
DQ327067.1 gg_id:150231 Metagenomic gut microbiome healthy human stool clone E575 DQ327
DQ796291.1 gg_id:185492 human fecal clone RL179_aah25c11 DQ796

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DQ803488.1 gg_id:194155 human fecal clone RL251_aaj86e01 DQ803
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GQ491945.1 gg_id:560070 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
DQ793395.1 gg_id:181678 human fecal clone RL199_aaj43b10 DQ793
FJ365331.1 gg_id:358442 feces adult twins and mothers; TS20 clone TS20_a01f04 FJ3653
FJ367717.1 gg_id:357170 feces adult twins and mothers; TS2 clone TS2_a02g06 FJ3677
DQ823900.1 gg_id:178122 human fecal clone RL250_aaj80f07 DQ823
DQ808806.1 gg_id:176621 human fecal clone RL243_aai85e04 DQ808
DQ807520.1 gg_id:193431 human fecal clone RL307_aam07f07 DQ807
FJ370181.1 gg_id:368835 feces adult twins and mothers; TS56 clone TS56_a01d07 FJ3701
DQ804460.1 gg_id:175586 human fecal clone RL187_aan80b09 DQ804
EF398689.1 gg_id:204315 human fecal clone SJTU_F_05_07 EF3986
FJ679312.1 gg_id:524376 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6793
FJ368258.1 gg_id:367873 feces adult twins and mothers; TS3 clone TS3_a02b04 FJ3682
DQ808355.1 gg_id:187289 human fecal clone RL180_aao75f07 DQ808
FJ833986.1 gg_id:589328 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P2Q202_82B11 FJ8339
DQ804066.1 gg_id:184882 human fecal clone RL187_aah68a02 DQ804
GQ090418.1 gg_id:449524 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw GQ090
FJ682063.1 gg_id:523934 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6820
DQ808292.1 gg_id:187565 human fecal clone RL180_aao74h05 DQ808
FJ368724.1 gg_id:358242 feces adult twins and mothers; TS49 clone TS49_a03g02 FJ3687
EU779376.1 gg_id:341433 Somali Wild Ass feces clone WA_aaa01e03 EU779
DQ807930.1 gg_id:194523 human fecal clone RL180_aan69c06 DQ807
DQ807157.1 gg_id:177252 human fecal clone RL244_aaj47a02 DQ807
DQ803367.1 gg_id:178494 human fecal clone RL311_aam24f12 DQ803
FJ369515.1 gg_id:361740 feces adult twins and mothers; TS51 clone TS51_a01e03 FJ3695
FJ674140.1 gg_id:532103 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6741
AY960566.1 gg_id:115149 Clostridium sp. str. IE5 AY9605
FJ364769.1 gg_id:364891 feces adult twins and mothers; TS19 clone TS19_a02h04 FJ3647
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DQ804978.1 gg_id:185255 human fecal clone RL385_aao83e08 DQ804
DQ797797.1 gg_id:184290 human fecal clone RL206_aaj16a02 DQ797
FJ368622.1 gg_id:369716 feces adult twins and mothers; TS49 clone TS49_a02e03 FJ3686
DQ905909.1 gg_id:169429 human fecal clone 29c-e10 DQ905
EU842917.1 gg_id:351299 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
FJ673517.1 gg_id:521392 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6735
DQ807843.1 gg_id:180481 human fecal clone RL180_aah37h04 DQ807
FJ372363.1 gg_id:364213 feces adult twins and mothers; TS9 clone TS9_a04g03 FJ3723

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DQ807941.1 gg_id:197208 human fecal clone RL180_aan69e04 DQ807
FJ673378.1 gg_id:515300 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6733
DQ800119.1 gg_id:192899 human fecal clone RL247_aaj24d07 DQ800
GQ493994.1 gg_id:583043 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
DQ804040.1 gg_id:194148 human fecal clone RL187_aah67e08 DQ804
FJ369151.1 gg_id:362193 feces adult twins and mothers; TS4 clone TS4_a04h05 FJ3691
AF371547.1 gg_id:22923 swine intestine clone p-2465-18B5 AF3715
FJ680876.1 gg_id:518515 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6808
DQ794465.1 gg_id:175434 human fecal clone RL197_aah88c03 DQ794
DQ795202.1 gg_id:179436 human fecal clone RL178_aah51e01 DQ795
DQ794420.1 gg_id:181675 human fecal clone RL197_aah87e07 DQ794
FJ363299.1 gg_id:358542 feces adult twins and mothers; TS149 clone TS149_a01f02 FJ3632
EU466833.1 gg_id:299620 African elephant feces clone AFEL2_aao30b02 EU4668
EU469499.1 gg_id:288896 black lemur feces clone BKLE_a01_2 EU4694
FJ680899.1 gg_id:531159 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6808
DQ799771.1 gg_id:184890 human fecal clone RL182_aah33c01 DQ799
EU462827.1 gg_id:290477 southern three-banded armadillo feces clone arma_aaj53f10 EU4628
DQ799073.1 gg_id:192246 human fecal clone RL205_aaj17c03 DQ799
GQ896789.1 gg_id:574406 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do GQ896
DQ804493.1 gg_id:188479 human fecal clone RL187_aan80g04 DQ804
AY983069.1 gg_id:122341 human descending colon mucosal biopsy clone L312 AY9830
DQ801581.1 gg_id:173802 human fecal clone RL117_aae91h12 DQ801
DQ326186.1 gg_id:148423 Metagenomic gut microbiome healthy human stool clone C092 DQ326
FJ677211.1 gg_id:514970 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6772
FJ367463.1 gg_id:363302 feces adult twins and mothers; TS29 clone TS29_a03h04 FJ3674
FJ365713.1 gg_id:359758 feces adult twins and mothers; TS21 clone TS21_a02b04 FJ3657
FJ369196.1 gg_id:357975 feces adult twins and mothers; TS50 clone TS50_a01d06 FJ3691
EF398925.1 gg_id:204830 human fecal clone SJTU_F_09_12 EF3989
EU462231.1 gg_id:294476 chimpanzee feces clone CHIMP1_aaj38a07 EU4622
FJ367949.1 gg_id:356869 feces adult twins and mothers; TS30 clone TS30_a01f03 FJ3679
DQ804026.1 gg_id:186234 human fecal clone RL187_aah67c08 DQ804
DQ794963.1 gg_id:178221 human fecal clone RL310_aam38e05 DQ794
FJ681816.1 gg_id:516988 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6818
FJ682724.1 gg_id:511020 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6827
FJ369965.1 gg_id:366165 feces adult twins and mothers; TS55 clone TS55_a02g10 FJ3699
EF398293.1 gg_id:208184 human fecal clone SJTU_F_01_72 EF3982
DQ805689.1 gg_id:178495 human fecal clone RL306aal89g12 DQ805
DQ804024.1 gg_id:179715 human fecal clone RL187_aah67c06 DQ804
FJ879925.1 gg_id:413935 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8799
DQ806925.1 gg_id:195679 human fecal clone RL198_aaj75e07 DQ806

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EU762797.1 gg_id:305632 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU762
EU465456.1 gg_id:295217 lion feces clone LI3_aah77f05 EU465
DQ824386.1 gg_id:198143 human fecal clone RL304_aal75d10 DQ824
FJ366844.1 gg_id:365869 feces adult twins and mothers; TS27 clone TS27_a04e06 FJ3668
EU472527.1 gg_id:292228 Angola colobus feces clone EAC_2_aaa01b11 EU472
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FJ679798.1 gg_id:524019 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6797
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EU458491.1 gg_id:299304 spotted hyena feces clone HY2_a04_1 EU458
FJ678819.1 gg_id:517547 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6788
FJ368482.1 gg_id:367763 feces adult twins and mothers; TS3 clone TS3_a04h07 FJ3684
DQ795187.1 gg_id:174286 human fecal clone RL178_aah51c05 DQ795
DQ805632.1 gg_id:187239 human fecal clone RL306aal89b12 DQ805
EU778834.1 gg_id:333694 Black-handed Spider Monkey feces clone SPIM_aaj35b11 EU778
FJ678972.1 gg_id:524202 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6789
DQ794571.1 gg_id:192840 human fecal clone RL240_aaj29g04 DQ794
FJ367473.1 gg_id:366237 feces adult twins and mothers; TS29 clone TS29_a04a02 FJ3674
FJ368067.1 gg_id:362389 feces adult twins and mothers; TS30 clone TS30_a03f01 FJ3680
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DQ798248.1 gg_id:195606 human fecal clone RL181_aah39e05 DQ798
DQ803705.1 gg_id:199487 human fecal clone RL200_aai57d05 DQ803
FJ369569.1 gg_id:361208 feces adult twins and mothers; TS51 clone TS51_a02b04 FJ3695
DQ804787.1 gg_id:174796 human fecal clone RL187_aao72f12 DQ804
DQ809680.1 gg_id:190956 human fecal clone RL184_aan82e07 DQ809
DQ800120.1 gg_id:174967 human fecal clone RL247_aaj24d08 DQ800
EU467144.1 gg_id:292859 mongoose lemur feces clone ML_aae89e06 EU467
GQ492618.1 gg_id:572387 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
DQ799584.1 gg_id:198805 human fecal clone RL305aal88a01 DQ799
EU462126.1 gg_id:300629 black-handed spider monkey feces clone SPIM_aaj35d04 EU462
EU778853.1 gg_id:343716 Black-handed Spider Monkey feces clone SPIM_aaj34h02 EU778
FJ368580.1 gg_id:364581 feces adult twins and mothers; TS49 clone TS49_a02a03 FJ3685
EU778515.1 gg_id:317113 Red river hog feces clone RRH_aaa03d05 EU778
DQ801893.1 gg_id:176898 human fecal clone RL201_aai48b10 DQ801
GQ002337.1 gg_id:507325 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu176c02 GQ002
EU764414.1 gg_id:334570 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1 EU764
FJ680085.1 gg_id:516004 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6800
DQ824108.1 gg_id:184288 human fecal clone RL204_aaj59d11 DQ824
EU776698.1 gg_id:303452 Lion feces clone LI3_aah78h03 EU776

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DQ809417.1 gg_id:188472 human fecal clone RL184_aah20f03 DQ809
DQ805441.1 gg_id:184344 human fecal clone RL203_aai62f08 DQ805
AF357567.1 gg_id:73388 mpn-isolate group 19 AF3575
FJ676500.1 gg_id:510563 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6765
AF132274.1 gg_id:72420 adult human fecal matter clone adhufec52 AF1322
DQ804933.1 gg_id:196581 human fecal clone RL385_aao82g10 DQ804
DQ804952.1 gg_id:187432 human fecal clone RL385_aao83b03 DQ804
EU462096.1 gg_id:287668 black-handed spider monkey feces clone SPIM_aaj34h11 EU462
FJ673623.1 gg_id:509645 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6736
DQ801879.1 gg_id:174348 human fecal clone RL201_aai48a04 DQ801
AF153853.1 gg_id:13992 faecal clone adhufec35.25 AF1538
DQ796760.1 gg_id:194745 human fecal clone RL179_aao54b03 DQ796
FJ363676.1 gg_id:362514 feces adult twins and mothers; TS14 clone TS14_a02a05 FJ3636
FJ366409.1 gg_id:358537 feces adult twins and mothers; TS26 clone TS26_a02g06 FJ3664
DQ808220.1 gg_id:197652 human fecal clone RL180_aao74a10 DQ808
FJ682086.1 gg_id:531472 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6820
DQ904728.1 gg_id:166362 human fecal clone 001-h6 DQ904
DQ804935.1 gg_id:182308 human fecal clone RL385_aao82h01 DQ804
DQ796155.1 gg_id:178646 human fecal clone RL202_aai52d05 DQ796
GQ492609.1 gg_id:553609 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
DQ326200.1 gg_id:145758 Metagenomic gut microbiome healthy human stool clone C115 DQ326
DQ798716.1 gg_id:198766 human fecal clone RL181_aao00e02 DQ798
FJ371877.1 gg_id:365497 feces adult twins and mothers; TS8 clone TS8_a03c04 FJ3718
NZ_AAVO02000004.1 gg_id:470971 Ruminococcus obeum str. ATCC 29174 NZ_AA
EU776277.1 gg_id:340251 Red Kangaroo feces clone KO1_aai41g04 EU776
FJ364807.1 gg_id:358558 feces adult twins and mothers; TS19 clone TS19_a03d03 FJ3648
AY981223.1 gg_id:126425 human sigmoid colon mucosal biopsy clone G186 AY9812
DQ807835.1 gg_id:198325 human fecal clone RL180_aah37g06 DQ807
FJ368592.1 gg_id:368630 feces adult twins and mothers; TS49 clone TS49_a02b05 FJ3685
EF401712.1 gg_id:208349 human fecal clone SJTU_D_14_18 EF4017
EU468139.1 gg_id:290228 lion feces clone LI1_c04 EU468
DQ807766.1 gg_id:193852 human fecal clone RL180_aah37a01 DQ807
FJ366613.1 gg_id:364141 feces adult twins and mothers; TS27 clone TS27_a01g04 FJ3666
DQ799635.1 gg_id:192476 human fecal clone RL305aal88e08 DQ799
DQ795414.1 gg_id:174625 human fecal clone RL178_aah54a12 DQ795
DQ808431.1 gg_id:176519 human fecal clone RL180_aao76e04 DQ808
FJ364646.1 gg_id:364097 feces adult twins and mothers; TS19 clone TS19_a01d06 FJ3646
DQ796801.1 gg_id:191021 human fecal clone RL179_aao54f11 DQ796
FJ678562.1 gg_id:517282 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6785
AY983064.1 gg_id:125001 human descending colon mucosal biopsy clone L306 AY983

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FJ369162.1 gg_id:357114 feces adult twins and mothers; TS50 clone TS50_a01a06	FJ3691
DQ802535.1 gg_id:197244 human fecal clone RL188_aan93b03	DQ802
DQ804262.1 gg_id:196986 human fecal clone RL187_aan77b05	DQ804
DQ805430.1 gg_id:185521 human fecal clone RL203_aai62e04	DQ805
FJ367768.1 gg_id:362466 feces adult twins and mothers; TS2 clone TS2_a03d05	FJ3677
FJ369199.1 gg_id:370044 feces adult twins and mothers; TS50 clone TS50_a01d09	FJ3691
DQ805300.1 gg_id:199508 human fecal clone RL249_aaj84g06	DQ805
AJ133124.1 gg_id:22899 Ruminococcus luti str. bln9	AJ1331
DQ801236.1 gg_id:182962 human fecal clone RL116_aaf02b10	DQ801
FJ362873.1 gg_id:368307 feces adult twins and mothers; TS13 clone TS13_a04c03	FJ3628
DQ825010.1 gg_id:187491 human fecal clone RL185_aao72c01	DQ825
DQ806646.1 gg_id:188588 human fecal clone RL186_aao47b05	DQ806
DQ905659.1 gg_id:163685 human fecal clone 014C-D5	DQ905
DQ057417.1 gg_id:134268 chicken ileum/cecum clone oc44	DQ057
DQ807155.1 gg_id:181330 human fecal clone RL244_aaj46h12	DQ807
DQ797201.1 gg_id:187271 human fecal clone RL386_aao88c09	DQ797
DQ804499.1 gg_id:185360 human fecal clone RL187_aan80h04	DQ804
FJ367409.1 gg_id:361412 feces adult twins and mothers; TS29 clone TS29_a03b08	FJ3674
FJ363998.1 gg_id:358181 feces adult twins and mothers; TS150 clone TS150_a01g10	FJ3639
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FJ370034.1 gg_id:368166 feces adult twins and mothers; TS55 clone TS55_a03f10	FJ3700
DQ805353.1 gg_id:196792 human fecal clone RL203_aai61e09	DQ805
GQ493491.1 gg_id:545944 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice	GQ493
EU774067.1 gg_id:324163 Chimpanzee feces clone CHIMP1_c12	EU774
DQ798308.1 gg_id:188852 human fecal clone RL181_aah40e02	DQ798
FJ363960.1 gg_id:369883 feces adult twins and mothers; TS150 clone TS150_a01d04	FJ3639
DQ802328.1 gg_id:182581 human fecal clone RL188_aah16b05	DQ802
FJ366920.1 gg_id:360553 feces adult twins and mothers; TS28 clone TS28_a01d05	FJ3669
DQ803447.1 gg_id:196353 human fecal clone RL251_aaj85h09	DQ803
DQ825323.1 gg_id:176089 human fecal clone RL185_aan88e07	DQ825
DQ808188.1 gg_id:186103 human fecal clone RL180_aao73f09	DQ808
DQ800214.1 gg_id:184636 human fecal clone RL303_aal69g02	DQ800
FJ368971.1 gg_id:366601 feces adult twins and mothers; TS4 clone TS4_a02g01	FJ3689
EU475728.1 gg_id:300551 white-faced saki feces clone Saki_aaj63c03	EU475
FJ678854.1 gg_id:515724 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee	FJ6788
FJ364216.1 gg_id:359342 feces adult twins and mothers; TS150 clone TS150_a04c10	FJ3642
DQ799793.1 gg_id:197502 human fecal clone RL182_aah33f10	DQ799
FJ368939.1 gg_id:363739 feces adult twins and mothers; TS4 clone TS4_a02c12	FJ3689

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AY442822.1 gg_id:99566 Ruminococcus sp. YE58 AY442
FJ370524.1 gg_id:368808 feces adult twins and mothers; TS57 clone TS57_a02a12 FJ3705
FJ365661.1 gg_id:365684 feces adult twins and mothers; TS21 clone TS21_a01e06 FJ3656
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FJ363916.1 gg_id:370410 feces adult twins and mothers; TS14 clone TS14_a04h04 FJ3639
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DQ803372.1 gg_id:191062 human fecal clone RL311_aam24g08 DQ803
FJ681121.1 gg_id:519761 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6811
EU728792.1 gg_id:344947 Ruminococcus sp. str. DJF_VR70k1 EU728
FJ364765.1 gg_id:361855 feces adult twins and mothers; TS19 clone TS19_a02g10 FJ3647
DQ799858.1 gg_id:176933 human fecal clone RL247_aaj21a07 DQ799
FJ365546.1 gg_id:369247 feces adult twins and mothers; TS20 clone TS20_a04b07 FJ3655
EU763193.1 gg_id:334957 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A> EU763
FJ367161.1 gg_id:361308 feces adult twins and mothers; TS28 clone TS28_a04c03 FJ3671
GQ492131.1 gg_id:578713 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492

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FJ682155.1 gg_id:519441 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6821
DQ797815.1 gg_id:173975 human fecal clone RL206_aaj16b08 DQ797
GQ492839.1 gg_id:585610 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
DQ799779.1 gg_id:189842 human fecal clone RL182_aah33d09 DQ799
DQ326493.1 gg_id:148279 Metagenomic gut microbiome healthy human stool clone C591 DQ326
DQ326406.1 gg_id:149236 Metagenomic gut microbiome healthy human stool clone C448 DQ326
FJ677824.1 gg_id:529004 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6778
DQ327590.1 gg_id:145858 Metagenomic gut microbiome healthy human stool clone EB76 DQ327
GQ491902.1 gg_id:576504 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
EU773407.1 gg_id:311080 Black lemur feces clone BKLE_c10_3 EU773
DQ804121.1 gg_id:175988 human fecal clone RL187_aah68h08 DQ804
DQ808356.1 gg_id:181831 human fecal clone RL180_aao75f08 DQ808
DQ795593.1 gg_id:194234 human fecal clone RL178_aan66g03 DQ795
DQ803639.1 gg_id:187496 human fecal clone RL251_aaj88e10 DQ803
DQ800645.1 gg_id:180900 human fecal clone RL183_aao01e03 DQ800
DQ825047.1 gg_id:191384 human fecal clone RL185_aao72f11 DQ825
DQ808011.1 gg_id:174599 human fecal clone RL180_aan70f05 DQ808
FJ367398.1 gg_id:368950 feces adult twins and mothers; TS29 clone TS29_a03a08 FJ3673
FJ370628.1 gg_id:362215 feces adult twins and mothers; TS57 clone TS57_a03d01 FJ3706
EU773503.1 gg_id:312986 Bonobo feces clone BNO_aaa01a01 EU773
GQ052306.1 gg_id:429460 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu534a05 GQ052
DQ805014.1 gg_id:194889 human fecal clone RL385_aao84a11 DQ805
DQ825038.1 gg_id:187583 human fecal clone RL185_aao72e12 DQ825
EU344383.1 gg_id:258461 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU344
EF403780.1 gg_id:204996 human fecal clone SJTU_A2_02_06 EF4037
DQ808990.1 gg_id:184545 human fecal clone RL243_aai87h08 DQ808
DQ807910.1 gg_id:180777 human fecal clone RL180_aah38h03 DQ807
FJ363776.1 gg_id:362510 feces adult twins and mothers; TS14 clone TS14_a03c02 FJ3637
FJ674058.1 gg_id:531865 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6740
DQ806218.1 gg_id:190648 human fecal clone RL186_aah62g11 DQ806
FJ683556.1 gg_id:521865 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6835
DQ798341.1 gg_id:175589 human fecal clone RL181_aah41b11 DQ798
EU467251.1 gg_id:296692 black-handed spider monkey feces clone SPIM_a03_1 EU467
DQ804949.1 gg_id:195941 human fecal clone RL385_aao83a10 DQ804
FJ684827.1 gg_id:513226 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6848
FJ370430.1 gg_id:358419 feces adult twins and mothers; TS57 clone TS57_a01a05 FJ3704
DQ795634.1 gg_id:199010 human fecal clone RL178_aan67d07 DQ795
DQ802591.1 gg_id:195295 human fecal clone RL188_aan93g08 DQ802
FJ364772.1 gg_id:357464 feces adult twins and mothers; TS19 clone TS19_a02h08 FJ3647
DQ804278.1 gg_id:187591 human fecal clone RL187_aan77c12 DQ804

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FJ366169.1 gg_id:357289 feces adult twins and mothers; TS25 clone TS25_a03e06 FJ3661
FJ678441.1 gg_id:519063 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6784
EU467416.1 gg_id:296514 chimpanzee feces clone CHIMP12_c03 EU467
GQ491331.1 gg_id:575263 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
GQ492790.1 gg_id:580891 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
FJ364998.1 gg_id:362334 feces adult twins and mothers; TS1 clone TS1_a01f06 FJ3649
AF349421.1 gg_id:77371 pig feces clone AF3494
FJ364211.1 gg_id:366259 feces adult twins and mothers; TS150 clone TS150_a04c05 FJ3642
FJ677875.1 gg_id:514708 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6778
FJ370381.1 gg_id:360033 feces adult twins and mothers; TS56 clone TS56_a04c02 FJ3703
DQ798463.1 gg_id:191746 human fecal clone RL181_aan97a06 DQ798
FJ678829.1 gg_id:528093 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6788
GQ491285.1 gg_id:587632 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
FJ370535.1 gg_id:365441 feces adult twins and mothers; TS57 clone TS57_a02b11 FJ3705
FJ367412.1 gg_id:365431 feces adult twins and mothers; TS29 clone TS29_a03c02 FJ3674
DQ809682.1 gg_id:195537 human fecal clone RL184_aan82e09 DQ809
DQ804413.1 gg_id:173896 human fecal clone RL187_aan79e02 DQ804
X95624.1 gg_id:13997 Ruminococcus hydrogenotrophicus str. S5a36 X95624
FJ366380.1 gg_id:360776 feces adult twins and mothers; TS26 clone TS26_a02c11 FJ3663
FJ365881.1 gg_id:364310 feces adult twins and mothers; TS21 clone TS21_a04b07 FJ3658
AY982924.1 gg_id:122998 human descending colon mucosal biopsy clone L118 AY9829
FJ369197.1 gg_id:357853 feces adult twins and mothers; TS50 clone TS50_a01d07 FJ3691
AY974849.1 gg_id:118782 human ascending colon mucosal biopsy clone KG89 AY9748
EU462164.1 gg_id:302830 black-handed spider monkey feces clone SPIM_aaj36c04 EU4621
DQ801948.1 gg_id:193284 human fecal clone RL201_aai48h05 DQ801
GQ898643.1 gg_id:569010 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ898
DQ802277.1 gg_id:198083 human fecal clone RL188_aah15e06 DQ802
DQ802736.1 gg_id:180297 human fecal clone RL188_aan95h08 DQ802
EU462179.1 gg_id:303169 black-handed spider monkey feces clone SPIM_aaj36f06 EU4621
DQ801357.1 gg_id:193389 human fecal clone RL388_aao94d11 DQ801
FJ678267.1 gg_id:529473 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6782
AB218345.1 gg_id:150230 Fecal microbial (dugong dugon) determined genes Dugong feces clone dgC-129 AB2183
DQ799789.1 gg_id:180169 human fecal clone RL182_aah33f04 DQ799
AY977739.1 gg_id:121304 human cecum mucosal biopsy clone LE08 AY9777
DQ799700.1 gg_id:188200 human fecal clone RL182_aah31f10 DQ799
EU768469.1 gg_id:336275 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C5 EU7684
DQ807542.1 gg_id:197222 human fecal clone RL307_aam07h12 DQ807
GQ491581.1 gg_id:567715 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
DQ801753.1 gg_id:196693 human fecal clone RL201_aai46d04 DQ801
FJ363021.1 gg_id:367919 feces adult twins and mothers; TS148 clone TS148_a02a07 FJ3630

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FJ369206.1 gg_id:364996 feces adult twins and mothers; TS50 clone TS50_a01e07 FJ3692
FJ880511.1 gg_id:384505 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8805
FJ683509.1 gg_id:531675 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6835
DQ803719.1 gg_id:177307 human fecal clone RL200_aai57e08 DQ803
DQ809757.1 gg_id:183040 human fecal clone RL184_aan83g05 DQ809
DQ796661.1 gg_id:193951 human fecal clone RL179aan76g10 DQ796
DQ794215.1 gg_id:194994 human fecal clone RL176_aan59e11 DQ794
EU530217.1 gg_id:262919 mucosa adherent and invasive microbes profile adenoma colorectal cancer clone M1 EU530
DQ807936.1 gg_id:193031 human fecal clone RL180_aan69d10 DQ807
DQ801248.1 gg_id:180078 human fecal clone RL116_aaf02h09 DQ801
FJ674092.1 gg_id:517703 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6740
GQ079643.1 gg_id:392131 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1232e GQ079
EU772296.1 gg_id:310490 Argali sheep feces clone AS1_aao37b06.Contig1 EU772
DQ326182.1 gg_id:148131 Metagenomic gut microbiome healthy human stool clone C085 DQ326
EU766231.1 gg_id:351847 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU766
FJ365593.1 gg_id:365207 feces adult twins and mothers; TS20 clone TS20_a04f12 FJ3655
DQ799673.1 gg_id:196932 human fecal clone RL305aal88h11 DQ799
DQ804111.1 gg_id:174535 human fecal clone RL187_aah68f11 DQ804
DQ794385.1 gg_id:184488 human fecal clone RL197_aah87a12 DQ794
GQ493579.1 gg_id:580685 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
FJ675878.1 gg_id:524722 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6758
DQ799473.1 gg_id:194586 human fecal clone RL305aal86f12 DQ799
EF399628.1 gg_id:205950 human fecal clone SJTU_E_01_40 EF3996
FJ364795.1 gg_id:365988 feces adult twins and mothers; TS19 clone TS19_a03c02 FJ3647
EF403194.1 gg_id:215270 human fecal clone SJTU_A1_6_25 EF4031
EU468183.1 gg_id:295586 lion feces clone LI1_e03_1 EU468
DQ804318.1 gg_id:183528 human fecal clone RL187_aan77h08 DQ804
DQ804781.1 gg_id:189687 human fecal clone RL187_aao72f05 DQ804
DQ800464.1 gg_id:183252 human fecal clone RL183_aah24h07 DQ800
FJ369439.1 gg_id:359096 feces adult twins and mothers; TS50 clone TS50_a04e06 FJ3694
DQ801547.1 gg_id:183577 human fecal clone RL388_aao96h06 DQ801
DQ804005.1 gg_id:198999 human fecal clone RL187_aah67a02 DQ804
DQ057397.1 gg_id:131559 chicken ileum/cecum clone cc361 DQ057
DQ803204.1 gg_id:191545 human fecal clone RL311_aam22b01 DQ803
EU459628.1 gg_id:292800 ring-tailed lemur feces clone RT_aai09e08 EU459
FJ673676.1 gg_id:531582 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6736
FJ368296.1 gg_id:359143 feces adult twins and mothers; TS3 clone TS3_a02f02 FJ3682
AY976522.1 gg_id:124583 human cecum mucosal biopsy clone K047 AY9765
FJ368201.1 gg_id:370186 feces adult twins and mothers; TS3 clone TS3_a01d08 FJ3682
DQ795062.1 gg_id:194595 human fecal clone RL310_aam39g01 DQ795
DQ807718.1 gg_id:175548 human fecal clone RL180_aah36d05 DQ807

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FJ673048.1 gg_id:522463 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6730
FJ367338.1 gg_id:359066 feces adult twins and mothers; TS29 clone TS29_a02c11 FJ3673
DQ802497.1 gg_id:178768 human fecal clone RL188_aah18e07 DQ802
EU776600.1 gg_id:331271 Lion feces clone LI2_aae50f03 EU776
EU777561.1 gg_id:337080 Sumatran orangutan feces clone orang1_aai55e12 EU777
DQ824090.1 gg_id:176724 human fecal clone RL204_aaj59b12 DQ824
FJ370157.1 gg_id:367719 feces adult twins and mothers; TS56 clone TS56_a01b02 FJ3701
FJ364096.1 gg_id:365980 feces adult twins and mothers; TS150 clone TS150_a02h11 FJ3640
FJ367236.1 gg_id:360886 feces adult twins and mothers; TS29 clone TS29_a01b07 FJ3672
FJ674006.1 gg_id:531328 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6740
DQ793750.1 gg_id:181927 human fecal clone RL246_aai76f11 DQ793
FJ678797.1 gg_id:529608 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6787
GQ175502.1 gg_id:544532 Chicken intestinal microbiota modulations various feed supplementations DGGE anc GQ175
FJ673697.1 gg_id:518146 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6736
DQ807587.1 gg_id:188805 human fecal clone RL307_aam08f01 DQ807
DQ804414.1 gg_id:198951 human fecal clone RL187_aan79e03 DQ804
FJ879848.1 gg_id:464311 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8798
DQ824766.1 gg_id:176450 human fecal clone RL185_aao69a01 DQ824
FJ370129.1 gg_id:365387 feces adult twins and mothers; TS55 clone TS55_a04g02 FJ3701
DQ824815.1 gg_id:197379 human fecal clone RL185_aao69f03 DQ824
FJ679957.1 gg_id:520155 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6799
DQ798965.1 gg_id:193337 human fecal clone RL242_aaj99g03 DQ798
FJ372063.1 gg_id:361345 feces adult twins and mothers; TS9 clone TS9_a01d02 FJ3720
DQ806358.1 gg_id:176330 human fecal clone RL186_aan91b11 DQ806
GQ896722.1 gg_id:585057 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do GQ896
EF405003.1 gg_id:216807 human fecal clone SJTU_G_05_74 EF405
DQ823723.1 gg_id:177005 human fecal clone RL250_aaj78b10 DQ823
DQ806093.1 gg_id:183145 human fecal clone RL186_aah61a12 DQ806
GQ493166.1 gg_id:583059 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
FJ367354.1 gg_id:363558 feces adult twins and mothers; TS29 clone TS29_a02e05 FJ3673
FJ680513.1 gg_id:514809 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6805
GQ493777.1 gg_id:587010 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
DQ798694.1 gg_id:190120 human fecal clone RL181_aao00b12 DQ798
FJ369874.1 gg_id:358576 feces adult twins and mothers; TS55 clone TS55_a01g07 FJ3698
DQ825195.1 gg_id:185845 human fecal clone RL185_aan86e08 DQ825
EF399515.1 gg_id:204058 human fecal clone SJTU_F_11_92 EF3995
GQ493460.1 gg_id:539851 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
EU462101.1 gg_id:288684 black-handed spider monkey feces clone SPIM_aaj35a05 EU462
EU344285.1 gg_id:264113 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU344
EU469501.1 gg_id:292310 black lemur feces clone BKLE_a03_2 EU469

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DQ824491.1 gg_id:178952 human fecal clone RL304_aal76f09 DQ824
GQ897401.1 gg_id:562918 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do GQ897
EU467434.1 gg_id:302049 chimpanzee feces clone CHIMP12_h05_2 EU467
DQ803247.1 gg_id:182728 human fecal clone RL311_aam22h02 DQ803
GQ492415.1 gg_id:580087 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
DQ325573.1 gg_id:146093 Metagenomic gut microbiome healthy human stool clone B068 DQ325
FJ368900.1 gg_id:361009 feces adult twins and mothers; TS4 clone TS4_a01h05 FJ3689
FJ679103.1 gg_id:527140 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6791
EU467241.1 gg_id:287583 black-handed spider monkey feces clone SPIM_d07 EU467
DQ326151.1 gg_id:150033 Metagenomic gut microbiome healthy human stool clone C045 DQ326
DQ806462.1 gg_id:195972 human fecal clone RL186_aao45a02 DQ806
DQ798304.1 gg_id:184228 human fecal clone RL181_aah40d07 DQ798
GQ493558.1 gg_id:539526 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
FJ365989.1 gg_id:361245 feces adult twins and mothers; TS25 clone TS25_a01d12 FJ3659
DQ793371.1 gg_id:192937 human fecal clone RL199_aaj42h06 DQ793
FJ362957.1 gg_id:365345 feces adult twins and mothers; TS148 clone TS148_a01c04 FJ3629
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DQ805900.1 gg_id:184238 human fecal clone RL306aal92d10 DQ805
EF398596.1 gg_id:217110 human fecal clone SJTU_F_04_21 EF3985
DQ805654.1 gg_id:198983 human fecal clone RL306aal89d10 DQ805
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AY977207.1 gg_id:115602 human cecum mucosal biopsy clone MT17 AY977
EF401997.1 gg_id:206178 human fecal clone SJTU_B_02_27 EF4019
EU459666.1 gg_id:300510 ring-tailed lemur feces clone RT_aai10d12 EU459
FJ683591.1 gg_id:528355 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6835
DQ802605.1 gg_id:174714 human fecal clone RL188_aan94a06 DQ802
DQ793844.1 gg_id:192433 human fecal clone RL176_aah44c02 DQ793
FJ362761.1 gg_id:357683 feces adult twins and mothers; TS13 clone TS13_a02g10 FJ3627
DQ804255.1 gg_id:186416 human fecal clone RL187_aan77a07 DQ804
DQ800776.1 gg_id:193211 human fecal clone RL183_aao03c12 DQ800
DQ795338.1 gg_id:182672 human fecal clone RL178_aah53b06 DQ795
DQ801899.1 gg_id:185135 human fecal clone RL201_aai48c04 DQ801
FJ880520.1 gg_id:436032 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8805
DQ809688.1 gg_id:187533 human fecal clone RL184_aan82f07 DQ809
DQ810008.1 gg_id:174624 human fecal clone RL184_aao67a03 DQ810
DQ804959.1 gg_id:186381 human fecal clone RL385_aao83c01 DQ804
FJ363959.1 gg_id:362856 feces adult twins and mothers; TS150 clone TS150_a01d03 FJ3639
DQ804062.1 gg_id:177461 human fecal clone RL187_aah67h09 DQ804
FJ367854.1 gg_id:369480 feces adult twins and mothers; TS2 clone TS2_a04d03 FJ3678
DQ905094.1 gg_id:170387 human fecal clone 2-002-h6 DQ905

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DQ327198.1 gg_id:149658 Metagenomic gut microbiome healthy human stool clone E729 DQ327
DQ802779.1 gg_id:187866 human fecal clone RL188_aan96e01 DQ802
FJ368606.1 gg_id:362131 feces adult twins and mothers; TS49 clone TS49_a02c08 FJ3686
DQ805395.1 gg_id:198771 human fecal clone RL203_aai62a11 DQ805
DQ794663.1 gg_id:190108 human fecal clone RL240_aaj30g12 DQ794
GQ492387.1 gg_id:587729 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
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DQ808174.1 gg_id:195511 human fecal clone RL180_aao73e06 DQ808
FJ370752.1 gg_id:360353 feces adult twins and mothers; TS57 clone TS57_a04h02 FJ3707
GQ492049.1 gg_id:537067 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
FJ833196.1 gg_id:589215 Microbial Ecology Crop Folivorous Hoatzin crop contents clone A3Q102_21E03 FJ8331
DQ905209.1 gg_id:166627 human fecal clone 013-b6 DQ905
DQ806393.1 gg_id:185655 human fecal clone RL186_aan91f10 DQ806
FJ673686.1 gg_id:526313 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6736
DQ805059.1 gg_id:187040 human fecal clone RL385_aao84f06 DQ805
EU776195.1 gg_id:338657 Spotted hyena feces clone HY2_c05 EU776
DQ802126.1 gg_id:185798 human fecal clone RL241_aaj03d06 DQ802
FJ367229.1 gg_id:367427 feces adult twins and mothers; TS29 clone TS29_a01a09 FJ3672
DQ824785.1 gg_id:184926 human fecal clone RL185_aao69c04 DQ824
FJ684853.1 gg_id:526044 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6848
FJ370795.1 gg_id:359557 feces adult twins and mothers; TS5 clone TS5_a01d03 FJ3707
EU763793.1 gg_id:318944 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A5 EU763
FJ370583.1 gg_id:359794 feces adult twins and mothers; TS57 clone TS57_a02g05 FJ3705
EU469566.1 gg_id:289089 flying fox feces clone FF_a05 EU469
FJ370920.1 gg_id:370338 feces adult twins and mothers; TS5 clone TS5_a02g10 FJ3709
DQ795286.1 gg_id:199065 human fecal clone RL178_aah52e04 DQ795
DQ806583.1 gg_id:194217 human fecal clone RL186_aao46d03 DQ806
DQ803474.1 gg_id:176483 human fecal clone RL251_aaj86c05 DQ803
DQ823702.1 gg_id:196262 human fecal clone RL250_aaj77h05 DQ823
FJ363706.1 gg_id:365327 feces adult twins and mothers; TS14 clone TS14_a02c11 FJ3637
EU463322.1 gg_id:302321 bush dog feces clone bdog1_aai78c06 EU463
DQ804117.1 gg_id:189289 human fecal clone RL187_aah68g09 DQ804
GQ491877.1 gg_id:551761 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
DQ057452.1 gg_id:131571 str. ic1272 DQ057
FJ673904.1 gg_id:516385 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6739
DQ325682.1 gg_id:149909 Metagenomic gut microbiome healthy human stool clone B281 DQ325
EU774663.1 gg_id:347115 Angola Colobus feces clone EAC_1aaa03b04 EU774
FJ676585.1 gg_id:525814 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6765
DQ798720.1 gg_id:192200 human fecal clone RL181_aao00e06 DQ798

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FJ368118.1 gg_id:367639 feces adult twins and mothers; TS30 clone TS30_a04c07 FJ3681
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DQ804486.1 gg_id:183159 human fecal clone RL187_aan80f05 DQ804
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DQ804248.1 gg_id:194327 human fecal clone RL187_aah70h04 DQ804
DQ808467.1 gg_id:185180 human fecal clone RL180_aao76h06 DQ808
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FJ367468.1 gg_id:363767 feces adult twins and mothers; TS29 clone TS29_a03h09 FJ3674
DQ804281.1 gg_id:192533 human fecal clone RL187_aan77d07 DQ804
FJ682467.1 gg_id:524374 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6824
AJ408999.1 gg_id:16475 human colonic clone HuCB25 AJ4089
AY981581.1 gg_id:126684 human sigmoid colon mucosal biopsy clone L764 AY9815
EF404178.1 gg_id:207790 human fecal clone SJTU_C_05_79 EF4041
EU459398.1 gg_id:294439 cheetah feces clone CE3_aai07c06 EU4593
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FJ681290.1 gg_id:528650 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6812
DQ806327.1 gg_id:174763 human fecal clone RL186_aan90f07 DQ806
FJ833830.1 gg_id:543708 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J2Q402_07G01 FJ8338
EU776912.1 gg_id:321453 Mongoose lemur feces clone ML_aaj28d01 EU7769
GQ077026.1 gg_id:409732 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1205h GQ077
GQ491288.1 gg_id:583454 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
FJ683504.1 gg_id:531001 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6835
DQ803389.1 gg_id:186324 human fecal clone RL251_aaj85a10 DQ803
FJ673117.1 gg_id:517348 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6731
FJ673669.1 gg_id:515203 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6736
EU764302.1 gg_id:336328 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A5 EU7643
FJ674047.1 gg_id:517387 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6740
DQ797638.1 gg_id:181387 human fecal clone RL206_aaj14a12 DQ797
DQ905829.2 gg_id:165922 human fecal clone 29E-d8 DQ905
DQ805269.1 gg_id:189310 human fecal clone RL249_aaj84b03 DQ805
GQ897352.1 gg_id:566202 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do s GQ897
DQ824909.1 gg_id:190610 human fecal clone RL185_aao70h05 DQ824

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DQ825227.1 gg_id:194540 human fecal clone RL185_aan86h11	DQ825
FM872529.1 gg_id:358675 occupant source house floor dust clone FA01F10	FM872
EU469676.1 gg_id:292633 flying fox feces clone FF_-aag84h04	EU469
FJ364608.1 gg_id:369728 feces adult twins and mothers; TS19 clone TS19_a01a03	FJ3646
DQ807273.1 gg_id:175296 human fecal clone RL244_aaj48d10	DQ807
FJ363614.1 gg_id:365076 feces adult twins and mothers; TS14 clone TS14_a01d02	FJ3636
DQ824897.1 gg_id:181054 human fecal clone RL185_aao70f09	DQ824
DQ806731.1 gg_id:174501 human fecal clone RL186_aao48a10	DQ806
DQ905045.1 gg_id:165102 human fecal clone 2-002-d3	DQ905
FJ364581.1 gg_id:366418 feces adult twins and mothers; TS15 clone TS15_a04f07	FJ3645
EU459631.1 gg_id:292864 ring-tailed lemur feces clone RT_aai09f02	EU459
DQ799731.1 gg_id:189522 human fecal clone RL182_aah32c08	DQ799
DQ325939.1 gg_id:149178 Metagenomic gut microbiome healthy human stool clone B807	DQ325
EU469413.1 gg_id:296007 black lemur feces clone BKLE_d08	EU469
FJ369499.1 gg_id:361773 feces adult twins and mothers; TS51 clone TS51_a01c10	FJ3694
EF401262.1 gg_id:211501 human fecal clone SJTU_D_08_02	EF4012
FJ370165.1 gg_id:361226 feces adult twins and mothers; TS56 clone TS56_a01b10	FJ3701
GQ492725.1 gg_id:560281 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice	GQ492
GQ493627.1 gg_id:569232 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice	GQ493
FJ364178.1 gg_id:359500 feces adult twins and mothers; TS150 clone TS150_a03h05	FJ3641
DQ799855.1 gg_id:179980 human fecal clone RL247_aaj21a03	DQ799
DQ802334.1 gg_id:183044 human fecal clone RL188_aah16c05	DQ802
EU778311.1 gg_id:355874 feces clone RL387_aao91d11	EU778
DQ905629.1 gg_id:168527 human fecal clone 014C-A4	DQ905
AB185576.1 gg_id:102704 rumen clone F24-A02	AB185
FJ680469.1 gg_id:528843 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee	FJ6804
DQ796458.1 gg_id:177101 human fecal clone RL179_aah28f09	DQ796
FJ369472.1 gg_id:365941 feces adult twins and mothers; TS50 clone TS50_a04h10	FJ3694
FJ370160.1 gg_id:370278 feces adult twins and mothers; TS56 clone TS56_a01b05	FJ3701
EU774103.1 gg_id:336133 Chimpanzee feces clone CHIMP1_f08	EU774
DQ795672.1 gg_id:174801 human fecal clone RL178_aan68b10	DQ795
EU773420.1 gg_id:340910 Black lemur feces clone BKLE_f01_1	EU773
FJ975983.1 gg_id:572109 Human gut microbiome adopts alternative state bowel transplantation ileum effluent	FJ9759
DQ825217.1 gg_id:190683 human fecal clone RL185_aan86g10	DQ825
DQ794691.1 gg_id:186166 human fecal clone RL240_aaj31b11	DQ794
FJ367085.1 gg_id:356822 feces adult twins and mothers; TS28 clone TS28_a03d04	FJ3670
DQ805508.1 gg_id:188525 human fecal clone RL203_aai63e10	DQ805
DQ806426.1 gg_id:187597 human fecal clone RL186_aan92c03	DQ806
GQ491899.1 gg_id:534865 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice	GQ491
FJ367501.1 gg_id:364982 feces adult twins and mothers; TS29 clone TS29_a04c08	FJ3675
AY169424.1 gg_id:81152 Ruminococcus obeum	AY169

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o__Clostridiales	f__Lachnospiraceae

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FJ364389.1 gg_id:368235 feces adult twins and mothers; TS15 clone TS15_a02d01 FJ3643
GQ898361.1 gg_id:581094 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ898
DQ794403.1 gg_id:191306 human fecal clone RL197_aah87c10 DQ794
DQ808364.1 gg_id:176416 human fecal clone RL180_aao75g04 DQ808
DQ807968.1 gg_id:181844 human fecal clone RL180_aan69h11 DQ807
FJ365929.1 gg_id:369888 feces adult twins and mothers; TS21 clone TS21_a04g07 FJ3659
DQ804897.1 gg_id:180401 human fecal clone RL385_aao82c02 DQ804
EU463335.1 gg_id:289863 bush dog feces clone bdog1_aai78h02 EU463
DQ796672.1 gg_id:190370 human fecal clone RL179_aao53a06 DQ796
FJ362616.1 gg_id:365574 feces adult twins and mothers; TS13 clone TS13_a01b04 FJ3626
DQ905859.2 gg_id:167403 human fecal clone 29E-g4 DQ905
DQ803223.1 gg_id:177941 human fecal clone RL311_aam22d08 DQ803
FJ879477.1 gg_id:449983 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8794
GQ898276.1 gg_id:549857 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do s GQ898
DQ806568.1 gg_id:181584 human fecal clone RL186_aao46b10 DQ806
DQ905381.1 gg_id:162651 human fecal clone 013C-A12 DQ905
DQ802069.1 gg_id:175754 human fecal clone RL241_aaj02f11 DQ802
EU776809.1 gg_id:354131 Mongoose lemur feces clone ML_aae88d12 EU776
EF399954.1 gg_id:211432 human fecal clone SJTU_E_06_47 EF3999
FJ366059.1 gg_id:362157 feces adult twins and mothers; TS25 clone TS25_a02c02 FJ3660
DQ807356.1 gg_id:190415 human fecal clone RL307_aam05e05 DQ807
FJ368244.1 gg_id:359889 feces adult twins and mothers; TS3 clone TS3_a01h09 FJ3682
FJ673226.1 gg_id:519792 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6732
FJ673404.1 gg_id:516361 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6734
AY981104.1 gg_id:123256 human sigmoid colon mucosal biopsy clone G018 AY981
DQ809635.1 gg_id:190191 human fecal clone RL184_aan81h05 DQ809
DQ804289.1 gg_id:175766 human fecal clone RL187_aan77e06 DQ804
DQ805215.1 gg_id:179077 human fecal clone RL249_aaj83b11 DQ805
EU728791.1 gg_id:328717 Ruminococcus sp. str. DJF_VR67 EU728
FJ679970.1 gg_id:523939 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6799
EU530242.1 gg_id:262753 mucosa adherent and invasive microbes adenoma colorectal cancer profile non-ader EU530
DQ806890.1 gg_id:185969 human fecal clone RL198_aaj74g10 DQ806
FJ369700.1 gg_id:367283 feces adult twins and mothers; TS51 clone TS51_a03g05 FJ3697
GQ492798.1 gg_id:557714 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
EU774068.1 gg_id:304108 Chimpanzee feces clone CHIMP1_g12 EU774
DQ806715.1 gg_id:184849 human fecal clone RL186_aao47h05 DQ806
FJ364854.1 gg_id:362009 feces adult twins and mothers; TS19 clone TS19_a03h11 FJ3648
GQ491341.1 gg_id:563161 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
FJ674265.1 gg_id:530490 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6742
FJ674119.1 gg_id:519474 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6741
FJ673319.1 gg_id:518746 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6733

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FJ673550.1 gg_id:524819 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6735
AY858435.2 gg_id:111427 gastrointestinal tract Grant's gazelle clone GRANT16 AY8584
EU381909.1 gg_id:267626 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU381
DQ673495.1 gg_id:164906 rumen fluid clone GRC30 DQ673
AB270010.1 gg_id:172308 Influence temperature and humidity on heifers rumen contents Holstein heifer (Bos AB270
EU844557.1 gg_id:310999 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
EU844013.1 gg_id:322677 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
EU468887.1 gg_id:290501 Speke's gazelle feces clone SP2_f07 EU468
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DQ799482.1 gg_id:193685 human fecal clone RL305aal86g09 DQ799
EU771915.1 gg_id:312589 Southern three-banded armadillo feces clone arma_g06_1 EU771
EU462163.1 gg_id:291179 black-handed spider monkey feces clone SPIM_aaj36c02 EU462
DQ804800.1 gg_id:184327 human fecal clone RL187_aao72h04 DQ804
FJ369853.1 gg_id:360784 feces adult twins and mothers; TS55 clone TS55_a01e09 FJ3698
AJ318527.2 gg_id:94718 Bryantella formatexigens I-52 AJ3185
FJ794074.1 gg_id:576531 Butyrivibrio hungatei str. AR10 FJ7940
X89972.1 gg_id:13946 Butyrivibrio fibrisolvens str. NCDO 2398 X89972
AJ428553.1 gg_id:41384 Butyrivibrio hungatei str. JK 615 AJ4285
AF001772.1 gg_id:13940 rumen clone RFP4 AF001
EU844037.1 gg_id:303813 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
EF436377.1 gg_id:217025 library-based ruminal water buffalo (Bubalus bubalis) rumen fluid clone BRC91 EF4363
EF686628.1 gg_id:247786 Sequences Manifest Rumen Yunnan Yel Cattle (Bos Taurus) rumen fluid clone YNRC1 EF6866
EU842438.1 gg_id:312418 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU8424
GU174088.1 gg_id:569196 Microbial Bactrian camel estimated rumen clone XJC46 GU174
DQ518911.1 gg_id:227475 Butyrivibrio hungatei str. OV109 DQ518
DQ392992.1 gg_id:154939 -Arctic peninsula Svalbard Norway determined genes and rumen isolates reindeer o DQ392
AY178635.1 gg_id:98638 Butyrivibrio hungatei str. Su6 AY1786

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EF686606.1 gg_id:248567 Sequences Manifest Rumen Yunnan Yel Cattle (Bos Taurus) rumen fluid clone YNRC9 EF6866
EU259429.1 gg_id:244932 Rumen yak (Bos grunniens) sequences rumen fluid clone YRC53 EU2594
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FJ833278.1 gg_id:510595 Microbial Ecology Crop Folivorous Hoatzin crop contents clone A3Q302_79G10 FJ8332
EF445246.1 gg_id:212281 dairy cow rumen clone NED4C4 EF4452
AB185815.1 gg_id:107748 rumen clone U29-H10 AB1858
AB494789.1 gg_id:554405 Fibrobacter succinogenes dominated consortium on hay stems sheep rumen clone A AB4947
AB494805.1 gg_id:589848 Fibrobacter succinogenes dominated consortium on hay stems sheep rumen clone A AB4948
FJ833585.1 gg_id:560025 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J1Q401_59C08 FJ8335
EU748391.1 gg_id:334520 neotropical folivorous flying bird adult hoatzin crop clone hoa5_07c03 EU7483
EU382023.1 gg_id:263296 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU3820
AB494829.1 gg_id:562425 Fibrobacter succinogenes dominated consortium on hay stems sheep rumen clone A AB4948
AB185609.1 gg_id:100426 rumen clone F24-D09 AB1856
AB034111.1 gg_id:45716 rumen clone 4C28d-22 AB0341
FJ685127.1 gg_id:529667 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6851
EF686550.1 gg_id:237534 Sequences Manifest Rumen Yunnan Yel Cattle (Bos Taurus) rumen fluid clone YNRC3 EF6865
AY858397.2 gg_id:111923 gastrointestinal tract Grant's gazelle clone GRANT63 AY8583
AB185548.1 gg_id:105647 rumen clone F23-E11 AB1855
EU845063.1 gg_id:330080 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8450
FJ832174.1 gg_id:593439 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P1Q101_33A05 FJ8321
DQ393006.1 gg_id:155107 on -Arctic peninsula Svalbard Norway determined genes and rumen isolates reindee DQ393
FJ673134.1 gg_id:518548 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6731
DQ673488.1 gg_id:171181 rumen fluid clone GRC23 DQ673
AM039826.1 gg_id:151973 Butyrivibrio hungatei str. JK684 AM039
EU998648.1 gg_id:344220 Anaerobic bio-energy process study on bioreactor fermentative hydrogen productio EU9986
AF018563.1 gg_id:13983 rumen fluid clone 12-116 AF0185
EU259455.1 gg_id:250378 Rumen yak (Bos grunniens) sequences rumen fluid clone YRC79 EU2594
AF396927.1 gg_id:46567 Butyrivibrio fibrisolvens str. WV1 AF3969

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EU381935.1 gg_id:272045 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU381
EU887842.1 gg_id:313349 Butyrivibrio fibrisolvens str. H15 EU887
GU303723.1 gg_id:583937 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU303
EU845522.1 gg_id:317020 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU845
EU259488.1 gg_id:251666 Rumen yak (Bos grunniens) sequences rumen fluid clone YRC112 EU259
FJ832546.1 gg_id:551295 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P3Q301_19C03 FJ8325
EU344292.1 gg_id:273016 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU344
X89973.1 gg_id:13947 Butyrivibrio fibrisolvens str. NCDO 2432 X89973
GQ402115.1 gg_id:572392 alpacas and sheep forestomach clone ALP7 GQ402
FJ833317.1 gg_id:508957 Microbial Ecology Crop Folivorous Hoatzin crop contents clone A3Q401_47G06 FJ8333
EU845719.1 gg_id:329343 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU845
EF686570.1 gg_id:257136 Sequences Manifest Rumen Yunnan Yel Cattle (Bos Taurus) rumen fluid clone YNRC5 EF6865
EU845411.1 gg_id:355326 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU845
EU468953.1 gg_id:303390 Speke's gazelle feces clone SP2_h03_1 EU468
FJ832450.1 gg_id:590844 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P3Q101_35C05 FJ8324
GU303299.1 gg_id:562486 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU303
EU344321.1 gg_id:266983 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU344
FJ172805.1 gg_id:310869 Qinghai Yak Ruminal and Fungi China rumen clone RB-2E2 FJ1728
AB185626.1 gg_id:101165 rumen clone F24-F04 AB185
AB034057.1 gg_id:53486 rumen clone 4C3d-2 AB034
AF084837.1 gg_id:13951 Eubacterium sp. str. TW2 AF084
EU843480.1 gg_id:333462 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
FJ832235.1 gg_id:538459 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P1Q102_57A08 FJ8322
EU469799.1 gg_id:295622 western lowland gorilla feces clone GOR_aag71b07 EU469
AY699275.1 gg_id:105974 Butyrivibrio fibrisolvens L10 AY699
DQ673500.1 gg_id:173319 rumen fluid clone GRC35 DQ673
FJ684664.1 gg_id:515496 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6846
EU844205.1 gg_id:350862 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
AB494756.1 gg_id:550436 Fibrobacter succinogenes dominated consortium on hay stems sheep rumen clone A AB494
X89976.1 gg_id:13950 Butyrivibrio fibrisolvens str. Bu 43 X89976
FJ678988.1 gg_id:511462 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6789
FJ832270.1 gg_id:587175 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P1Q201_33A05 FJ8322
EU748148.1 gg_id:313865 neotropical folivorous flying bird adult hoatzin crop clone hoa32_08H01.F EU748
EU844744.1 gg_id:324284 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844

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EF436289.1 gg_id:212460 library-based ruminal water buffalo (Bubalus bubalis) rumen fluid clone BRC03 EF4362
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X89975.1 gg_id:13949 Butyrivibrio fibrisolvens str. NCDO 2435 X89975
DQ256289.1 gg_id:142613 Rumen fermentation and dynamics during stepwise adaptation -concentrate diet gc DQ256
EF436453.1 gg_id:208144 library-based ruminal water buffalo (Bubalus bubalis) rumen fluid clone BRC167 EF4364
EU344334.1 gg_id:260128 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU3443
AF396926.1 gg_id:37898 Butyrivibrio fibrisolvens str. C211 AF3969
EU468849.1 gg_id:287834 Speke's gazelle feces clone SP2_a02 EU4688
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FJ833856.1 gg_id:578507 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J2Q402_60D08 FJ8338
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FJ833619.1 gg_id:591679 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J1Q402_08H01 FJ8336
GU303967.1 gg_id:544678 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU303
FJ834274.1 gg_id:584208 Microbial Ecology Crop Folivorous Hoatzin crop contents clone A2Q401_73A10 FJ8342
EU843301.1 gg_id:306119 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8433
DQ278862.1 gg_id:155730 Clostridium aminophilum 152R-1b DQ278
FJ833697.1 gg_id:551575 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J2Q101_44D06 FJ8336
EU998650.1 gg_id:304850 Anaerobic bio-energy process study on bioreactor fermentative hydrogen productio EU998
GU302568.1 gg_id:557599 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU302
GQ115584.1 gg_id:382807 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw687h1 GQ115
AM420037.1 gg_id:239814 Noma subgingival plaque clone 202A08(oral) AM420
GU407024.1 gg_id:571776 Human Oral Microbiome oral cavity GU407
X87151.1 gg_id:14096 Catonella morbi str. ATCC 51271 X87151
AF385556.1 gg_id:48583 crevicular epithelial cells clone BR063 AF3855
NZ_ACIN02000016.1 gg_id:469479 Abiotrophia defectiva str. ATCC 49176 NZ_AC
NZ_ABCC02000039.1 gg_id:469991 Clostridium bolteae str. ATCC BAA-613 NZ_AB
FJ371143.1 gg_id:360723 feces adult twins and mothers; TS6 clone TS6_a01d12 FJ3711
AJ508452.1 gg_id:83226 Clostridium bolteae str. 16351 AJ5084
DQ479412.1 gg_id:157999 Clostridium sp. CYP2 DQ479
FM994938.1 gg_id:537456 Clostridium celerecrescens str. HP2 FM994
AB117568.1 gg_id:111552 Clostridium hylemonae str. CT-30 AB117
D14638.1 gg_id:14113 Clostridium piliforme str. RJ D14638
DQ352808.1 gg_id:151298 Clostridium piliforme CRL-K DQ352
DQ352807.1 gg_id:155362 Clostridium piliforme 7MTS DQ352
DQ352806.1 gg_id:153965 Clostridium piliforme DQ352
DQ352811.1 gg_id:153952 Clostridium piliforme R1 DQ352
DQ352810.1 gg_id:153713 Clostridium piliforme CRL DQ352
AY244789.1 gg_id:86360 Clostridium scindens str. 2002-69680 AY2447

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DQ801189.1 gg_id:179381 human fecal clone RL116_aaf00c04 DQ801
FJ678914.1 gg_id:522609 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6789
EU451069.1 gg_id:322062 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H74N EU451
AY984751.1 gg_id:122545 human stool clone B711 AY9847
GQ492488.1 gg_id:584140 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
EU462089.1 gg_id:292294 black-handed spider monkey feces clone SPIM_aaj34g08 EU462
EU504811.1 gg_id:273376 cecal contents Mus musculus strain C57BL/6J; myd2 clone myd2_aaa02e11 EU5048
DQ823839.1 gg_id:185281 human fecal clone RL250_aaj79g08 DQ823
DQ456402.1 gg_id:157112 pre-adolescent turkey cecum clone CFT214H8 DQ456
DQ801439.1 gg_id:185174 human fecal clone RL388_aao95e09 DQ801
DQ799332.1 gg_id:179876 human fecal clone RL305aal85a06 DQ799
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EU778887.1 gg_id:306692 Black-handed Spider Monkey feces clone SPIM_f10 EU778
FJ685196.1 gg_id:531394 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6851
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FJ879747.1 gg_id:419244 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8797
EU779009.1 gg_id:341752 Prevost's squirrel feces clone SQ_aah80e08 EU779
FJ371024.1 gg_id:360061 feces adult twins and mothers; TS5 clone TS5_a04a08 FJ3710
GQ156416.1 gg_id:558831 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
FJ683057.1 gg_id:528893 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6830
EU509444.1 gg_id:267886 cecal contents Mus musculus strain C57BL/6J; MD9 clone MD9_aap58e03 EU509
DQ805861.1 gg_id:184155 human fecal clone RL306aal92a04 DQ805
GQ491719.1 gg_id:560908 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
FJ369253.1 gg_id:363341 feces adult twins and mothers; TS50 clone TS50_a02b02 FJ3692
EU510715.1 gg_id:269586 cecal contents Mus musculus strain C57BL/6J; WD5 clone WD5_aak39g09 EU510
DQ801354.1 gg_id:188674 human fecal clone RL388_aao94d08 DQ801
DQ057375.1 gg_id:130277 chicken ileum/cecum clone cc152 DQ057
DQ805819.1 gg_id:182430 human fecal clone RL306aal91e02 DQ805
EU451541.1 gg_id:349757 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H74N EU451
EU508869.1 gg_id:270015 cecal contents Mus musculus strain C57BL/6J; MD6 clone MD6_aap37d12 EU5088
EU766372.1 gg_id:328667 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU7663
DQ825256.1 gg_id:182940 human fecal clone RL185_aan87d04 DQ825
EU470204.1 gg_id:297920 trancaspain urial feces clone TU2_aaa04b02 EU470
FJ367980.1 gg_id:358986 feces adult twins and mothers; TS30 clone TS30_a02b03 FJ3679
FJ678396.1 gg_id:513429 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6783
EU455270.1 gg_id:340600 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K77S EU455
EU763188.1 gg_id:323777 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A> EU7631
EF399125.1 gg_id:205476 human fecal clone SJTU_F_12_07 EF3991

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EU468527.1 gg_id:290934 okapi feces clone OK1_a07_2 EU468
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GQ492164.1 gg_id:534016 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
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DQ801933.1 gg_id:190188 human fecal clone RL201_aai48f09 DQ801
GQ493000.1 gg_id:537661 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
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FJ368654.1 gg_id:368572 feces adult twins and mothers; TS49 clone TS49_a02h04 FJ3686
FJ680491.1 gg_id:519396 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6804
FJ366657.1 gg_id:362539 feces adult twins and mothers; TS27 clone TS27_a02c07 FJ3666
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EF404404.1 gg_id:209847 human fecal clone SJTU_C_09_53 EF4044
FJ679391.1 gg_id:518431 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6793
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EU462022.1 gg_id:291771 black-handed spider monkey feces clone SPIM_aaj33d11 EU462
AB234508.1 gg_id:147442 termite gut homogenate clone MgMjW-19 AB2345
EU463310.1 gg_id:291477 bush dog feces clone bdog1_aai77g06 EU463
FJ676399.1 gg_id:522177 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6763
FJ364631.1 gg_id:366411 feces adult twins and mothers; TS19 clone TS19_a01c03 FJ3646
FJ677673.1 gg_id:517081 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6776
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GQ016102.1 gg_id:493565 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw GQ016
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EU459637.1 gg_id:298788 ring-tailed lemur feces clone RT_aai09g03 EU459
GQ493802.1 gg_id:566459 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
EU459728.1 gg_id:292544 ring-tailed lemur feces clone RT_aai11f10 EU459
EU462186.1 gg_id:295683 black-handed spider monkey feces clone SPIM_aaj36g03 EU462
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DQ808211.1 gg_id:193699 human fecal clone RL180_aao73h09 DQ808
EF401865.1 gg_id:210965 human fecal clone SJTU_D_04_32 EF4018

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AY916317.1 gg_id:113422 human stool clone B395 AY9163
EU510296.1 gg_id:259056 cecal contents Mus musculus strain C57BL/6J; WD3 clone WD3_aak04c08 EU5102
FJ368701.1 gg_id:368980 feces adult twins and mothers; TS49 clone TS49_a03e03 FJ3687
AM405126.2 gg_id:573969 percent G+C fraction libraries number Actinobacteria human faecal clone AP11K.76 AM405
EU456172.1 gg_id:311674 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU4561
AY984289.1 gg_id:117903 human stool clone B182 AY9842
DQ808725.1 gg_id:198434 human fecal clone RL239_aaj12d08 DQ808
FJ676459.1 gg_id:531723 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6764
EU510783.1 gg_id:259781 cecal contents Mus musculus strain C57BL/6J; WD6 clone WD6_aak49c02 EU5107
EU761737.1 gg_id:349087 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1 EU7617
EU009784.1 gg_id:256807 intestinal microbiota domestic and wild turkeys turkey cecum clone DTB_R38 EU0097
EU463311.1 gg_id:298468 bush dog feces clone bdog1_aai77g08 EU4633
EU771786.1 gg_id:313144 African elephant feces clone AFYEL_aaj65g01 EU7717
EF096345.1 gg_id:185355 mouse cecum clone obob2_aaa01c07 EF0963
DQ809008.1 gg_id:187682 human fecal clone RL243_aai88b05 DQ809
DQ799785.1 gg_id:178610 human fecal clone RL182_aah33e05 DQ799
DQ342332.1 gg_id:174153 Effect probiotics and synbiotics on gastrointestinal broilers broiler chicken intestine DQ342
GQ492903.1 gg_id:593444 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
EF399415.1 gg_id:207651 human fecal clone SJTU_F_15_57 EF3994
DQ809996.1 gg_id:198555 human fecal clone RL184_aao66h02 DQ809
FJ364704.1 gg_id:358447 feces adult twins and mothers; TS19 clone TS19_a02a09 FJ3647
FJ680441.1 gg_id:527271 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6804
FJ362631.1 gg_id:361732 feces adult twins and mothers; TS13 clone TS13_a01c08 FJ3626
EU459643.1 gg_id:293128 ring-tailed lemur feces clone RT_aai09h03 EU4596
FJ680851.1 gg_id:521515 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6808
EU778329.1 gg_id:313557 feces clone RL116_aaf01d03 EU7783
EU459610.1 gg_id:301862 ring-tailed lemur feces clone RT_aai09c01 EU4596
EU009777.1 gg_id:239053 intestinal microbiota domestic and wild turkeys turkey cecum clone DTB_I27 EU0097
FJ367490.1 gg_id:359444 feces adult twins and mothers; TS29 clone TS29_a04b09 FJ3674
NZ_AAXB02000032.1 gg_id:470236 Dorea longicatena str. DSM 13814 NZ_AA
FJ371029.1 gg_id:356903 feces adult twins and mothers; TS5 clone TS5_a04b02 FJ3710
EF604799.1 gg_id:234097 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6047
DQ798501.1 gg_id:181434 human fecal clone RL181_aan97e05 DQ798
DQ796631.1 gg_id:199154 human fecal clone RL179aan76c06 DQ796
DQ803468.1 gg_id:188970 human fecal clone RL251_aaj86b09 DQ803
DQ014717.1 gg_id:130551 mouse cecum clone M1_h04_1 DQ014
EU767921.1 gg_id:306209 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C3 EU7679
DQ809818.1 gg_id:188194 human fecal clone RL184_aan84f06 DQ809
EU453069.1 gg_id:355468 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU4530
FJ680448.1 gg_id:515629 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6804
NZ_ACCJ01000522.1 gg_id:469972 Clostridium asparagiforme str. DSM 15981 NZ_AC

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DQ905776.1 gg_id:167098 human fecal clone 29A-g7 DQ905
DQ807951.1 gg_id:196160 human fecal clone RL180_aan69f04 DQ807
FJ676983.1 gg_id:525798 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6769
FJ681024.1 gg_id:515999 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6810
EU456668.1 gg_id:335149 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H78 EU456
EU767879.1 gg_id:350481 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C EU767
FJ364032.1 gg_id:364034 feces adult twins and mothers; TS150 clone TS150_a02b10 FJ3640
DQ796690.1 gg_id:198124 human fecal clone RL179_aao53c04 DQ796
EU509687.1 gg_id:261368 cecal contents Mus musculus strain C57BL/6J; WD10 clone WD10_aak47b05 EU509
EU463375.1 gg_id:298858 bush dog feces clone bdog1_aai80e02 EU463
FJ367507.1 gg_id:358064 feces adult twins and mothers; TS29 clone TS29_a04d03 FJ3675
DQ805157.1 gg_id:193769 human fecal clone RL249_aaj82b11 DQ805
FJ370811.1 gg_id:362280 feces adult twins and mothers; TS5 clone TS5_a01e09 FJ3708
EU510136.1 gg_id:261334 cecal contents Mus musculus strain C57BL/6J; WD3 clone WD3_aak01h03 EU510
EF098609.1 gg_id:197240 mouse cecum clone SWPT16_aaa02b03 EF0986
EF098496.1 gg_id:189905 mouse cecum clone SWPT15_aaa04c05 EF0984
EU461086.1 gg_id:297708 red kangaroo feces clone KO1_aai43h08 EU461
EF098635.1 gg_id:191772 mouse cecum clone SWPT16_aaa02e02 EF0986
EU467257.1 gg_id:299536 black-handed spider monkey feces clone SPIM_d12_1 EU467
FJ363999.1 gg_id:370424 feces adult twins and mothers; TS150 clone TS150_a01g11 FJ3639
DQ799835.1 gg_id:197134 human fecal clone RL182_aah34f05 DQ799
GQ492902.1 gg_id:550531 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
EF025255.1 gg_id:177762 Examination microbial ecology avian vivo bromodeoxyuridine intestine clone B5_F17 EF0252
DQ456162.1 gg_id:158542 pre-adolescent turkey cecum clone CFT29B5 DQ456
EU767769.1 gg_id:352786 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C EU767
AF499906.1 gg_id:83271 human colonic mucosal biopsy clone ABLCf11 AF499
EU794106.1 gg_id:334661 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_U22 EU794
FJ678586.1 gg_id:522277 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6785
DQ057365.1 gg_id:132892 chicken ileum/cecum clone cc112 DQ057
DQ325863.1 gg_id:149131 Metagenomic gut microbiome healthy human stool clone B647 DQ325
EU768387.1 gg_id:322204 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C EU768
FJ673162.1 gg_id:522205 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6731
FJ370677.1 gg_id:356832 feces adult twins and mothers; TS57 clone TS57_a03h07 FJ3706
EU459600.1 gg_id:294988 ring-tailed lemur feces clone RT_aai09a08 EU459
GQ491319.1 gg_id:542096 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
EU459747.1 gg_id:296770 ring-tailed lemur feces clone RT_aai12b05 EU459
EF098200.1 gg_id:183362 mouse cecum clone SWPT14_aaa02h11 EF0982
FJ685226.1 gg_id:512257 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6852
EU503833.1 gg_id:269103 cecal contents Mus musculus strain C57BL/6J; CRWD4 clone CRWD4_aaa01c06 EU503
DQ799122.1 gg_id:197783 human fecal clone RL205_aaj17h06 DQ799

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EU768430.1 gg_id:326928 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C5 EU7684
FJ675705.1 gg_id:517846 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6757
DQ824939.1 gg_id:180216 human fecal clone RL185_aao71c05 DQ824
EU775513.1 gg_id:323595 Western lowland gorilla feces clone GORSD_aaa01c09 EU7755
EU778621.1 gg_id:316740 Ring-tailed lemur feces clone RT_aai10e02 EU7786
EF095977.1 gg_id:181683 mouse cecum clone lean2_aaa01c05 EF0959
DQ797241.1 gg_id:184394 human fecal clone RL386_aao88g09 DQ797
GQ896927.1 gg_id:554259 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do GQ896
EU772874.1 gg_id:316781 Bush dog feces clone bdog1_aai79d12 EU7728
AY978223.1 gg_id:117538 human transverse colon mucosal biopsy clone F032 AY9782
EU451143.1 gg_id:351734 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83M EU4511
DQ798482.1 gg_id:180957 human fecal clone RL181_aan97c07 DQ798
DQ806976.1 gg_id:197405 human fecal clone RL198_aaj76d11 DQ806
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EU454651.1 gg_id:352861 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75M EU4546
AY984335.1 gg_id:125016 human stool clone B234 AY9843
EF098022.1 gg_id:199550 mouse cecum clone SWPT12_aaa04b11 EF0980
EU454185.1 gg_id:335430 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H79S EU4541
DQ794783.1 gg_id:187360 human fecal clone RL240_aaj32c10 DQ794
DQ279737.1 gg_id:141412 Clostridium citroniae str. RMA 16102 DQ279
EF098354.1 gg_id:190273 mouse cecum clone SWPT15_aaa01d07 EF0983
AB234505.1 gg_id:149725 termite gut homogenate clone MgMjW-36 AB2345
GQ047220.1 gg_id:424615 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1010b GQ047
DQ353932.1 gg_id:146448 Fecal Wild Gorilla (Gorilla beringei) wild gorilla feces clone Z86 DQ353
DQ456197.1 gg_id:157470 pre-adolescent turkey cecum clone CFT29E6 DQ456
GQ867559.1 gg_id:573341 and prevalence blaTEM genes Arctic seals colon content clone CSH64 GQ867
EU531926.1 gg_id:258392 Predominant role host genetics controlling gut microbiota FMF remission stool clone EU5319
EF025272.1 gg_id:175640 Examination microbial ecology avian vivo bromodeoxyuridine intestine clone B5_N3 EF0252
EU452062.1 gg_id:352160 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H79S EU4520
DQ014807.1 gg_id:132092 mouse cecum clone M1_h08_2 DQ014
AY978473.1 gg_id:119101 human transverse colon mucosal biopsy clone KP30 AY9784
EF097959.1 gg_id:180717 mouse cecum clone SWPT12_aaa02h07 EF0979
EF098965.1 gg_id:181568 mouse cecum clone SWPT1_aaa04a07 EF0989
DQ797248.1 gg_id:198490 human fecal clone RL386_aao88h07 DQ797
EF614514.1 gg_id:230096 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o EF6145
EF614857.1 gg_id:232638 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o EF6148
DQ815496.1 gg_id:171989 mouse cecum clone aab41f05 DQ815
GQ491971.1 gg_id:559976 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
AY975738.1 gg_id:125725 human ascending colon mucosal biopsy clone Y188 AY9757

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FJ440041.1 gg_id:510813 Megamonas hypermegale colonization correlates Campylobacter jejuni exclusion pou FJ4400
EF096677.1 gg_id:192991 mouse cecum clone SWPT11_aaa03a03 EF0966
EU452637.1 gg_id:314945 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU4526
EU457171.1 gg_id:311466 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83N EU4571
EU508167.1 gg_id:276240 cecal contents Mus musculus strain C57BL/6J; MD26 clone MD26_aaa02c06 EU5081
NR_026409.1 gg_id:559837 Desulfotomaculum guttoideum str. DSM 4024 NR_026
AY977745.1 gg_id:123816 human cecum mucosal biopsy clone LE16 AY9777
FJ880789.1 gg_id:458831 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8807
EU776090.1 gg_id:346658 Spotted hyena feces clone HY1_e08_2 EU7760
EF614550.1 gg_id:229302 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o EF6145
EU767569.1 gg_id:311176 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C3 EU7675
EU510621.1 gg_id:263896 cecal contents Mus musculus strain C57BL/6J; WD5 clone WD5_aak38d01 EU5106
AF092549.1 gg_id:52289 Clostridium algidixylanolyticum str. SPL73 AF0925
EU457056.1 gg_id:318912 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83N EU4570
EU776542.1 gg_id:319417 Lion feces clone LI3_aah77g11 EU7765
DQ798202.1 gg_id:182631 human fecal clone RL302_aal96g08 DQ798
EU511054.1 gg_id:264774 cecal contents Mus musculus strain C57BL/6J; WD7 clone WD7_aal02a07 EU5110
GQ493516.1 gg_id:542055 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
AY992804.1 gg_id:131095 mouse cecum clone C22_c07 AY9928
AY991713.1 gg_id:135440 mouse cecum clone C20_a06 AY9917
GQ492799.1 gg_id:583974 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
EF099655.1 gg_id:177473 mouse cecum clone SWPT4_aaa02e04 EF0996
EF096370.1 gg_id:183391 mouse cecum clone obob2_aaa01f11 EF0963
FJ680759.1 gg_id:514398 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6807
GQ867532.1 gg_id:587724 and prevalence blaTEM genes Arctic seals colon content clone CSH36 GQ867
AY353957.1 gg_id:103489 Clostridium amygdalinum str. BR-10 AY3539
EF098651.1 gg_id:197167 mouse cecum clone SWPT16_aaa02g06 EF0986
EU451387.1 gg_id:351209 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU4513
EF097514.1 gg_id:189187 mouse cecum clone SWPT19_aaa03f12 EF0975
EF098106.1 gg_id:174540 mouse cecum clone SWPT14_aaa01e12 EF0981
EU507818.1 gg_id:272778 cecal contents Mus musculus strain C57BL/6J; MD24 clone MD24_aaa01d02 EU5078
EF614747.1 gg_id:233250 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o EF6147
FJ365805.1 gg_id:361998 feces adult twins and mothers; TS21 clone TS21_a03c06 FJ3658
AY984860.1 gg_id:119032 human stool clone B831 AY9848
DQ015443.1 gg_id:135545 mouse cecum clone M3_b07_1 DQ015
AB234506.1 gg_id:146502 termite gut homogenate clone MgMjW-10 AB2345
EU509027.1 gg_id:261702 cecal contents Mus musculus strain C57BL/6J; MD7 clone MD7_aap42c01 EU5090
FJ370740.1 gg_id:357463 feces adult twins and mothers; TS57 clone TS57_a04f09 FJ3707
EU457966.1 gg_id:330827 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU4579
DQ800914.1 gg_id:187219 human fecal clone RL387_aao89c01 DQ800

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EU768688.1 gg_id:353667 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C5 EU768
GQ491558.1 gg_id:586550 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
DQ801140.1 gg_id:195881 human fecal clone RL387_aao92h01 DQ801
FJ370445.1 gg_id:365964 feces adult twins and mothers; TS57 clone TS57_a01b09 FJ3704
EU773398.1 gg_id:336380 Black lemur feces clone BKLE_a10_2 EU773
EU509201.1 gg_id:263138 cecal contents Mus musculus strain C57BL/6J; MD8 clone MD8_aap45g06 EU509
DQ905099.1 gg_id:161968 human fecal clone 002C-a12 DQ905
EU778925.1 gg_id:320055 Black-handed Spider Monkey feces clone SPIM_f09 EU778
AY993032.1 gg_id:129499 mouse cecum clone C22_p16 AY993
EU455030.1 gg_id:348772 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75M EU455
DQ326829.1 gg_id:146345 Metagenomic gut microbiome healthy human stool clone E306 DQ326
EU509143.1 gg_id:259818 cecal contents Mus musculus strain C57BL/6J; MD7 clone MD7_aap44g03 EU509
EF096881.1 gg_id:187921 mouse cecum clone SWPT13_aaa02b10 EF0968
EU474306.1 gg_id:301475 western lowland gorilla feces clone GORSD_aaa02a05 EU474
EU457851.1 gg_id:308032 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74M EU457
EF096575.1 gg_id:173922 mouse cecum clone SWPT11_aaa01c11 EF0965
EU508162.1 gg_id:261380 cecal contents Mus musculus strain C57BL/6J; MD26 clone MD26_aaa02b10 EU508
EF096197.1 gg_id:186792 mouse cecum clone obob1_aaa02d03 EF0961
EU455805.1 gg_id:346278 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75M EU455
EU510123.1 gg_id:272390 cecal contents Mus musculus strain C57BL/6J; WD3 clone WD3_aak01f11 EU510
EU457007.1 gg_id:346275 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75M EU457
EU459640.1 gg_id:296042 ring-tailed lemur feces clone RT_aai09g10 EU459
EF098240.1 gg_id:196497 mouse cecum clone SWPT14_aaa03e03 EF0982
EU508949.1 gg_id:259909 cecal contents Mus musculus strain C57BL/6J; MD6 clone MD6_aap40a10 EU508
GQ493246.1 gg_id:545473 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
Y18184.1 gg_id:26602 Clostridium indolis str. DSM 755 Y18184
EU506499.1 gg_id:259653 cecal contents Mus musculus strain C57BL/6J; MD19 clone MD19_aaa03a06 EU506
FJ369112.1 gg_id:367707 feces adult twins and mothers; TS4 clone TS4_a04d05 FJ3691
EF096597.1 gg_id:178199 mouse cecum clone SWPT11_aaa01f04 EF0965
EU511885.1 gg_id:261220 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_aaf10e04 EU511
EU454984.1 gg_id:328536 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU454
FJ370230.1 gg_id:359949 feces adult twins and mothers; TS56 clone TS56_a02b02 FJ3702
EF098306.1 gg_id:181133 mouse cecum clone SWPT14_aaa04e07 EF0983
AY993145.1 gg_id:135431 mouse cecum clone C21_g02 AY993
EU458073.1 gg_id:315358 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU458
GQ491281.1 gg_id:583045 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
EU509952.1 gg_id:269949 cecal contents Mus musculus strain C57BL/6J; WD11 clone WD11_aak24c03 EU509
EU504399.1 gg_id:266896 cecal contents Mus musculus strain C57BL/6J; CRWD6 clone CRWD6_aaa03f03 EU504
EU457908.1 gg_id:309360 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K79S EU457
EU450910.1 gg_id:333069 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU450

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AY992008.1 gg_id:134549 mouse cecum clone C20_p10 AY9920
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EF096277.1 gg_id:199341 mouse cecum clone obob1_aaa04a05 EF0962
EU452590.1 gg_id:312205 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75M EU4525
EF099536.1 gg_id:186085 mouse cecum clone SWPT3_aaa04f01 EF0995
EF604514.1 gg_id:234516 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6045
EF614877.1 gg_id:233595 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o EF6148
DQ815426.1 gg_id:166609 mouse cecum clone aab48b10 DQ815
GQ492112.1 gg_id:593369 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
FJ957873.1 gg_id:461989 Clostridium saccharolyticum str. JPL_21 FJ9578
EF404438.1 gg_id:209193 human fecal clone SJTU_C_10_05 EF4044
FJ370463.1 gg_id:362460 feces adult twins and mothers; TS57 clone TS57_a01d06 FJ3704
FJ370529.1 gg_id:357221 feces adult twins and mothers; TS57 clone TS57_a02b05 FJ3705
FJ680978.1 gg_id:527327 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6809
AJ311620.2 gg_id:90431 Clostridium hathewayi str. DSM 13479 = CCUG 43 AJ3116
AJ408971.1 gg_id:69958 human colonic clone HuCA19 AJ4089
EU463123.1 gg_id:296872 naked mole-rat feces clone molerat_aai70c02 EU4631
EU509115.1 gg_id:276941 cecal contents Mus musculus strain C57BL/6J; MD7 clone MD7_aap44a08 EU5091
EF099826.1 gg_id:193023 mouse cecum clone SWPT4_aaa04h05 EF0998
EU510090.1 gg_id:270627 cecal contents Mus musculus strain C57BL/6J; WD3 clone WD3_aak01b12 EU5100
DQ815622.1 gg_id:169045 mouse cecum clone aab43f10 DQ815
DQ801685.1 gg_id:181521 human fecal clone RL201_aai45e03 DQ801
FJ370676.1 gg_id:361375 feces adult twins and mothers; TS57 clone TS57_a03h06 FJ3706
DQ904855.1 gg_id:173777 human fecal clone 001C-c6 DQ904
EU452655.1 gg_id:321921 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU4526
EU511980.1 gg_id:267783 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_aak12c04 EU5119
EF406450.1 gg_id:211001 mouse colon clone control_14days-A1 EF4064
EF095970.1 gg_id:178026 mouse cecum clone lean2_aaa01b07 EF0959
EU450991.1 gg_id:350064 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74M EU4509
DQ815701.1 gg_id:164638 mouse cecum clone aab21b07 DQ815
EF604630.1 gg_id:231997 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6046
EU511917.1 gg_id:274132 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_aak11c02 EU5119
FJ370659.1 gg_id:367027 feces adult twins and mothers; TS57 clone TS57_a03f09 FJ3706
EF096886.1 gg_id:175986 mouse cecum clone SWPT13_aaa02c04 EF0968
DQ015121.1 gg_id:131793 mouse cecum clone M2_f12_1 DQ015
AY993011.1 gg_id:130465 mouse cecum clone C22_o10 AY9930
EF098094.1 gg_id:184695 mouse cecum clone SWPT14_aaa01d09 EF0980
FJ880800.1 gg_id:429698 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8808

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DQ507245.1 gg_id:159259 Clostridium sp. str. AIP 321.05 DQ507
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EU511227.1 gg_id:273077 cecal contents Mus musculus strain C57BL/6J; WD7 clone WD7_aal04f11 EU511
EU510407.1 gg_id:270065 cecal contents Mus musculus strain C57BL/6J; WD4 clone WD4_aal38b01 EU510
DQ803584.1 gg_id:179758 human fecal clone RL251_aaj87g05 DQ803
DQ800728.1 gg_id:183498 human fecal clone RL183_aao02f09 DQ800
FJ370516.1 gg_id:368577 feces adult twins and mothers; TS57 clone TS57_a02a04 FJ3705
EF098834.1 gg_id:181808 mouse cecum clone SWPT1_aaa01f07 EF0988
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EU508759.1 gg_id:271646 cecal contents Mus musculus strain C57BL/6J; MD4 clone MD4_aap50e12 EU508
EU504370.1 gg_id:260529 cecal contents Mus musculus strain C57BL/6J; CRWD6 clone CRWD6_aaa03b11 EU504
EU776687.1 gg_id:331571 Lion feces clone LI3_aah76a12 EU776
EF098153.1 gg_id:181711 mouse cecum clone SWPT14_aaa02c08 EF0981
EU451008.1 gg_id:345101 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU451
EU776759.1 gg_id:310803 Mongoose lemur feces clone ML_aaj25c02 EU776
FJ364698.1 gg_id:362665 feces adult twins and mothers; TS19 clone TS19_a02a02 FJ3646
EU778969.1 gg_id:331575 Prevost's squirrel feces clone SQ_aah82g09 EU778
EU452394.1 gg_id:352370 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU452
EU767660.1 gg_id:304352 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C EU767
DQ815778.1 gg_id:167848 mouse cecum clone aab22b11 DQ815
EU862317.1 gg_id:344422 Clostridium sp. str. C9 EU862
EU451858.1 gg_id:326644 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H79 EU451
EF614479.1 gg_id:234428 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o EF6144
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EU454659.1 gg_id:313237 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N EU454
EF099107.1 gg_id:196760 mouse cecum clone SWPT2_aaa02d03 EF0991
EU456764.1 gg_id:311165 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU456

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EU766772.1 gg_id:332005 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU7667
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AM183091.1 gg_id:253465 and its spatial composts compost clone SMC62 AM183
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EU764399.1 gg_id:321397 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1 EU7643
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FJ364572.1 gg_id:362759 feces adult twins and mothers; TS15 clone TS15_a04e07 FJ3645
EF099498.1 gg_id:191020 mouse cecum clone SWPT3_aaa04a04 EF0994
AF357570.1 gg_id:71692 mpn-isolate group 22 AF3575
EU504147.1 gg_id:263865 cecal contents Mus musculus strain C57BL/6J; CRWD5 clone CRWD5_aaa02c04 EU5041
GQ492220.1 gg_id:592784 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
EU506722.1 gg_id:265652 cecal contents Mus musculus strain C57BL/6J; MD20 clone MD20_aap55b07 EU5067
EU452778.1 gg_id:312718 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU4527
FJ370778.1 gg_id:370100 feces adult twins and mothers; TS5 clone TS5_a01b08 FJ3707
EU504001.1 gg_id:268581 cecal contents Mus musculus strain C57BL/6J; CRWD4 clone CRWD4_aaa03h01 EU5040

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EU503912.1 gg_id:267090 cecal contents Mus musculus strain C57BL/6J; CRWD4 clone CRWD4_aaa02e02 EU503
EF098723.1 gg_id:199322 mouse cecum clone SWPT16_aaa04a02 EF0987
FJ371935.1 gg_id:358495 feces adult twins and mothers; TS8 clone TS8_a03h06 FJ3719
DQ808448.1 gg_id:180386 human fecal clone RL180_aao76f10 DQ808
EU503586.1 gg_id:266131 cecal contents Mus musculus strain C57BL/6J; CRWD2 clone CRWD2_aaa01f02 EU503
FM204998.1 gg_id:564961 Prokaryote shifts and reductive dehalogenase redundancy response electron donor FM204
EU451441.1 gg_id:355374 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H79 EU451
EU510210.1 gg_id:258218 cecal contents Mus musculus strain C57BL/6J; WD3 clone WD3_aak02h12 EU510
EU508100.1 gg_id:276628 cecal contents Mus musculus strain C57BL/6J; MD25 clone MD25_aaa04a04 EU508
DQ807984.1 gg_id:177535 human fecal clone RL180_aan70b12 DQ807
EF097084.1 gg_id:175044 mouse cecum clone SWPT18_aaa01b09 EF097
EU453023.1 gg_id:331317 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77 EU453
EF099459.1 gg_id:188117 mouse cecum clone SWPT3_aaa03e02 EF0994
EU474426.1 gg_id:292669 western lowland gorilla feces clone GORSD_aaa01a07 EU474
EF096430.1 gg_id:182604 mouse cecum clone obob2_aaa02f12 EF0964
EF398816.1 gg_id:213808 human fecal clone SJTU_F_07_51 EF3988
DQ795209.1 gg_id:182723 human fecal clone RL178_aah51e09 DQ795
EU511939.1 gg_id:263503 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_aak11e10 EU511
EF025256.1 gg_id:185151 Examination microbial ecology avian vivo bromodeoxyuridine intestine clone B5_F18 EF0252
EF098495.1 gg_id:181368 mouse cecum clone SWPT15_aaa04c02 EF0984
EU506432.1 gg_id:270960 cecal contents Mus musculus strain C57BL/6J; MD19 clone MD19_aaa01f09 EU506
EU511857.1 gg_id:260996 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_aaf10a07 EU511
EU773389.1 gg_id:332584 BigHorn sheep feces clone BH1_aao26e10 EU773
EU456147.1 gg_id:316007 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75 EU456
EU508222.1 gg_id:275907 cecal contents Mus musculus strain C57BL/6J; MD26 clone MD26_aaa03f09 EU508
GQ897835.1 gg_id:557850 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ897
AB114225.1 gg_id:97871 Clostridium sp. str. B556-1 AB114
X71855.1 gg_id:13973 Clostridium xylanolyticum str. ATCC 4963 X71855
EF604530.1 gg_id:233313 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6045
DQ014635.1 gg_id:134263 mouse cecum clone M1_h08 DQ014
DQ799555.1 gg_id:184320 human fecal clone RL305aal87f04 DQ799
EF099548.1 gg_id:185301 mouse cecum clone SWPT3_aaa04g06 EF0995
EU506240.1 gg_id:261109 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aap61c06 EU506
FJ880755.1 gg_id:416185 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8807
EU455733.1 gg_id:321446 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77 EU455
EU508176.1 gg_id:272386 cecal contents Mus musculus strain C57BL/6J; MD26 clone MD26_aaa02e07 EU508
EF098641.1 gg_id:183428 mouse cecum clone SWPT16_aaa02e12 EF0986
EU504073.1 gg_id:272742 cecal contents Mus musculus strain C57BL/6J; CRWD4 clone CRWD4_aaa04h05 EU504
DQ798869.1 gg_id:177286 human fecal clone RL242_aaj98d09 DQ798
EF096053.1 gg_id:177043 mouse cecum clone lean2_aaa03a06 EF0960
EU456428.1 gg_id:347190 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80 EU456

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AB114231.1 gg_id:95658 Clostridium sp. str. Kas401-4	AB114
EF098553.1 gg_id:185587 mouse cecum clone SWPT16_aaa01c07	EF0985
EU506380.1 gg_id:275913 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aap64e10	EU5063
EF096792.1 gg_id:173865 mouse cecum clone SWPT11_aaa04g04	EF0967
DQ015610.1 gg_id:129538 mouse cecum clone M3_b09_3	DQ015
DQ798924.1 gg_id:176924 human fecal clone RL242_aaj99b07	DQ798
EF098774.1 gg_id:188527 mouse cecum clone SWPT16_aaa04g01	EF0987
EU511784.1 gg_id:275362 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_aaf09b12.Contig2	EU5117
EU777890.1 gg_id:333030 European rabbit feces clone RA_c12	EU7778
EU777843.1 gg_id:317693 European rabbit feces clone RA_d04	EU7778
EU771662.1 gg_id:324837 African elephant feces clone AFYEL_aaj67h11	EU7716
EU450997.1 gg_id:351184 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S	EU4509
EF097574.1 gg_id:193509 mouse cecum clone SWPT19_aaa04f03	EF0975
EU777852.1 gg_id:353339 European rabbit feces clone RA_c07	EU7778
EU458606.1 gg_id:302763 European rabbit feces clone RA_c11	EU4586
EU453414.1 gg_id:304920 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N	EU4534
EF099092.1 gg_id:189272 mouse cecum clone SWPT2_aaa02b04	EF0990
EU454774.1 gg_id:314424 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S	EU4547
EU506185.1 gg_id:274509 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aaa02f05	EU5061
EF097951.1 gg_id:188402 mouse cecum clone SWPT12_aaa02g05	EF0979
EU506150.1 gg_id:276190 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aaa01a10	EU5061
EU530312.1 gg_id:259761 mucosa adherent and invasive microbes profile adenoma colorectal cancer clone M4	EU5303
DQ807567.1 gg_id:196575 human fecal clone RL307_aam08d02	DQ807
DQ904659.1 gg_id:163667 human fecal clone 001-b9	DQ904
DQ815335.1 gg_id:165437 mouse cecum clone aab45g07	DQ815
EU511089.1 gg_id:274060 cecal contents Mus musculus strain C57BL/6J; WD7 clone WD7_aal02e08	EU5110
EF098104.1 gg_id:186332 mouse cecum clone SWPT14_aaa01e09	EF0981
FJ364077.1 gg_id:367361 feces adult twins and mothers; TS150 clone TS150_a02g01	FJ3640
AY984246.1 gg_id:125031 human stool clone B137	AY9842
DQ802434.1 gg_id:196091 human fecal clone RL188_aah17f09	DQ802
DQ014768.1 gg_id:131073 mouse cecum clone M1_e02_2	DQ014
EU453995.1 gg_id:338442 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S	EU4539
FJ367695.1 gg_id:367805 feces adult twins and mothers; TS2 clone TS2_a02e03	FJ3676
DQ825146.1 gg_id:185864 human fecal clone RL185_aan85h06	DQ825
FJ371087.1 gg_id:369473 feces adult twins and mothers; TS5 clone TS5_a04g05	FJ3710
AY977088.1 gg_id:118015 human cecum mucosal biopsy clone K778	AY9770
DQ808251.1 gg_id:198086 human fecal clone RL180_aao74d08	DQ808
FJ369137.1 gg_id:361894 feces adult twins and mothers; TS4 clone TS4_a04f10	FJ3691
FJ369095.1 gg_id:357512 feces adult twins and mothers; TS4 clone TS4_a04b08	FJ3690
FJ368954.1 gg_id:359028 feces adult twins and mothers; TS4 clone TS4_a02e06	FJ3689
DQ807363.1 gg_id:187991 human fecal clone RL307_aam05f02	DQ807

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FJ371331.1 gg_id:370049 feces adult twins and mothers; TS6 clone TS6_a03f11 FJ3713
AY994021.1 gg_id:136633 Abundant and fungal microbiota murine intestine clone 41-1 AY994
DQ799304.1 gg_id:181834 human fecal clone RL205_aaj20e03 DQ799
FJ369123.1 gg_id:365644 feces adult twins and mothers; TS4 clone TS4_a04e06 FJ3691
AY981455.1 gg_id:122012 human sigmoid colon mucosal biopsy clone L545 AY981
EU766751.1 gg_id:329944 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU766
AY984564.1 gg_id:123233 human stool clone B503 AY984
EF098881.1 gg_id:187852 mouse cecum clone SWPT1_aaa02e12 EF0988
FJ367781.1 gg_id:357957 feces adult twins and mothers; TS2 clone TS2_a03e07 FJ3677
DQ904722.1 gg_id:171410 human fecal clone 001-h12 DQ904
AY984690.1 gg_id:121570 human stool clone B642 AY984
EF099816.1 gg_id:192408 mouse cecum clone SWPT4_aaa04g01 EF0998
FJ369040.1 gg_id:365086 feces adult twins and mothers; TS4 clone TS4_a03e09 FJ3690
DQ823933.1 gg_id:196107 human fecal clone RL204_aaj57b03 DQ823
FJ368977.1 gg_id:358255 feces adult twins and mothers; TS4 clone TS4_a02g07 FJ3689
EU504262.1 gg_id:275676 cecal contents Mus musculus strain C57BL/6J; CRWD6 clone CRWD6_aaa01c09 EU504
DQ905526.1 gg_id:162294 human fecal clone 014-g1 DQ905
EU508369.1 gg_id:258165 cecal contents Mus musculus strain C57BL/6J; MD27 clone MD27_aaa04a08 EU508
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FJ370956.1 gg_id:363515 feces adult twins and mothers; TS5 clone TS5_a03c03 FJ3709
EF404993.1 gg_id:216746 human fecal clone SJTU_G_05_59 EF4049
FJ369087.1 gg_id:357218 feces adult twins and mothers; TS4 clone TS4_a04a12 FJ3690
DQ904930.1 gg_id:171783 human fecal clone 002-b1 DQ904
AY978695.1 gg_id:119824 human transverse colon mucosal biopsy clone KT72 AY978
EU453964.1 gg_id:318008 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU453
EF403201.1 gg_id:210539 human fecal clone SJTU_A1_6_40 EF4032
AY984776.1 gg_id:116238 human stool clone B738 AY984
AY975938.1 gg_id:120535 human ascending colon mucosal biopsy clone LS45 AY975
AY982876.1 gg_id:120781 human descending colon mucosal biopsy clone L046 AY982
AY983028.1 gg_id:123310 human descending colon mucosal biopsy clone L258 AY983
AY980512.1 gg_id:127137 human rectum mucosal biopsy clone X243 AY980
FJ368858.1 gg_id:364039 feces adult twins and mothers; TS4 clone TS4_a01d09 FJ3688
AY982766.1 gg_id:126286 human descending colon mucosal biopsy clone KZ01 AY982
EU508235.1 gg_id:275799 cecal contents Mus musculus strain C57BL/6J; MD26 clone MD26_aaa04a07 EU508
FJ368923.1 gg_id:366377 feces adult twins and mothers; TS4 clone TS4_a02b08 FJ3689
DQ802136.1 gg_id:176587 human fecal clone RL241_aaj03e08 DQ802
FJ371276.1 gg_id:357312 feces adult twins and mothers; TS6 clone TS6_a03a10 FJ3712
EF400450.1 gg_id:212481 human fecal clone SJTU_E_13_50 EF4004
EF401232.1 gg_id:206701 human fecal clone SJTU_D_07_54 EF4012

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DQ823905.1 gg_id:197197 human fecal clone RL250_aaj80g04 DQ823
AY916166.1 gg_id:114387 human transverse colon biopsy clone M629 AY916
EU776782.1 gg_id:321095 Mongoose lemur feces clone ML_aaj28f07 EU776
FJ369014.1 gg_id:370235 feces adult twins and mothers; TS4 clone TS4_a03c07 FJ3690
FJ369150.1 gg_id:367923 feces adult twins and mothers; TS4 clone TS4_a04h04 FJ3691
AY985171.1 gg_id:116565 human stool clone BB95 AY985
DQ801872.1 gg_id:183711 human fecal clone RL201_aai47h08 DQ801
AY982502.1 gg_id:123023 human sigmoid colon mucosal biopsy clone MN06 AY982
EF604966.1 gg_id:235081 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF604
EF604534.1 gg_id:234956 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6045
EF097988.1 gg_id:181415 mouse cecum clone SWPT12_aaa03f06 EF0979
EU511999.1 gg_id:271804 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_aak12e04 EU511
EF099490.1 gg_id:174338 mouse cecum clone SWPT3_aaa03g12 EF0994
EF602819.1 gg_id:228836 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6028
EU457160.1 gg_id:352799 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H79 EU457
EU451365.1 gg_id:327720 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83 EU451
EU452796.1 gg_id:315001 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU452
EU776507.1 gg_id:325848 Lion feces clone LI3_aah76a09 EU776
EF098165.1 gg_id:197600 mouse cecum clone SWPT14_aaa02e04 EF0981
EU454540.1 gg_id:305112 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83 EU454
EU453875.1 gg_id:307093 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75 EU453
EF098455.1 gg_id:197759 mouse cecum clone SWPT15_aaa03e04 EF0984
EU509194.1 gg_id:272159 cecal contents Mus musculus strain C57BL/6J; MD8 clone MD8_aap45f11 EU509
EU504518.1 gg_id:267353 cecal contents Mus musculus strain C57BL/6J; myd1 clone myd1_aaa01g04 EU504
EU454074.1 gg_id:353177 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75 EU454
EF605183.1 gg_id:228046 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6051
EU509790.1 gg_id:275349 cecal contents Mus musculus strain C57BL/6J; WD11 clone WD11_aak21b01 EU509
AY992530.1 gg_id:132673 mouse cecum clone C23_h21 AY992
EU506415.1 gg_id:259154 cecal contents Mus musculus strain C57BL/6J; MD19 clone MD19_aaa01d10 EU506
EU455283.1 gg_id:345503 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU455
EF098479.1 gg_id:190699 mouse cecum clone SWPT15_aaa03h11 EF0984
EF097776.1 gg_id:192131 mouse cecum clone SWPT20_aaa03f01 EF0977
EF097342.1 gg_id:176950 mouse cecum clone SWPT19_aaa01c11 EF0973
AY991902.1 gg_id:135378 mouse cecum clone C20_k03 AY991
EU504157.1 gg_id:266061 cecal contents Mus musculus strain C57BL/6J; CRWD5 clone CRWD5_aaa02e02 EU504
EU510843.1 gg_id:277200 cecal contents Mus musculus strain C57BL/6J; WD6 clone WD6_aak50b04 EU510
EU474262.1 gg_id:296041 western lowland gorilla feces clone GORSD_aaa01e03 EU474
EU453646.1 gg_id:315974 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77 EU453
EF602818.1 gg_id:228511 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6028
EF604535.1 gg_id:235067 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6045
FJ881305.1 gg_id:428954 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8813

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EU455602.1 gg_id:330278 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H79S EU455
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EF098746.1 gg_id:199211 mouse cecum clone SWPT16_aaa04c10 EF0987
EF096344.1 gg_id:180694 mouse cecum clone obob2_aaa01c06 EF0963
EU510446.1 gg_id:274237 cecal contents Mus musculus strain C57BL/6J; WD4 clone WD4_aal38g05 EU510
EU453143.1 gg_id:352769 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU453
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EU451037.1 gg_id:352146 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU451
EF604634.1 gg_id:232681 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6046
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EU451512.1 gg_id:341100 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU451
EU503823.1 gg_id:264544 cecal contents Mus musculus strain C57BL/6J; CRWD4 clone CRWD4_aaa01b06 EU503
EU510959.1 gg_id:258626 cecal contents Mus musculus strain C57BL/6J; WD6 clone WD6_aak52d07 EU510
EF098083.1 gg_id:194848 mouse cecum clone SWPT14_aaa01c05 EF0980
EU506320.1 gg_id:273558 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aap63b10 EU506
AY992877.1 gg_id:130280 mouse cecum clone C22_g16 AY9928
AM932538.1 gg_id:567954 microbiota Toll-like receptor 2 deficient mice exhibits lineage specific modifications AM932
DQ015189.1 gg_id:132741 mouse cecum clone M2_g02_2 DQ015
EF095964.1 gg_id:187871 mouse cecum clone lean2_aaa01a05 EF0959
EU457571.1 gg_id:349645 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H78S EU457
EU474428.1 gg_id:287507 western lowland gorilla feces clone GORSD_aaa01a10 EU4744
EF096058.1 gg_id:190496 mouse cecum clone lean2_aaa03b08 EF0960
AY991913.1 gg_id:129978 mouse cecum clone C20_k14 AY9919
AM932611.1 gg_id:537301 microbiota Toll-like receptor 2 deficient mice exhibits lineage specific modifications AM932
FJ879176.1 gg_id:403497 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8791
EU504967.1 gg_id:273683 cecal contents Mus musculus strain C57BL/6J; myd2 clone myd2_aaa04h09 EU5049
EF098676.1 gg_id:180508 mouse cecum clone SWPT16_aaa03c07 EF0986
DQ014804.1 gg_id:131642 mouse cecum clone M1_h04_2 DQ014
DQ815639.1 gg_id:163445 mouse cecum clone aab44b08 DQ815
DQ014926.1 gg_id:133348 mouse cecum clone M1_1e10 DQ014
EU454486.1 gg_id:311129 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K79S EU4544
EF099794.1 gg_id:197183 mouse cecum clone SWPT4_aaa04d06 EF0997
EU511991.1 gg_id:262335 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_aak12d06 EU5119
EU006205.1 gg_id:240405 Salmonella enterica serovar typhimurium exploits inflammation compete intestinal r EU0062
EF098596.1 gg_id:174631 mouse cecum clone SWPT16_aaa01h10 EF0985
EU454164.1 gg_id:321642 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU4541
EU504734.1 gg_id:260278 cecal contents Mus musculus strain C57BL/6J; myd2 clone myd2_aaa01c09 EU5047

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EU454820.1 gg_id:316984 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU4548
EU506201.1 gg_id:264427 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aaa03e06 EU5062
EU451646.1 gg_id:343917 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N EU4516
EU776893.1 gg_id:350052 Mongoose lemur feces clone ML_aae87d11 EU7768
EU766933.1 gg_id:352649 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU7669
DQ824440.1 gg_id:197356 human fecal clone RL304_aal76a10 DQ824
GQ503859.1 gg_id:564639 Captain bheri clone Ecwsrb022 GQ503
AB234493.1 gg_id:146488 termite gut homogenate clone MgMjR-083 AB2344
EU768108.1 gg_id:329703 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C4 EU7681
AB234484.1 gg_id:147741 termite gut homogenate clone MgMjR-030 AB2344
EU504190.1 gg_id:258283 cecal contents Mus musculus strain C57BL/6J; CRWD5 clone CRWD5_aaa03g02 EU5041
DQ798696.1 gg_id:198678 human fecal clone RL181_aao00c02 DQ798
AY349389.1 gg_id:92430 human oral cavity clone JM048 AY3493
FJ978593.1 gg_id:384675 feces clone CL_F_197 FJ9785
FJ676837.1 gg_id:525104 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6768
DQ802531.1 gg_id:187163 human fecal clone RL188_aan93a09 DQ802
DQ905267.1 gg_id:171220 human fecal clone 013-g8 DQ905
AB088949.1 gg_id:77909 termite gut homogenate clone Rs-D68 bacterium AB0889
AY974898.1 gg_id:116267 human ascending colon mucosal biopsy clone KH90 AY9748
DQ802285.1 gg_id:181634 human fecal clone RL188_aah15f04 DQ802
AY975299.1 gg_id:124921 human ascending colon mucosal biopsy clone N540 AY9752
DQ803552.1 gg_id:199212 human fecal clone RL251_aaj87d02 DQ803
NR_029269.1 gg_id:584986 Clostridium propionicum str. X2; DSM 1682 NR_029
GQ448418.1 gg_id:557186 Microbiome neonatal calves: shedding microorganisms fecal clone calf783_10wks_g GQ448
FJ362869.1 gg_id:363216 feces adult twins and mothers; TS13 clone TS13_a04b10 FJ3628
EU748174.1 gg_id:321561 neotropical folivorous flying bird adult hoatzin crop clone hoa31_73A10.F EU7481
EF399587.1 gg_id:205933 human fecal clone SJTU_F_06_63 EF3995
AY992923.1 gg_id:130491 mouse cecum clone C22_i22 AY9929
GU304319.1 gg_id:563613 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU304
DQ799077.1 gg_id:180319 human fecal clone RL205_aaj17c08 DQ799
DQ327495.1 gg_id:150500 Metagenomic gut microbiome healthy human stool clone EA67 DQ327
EF402203.1 gg_id:204121 human fecal clone SJTU_B_04_90 EF4022
DQ804300.1 gg_id:197231 human fecal clone RL187_aan77f07 DQ804
EU763532.1 gg_id:327125 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A4 EU7635
EU472163.1 gg_id:295754 francois langur feces clone FL_2aaa03h11 EU4721
EF434346.1 gg_id:210179 human infant gastrointestinal tract microbiota stool baby 3 12 weeks old clone 10999 EF4343
DQ799640.1 gg_id:175400 human fecal clone RL305aal88f01 DQ799
EU761814.1 gg_id:347117 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1 EU7618
EU250957.1 gg_id:370405 degraded cellulose lindane NSC-7 NFC-7 grown 50 degrees Celsius compost compose EU2509

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AB185777.1 gg_id:105659 rumen clone U29-D06 AB185
FJ368953.1 gg_id:358649 feces adult twins and mothers; TS4 clone TS4_a02e05 FJ3689
FJ364499.1 gg_id:365900 feces adult twins and mothers; TS15 clone TS15_a03f08 FJ3644
AB288892.1 gg_id:201079 termite gut homogenate clone BOf2-23 AB288
DQ799135.1 gg_id:185370 human fecal clone RL205_aaj18a11 DQ799
EU763056.1 gg_id:313769 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU763
DQ803148.1 gg_id:182190 human fecal clone RL311_aam21b06 DQ803
AM275397.2 gg_id:231161 fecal microbiota irritable bowel syndrome patients significantly that healthy subject AM275
AF371679.1 gg_id:32467 swine intestine clone p-4247-4Wa3 AF371
AB234448.1 gg_id:148473 termite gut homogenate clone MgMjR-070 AB234
AB192216.1 gg_id:143980 termite gut homogenate clone RsTu1-66 AB192
GQ449057.1 gg_id:547906 Microbiome neonatal calves: shedding microorganisms fecal clone calf783_10wks_g GQ449
EF603661.1 gg_id:229062 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6036
GQ502561.1 gg_id:563998 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf4- GQ502
EU763577.1 gg_id:308853 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU763
EF097077.1 gg_id:175307 mouse cecum clone SWPT18_aaa01a12 EF097
AM420271.1 gg_id:251150 Noma subgingival plaque clone 702B06(oral) AM420
AY986119.1 gg_id:118835 human stool clone D461 AY986
EU510399.1 gg_id:268620 cecal contents Mus musculus strain C57BL/6J; WD4 clone WD4_aal37h12 EU510
AB198664.1 gg_id:135632 termite gut fluid and protists fraction clone RsC01-098 AB198
EU472066.1 gg_id:289449 francois langur feces clone FL_1aaa03g05 EU472
AY684405.2 gg_id:110059 mucosal biopsies human intestine clone HuDI72 AY684
DQ807168.1 gg_id:176088 human fecal clone RL244_aaj47b01 DQ807
AY916283.1 gg_id:113415 human sigmoid colon biopsy clone G075 AY916
AY984500.1 gg_id:121072 human stool clone B424 AY984
DQ797242.1 gg_id:174520 human fecal clone RL386_aao88g10 DQ797
FJ366310.1 gg_id:361864 feces adult twins and mothers; TS26 clone TS26_a01b09 FJ3663
DQ825193.1 gg_id:188567 human fecal clone RL185_aan86e06 DQ825
GQ175485.1 gg_id:591118 Chicken intestinal microbiota modulations various feed supplementations DGGE an GQ175
NR_026151.1 gg_id:539658 Clostridium colinum str. DSM 6011 NR_02
EU850560.1 gg_id:347796 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF369 EU850
EU768799.1 gg_id:318400 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C EU768
EU283547.1 gg_id:277790 Model Early Earth Harbors Deeply Divergent Divisions Anderson Lake clone A889 EU283
EU842731.1 gg_id:318679 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
EF603946.1 gg_id:233761 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6039
AB192057.1 gg_id:142092 termite gut homogenate clone M1NP2-32 AB192
AJ811979.1 gg_id:196159 human biopsies Human ulcerative colitis biopsy clone UC9-31 AJ8119
DQ647100.1 gg_id:256583 Microbial structure -temperature oil-field produced water Troll formations North Se DQ647
EU764416.1 gg_id:329193 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B EU764
DQ456412.1 gg_id:157611 pre-adolescent turkey cecum clone CFT214G6 DQ456

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FJ684344.1 gg_id:520882 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6843
FJ879150.1 gg_id:430468 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8791
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EU505619.1 gg_id:262012 cecal contents Mus musculus strain C57BL/6J; myd5 clone myd5_aaa03e07 EU5056
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AB062772.1 gg_id:37128 termite gut homogenate clone BCf1-11 AB0627
AB234445.1 gg_id:145498 termite gut homogenate clone MgMjD-060 AB2344
DQ802465.1 gg_id:178262 human fecal clone RL188_aah18b04 DQ802
AY981965.1 gg_id:127759 human sigmoid colon mucosal biopsy clone P096 AY9819
FJ365463.1 gg_id:362977 feces adult twins and mothers; TS20 clone TS20_a03b11 FJ3654
EU765802.1 gg_id:317793 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B4 EU7658
EU475248.1 gg_id:298150 bonobo feces clone BNO_aaa03f12 EU4752
FJ366941.1 gg_id:360303 feces adult twins and mothers; TS28 clone TS28_a01f02 FJ3669
EU488294.1 gg_id:540852 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU4882
DQ206415.1 gg_id:140502 microbial mediates arsenate reduction soda lake water clone ML-AsS-9 DQ206
EF096990.1 gg_id:187515 mouse cecum clone SWPT13_aaa03g10 EF0969
EU768713.1 gg_id:339985 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C5 EU7687
EU344547.1 gg_id:263432 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU3445
DQ904757.1 gg_id:162278 human fecal clone 001B-c11 DQ904
GQ493719.1 gg_id:578445 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
AJ576348.1 gg_id:102471 hindgut homogenate Pachnoda ephippiata larva clone PeH31 AJ5763
EU775142.1 gg_id:348992 Francois Langur feces clone FL_1aaa04a08 EU7751
AB192223.1 gg_id:142182 termite gut homogenate clone RsTu1-83 AB1922
FJ679144.1 gg_id:524841 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6791

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GQ502538.1 gg_id:552353 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf4- GQ502
GQ249495.1 gg_id:587669 Microbial anaerobic sediments Bay Cadiz (Spain) marine sediment: 0-2 cm layer clor GQ249
DQ905185.1 gg_id:168289 human fecal clone 002C-h6 DQ905
FJ681873.1 gg_id:509718 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6818
DQ802242.1 gg_id:184702 human fecal clone RL188_aah15a02 DQ802
DQ804469.1 gg_id:195799 human fecal clone RL187_aan80d02 DQ804
AB198449.1 gg_id:135337 termite gut wall fraction clone RsW01-009 AB1984
EU843061.1 gg_id:345031 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
DQ802280.1 gg_id:195605 human fecal clone RL188_aah15e10 DQ802
EU508139.1 gg_id:269912 cecal contents Mus musculus strain C57BL/6J; MD26 clone MD26_aaa01c09 EU508
EF402988.1 gg_id:206523 human fecal clone SJTU_B_15_24 EF4029
DQ824134.1 gg_id:177731 human fecal clone RL204_aaj59g08 DQ824
AY984216.1 gg_id:119151 human stool clone B105 AY9842
AY974917.1 gg_id:121020 human ascending colon mucosal biopsy clone KI37 AY9749
EU765496.1 gg_id:354397 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B EU7654
AY571393.1 gg_id:114620 termite gut clone RsaHf312 AY5713
EU777270.1 gg_id:351986 Okapi feces clone OK3_b06_1 EU777
EU762778.1 gg_id:320202 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU762
DQ327161.1 gg_id:148112 Metagenomic gut microbiome healthy human stool clone E682 DQ327
DQ804246.1 gg_id:181537 human fecal clone RL187_aah70g10 DQ804
AY667250.1 gg_id:105725 TCE-dechlorinating groundwater clone TANB5 AY667
EU344412.1 gg_id:275216 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU344
DQ799449.1 gg_id:192133 human fecal clone RL305aal86d08 DQ799
FJ833638.1 gg_id:549831 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J1Q402_36D05 FJ8336
EF123527.1 gg_id:242805 Microbial disease microbial mats on Siderastrea siderea three regions wider Caribbe EF1235
AY985856.1 gg_id:126931 human stool clone D130 AY9858
EF559166.1 gg_id:218171 mesophilic anaerobic digester clone G35_D8_H_B_B09 EF5591
AB198443.1 gg_id:135362 termite gut wall fraction clone RsW01-001 AB1984
EU765511.1 gg_id:304969 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B EU765
FJ372276.1 gg_id:366470 feces adult twins and mothers; TS9 clone TS9_a03g02 FJ3722
DQ905850.2 gg_id:168659 human fecal clone 29E-f6 DQ905
EF400772.1 gg_id:213176 human fecal clone SJTU_D_01_33 EF4007
EF097198.1 gg_id:177969 mouse cecum clone SWPT18_aaa02h12 EF0971
EU850609.1 gg_id:324705 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF444 EU850
EU765712.1 gg_id:354597 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B EU765
FJ365526.1 gg_id:358859 feces adult twins and mothers; TS20 clone TS20_a03h07 FJ3655
EU762397.1 gg_id:345086 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU762
DQ904836.1 gg_id:167327 human fecal clone 001C-b10 DQ904
DQ815362.1 gg_id:171881 mouse cecum clone aab46f02 DQ815
EU762524.1 gg_id:344336 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU762

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EU766596.1 gg_id:308206 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU7665
AY984211.1 gg_id:124785 human stool clone B096 AY9842
GQ503877.1 gg_id:587633 Captain bheri clone Ecwsrb040 GQ503
EU772692.1 gg_id:303460 Bush dog feces clone bdog1_g03_1 EU7726
GQ896694.1 gg_id:572516 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do s GQ896
FJ363376.1 gg_id:367825 feces adult twins and mothers; TS149 clone TS149_a02e04 FJ3633
AB192032.1 gg_id:141363 termite gut homogenate clone M2PB4-29 AB1920
AB031328.1 gg_id:51807 Clostridium sp. str. NT-2 AB0313
AB031327.1 gg_id:42607 Clostridium sp. str. NT-1 AB0313
AB192044.1 gg_id:142702 termite gut homogenate clone M2PT2-80 AB1920
AB192040.1 gg_id:144949 termite gut homogenate clone M1NP1-74 AB1920
AB192050.1 gg_id:141770 termite gut homogenate clone M1PT4-74 AB1920
NC_010001.1 gg_id:235413 Clostridium phytofermentans str. ISDg NC_010
AY984142.1 gg_id:117209 human stool clone B024 AY9841
DQ799529.1 gg_id:197814 human fecal clone RL305aal87d02 DQ799
AY974814.1 gg_id:115535 human ascending colon mucosal biopsy clone KG10 AY9748
EU767854.1 gg_id:355893 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C3 EU7678
DQ801417.1 gg_id:180622 human fecal clone RL388_aao95c05 DQ801
DQ325736.1 gg_id:149889 Metagenomic gut microbiome healthy human stool clone B384 DQ325
DQ799434.1 gg_id:198495 human fecal clone RL305aal86c03 DQ799
AY982887.1 gg_id:123174 human descending colon mucosal biopsy clone L059 AY9828
DQ802029.1 gg_id:187229 human fecal clone RL241_aaj02a12 DQ802
EU767909.1 gg_id:332048 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C3 EU7679
GQ897100.1 gg_id:576132 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ897
AY974968.1 gg_id:116469 human ascending colon mucosal biopsy clone KJ23 AY9749
AY979886.1 gg_id:118682 human rectum mucosal biopsy clone E169 AY9798
EU466940.1 gg_id:302490 African elephant feces clone AFEL2_aao31f06 EU4669
GQ896926.1 gg_id:544108 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do s GQ896
FJ365323.1 gg_id:369831 feces adult twins and mothers; TS20 clone TS20_a01e07 FJ3653
DQ799405.1 gg_id:194052 human fecal clone RL305aal85h02 DQ799
FJ367911.1 gg_id:362741 feces adult twins and mothers; TS30 clone TS30_a01a05 FJ3679
EU766707.1 gg_id:342338 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU7667
AY985965.1 gg_id:126527 human stool clone D264 AY9859
FJ366554.1 gg_id:357369 feces adult twins and mothers; TS27 clone TS27_a01b03 FJ3665
FJ371073.1 gg_id:368129 feces adult twins and mothers; TS5 clone TS5_a04f02 FJ3710
DQ801052.1 gg_id:183701 human fecal clone RL387_aao91d12 DQ801
FJ369451.1 gg_id:363138 feces adult twins and mothers; TS50 clone TS50_a04f10 FJ3694
AY981557.1 gg_id:116122 human sigmoid colon mucosal biopsy clone L712 AY9815
EU764116.1 gg_id:346508 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A5 EU7641
FJ364563.1 gg_id:357007 feces adult twins and mothers; TS15 clone TS15_a04d09 FJ3645
EU768317.1 gg_id:323354 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C5 EU7683

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EU764418.1 gg_id:343960 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1 EU7644
DQ802338.1 gg_id:187157 human fecal clone RL188_aah16d02 DQ802
DQ326159.1 gg_id:149198 Metagenomic gut microbiome healthy human stool clone C054 DQ326
GQ896992.1 gg_id:583202 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ896
FJ365267.1 gg_id:362811 feces adult twins and mothers; TS1 clone TS1_a04h01 FJ3652
GQ077508.1 gg_id:412854 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1209f0 GQ077
AY978337.1 gg_id:121737 human transverse colon mucosal biopsy clone F244 AY9783
EU763747.1 gg_id:341629 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A4 EU7637
GQ079269.1 gg_id:437713 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1230f0 GQ079
ABGC03000035.1 gg_id:268313 Clostridium sp. str. SS2/1 ABGC0
AY982970.1 gg_id:122388 human descending colon mucosal biopsy clone L179 AY9829
FJ367689.1 gg_id:358527 feces adult twins and mothers; TS2 clone TS2_a02d07 FJ3676
DQ797631.1 gg_id:183214 human fecal clone RL206_aaj13h11 DQ797
AY981134.1 gg_id:122205 human sigmoid colon mucosal biopsy clone G056 AY9811
GQ896955.1 gg_id:573003 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ896
AY979901.1 gg_id:119323 human rectum mucosal biopsy clone E209 AY9799
GQ897021.1 gg_id:538339 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ897
AY977059.1 gg_id:124905 human cecum mucosal biopsy clone K747 AY9770
FJ365360.1 gg_id:367646 feces adult twins and mothers; TS20 clone TS20_a02a03 FJ3653
AY981748.1 gg_id:124788 human sigmoid colon mucosal biopsy clone LB84 AY9817
FJ370820.1 gg_id:368282 feces adult twins and mothers; TS5 clone TS5_a01f06 FJ3708
DQ326449.1 gg_id:148389 Metagenomic gut microbiome healthy human stool clone C521 DQ326
FJ366327.1 gg_id:367179 feces adult twins and mothers; TS26 clone TS26_a01d10 FJ3663
DQ798712.1 gg_id:176221 human fecal clone RL181_aao00d10 DQ798
FJ368314.1 gg_id:356764 feces adult twins and mothers; TS3 clone TS3_a02g10 FJ3683
DQ905606.1 gg_id:166598 human fecal clone 014B-G2 DQ905
DQ803327.1 gg_id:187518 human fecal clone RL311_aam24a11 DQ803
DQ795759.1 gg_id:179147 human fecal clone RL245_aai81h08 DQ795
AY983324.1 gg_id:125323 human descending colon mucosal biopsy clone A386 AY9833
AY977551.1 gg_id:121101 human cecum mucosal biopsy clone W357 AY9775
EU768039.1 gg_id:331250 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C4 EU7680
DQ807186.1 gg_id:188131 human fecal clone RL244_aaj47c10 DQ807
DQ823980.1 gg_id:181649 human fecal clone RL204_aaj57g01 DQ823
DQ799470.1 gg_id:198583 human fecal clone RL305aal86f09 DQ799
AB494744.1 gg_id:589475 Fibrobacter succinogenes dominated consortium on hay stems sheep rumen clone A AB4947
DQ796782.1 gg_id:185703 human fecal clone RL179_aao54d08 DQ796
FJ879449.1 gg_id:382721 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8794
AY975195.1 gg_id:121393 human ascending colon mucosal biopsy clone KN24 AY9751
FJ364970.1 gg_id:365093 feces adult twins and mothers; TS1 clone TS1_a01d01 FJ3649
FJ024722.1 gg_id:330731 Copper affects reduction and genetic enriched sulfate reducing coastal sediments exp FJ0247

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EF098253.1 gg_id:188643 mouse cecum clone SWPT14_aaa03f07 EF0982
EU504306.1 gg_id:259989 cecal contents Mus musculus strain C57BL/6J; CRWD6 clone CRWD6_aaa02b02 EU5043
EU473641.1 gg_id:299118 banteng feces clone BG_aaa04d05.Contig1 EU4736
AY756592.1 gg_id:108706 Siwhaho sediment clone LJ3 AY7565
FJ880192.1 gg_id:434572 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8801
FJ880748.1 gg_id:378068 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8807
EU778880.1 gg_id:353577 Black-handed Spider Monkey feces clone SPIM_aaj36b05 EU7788
EU507949.1 gg_id:265576 cecal contents Mus musculus strain C57BL/6J; MD24 clone MD24_aaa04b05 EU5079
EU507971.1 gg_id:277133 cecal contents Mus musculus strain C57BL/6J; MD25 clone MD25_aaa01a03 EU5079
EU771949.1 gg_id:319153 Southern three-banded armadillo feces clone arma_aaj53g07 EU7719
EU508268.1 gg_id:266726 cecal contents Mus musculus strain C57BL/6J; MD26 clone MD26_aaa04h08 EU5082
DQ105656.1 gg_id:137353 pig feces clone DGGE band K2 DQ105
FJ879330.1 gg_id:441799 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8793
EF655642.1 gg_id:245596 dye containing wastewater treatment biofilm reactor clone B29 EF6556
EU508881.1 gg_id:263014 cecal contents Mus musculus strain C57BL/6J; MD6 clone MD6_aap37f10 EU5088
DQ815812.1 gg_id:172622 mouse cecum clone aab22f06 DQ815
EU794200.1 gg_id:355318 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_K22 EU7942
EU456821.1 gg_id:312892 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU4568
EU504348.1 gg_id:262939 cecal contents Mus musculus strain C57BL/6J; CRWD6 clone CRWD6_aaa02g11 EU5043
EU452929.1 gg_id:309206 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU4529
EF632747.1 gg_id:237273 Unique microbial contrasting aquatic altitude Andean Altiplano (northern Chile) fresh EF6327
GQ493671.1 gg_id:574714 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
AF349416.1 gg_id:77449 pig feces clone AF3494
EU773327.1 gg_id:322137 BigHorn sheep feces clone BH1_aao26e11 EU7733
FJ679990.1 gg_id:531052 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6799
DQ793657.1 gg_id:178682 human fecal clone RL246_aai75b10 DQ793
FJ879661.1 gg_id:418999 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8796
AB486484.1 gg_id:561193 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC AB4864
EU850551.1 gg_id:326833 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF351 EU8505
GQ491405.1 gg_id:583711 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
X71853.1 gg_id:14099 Clostridium populeti str. ATCC 35295 X71853
AY212660.1 gg_id:99173 water 20 m downstream manure clone 213ds20 AY2126
EU466237.1 gg_id:291890 bighorn sheep feces clone BH1_aao28e12 EU4662
EU506241.1 gg_id:272369 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aap61c07 EU5062
EF602871.1 gg_id:232283 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6028
AY977415.1 gg_id:122556 human cecum mucosal biopsy clone W090 AY9774
FJ879205.1 gg_id:423041 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8792
EU470217.1 gg_id:302864 trancaspain urial feces clone TU2_aaa03h09 EU4702
DQ071475.1 gg_id:231128 microbial cecum captive and free-living capercaillies (Tetrao urogallus) clone TuCc10 DQ071
EU794284.1 gg_id:322231 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_N36 EU7942
DQ803800.1 gg_id:177788 human fecal clone RL200_aai58e10 DQ803

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EF095995.1 gg_id:182621 mouse cecum clone lean2_aaa01f04 EF0959
EU779113.1 gg_id:308857 Takin feces clone TAK_aaa03e11 EU779
FJ366481.1 gg_id:358834 feces adult twins and mothers; TS26 clone TS26_a03h07 FJ3664
DQ815966.1 gg_id:169701 mouse cecum clone aab24h11 DQ815
FJ365126.1 gg_id:370305 feces adult twins and mothers; TS1 clone TS1_a03b10 FJ3651
EU508740.1 gg_id:267400 cecal contents Mus musculus strain C57BL/6J; MD4 clone MD4_aap50c10 EU508
FJ679327.1 gg_id:515632 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6793
EU452548.1 gg_id:315309 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU4525
EU509492.1 gg_id:273301 cecal contents Mus musculus strain C57BL/6J; MD9 clone MD9_aap59c09 EU509
EU456838.1 gg_id:324615 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU4568
GQ491245.1 gg_id:538885 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
EU774776.1 gg_id:311610 Angola Colobus feces clone EAC_1aaa01e03 EU774
FJ672488.1 gg_id:531825 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6724
EU460964.1 gg_id:301879 red kangaroo feces clone KO1_aai41b07 EU460
DQ808993.1 gg_id:175596 human fecal clone RL243_aai87h11 DQ808
AY534872.1 gg_id:102328 Clostridium sp. str. IMSNU 40011 AY5348
EU508308.1 gg_id:274455 cecal contents Mus musculus strain C57BL/6J; MD27 clone MD27_aaa02d01 EU508
EU461740.1 gg_id:294791 mongoose lemur feces clone ML_aaj28b01 EU461
DQ793567.1 gg_id:184905 human fecal clone RL246_aai73f04 DQ793
FJ678549.1 gg_id:519866 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6785
GQ868402.1 gg_id:580793 Fungal and Structure Bioaerosols Pig Stable pig stable bioaerosols clone BBC81 GQ868
DQ800844.1 gg_id:178970 human fecal clone RL183_aao04c02 DQ800
FJ542922.1 gg_id:520231 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone B FJ5429
EF515538.1 gg_id:225599 Electricigen Enrichment MFC full-scale anaerobic bioreactor sludge treating brewery EF5155
EU509215.1 gg_id:268028 cecal contents Mus musculus strain C57BL/6J; MD8 clone MD8_aap46a03 EU509
EU773313.1 gg_id:323365 BigHorn sheep feces clone BH1_aao25a09 EU773
EU466172.1 gg_id:291475 bighorn sheep feces clone BH1_aao27d08 EU466
EU453188.1 gg_id:328453 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU453
EU473636.1 gg_id:300295 banteng feces clone BG_aaa02h01.Contig1 EU473
FJ672606.1 gg_id:527413 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6726
NR_025796.1 gg_id:552538 Clostridium jejuense str. HY-35-12; IMSNU 40003 NR_02
GQ493826.1 gg_id:572045 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
EU509517.1 gg_id:274400 cecal contents Mus musculus strain C57BL/6J; MD9 clone MD9_aap59h07 EU509
FJ371671.1 gg_id:369597 feces adult twins and mothers; TS7 clone TS7_a04h09 FJ3716
FJ362613.1 gg_id:364756 feces adult twins and mothers; TS13 clone TS13_a01b01 FJ3626
EF071231.1 gg_id:195514 library survey and quantitative measurement major mucosa- IBD human colonic muc EF0712
EU462354.1 gg_id:288857 chimpanzee feces clone CHIMP1_aaj40g10 EU462
FJ363762.1 gg_id:365692 feces adult twins and mothers; TS14 clone TS14_a03a10 FJ3637
DQ327549.1 gg_id:145426 Metagenomic gut microbiome healthy human stool clone EB31 DQ327
DQ798564.1 gg_id:179518 human fecal clone RL181_aan98d01 DQ798

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AM277382.2 gg_id:229853 fecal microbiota irritable bowel syndrome patients significantly that healthy subject AM277
DQ802766.1 gg_id:183853 human fecal clone RL188_aan96c08 DQ802
FJ367837.1 gg_id:358360 feces adult twins and mothers; TS2 clone TS2_a04b07 FJ3678
DQ325827.1 gg_id:145051 Metagenomic gut microbiome healthy human stool clone B566 DQ325
FJ679258.1 gg_id:524214 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6792
AY976512.1 gg_id:119285 human cecum mucosal biopsy clone K034 AY9765
GQ896896.1 gg_id:580242 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do GQ896
DQ801081.1 gg_id:177184 human fecal clone RL387_aao91h04 DQ801
DQ796707.1 gg_id:183325 human fecal clone RL179_aao53d11 DQ796
EU762664.1 gg_id:318085 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU762
DQ801445.1 gg_id:175981 human fecal clone RL388_aao95f05 DQ801
DQ801596.1 gg_id:193594 human fecal clone RL117_aae92c08 DQ801
FJ367849.1 gg_id:370336 feces adult twins and mothers; TS2 clone TS2_a04c09 FJ3678
GQ897203.1 gg_id:545113 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ897
AF371638.1 gg_id:29079 swine intestine clone p-1894-s962-3 AF371
DQ801802.1 gg_id:189572 human fecal clone RL201_aai47a04 DQ801
EU762248.1 gg_id:346684 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU762
EF399973.1 gg_id:213155 human fecal clone SJTU_E_07_14 EF3999
FJ367910.1 gg_id:365889 feces adult twins and mothers; TS30 clone TS30_a01a04 FJ3679
AY976640.1 gg_id:116094 human cecum mucosal biopsy clone K204 AY9766
DQ327315.1 gg_id:147899 Metagenomic gut microbiome healthy human stool clone E863 DQ327
AM697161.1 gg_id:227258 sequencing libraries indoor dust clone BF0001C002 AM697
AY981729.1 gg_id:120484 human sigmoid colon mucosal biopsy clone LB21 AY9817
EU467096.1 gg_id:300902 mongoose lemur feces clone ML_aae88b05 EU467
DQ807097.1 gg_id:192077 human fecal clone RL244_aaj46b10 DQ807
FJ370064.1 gg_id:370074 feces adult twins and mothers; TS55 clone TS55_a04a07 FJ3700
FJ368444.1 gg_id:357429 feces adult twins and mothers; TS3 clone TS3_a04d09 FJ3684
DQ325631.1 gg_id:146452 Metagenomic gut microbiome healthy human stool clone B171 DQ325
DQ796741.1 gg_id:192388 human fecal clone RL179_aao53h04 DQ796
FJ371070.1 gg_id:364813 feces adult twins and mothers; TS5 clone TS5_a04e11 FJ3710
FJ682996.1 gg_id:519242 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6829
FJ678681.1 gg_id:528608 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6786
DQ806889.1 gg_id:190886 human fecal clone RL198_aaj74g09 DQ806
DQ798252.1 gg_id:176633 human fecal clone RL181_aah39e11 DQ798
GQ001531.1 gg_id:508130 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu174b11 GQ001
FJ363666.1 gg_id:357596 feces adult twins and mothers; TS14 clone TS14_a01h07 FJ3636
FJ367676.1 gg_id:368233 feces adult twins and mothers; TS2 clone TS2_a02c06 FJ3676
DQ799669.1 gg_id:197638 human fecal clone RL305aal88h07 DQ799
AY981488.1 gg_id:127177 human sigmoid colon mucosal biopsy clone L591 AY9814
FJ368089.1 gg_id:356961 feces adult twins and mothers; TS30 clone TS30_a03h04 FJ3680

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FJ370352.1 gg_id:360418 feces adult twins and mothers; TS56 clone TS56_a03h01 FJ3703
FJ365716.1 gg_id:357752 feces adult twins and mothers; TS21 clone TS21_a02b07 FJ3657
FJ366917.1 gg_id:368931 feces adult twins and mothers; TS28 clone TS28_a01d02 FJ3669
AM275455.2 gg_id:234340 fecal microbiota irritable bowel syndrome patients significantly that healthy subject AM275
DQ798714.1 gg_id:193231 human fecal clone RL181_aao00d12 DQ798
EU466792.1 gg_id:303125 African elephant feces clone AFEL2_aao29e11 EU466
FJ363689.1 gg_id:357535 feces adult twins and mothers; TS14 clone TS14_a02b06 FJ3636
DQ807937.1 gg_id:195481 human fecal clone RL180_aan69d11 DQ807
DQ326713.1 gg_id:148649 Metagenomic gut microbiome healthy human stool clone E168 DQ326
DQ797422.1 gg_id:190985 human fecal clone RL248_aai99b08 DQ797
EU763441.1 gg_id:330946 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A4 EU7634
AY979955.1 gg_id:119081 human rectum mucosal biopsy clone K838 AY9799
AY981292.1 gg_id:120019 human sigmoid colon mucosal biopsy clone G288 AY9812
EU466835.1 gg_id:303384 African elephant feces clone AFEL2_aao30b04 EU4668
FJ368522.1 gg_id:368771 feces adult twins and mothers; TS49 clone TS49_a01d01 FJ3685
FJ368896.1 gg_id:358153 feces adult twins and mothers; TS4 clone TS4_a01h01 FJ3688
DQ327483.1 gg_id:146465 Metagenomic gut microbiome healthy human stool clone EA53 DQ327
AY977072.1 gg_id:123375 human cecum mucosal biopsy clone K760 AY9770
FJ676090.1 gg_id:521570 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6760
FJ367114.1 gg_id:360063 feces adult twins and mothers; TS28 clone TS28_a03f09 FJ3671
FJ679823.1 gg_id:516527 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6798
FJ369460.1 gg_id:358560 feces adult twins and mothers; TS50 clone TS50_a04g09 FJ3694
DQ801252.1 gg_id:189002 human fecal clone RL388_aao93a04 DQ801
FJ369397.1 gg_id:368336 feces adult twins and mothers; TS50 clone TS50_a04a04 FJ3693
DQ071523.1 gg_id:230528 microbial cecum captive and free-living capercaillies (Tetrao urogallus) clone TuCc31 DQ071
AY981621.1 gg_id:122358 human sigmoid colon mucosal biopsy clone L858 AY9816
DQ795404.1 gg_id:198270 human fecal clone RL178_aah53h12 DQ795
AY981324.1 gg_id:120304 human sigmoid colon mucosal biopsy clone G341 AY9813
AY976872.1 gg_id:120572 human cecum mucosal biopsy clone K513 AY9768
FJ370090.1 gg_id:363987 feces adult twins and mothers; TS55 clone TS55_a04c10 FJ3700
DQ795084.1 gg_id:174110 human fecal clone RL310_aam40a06 DQ795
FJ676204.1 gg_id:527356 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6762
FJ679996.1 gg_id:521075 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6799
DQ807278.1 gg_id:177041 human fecal clone RL244_aaj48e06 DQ807
EU761890.1 gg_id:341191 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1 EU7618
EU762096.1 gg_id:356215 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1 EU7620
FJ368085.1 gg_id:363354 feces adult twins and mothers; TS30 clone TS30_a03g10 FJ3680
DQ796540.1 gg_id:189217 human fecal clone RL179aan74d05 DQ796
FJ370864.1 gg_id:358427 feces adult twins and mothers; TS5 clone TS5_a02b07 FJ3708

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FJ370346.1 gg_id:361594 feces adult twins and mothers; TS56 clone TS56_a03g04 FJ3703
AY974859.1 gg_id:118535 human ascending colon mucosal biopsy clone KH11 AY9748
AY983020.1 gg_id:125747 human descending colon mucosal biopsy clone L248 AY9830
FJ370319.1 gg_id:363682 feces adult twins and mothers; TS56 clone TS56_a03d07 FJ3703
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DQ327031.1 gg_id:148868 Metagenomic gut microbiome healthy human stool clone E536 DQ327
AY974985.1 gg_id:124294 human ascending colon mucosal biopsy clone KJ58 AY9749
FJ364648.1 gg_id:369711 feces adult twins and mothers; TS19 clone TS19_a01d08 FJ3646
AY960568.1 gg_id:114994 Anaerostipes sp. str. IE4 AY9605
GQ002290.1 gg_id:507372 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu175f09 GQ002
DQ326965.1 gg_id:146256 Metagenomic gut microbiome healthy human stool clone E458 DQ326
DQ805381.1 gg_id:197515 human fecal clone RL203_aai61h08 DQ805
EU762235.1 gg_id:349852 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A› EU7622
FJ679950.1 gg_id:513542 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6799
FJ678623.1 gg_id:513783 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6786
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FJ369427.1 gg_id:368844 feces adult twins and mothers; TS50 clone TS50_a04d03 FJ3694
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EU767808.1 gg_id:356162 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C3 EU7678
DQ796479.1 gg_id:192913 human fecal clone RL179_aah28h11 DQ796
AY984899.1 gg_id:122801 human stool clone B880 AY9848
DQ795217.1 gg_id:178717 human fecal clone RL178_aah51f05 DQ795
DQ327118.1 gg_id:145284 Metagenomic gut microbiome healthy human stool clone E636 DQ327
FJ368110.1 gg_id:360474 feces adult twins and mothers; TS30 clone TS30_a04b09 FJ3681
DQ807820.1 gg_id:184457 human fecal clone RL180_aah37f02 DQ807
FJ362753.1 gg_id:363486 feces adult twins and mothers; TS13 clone TS13_a02g02 FJ3627
DQ326681.1 gg_id:147258 Metagenomic gut microbiome healthy human stool clone E128 DQ326
DQ807882.1 gg_id:182054 human fecal clone RL180_aah38d06 DQ807
DQ326470.1 gg_id:147326 Metagenomic gut microbiome healthy human stool clone C559 DQ326
GQ047165.1 gg_id:402005 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1009d GQ047
GQ047276.1 gg_id:402052 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1010g GQ047
DQ801729.1 gg_id:184590 human fecal clone RL201_aai46b03 DQ801
DQ804603.1 gg_id:193691 human fecal clone RL187_aao70c01 DQ804
DQ327576.1 gg_id:150150 Metagenomic gut microbiome healthy human stool clone EB60 DQ327
AY983034.1 gg_id:127613 human descending colon mucosal biopsy clone L265 AY9830
FJ367163.1 gg_id:359737 feces adult twins and mothers; TS28 clone TS28_a04c05 FJ3671
DQ798590.1 gg_id:195395 human fecal clone RL181_aan98f09 DQ798

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DQ905930.1 gg_id:173503 human fecal clone 29c-h8 DQ905
FJ683219.1 gg_id:515754 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6832
DQ795343.1 gg_id:182566 human fecal clone RL178_aah53b12 DQ795
FJ363496.1 gg_id:366870 feces adult twins and mothers; TS149 clone TS149_a03h09 FJ3634
FJ365779.1 gg_id:362106 feces adult twins and mothers; TS21 clone TS21_a02h08 FJ3657
FJ369957.1 gg_id:361190 feces adult twins and mothers; TS55 clone TS55_a02g02 FJ3699
EU766947.1 gg_id:348387 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU766
FJ364681.1 gg_id:357195 feces adult twins and mothers; TS19 clone TS19_a01g07 FJ3646
DQ796685.1 gg_id:194298 human fecal clone RL179_aao53b07 DQ796
FJ364929.1 gg_id:361669 feces adult twins and mothers; TS19 clone TS19_a04h04 FJ3649
AY978349.1 gg_id:119014 human transverse colon mucosal biopsy clone F280 AY978
FJ679203.1 gg_id:512803 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6792
FJ365787.1 gg_id:364446 feces adult twins and mothers; TS21 clone TS21_a03a06 FJ3657
DQ806364.1 gg_id:175387 human fecal clone RL186_aan91c08 DQ806
DQ798516.1 gg_id:194999 human fecal clone RL181_aan97f11 DQ798
FJ371032.1 gg_id:366081 feces adult twins and mothers; TS5 clone TS5_a04b06 FJ3710
FJ367605.1 gg_id:368886 feces adult twins and mothers; TS2 clone TS2_a01e01 FJ3676
EF400396.1 gg_id:214689 human fecal clone SJTU_E_12_81 EF4003
FJ367811.1 gg_id:359780 feces adult twins and mothers; TS2 clone TS2_a03h03 FJ3678
AY983090.1 gg_id:117012 human descending colon mucosal biopsy clone L337 AY983
AY976510.1 gg_id:122853 human cecum mucosal biopsy clone K032 AY976
FJ365724.1 gg_id:365011 feces adult twins and mothers; TS21 clone TS21_a02c05 FJ3657
FJ363664.1 gg_id:357558 feces adult twins and mothers; TS14 clone TS14_a01h05 FJ3636
DQ326796.1 gg_id:146454 Metagenomic gut microbiome healthy human stool clone E265 DQ326
FJ368651.1 gg_id:359189 feces adult twins and mothers; TS49 clone TS49_a02g11 FJ3686
FJ679210.1 gg_id:516896 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6792
DQ796804.1 gg_id:176547 human fecal clone RL179_aao54g05 DQ796
FJ363631.1 gg_id:360786 feces adult twins and mothers; TS14 clone TS14_a01e08 FJ3636
FJ679121.1 gg_id:531815 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6791
FJ370243.1 gg_id:364800 feces adult twins and mothers; TS56 clone TS56_a02c06 FJ3702
DQ326407.1 gg_id:146736 Metagenomic gut microbiome healthy human stool clone C450 DQ326
FJ369995.1 gg_id:367250 feces adult twins and mothers; TS55 clone TS55_a03c04 FJ3699
EU466813.1 gg_id:295177 African elephant feces clone AFEL2_aao29g10 EU466
AY984705.1 gg_id:126730 human stool clone B658 AY984
DQ326469.1 gg_id:147499 Metagenomic gut microbiome healthy human stool clone C556 DQ326
DQ803244.1 gg_id:174137 human fecal clone RL311_aam22g08 DQ803
DQ795368.1 gg_id:192243 human fecal clone RL178_aah53e04 DQ795
FJ369837.1 gg_id:359199 feces adult twins and mothers; TS55 clone TS55_a01d04 FJ3698
DQ801534.1 gg_id:174920 human fecal clone RL388_aao96g04 DQ801
DQ807884.1 gg_id:192300 human fecal clone RL180_aah38d09 DQ807

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DQ798578.1 gg_id:181113 human fecal clone RL181_aan98e05 DQ798
GQ898585.1 gg_id:553014 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ898
AY981405.1 gg_id:126052 human sigmoid colon mucosal biopsy clone L458 AY9814
FJ367771.1 gg_id:363066 feces adult twins and mothers; TS2 clone TS2_a03d08 FJ3677
FJ370019.1 gg_id:357288 feces adult twins and mothers; TS55 clone TS55_a03e05 FJ3700
FJ364702.1 gg_id:360169 feces adult twins and mothers; TS19 clone TS19_a02a07 FJ3647
FJ370368.1 gg_id:363012 feces adult twins and mothers; TS56 clone TS56_a04a07 FJ3703
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AY977058.1 gg_id:121722 human cecum mucosal biopsy clone K746 AY977(
DQ795245.1 gg_id:189081 human fecal clone RL178_aah51h10 DQ795
FJ370088.1 gg_id:368843 feces adult twins and mothers; TS55 clone TS55_a04c08 FJ3700
FJ678759.1 gg_id:527751 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6787
DQ794536.1 gg_id:194931 human fecal clone RL240_aaj29c07 DQ794
DQ327360.1 gg_id:146102 Metagenomic gut microbiome healthy human stool clone E916 DQ327
FJ365088.1 gg_id:356729 feces adult twins and mothers; TS1 clone TS1_a02f10 FJ3650
FJ369862.1 gg_id:363055 feces adult twins and mothers; TS55 clone TS55_a01f07 FJ3698
FJ372207.1 gg_id:360381 feces adult twins and mothers; TS9 clone TS9_a03a02 FJ3722
GQ090517.1 gg_id:401779 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw GQ090
DQ801721.1 gg_id:199183 human fecal clone RL201_aai46a06 DQ801
FJ369989.1 gg_id:363307 feces adult twins and mothers; TS55 clone TS55_a03b09 FJ3699
FJ366965.1 gg_id:367240 feces adult twins and mothers; TS28 clone TS28_a01h03 FJ3669
FJ363816.1 gg_id:370034 feces adult twins and mothers; TS14 clone TS14_a03f11 FJ3638
DQ796388.1 gg_id:185876 human fecal clone RL179_aah26e12 DQ796
FJ370071.1 gg_id:361092 feces adult twins and mothers; TS55 clone TS55_a04b03 FJ3700
AY979995.1 gg_id:118321 human rectum mucosal biopsy clone K936 AY9799
DQ799666.1 gg_id:199237 human fecal clone RL305aal88h04 DQ799
DQ325976.1 gg_id:147194 Metagenomic gut microbiome healthy human stool clone B875 DQ325
AY981491.1 gg_id:126530 human sigmoid colon mucosal biopsy clone L595 AY9814
DQ795475.1 gg_id:180860 human fecal clone RL178_aah54g11 DQ795
FJ365982.1 gg_id:364181 feces adult twins and mothers; TS25 clone TS25_a01d05 FJ3659
DQ327604.1 gg_id:148762 Metagenomic gut microbiome healthy human stool clone EB94 DQ327
AY981519.1 gg_id:115463 human sigmoid colon mucosal biopsy clone L646 AY9815
FJ367595.1 gg_id:365617 feces adult twins and mothers; TS2 clone TS2_a01d03 FJ3675
DQ327512.1 gg_id:147432 Metagenomic gut microbiome healthy human stool clone EA87 DQ327
AY980228.1 gg_id:119170 human rectum mucosal biopsy clone KF73 AY9802
EU530468.1 gg_id:269215 mucosa adherent and invasive microbes profile adenoma colorectal cancer clone M7 EU5304
DQ795430.1 gg_id:187643 human fecal clone RL178_aah54c07 DQ795

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GQ897929.1 gg_id:586117 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ897
DQ803171.1 gg_id:185017 human fecal clone RL311_aam21e05 DQ803
AY983132.1 gg_id:115404 human descending colon mucosal biopsy clone L392 AY9831
FJ365852.1 gg_id:366076 feces adult twins and mothers; TS21 clone TS21_a03g11 FJ3658
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DQ799778.1 gg_id:184382 human fecal clone RL182_aah33d02 DQ799
AY982803.1 gg_id:118990 human descending colon mucosal biopsy clone KZ48 AY9828
AY982947.1 gg_id:120341 human descending colon mucosal biopsy clone L150 AY9829
FJ367115.1 gg_id:361458 feces adult twins and mothers; TS28 clone TS28_a03f10 FJ3671
FJ369352.1 gg_id:363050 feces adult twins and mothers; TS50 clone TS50_a03d11 FJ3693
DQ326570.1 gg_id:150134 Metagenomic gut microbiome healthy human stool clone E003 DQ326
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FJ370380.1 gg_id:366297 feces adult twins and mothers; TS56 clone TS56_a04c01 FJ3703
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AY981351.1 gg_id:118041 human sigmoid colon mucosal biopsy clone G370 AY9813
FJ672871.1 gg_id:518121 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6728
FJ365880.1 gg_id:369955 feces adult twins and mothers; TS21 clone TS21_a04b06 FJ3658
FJ368830.1 gg_id:367061 feces adult twins and mothers; TS4 clone TS4_a01b03 FJ3688
AY984592.1 gg_id:127691 human stool clone B532 AY9845
DQ807010.1 gg_id:199158 human fecal clone RL244_aaj45b01 DQ807
DQ803217.1 gg_id:190799 human fecal clone RL311_aam22c07 DQ803
FJ370984.1 gg_id:368313 feces adult twins and mothers; TS5 clone TS5_a03e10 FJ3709
DQ327407.1 gg_id:146980 Metagenomic gut microbiome healthy human stool clone E966 DQ327
AY982992.1 gg_id:122440 human descending colon mucosal biopsy clone L213 AY9829
DQ806816.1 gg_id:199262 human fecal clone RL198_aaj73b09 DQ806
FJ370062.1 gg_id:363104 feces adult twins and mothers; TS55 clone TS55_a04a05 FJ3700
FJ679229.1 gg_id:528140 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6792
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FJ367926.1 gg_id:357891 feces adult twins and mothers; TS30 clone TS30_a01c04 FJ3679
DQ802357.1 gg_id:178821 human fecal clone RL188_aah16f01 DQ802
FJ369824.1 gg_id:363186 feces adult twins and mothers; TS55 clone TS55_a01c03 FJ3698
FJ365682.1 gg_id:362783 feces adult twins and mothers; TS21 clone TS21_a01g06 FJ3656
DQ807636.1 gg_id:185429 human fecal clone RL180_aah35c05 DQ807
FJ365938.1 gg_id:367945 feces adult twins and mothers; TS21 clone TS21_a04h06 FJ3659
DQ798388.1 gg_id:183609 human fecal clone RL181_aah41h06 DQ798

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FJ364479.1 gg_id:367115 feces adult twins and mothers; TS15 clone TS15_a03d11 FJ3644
FJ678170.1 gg_id:520887 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6781
AY985660.1 gg_id:116406 human stool clone C666 AY9856
FJ363359.1 gg_id:367937 feces adult twins and mothers; TS149 clone TS149_a02c11 FJ3633
AY975186.1 gg_id:126668 human ascending colon mucosal biopsy clone KN08 AY9751
DQ808141.1 gg_id:179395 human fecal clone RL180_aao73b07 DQ808
FJ370188.1 gg_id:361470 feces adult twins and mothers; TS56 clone TS56_a01e05 FJ3701
GQ898491.1 gg_id:565351 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ898
FJ365837.1 gg_id:363010 feces adult twins and mothers; TS21 clone TS21_a03f06 FJ3658
FJ370337.1 gg_id:356973 feces adult twins and mothers; TS56 clone TS56_a03f06 FJ3703
DQ794645.1 gg_id:198329 human fecal clone RL240_aaj30f03 DQ794
DQ325767.1 gg_id:148012 Metagenomic gut microbiome healthy human stool clone B445 DQ325
FJ363137.1 gg_id:366756 feces adult twins and mothers; TS148 clone TS148_a03e08 FJ3631
FJ370944.1 gg_id:361071 feces adult twins and mothers; TS5 clone TS5_a03b02 FJ3709
EU466973.1 gg_id:290543 African elephant feces clone AFEL2_aao32b04 EU466
EU767156.1 gg_id:335982 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU767
DQ799484.1 gg_id:184523 human fecal clone RL305aal86h01 DQ799
AY978359.1 gg_id:121691 human transverse colon mucosal biopsy clone F306 AY9783
DQ325826.1 gg_id:147221 Metagenomic gut microbiome healthy human stool clone B565 DQ325
DQ823952.1 gg_id:188128 human fecal clone RL204_aaj57d04 DQ823
FJ371333.1 gg_id:367760 feces adult twins and mothers; TS6 clone TS6_a03g01 FJ3713
EU764364.1 gg_id:303428 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1 EU7643
DQ325851.1 gg_id:147212 Metagenomic gut microbiome healthy human stool clone B626 DQ325
GQ897976.1 gg_id:579613 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ897
EU762013.1 gg_id:350368 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1 EU762
FJ369357.1 gg_id:367975 feces adult twins and mothers; TS50 clone TS50_a03e06 FJ3693
DQ802600.1 gg_id:188331 human fecal clone RL188_aan93h09 DQ802
FJ369422.1 gg_id:360753 feces adult twins and mothers; TS50 clone TS50_a04c09 FJ3694
FJ370009.1 gg_id:363126 feces adult twins and mothers; TS55 clone TS55_a03d06 FJ3700
FJ369117.1 gg_id:366010 feces adult twins and mothers; TS4 clone TS4_a04d10 FJ3691
FJ372009.1 gg_id:358234 feces adult twins and mothers; TS8 clone TS8_a04g02 FJ3720
AM275420.2 gg_id:232700 fecal microbiota irritable bowel syndrome patients significantly that healthy subject AM275
AY979987.1 gg_id:116730 human rectum mucosal biopsy clone K910 AY9799
FJ365630.1 gg_id:365873 feces adult twins and mothers; TS21 clone TS21_a01b08 FJ3656
FJ683843.1 gg_id:529625 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6838
FJ678187.1 gg_id:519886 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6781
GQ016070.1 gg_id:493598 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw GQ016
EU466989.1 gg_id:291504 African elephant feces clone AFEL2_aao32d03 EU466
FJ368053.1 gg_id:364459 feces adult twins and mothers; TS30 clone TS30_a03d06 FJ3680
FJ367714.1 gg_id:361615 feces adult twins and mothers; TS2 clone TS2_a02g03 FJ3677
DQ798732.1 gg_id:186891 human fecal clone RL181_aao00f09 DQ798

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EU466881.1 gg_id:299300 African elephant feces clone AFEL2_aao30g08 EU466
DQ793763.1 gg_id:194417 human fecal clone RL246_aai76h08 DQ793
DQ327598.1 gg_id:147399 Metagenomic gut microbiome healthy human stool clone EB86 DQ327
EU766663.1 gg_id:353149 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU766
FJ368064.1 gg_id:358567 feces adult twins and mothers; TS30 clone TS30_a03e08 FJ3680
AY981109.1 gg_id:123392 human sigmoid colon mucosal biopsy clone G023 AY981
AY976729.1 gg_id:118744 human cecum mucosal biopsy clone K322 AY976
FJ362679.1 gg_id:361660 feces adult twins and mothers; TS13 clone TS13_a01h01 FJ3626
DQ797842.1 gg_id:198743 human fecal clone RL206_aaj16e03 DQ797
FJ363626.1 gg_id:358857 feces adult twins and mothers; TS14 clone TS14_a01e02 FJ3636
DQ807991.1 gg_id:195146 human fecal clone RL180_aan70c08 DQ807
FJ370084.1 gg_id:367682 feces adult twins and mothers; TS55 clone TS55_a04c04 FJ3700
DQ807187.1 gg_id:178805 human fecal clone RL244_aaj47c11 DQ807
FJ365909.1 gg_id:365938 feces adult twins and mothers; TS21 clone TS21_a04e01 FJ3659
FJ369328.1 gg_id:359727 feces adult twins and mothers; TS50 clone TS50_a03b08 FJ3693
FJ363648.1 gg_id:362322 feces adult twins and mothers; TS14 clone TS14_a01g01 FJ3636
DQ798687.1 gg_id:181548 human fecal clone RL181_aao00b04 DQ798
DQ799737.1 gg_id:189763 human fecal clone RL182_aah32d07 DQ799
FJ371007.1 gg_id:363139 feces adult twins and mothers; TS5 clone TS5_a03h03 FJ3710
FJ676935.1 gg_id:527583 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6769
AJ408972.1 gg_id:72481 human colonic clone HuCA20 AJ4089
AY977012.1 gg_id:115635 human cecum mucosal biopsy clone K686 AY977
FJ368155.1 gg_id:363118 feces adult twins and mothers; TS30 clone TS30_a04h05 FJ3681
EU768210.1 gg_id:310205 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C4 EU768
AY978510.1 gg_id:120323 human transverse colon mucosal biopsy clone KQ08 AY978
FJ366548.1 gg_id:365979 feces adult twins and mothers; TS27 clone TS27_a01a09 FJ3665
DQ796764.1 gg_id:195420 human fecal clone RL179_aao54b08 DQ796
GQ898666.1 gg_id:573178 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ898
FJ368131.1 gg_id:367336 feces adult twins and mothers; TS30 clone TS30_a04e04 FJ3681
AY981390.1 gg_id:123610 human sigmoid colon mucosal biopsy clone L434 AY981
EU767800.1 gg_id:335052 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C3 EU767
GQ898549.1 gg_id:538276 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ898
DQ795463.1 gg_id:195174 human fecal clone RL178_aah54f07 DQ795
FJ371311.1 gg_id:366504 feces adult twins and mothers; TS6 clone TS6_a03e02 FJ3713
GQ079184.1 gg_id:468250 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1229e GQ079
AY975126.1 gg_id:118960 human ascending colon mucosal biopsy clone KM16 AY975
FJ368054.1 gg_id:360490 feces adult twins and mothers; TS30 clone TS30_a03d07 FJ3680
FJ682827.1 gg_id:514693 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6828
FJ682413.1 gg_id:524658 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6824

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DQ794798.1 gg_id:178201 human fecal clone RL240_aaj32e03 DQ794
FJ370014.1 gg_id:363968 feces adult twins and mothers; TS55 clone TS55_a03d11 FJ3700
AY981272.1 gg_id:121932 human sigmoid colon mucosal biopsy clone G264 AY9812
EF399741.1 gg_id:214326 human fecal clone SJTU_E_02_80 EF3997
EU467094.1 gg_id:302260 mongoose lemur feces clone ML_aae88b02 EU467
FJ365465.1 gg_id:359239 feces adult twins and mothers; TS20 clone TS20_a03c02 FJ3654
DQ808298.1 gg_id:197637 human fecal clone RL180_aao75a02 DQ808
AY976950.1 gg_id:121006 human cecum mucosal biopsy clone K611 AY976
EU767253.1 gg_id:347629 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C2 EU767
DQ327506.1 gg_id:145154 Metagenomic gut microbiome healthy human stool clone EA80 DQ327
FJ370957.1 gg_id:369037 feces adult twins and mothers; TS5 clone TS5_a03c04 FJ3709
FJ370095.1 gg_id:357176 feces adult twins and mothers; TS55 clone TS55_a04d03 FJ3700
DQ795794.1 gg_id:198960 human fecal clone RL245_aai82e05 DQ795
DQ799849.1 gg_id:178896 human fecal clone RL182_aah34h07 DQ799
AY979988.1 gg_id:115875 human rectum mucosal biopsy clone K917 AY979
FJ367600.1 gg_id:362701 feces adult twins and mothers; TS2 clone TS2_a01d08 FJ3676
EU466760.1 gg_id:289045 African elephant feces clone AFEL2_aao29b01 EU466
EF399837.1 gg_id:215378 human fecal clone SJTU_E_03_90 EF3998
DQ905506.1 gg_id:173012 human fecal clone 014-d9 DQ905
DQ806249.1 gg_id:190058 human fecal clone RL186_aan89c09 DQ806
EU767773.1 gg_id:318758 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C3 EU767
DQ327206.1 gg_id:147131 Metagenomic gut microbiome healthy human stool clone E737 DQ327
EU451337.1 gg_id:330473 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU451
EU763884.1 gg_id:346114 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A5 EU763
AY975189.1 gg_id:121776 human ascending colon mucosal biopsy clone KN15 AY975
DQ795244.1 gg_id:195491 human fecal clone RL178_aah51h09 DQ795
DQ799441.1 gg_id:196073 human fecal clone RL305aal86c10 DQ799
EU762316.1 gg_id:328305 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A9 EU762
DQ326456.1 gg_id:146072 Metagenomic gut microbiome healthy human stool clone C531 DQ326
FJ370419.1 gg_id:357103 feces adult twins and mothers; TS56 clone TS56_a04h04 FJ3704
AY978700.1 gg_id:126318 human transverse colon mucosal biopsy clone KT78 AY978
GQ897549.1 gg_id:592235 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ897
DQ799818.1 gg_id:195604 human fecal clone RL182_aah34c02 DQ799
GQ001498.1 gg_id:508164 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu173g01 GQ001
GQ897613.1 gg_id:535749 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ897
DQ796531.1 gg_id:197819 human fecal clone RL179aan74c03 DQ796
FJ364639.1 gg_id:358860 feces adult twins and mothers; TS19 clone TS19_a01c11 FJ3646
EU762312.1 gg_id:317534 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A9 EU762
FJ367738.1 gg_id:361646 feces adult twins and mothers; TS2 clone TS2_a03a07 FJ3677
DQ327267.1 gg_id:145585 Metagenomic gut microbiome healthy human stool clone E811 DQ327

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DQ799325.1 gg_id:189701 human fecal clone RL205_aaj20h09 DQ799
DQ326644.1 gg_id:147888 Metagenomic gut microbiome healthy human stool clone E081 DQ326
AY978654.1 gg_id:117354 human transverse colon mucosal biopsy clone KS83 AY978
AY980149.1 gg_id:121657 human rectum mucosal biopsy clone KD47 AY980
DQ794967.1 gg_id:181815 human fecal clone RL310_aam38e09 DQ794
DQ808460.1 gg_id:184002 human fecal clone RL180_aao76g10 DQ808
DQ807035.1 gg_id:197041 human fecal clone RL244_aaj45d05 DQ807
DQ801333.1 gg_id:181853 human fecal clone RL388_aao94b05 DQ801
DQ809690.1 gg_id:174111 human fecal clone RL184_aan82f09 DQ809
DQ795390.1 gg_id:174199 human fecal clone RL178_aah53g06 DQ795
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AY981426.1 gg_id:117920 human sigmoid colon mucosal biopsy clone L493 AY981
FJ370030.1 gg_id:364149 feces adult twins and mothers; TS55 clone TS55_a03f06 FJ3700
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DQ796749.1 gg_id:190462 human fecal clone RL179_aao53h12 DQ796
DQ807697.1 gg_id:174347 human fecal clone RL180_aah36b03 DQ807
AY977087.1 gg_id:119004 human cecum mucosal biopsy clone K777 AY977
DQ327521.1 gg_id:148085 Metagenomic gut microbiome healthy human stool clone EB01 DQ327
DQ798618.1 gg_id:193664 human fecal clone RL181_aan99b01 DQ798
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DQ796228.1 gg_id:191484 human fecal clone RL179_aah23d06 DQ796
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DQ800930.1 gg_id:180095 human fecal clone RL387_aao89e01 DQ800
DQ809583.1 gg_id:182505 human fecal clone RL184_aan81b10 DQ809
EU762022.1 gg_id:306696 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1 EU762
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AY981259.1 gg_id:122690 human sigmoid colon mucosal biopsy clone G246 AY981
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DQ801679.1 gg_id:183837 human fecal clone RL201_aai45d03 DQ801
DQ327280.1 gg_id:145739 Metagenomic gut microbiome healthy human stool clone E824 DQ327
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DQ807958.1 gg_id:178681 human fecal clone RL180_aan69g07 DQ807
DQ807688.1 gg_id:178919 human fecal clone RL180_aah35h11 DQ807
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DQ796894.1 gg_id:185065 human fecal clone RL179_aao56a11 DQ796
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GQ897330.1 gg_id:547913 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ897
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EF602816.1 gg_id:233515 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6028
AY330126.1 gg_id:95597 methanogenic landfill leachate bioreactor clone AC036 AY330
AF371667.1 gg_id:32727 swine intestine clone p-1612-c5 AF371
AJ229203.1 gg_id:38211 anoxic bulk soil flooded rice microcosm clone BSV51 AJ2292
EF602953.1 gg_id:231295 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6029
EF602951.1 gg_id:232130 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6029
EU779322.1 gg_id:336501 Visayam Warty Pig feces clone VWP_aaa04d03 EU779
AM932651.1 gg_id:560203 microbiota Toll-like receptor 2 deficient mice exhibits lineage specific modifications AM932
DQ815773.1 gg_id:172705 mouse cecum clone aab22b06 DQ815
FJ365173.1 gg_id:364390 feces adult twins and mothers; TS1 clone TS1_a03g03 FJ3651
X77839.1 gg_id:14090 Clostridium polysaccharolyticum str. DSM 1801 X77839
AF371666.1 gg_id:25842 swine intestine clone p-204-o5 AF371
EU504957.1 gg_id:259762 cecal contents Mus musculus strain C57BL/6J; myd2 clone myd2_aaa04g09 EU504
AB488370.1 gg_id:532832 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSSUR0 AB488
AB264067.1 gg_id:196195 Fecal microbial (dugong dugon) determined genes Dugong feces clone dgD-50 AB264
EU656014.1 gg_id:283710 influence dietary flavonoid-containing extracts on gut microbiota mouse feces clone EU656
EU503974.1 gg_id:277385 cecal contents Mus musculus strain C57BL/6J; CRWD4 clone CRWD4_aaa03e03 EU503
AB264071.1 gg_id:177681 Fecal microbial (dugong dugon) determined genes Dugong feces clone dgD-96 AB264
EF559115.1 gg_id:222851 mesophilic anaerobic digester clone C35_D7_H_B_B05 EF5591
EU598268.1 gg_id:270815 Production purification and alkaliphilic xylanase microbial EMSD5 compost clone OTU EU598

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EU474886.1 gg_id:302836 red river hog feces clone RRH_aaa02c04 EU4748
EF559119.1 gg_id:220781 mesophilic anaerobic digester clone C35_D7_H_B_H01 EF5591
AJ229234.1 gg_id:14101 Clostridium sp. str. XB90 AJ2292
EU655971.1 gg_id:286598 influence dietary flavonoid-containing extracts on gut microbiota mouse feces clone EU6559
X71858.1 gg_id:14089 Clostridium polysaccharolyticum str. DSM 1801 X71858
AM982562.1 gg_id:278018 microbial and slurry pig saw dust spent bedding clone PISD-AIH08 AM982
AB487614.1 gg_id:541647 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNSR0 AB4876
EF603083.1 gg_id:233089 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6030
AB486227.1 gg_id:575834 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBAR0 AB4862
AJ229214.1 gg_id:23653 anoxic bulk soil flooded rice microcosm clone BSV70 clone AJ2292
EU358714.1 gg_id:308774 structure archaeal denaturing gel electrophoresis and sequencing mesophilic biogas EU3587
EF603181.1 gg_id:229938 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6031
AB487451.1 gg_id:540943 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNIR0 AB4874
EF445208.1 gg_id:205597 rabbit cecum clone NED2H8 EF4452
AM500788.1 gg_id:540532 proof spatial heterogeneity hot composting clone E72 AM500
FJ365944.1 gg_id:367453 feces adult twins and mothers; TS25 clone TS25_a01a03 FJ3659
DQ795967.1 gg_id:189870 human fecal clone RL202_aai49e10 DQ795
DQ798524.1 gg_id:182948 human fecal clone RL181_aan97g08 DQ798
AF371659.1 gg_id:25904 swine intestine clone p-197-o5 AF3716
DQ326932.1 gg_id:145977 Metagenomic gut microbiome healthy human stool clone E423 DQ326
DQ798374.1 gg_id:196045 human fecal clone RL181_aah41g01 DQ798
AY212770.1 gg_id:101237 equine manure clone wet68 AY2127
AB218343.1 gg_id:145097 Fecal microbial (dugong dugon) determined genes Dugong feces clone dgC-172 AB2183
DQ795043.1 gg_id:175342 human fecal clone RL310_aam39e04 DQ795
GQ040652.1 gg_id:446057 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw957b10 GQ040
EU777587.1 gg_id:312054 Sumatran orangutan feces clone orang1_aai56c10 EU7775
FJ370200.1 gg_id:361563 feces adult twins and mothers; TS56 clone TS56_a01f10 FJ3702
GQ040758.1 gg_id:439855 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw958d01 GQ040
FJ364231.1 gg_id:362190 feces adult twins and mothers; TS150 clone TS150_a04e04 FJ3642
FN563398.1 gg_id:594380 Impact changing HRT OLR on prokaryotes involved biomethanizitaion and fuzzy logic FN5633
AB185572.1 gg_id:102090 rumen clone F23-H10 AB1855
FJ368245.1 gg_id:365926 feces adult twins and mothers; TS3 clone TS3_a02a01 FJ3682
EU748480.1 gg_id:327697 neotropical folivorous flying bird adult hoatzin crop clone hoa61_09e11 EU7484
EU009810.1 gg_id:246937 intestinal microbiota domestic and wild turkeys turkey cecum clone WTB_E48 EU0098
DQ806056.1 gg_id:177612 human fecal clone RL186_aah60e10 DQ806
AF001738.1 gg_id:14079 rumen clone RF5 AF0017
DQ905358.1 gg_id:169063 human fecal clone 013B-G11 DQ905
DQ803139.1 gg_id:177960 human fecal clone RL311_aam21a01 DQ803
DQ325775.1 gg_id:148628 Metagenomic gut microbiome healthy human stool clone B461 DQ325
EU775348.1 gg_id:335703 Western lowland gorilla feces clone GOR_aag73h05 EU7753

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FJ363598.1 gg_id:363673 feces adult twins and mothers; TS14 clone TS14_a01b10 FJ3635
EU471606.1 gg_id:297180 Asiatic elephant feces clone AE1_aaa03b08 EU471
FJ369768.1 gg_id:368229 feces adult twins and mothers; TS51 clone TS51_a04e12 FJ3697
DQ797873.1 gg_id:174394 human fecal clone RL206_aaj16h04 DQ797
FJ369407.1 gg_id:368023 feces adult twins and mothers; TS50 clone TS50_a04b05 FJ3694
DQ797064.1 gg_id:198736 human fecal clone RL386_aao86e03 DQ797
DQ797794.1 gg_id:176294 human fecal clone RL206_aaj15h11 DQ797
DQ804235.1 gg_id:180498 human fecal clone RL187_aah70f08 DQ804
FM873638.1 gg_id:367860 occupant source house mattress dust clone MA01H09 FM873
AB218300.1 gg_id:148304 Fecal microbial (dugong dugon) determined genes Dugong feces clone dgA-73 AB218
DQ824467.1 gg_id:189373 human fecal clone RL304_aal76d03 DQ824
GQ897362.1 gg_id:566033 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do GQ897
FJ369269.1 gg_id:364786 feces adult twins and mothers; TS50 clone TS50_a02c08 FJ3692
DQ325553.1 gg_id:146945 Metagenomic gut microbiome healthy human stool clone B015 DQ325
DQ803271.1 gg_id:187948 human fecal clone RL311_aam23c01 DQ803
FJ362754.1 gg_id:363879 feces adult twins and mothers; TS13 clone TS13_a02g03 FJ3627
EU778160.1 gg_id:316598 feces clone RL388_aao96f07 EU778
DQ795004.1 gg_id:178146 human fecal clone RL310_aam39a05 DQ795
FJ369227.1 gg_id:367762 feces adult twins and mothers; TS50 clone TS50_a01g07 FJ3692
FJ832200.1 gg_id:560995 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P1Q101_82B11 FJ8322
FJ371026.1 gg_id:368983 feces adult twins and mothers; TS5 clone TS5_a04a11 FJ3710
DQ807249.1 gg_id:191769 human fecal clone RL244_aaj48b05 DQ807
DQ327417.1 gg_id:148635 Metagenomic gut microbiome healthy human stool clone E976 DQ327
DQ806335.1 gg_id:184069 human fecal clone RL186_aan90g07 DQ806
DQ116006.1 gg_id:130051 bovine teat canal clone D-51 DQ116
FJ673323.1 gg_id:515572 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6733
DQ326427.1 gg_id:147279 Metagenomic gut microbiome healthy human stool clone C482 DQ326
EU844987.1 gg_id:343667 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
AB218299.1 gg_id:145431 Fecal microbial (dugong dugon) determined genes Dugong feces clone dgA-71 AB218
DQ795466.1 gg_id:182270 human fecal clone RL178_aah54f12 DQ795
DQ804374.1 gg_id:174474 human fecal clone RL187_aan78h05 DQ804
FJ363791.1 gg_id:364298 feces adult twins and mothers; TS14 clone TS14_a03d05 FJ3637
EF436361.1 gg_id:205445 library-based ruminal water buffalo (Bubalus bubalis) rumen fluid clone BRC75 EF4363
DQ794583.1 gg_id:192428 human fecal clone RL240_aaj29h05 DQ794
DQ798651.1 gg_id:189815 human fecal clone RL181_aan99e10 DQ798
DQ800500.1 gg_id:179320 human fecal clone RL183_aah27e04 DQ800
DQ802270.1 gg_id:188481 human fecal clone RL188_aah15d08 DQ802
DQ803722.1 gg_id:181406 human fecal clone RL200_aai57e11 DQ803
FJ364143.1 gg_id:369413 feces adult twins and mothers; TS150 clone TS150_a03e05 FJ3641
DQ798129.1 gg_id:184829 human fecal clone RL302_aal95h02 DQ798

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FJ366225.1 gg_id:361112 feces adult twins and mothers; TS25 clone TS25_a04b10 FJ3662
DQ795259.1 gg_id:176125 human fecal clone RL178_aah52b08 DQ795
FJ370766.1 gg_id:359863 feces adult twins and mothers; TS5 clone TS5_a01a06 FJ3707
EU771423.1 gg_id:320284 Asiatic elephant feces clone AE2_aaa04e11 EU771
EU776147.1 gg_id:308045 Spotted hyena feces clone HY2_g06 EU776
DQ794005.1 gg_id:196443 human fecal clone RL176_aah46e07 DQ794
DQ796513.1 gg_id:194330 human fecal clone RL179aan73f11 DQ796
FJ369329.1 gg_id:368073 feces adult twins and mothers; TS50 clone TS50_a03b09 FJ3693
FJ363846.1 gg_id:358422 feces adult twins and mothers; TS14 clone TS14_a04a09 FJ3638
DQ794651.1 gg_id:185791 human fecal clone RL240_aaj30f09 DQ794
AF001702.1 gg_id:14091 rumen clone RC10 AF001
DQ806145.1 gg_id:197745 human fecal clone RL186_aah61g10 DQ806
DQ325786.1 gg_id:148837 Metagenomic gut microbiome healthy human stool clone B477 DQ325
GQ448774.1 gg_id:540224 Microbiome neonatal calves: shedding microorganisms fecal clone calf784_10wks_g GQ448
EU778980.1 gg_id:313823 Prevost's squirrel feces clone SQ_aah81a06 EU778
FJ371206.1 gg_id:363385 feces adult twins and mothers; TS6 clone TS6_a02b07 FJ3712
FJ364508.1 gg_id:361833 feces adult twins and mothers; TS15 clone TS15_a03g07 FJ3645
DQ803194.1 gg_id:183984 human fecal clone RL311_aam21h10 DQ803
AY960565.1 gg_id:114912 Clostridium sp. str. ID11 AY960
DQ796396.1 gg_id:190307 human fecal clone RL179_aah26f11 DQ796
FJ368662.1 gg_id:360088 feces adult twins and mothers; TS49 clone TS49_a03a04 FJ3686
DQ793914.1 gg_id:189485 human fecal clone RL176_aah45c03 DQ793
DQ795696.1 gg_id:191766 human fecal clone RL178_aan68g08 DQ795
GQ897258.1 gg_id:568646 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ897
EU344679.1 gg_id:275370 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU344
AF371665.1 gg_id:71089 swine intestine clone p-30-a5 AF371
EF445260.1 gg_id:211734 dairy cow rumen clone NED4D11 EF4452
EU622674.1 gg_id:279487 -feed administered sub-therapeutic chlorotetracycline alters structure and but not a EU622
FJ363493.1 gg_id:362863 feces adult twins and mothers; TS149 clone TS149_a03h05 FJ3634
FJ368627.1 gg_id:367884 feces adult twins and mothers; TS49 clone TS49_a02e08 FJ3686
DQ809618.1 gg_id:197865 human fecal clone RL184_aan81f05 DQ809
DQ795109.1 gg_id:176491 human fecal clone RL310_aam40d01 DQ795
DQ327256.1 gg_id:149461 Metagenomic gut microbiome healthy human stool clone E795 DQ327
DQ803199.1 gg_id:188592 human fecal clone RL311_aam22a05 DQ803
EU381987.1 gg_id:271750 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU381
DQ805127.1 gg_id:192315 human fecal clone RL249_aaj81f03 DQ805
EU762969.1 gg_id:315028 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU762
DQ796218.1 gg_id:174256 human fecal clone RL179_aah23c07 DQ796
EU473489.1 gg_id:296607 Somali wild ass feces clone WA_aaa01b03 EU473
DQ796700.1 gg_id:181100 human fecal clone RL179_aao53d03 DQ796
FJ368814.1 gg_id:366752 feces adult twins and mothers; TS49 clone TS49_a04h10 FJ3688

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DQ795156.1 gg_id:186048 human fecal clone RL310_aam40h03 DQ795
DQ824600.1 gg_id:185299 human fecal clone RL185_aaj70c05 DQ824
DQ803202.1 gg_id:189745 human fecal clone RL311_aam22a09 DQ803
GU303697.1 gg_id:570450 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU303
FJ362975.1 gg_id:362583 feces adult twins and mothers; TS148 clone TS148_a01d10 FJ3629
FJ364128.1 gg_id:362262 feces adult twins and mothers; TS150 clone TS150_a03c12 FJ3641
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FJ368288.1 gg_id:369224 feces adult twins and mothers; TS3 clone TS3_a02e04 FJ3682
EU774091.1 gg_id:315176 Chimpanzee feces clone CHIMP12_e08_1 EU774
FJ364204.1 gg_id:369896 feces adult twins and mothers; TS150 clone TS150_a04b09 FJ3642
DQ799390.1 gg_id:189715 human fecal clone RL305aal85f10 DQ799
EU775922.1 gg_id:331309 Horse feces clone horsej_aai90c10 EU775
DQ327173.1 gg_id:148579 Metagenomic gut microbiome healthy human stool clone E701 DQ327
GQ090630.1 gg_id:381579 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw GQ090
DQ802518.1 gg_id:190122 human fecal clone RL188_aah18h02 DQ802
FJ366839.1 gg_id:362391 feces adult twins and mothers; TS27 clone TS27_a04e01 FJ3668
EU845683.1 gg_id:311395 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU845
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FJ368263.1 gg_id:364272 feces adult twins and mothers; TS3 clone TS3_a02b09 FJ3682
DQ904646.1 gg_id:170104 human fecal clone 001-a7 DQ904
DQ327003.1 gg_id:147218 Metagenomic gut microbiome healthy human stool clone E504 DQ327
EU772020.1 gg_id:324961 Argali sheep feces clone AS1_aao38e09.Contig1 EU772
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FJ363898.1 gg_id:363738 feces adult twins and mothers; TS14 clone TS14_a04f08 FJ3638
DQ798645.1 gg_id:198540 human fecal clone RL181_aan99e03 DQ798
FJ833076.1 gg_id:510859 Microbial Ecology Crop Folivorous Hoatzin crop contents clone A1Q201_82B11 FJ8330
DQ794056.1 gg_id:177942 human fecal clone RL176_aan57d05 DQ794
DQ805407.1 gg_id:194366 human fecal clone RL203_aai62b11 DQ805
EU843494.1 gg_id:314618 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
FJ363471.1 gg_id:357829 feces adult twins and mothers; TS149 clone TS149_a03f03 FJ3634
EF404127.1 gg_id:215034 human fecal clone SJTU_C_05_14 EF4041
FJ368805.1 gg_id:361224 feces adult twins and mothers; TS49 clone TS49_a04g08 FJ3688
DQ326977.1 gg_id:149713 Metagenomic gut microbiome healthy human stool clone E472 DQ326
EU775401.1 gg_id:335601 Western lowland gorilla feces clone GOR_aag74d01 EU775
EU843844.1 gg_id:308974 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
DQ810039.1 gg_id:192338 human fecal clone RL184_aao67d03 DQ810
AF001756.1 gg_id:14080 rumen clone RF24 AF001
EU451291.1 gg_id:326416 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75 EU451
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DQ777934.1 gg_id:167252 rat feces clone R-1199(2) DQ777
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EU765884.1 gg_id:343785 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B EU765
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EU778332.1 gg_id:321304 feces clone RL388_aao93h04 EU778
EU456462.1 gg_id:313333 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K79 EU456
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FJ881245.1 gg_id:430739 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8812
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FJ681388.1 gg_id:515129 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6813
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FJ879304.1 gg_id:411214 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8793
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EU344224.1 gg_id:260496 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU344
EU455186.1 gg_id:333786 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H79 EU455
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FJ367885.1 gg_id:359911 feces adult twins and mothers; TS2 clone TS2_a04g01 FJ3678
FJ680195.1 gg_id:530278 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6801
EU452990.1 gg_id:332816 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83 EU452
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EU456680.1 gg_id:318224 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75 EU456
EF098586.1 gg_id:188120 mouse cecum clone SWPT16_aaa01g06 EF0985
FJ678722.1 gg_id:525789 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6787
DQ815697.1 gg_id:163142 mouse cecum clone aab21b02 DQ815
EU509978.1 gg_id:268910 cecal contents Mus musculus strain C57BL/6J; WD11 clone WD11_aak24h05 EU509
EU530167.1 gg_id:258321 mucosa adherent and invasive microbes profile adenoma colorectal cancer clone M1 EU530
EU748382.1 gg_id:323463 neotropical folivorous flying bird adult hoatzin crop clone hoa5_07h08 EU748
EU450938.1 gg_id:306993 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77 EU450

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EU455391.1 gg_id:329314 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU455
AF371675.1 gg_id:106258 swine intestine clone p-653-a5 AF3716
DQ799657.1 gg_id:173934 human fecal clone RL305aal88g06 DQ799
EU503857.1 gg_id:275869 cecal contents Mus musculus strain C57BL/6J; CRWD4 clone CRWD4_aaa01f04 EU5038
EU344496.1 gg_id:261381 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU344
EU450979.1 gg_id:356010 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU450
FJ685073.1 gg_id:517182 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6850
EU453671.1 gg_id:314503 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K79S EU453
FJ368515.1 gg_id:358624 feces adult twins and mothers; TS49 clone TS49_a01c05 FJ3685
EU456865.1 gg_id:337710 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU456
EF614592.1 gg_id:234914 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o EF6145
EU456162.1 gg_id:320303 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU456
FJ680692.1 gg_id:523749 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6806
FJ680968.1 gg_id:521604 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6809
EU457567.1 gg_id:336011 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU457
EU454285.1 gg_id:331683 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU454
FJ684591.1 gg_id:520237 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6845
FJ832915.1 gg_id:565563 Microbial Ecology Crop Folivorous Hoatzin crop contents clone A1Q101_13E02 FJ8329
FJ368425.1 gg_id:370307 feces adult twins and mothers; TS3 clone TS3_a04b11 FJ3684
EU457237.1 gg_id:339073 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU457
FJ678929.1 gg_id:519545 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6789
DQ801232.1 gg_id:192443 human fecal clone RL116_aaf02b01 DQ801
FJ681054.1 gg_id:521401 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6810
FM874014.1 gg_id:369502 occupant source house mattress dust clone MB05B06 FM874
FJ679944.1 gg_id:520788 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6799
EU467116.1 gg_id:297642 mongoose lemur feces clone ML_aae88f01 EU467
EU842491.1 gg_id:347828 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
EU006303.1 gg_id:257049 Salmonella enterica serovar typhimurium exploits inflammation compete intestinal r EU006
FJ364129.1 gg_id:366721 feces adult twins and mothers; TS150 clone TS150_a03d02 FJ3641
FJ880839.1 gg_id:435285 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8808
EU455671.1 gg_id:353454 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU455
EF098785.1 gg_id:182446 mouse cecum clone SWPT16_aaa04h06 EF0987
EU344398.1 gg_id:261634 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU344
FJ681916.1 gg_id:523731 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6819
EU457797.1 gg_id:319812 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75N EU457
DQ809672.1 gg_id:189574 human fecal clone RL184_aan82d09 DQ809
EU461523.1 gg_id:299398 black rhinoceros feces clone RH_aaj91f01 EU461
EU763756.1 gg_id:324502 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A4 EU763
FJ372350.1 gg_id:360928 feces adult twins and mothers; TS9 clone TS9_a04e12 FJ3723
EU505012.1 gg_id:272499 cecal contents Mus musculus strain C57BL/6J; myd3 clone myd3_aaa01f02 EU505

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FJ880110.1 gg_id:452592 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8801
EU766273.1 gg_id:306643 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU766
EU764369.1 gg_id:306379 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1 EU764
EU381441.1 gg_id:266392 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid p EU3814
DQ794425.1 gg_id:181500 human fecal clone RL197_aah87e12 DQ794
FJ833469.1 gg_id:584481 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J1Q201_61E08 FJ8334
DQ797246.1 gg_id:177482 human fecal clone RL386_aao88h04 DQ797
DQ794364.1 gg_id:188621 human fecal clone RL197_aah86e07 DQ794
EU844552.1 gg_id:319145 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8445
EU381898.1 gg_id:261290 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU3818
FJ363635.1 gg_id:366757 feces adult twins and mothers; TS14 clone TS14_a01e12 FJ3636
EU469257.1 gg_id:302339 Speke's gazelle feces clone SP3_h08_1 EU469
DQ797019.1 gg_id:199305 human fecal clone RL386_aao85h05 DQ797
EU778230.1 gg_id:339621 feces clone RL388_aao94f07 EU778
DQ794527.1 gg_id:186724 human fecal clone RL240_aaj29b08 DQ794
AB185762.1 gg_id:99824 rumen clone U29-C01 AB185
DQ794949.1 gg_id:180449 human fecal clone RL310_aam38c12 DQ794
AF371657.1 gg_id:20421 swine intestine clone p-444-o3 AF3716
DQ824117.1 gg_id:192060 human fecal clone RL204_aaj59e08 DQ824
FJ366191.1 gg_id:358337 feces adult twins and mothers; TS25 clone TS25_a03g05 FJ3661
EF686576.1 gg_id:253222 Sequences Manifest Rumen Yunnan Yel Cattle (Bos Taurus) rumen fluid clone YNRC6 EF6865
EU381470.1 gg_id:263808 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid p EU3814
EU766374.1 gg_id:325264 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU7663
DQ794376.1 gg_id:183192 human fecal clone RL197_aah86g11 DQ794
EU842292.1 gg_id:331206 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
AF371650.1 gg_id:34731 swine intestine clone p-1895-s962-3 AF3716
EU766433.1 gg_id:350577 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU7664
EU777196.1 gg_id:340572 Okapi feces clone OK1_g03_1 EU777
EU766213.1 gg_id:354961 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU766
EU381880.1 gg_id:260787 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU3818
NR_024661.1 gg_id:573803 Eubacterium ruminantium str. GA195; ATCC 17233 NR_024
FJ833266.1 gg_id:538611 Microbial Ecology Crop Folivorous Hoatzin crop contents clone A3Q302_49A07 FJ8332
EU843008.1 gg_id:343422 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8430
EU778151.1 gg_id:343981 feces clone RL388_aao96e11 EU778
DQ824189.1 gg_id:194572 human fecal clone RL204_aaj60f02 DQ824
AY854269.2 gg_id:109798 herbivore gastrointestinal tract clone CATTLE_7 AY8542
NZ_AAYW02000018.1 gg_id:469946 Clostridium sp. str. L2-50 NZ_AA
EU344603.1 gg_id:268215 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU3446
DQ824605.1 gg_id:177984 human fecal clone RL185_aaj70c10 DQ824
EU844383.1 gg_id:322159 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8443

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EU764626.1 gg_id:353279 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1 EU7646
FJ680393.1 gg_id:514136 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6803
EU764391.1 gg_id:340570 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1 EU7643
EU381742.1 gg_id:274577 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid EU3817
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EU771329.1 gg_id:346606 Asiatic elephant feces clone AE2_aaa04a09 EU7713
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DQ801418.1 gg_id:196850 human fecal clone RL388_aao95c06 DQ801
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EU381551.1 gg_id:274876 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid EU3815
EU842621.1 gg_id:342811 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU8426
EU381639.1 gg_id:266062 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid EU3816
EU766527.1 gg_id:345136 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU7665
EU622773.1 gg_id:278439 -feed administered sub-therapeutic chlorotetracycline alters structure and but not a EU6227
DQ794497.1 gg_id:174019 human fecal clone RL197_aah88f11 DQ794
FJ681890.1 gg_id:524260 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6818
DQ795023.1 gg_id:182681 human fecal clone RL310_aam39c06 DQ795
AY985444.1 gg_id:127752 human stool clone C391 AY9854
AB185807.1 gg_id:103066 rumen clone U29-G09 AB1858
EF436389.1 gg_id:209741 library-based ruminal water buffalo (Bubalus bubalis) rumen fluid clone BRC103 EF4363
EU843953.1 gg_id:324835 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8439
EU764717.1 gg_id:356540 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1 EU7647
FJ833666.1 gg_id:571186 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J1Q402_91C12 FJ8336
EU774771.1 gg_id:345211 Angola Colobus feces clone EAC_1aaa01e02 EU7747
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FJ364307.1 gg_id:357959 feces adult twins and mothers; TS15 clone TS15_a01d08 FJ3643
AY984686.1 gg_id:124107 human stool clone B638 AY9846
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AY976895.1 gg_id:127343 human cecum mucosal biopsy clone K540 AY9768
NZ_AAXA02000015.1 gg_id:470238 Dorea formicigenerans str. ATCC 27755 NZ_AA
NZ_AAXA02000016.1 gg_id:470230 Dorea formicigenerans str. ATCC 27755 NZ_AA
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AY979373.1 gg_id:117508 human transverse colon mucosal biopsy clone Z722 AY9793
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AY983685.1 gg_id:118813 human descending colon mucosal biopsy clone NP92 AY9836
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DQ327389.1 gg_id:145925 Metagenomic gut microbiome healthy human stool clone E947 DQ327
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FJ368583.1 gg_id:369057 feces adult twins and mothers; TS49 clone TS49_a02a06 FJ3685
AY981801.1 gg_id:127835 human sigmoid colon mucosal biopsy clone NU02 AY9818
FJ369873.1 gg_id:358282 feces adult twins and mothers; TS55 clone TS55_a01g06 FJ3698
AY977989.1 gg_id:115924 human cecum mucosal biopsy clone LH22 AY9779
AY983625.1 gg_id:116382 human descending colon mucosal biopsy clone NO65 AY9836
FJ371197.1 gg_id:359382 feces adult twins and mothers; TS6 clone TS6_a02a10 FJ3711
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AY978748.1 gg_id:123331 human transverse colon mucosal biopsy clone KU94 AY9787
FJ368698.1 gg_id:363888 feces adult twins and mothers; TS49 clone TS49_a03d10 FJ3686
AY975351.1 gg_id:116850 human ascending colon mucosal biopsy clone N632 AY9753
FJ365936.1 gg_id:365459 feces adult twins and mothers; TS21 clone TS21_a04h04 FJ3659
AY982434.1 gg_id:117037 human sigmoid colon mucosal biopsy clone ML48 AY9824
FJ365581.1 gg_id:359797 feces adult twins and mothers; TS20 clone TS20_a04e09 FJ3655

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DQ326308.1 gg_id:145731 Metagenomic gut microbiome healthy human stool clone C279	DQ326
FJ367538.1 gg_id:363533 feces adult twins and mothers; TS29 clone TS29_a04g03	FJ3675
AY976662.1 gg_id:119238 human cecum mucosal biopsy clone K229	AY9766
FJ369025.1 gg_id:360317 feces adult twins and mothers; TS4 clone TS4_a03d06	FJ3690
EU762250.1 gg_id:309236 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A>	EU762
FJ370139.1 gg_id:359846 feces adult twins and mothers; TS55 clone TS55_a04h02	FJ3701
AY982186.1 gg_id:119083 human sigmoid colon mucosal biopsy clone MG65	AY9821
AY979159.1 gg_id:119223 human transverse colon mucosal biopsy clone Z211	AY9791
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DQ327584.1 gg_id:150493 Metagenomic gut microbiome healthy human stool clone EB69	DQ327
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FJ365464.1 gg_id:367576 feces adult twins and mothers; TS20 clone TS20_a03c01	FJ3654
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AF067414.1 gg_id:14130 Epulopiscium fishelsoni str. Red Sea A2	AF0674
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AM500767.1 gg_id:558007 proof spatial heterogeneity hot composting clone E6	AM500
EU468764.1 gg_id:294143 okapi feces clone OK3_c09_1	EU4687
DQ113748.1 gg_id:136518 dog duodenum clone D1-26	DQ113
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EU475028.1 gg_id:291710 red river hog feces clone RRH_aaa02f06	EU4750
EU470379.1 gg_id:299376 Grevy's zebra feces clone GZ_aaa01c09	EU4703
U22332.1 gg_id:14127 "Metabacterium polyspora"	U22332
X71860.1 gg_id:13988 Eubacterium cellulosolvens 6 str. ATCC 43171	X71860
AB372004.1 gg_id:312201 Eubacterium cellulosolvens str. NE13	AB3720
DQ824305.1 gg_id:192536 human fecal clone RL304_aal74c01	DQ824
EU778103.1 gg_id:332313 feces clone RL387_aao89a11.Contig2	EU7781
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DQ805487.1 gg_id:189396 human fecal clone RL203_aai63c09	DQ805

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EU464298.1 gg_id:292341 hamadryas baboon feces clone AFBAB_aai02b02 EU4642
AY960569.1 gg_id:114929 Ruminococcus sp. str. ID1 AY9605
EU464283.1 gg_id:299741 hamadryas baboon feces clone AFBAB_aai01f10 EU4642
EU464338.1 gg_id:295189 hamadryas baboon feces clone AFBAB_aai03a06 EU4643
DQ804789.1 gg_id:182724 human fecal clone RL187_aao72g02 DQ804
FJ676752.1 gg_id:522551 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6767
EU381497.1 gg_id:275224 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid p EU3814
EU773576.1 gg_id:312780 Goeldi's Marmoset feces clone CAL_g05 EU7735
DQ085084.1 gg_id:137650 goat rumen clone A10 DQ085
EU530321.1 gg_id:273681 mucosa adherent and invasive microbes profile adenoma colorectal cancer clone M4 EU5303
DQ071485.1 gg_id:233103 microbial cecum captive and free-living capercaillies (Tetrao urogallus) clone TuCc8 DQ071
DQ797410.1 gg_id:195175 human fecal clone RL248_aai99a05 DQ797
EU466910.1 gg_id:288208 African elephant feces clone AFEL2_aao31c03 EU4669
FJ364061.1 gg_id:366656 feces adult twins and mothers; TS150 clone TS150_a02e06 FJ3640
FJ363785.1 gg_id:363228 feces adult twins and mothers; TS14 clone TS14_a03c11 FJ3637
FJ677666.1 gg_id:527303 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6776
DQ798613.1 gg_id:198740 human fecal clone RL181_aan99a06 DQ798
AJ408978.1 gg_id:111446 human colonic clone HuCA27 AJ4089
FJ362772.1 gg_id:357827 feces adult twins and mothers; TS13 clone TS13_a03a04 FJ3627
DQ824940.1 gg_id:181111 human fecal clone RL185_aao71c06 DQ824
GQ493324.1 gg_id:580898 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
AY977502.1 gg_id:127727 human cecum mucosal biopsy clone W257 AY9775
DQ796051.1 gg_id:177746 human fecal clone RL202_aai50g07 DQ796
DQ795677.1 gg_id:180329 human fecal clone RL178_aan68d01 DQ795
DQ823941.1 gg_id:174799 human fecal clone RL204_aaj57c01 DQ823
FJ372061.1 gg_id:366033 feces adult twins and mothers; TS9 clone TS9_a01c12 FJ3720
DQ797635.1 gg_id:180628 human fecal clone RL206_aaj14a05 DQ797
DQ795675.1 gg_id:190177 human fecal clone RL178_aan68c05 DQ795
DQ798351.1 gg_id:189315 human fecal clone RL181_aah41d03 DQ798
DQ795022.1 gg_id:176238 human fecal clone RL310_aam39c05 DQ795
GQ897243.1 gg_id:539595 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ897
FJ674180.1 gg_id:518553 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6741
DQ795460.1 gg_id:175261 human fecal clone RL178_aah54f04 DQ795
FJ683955.1 gg_id:529512 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6839
FJ679615.1 gg_id:512352 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6796
FJ685186.1 gg_id:516143 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6851
DQ794499.1 gg_id:184670 human fecal clone RL197_aah88g03 DQ794
DQ801131.1 gg_id:189661 human fecal clone RL387_aao92g01 DQ801
DQ796378.1 gg_id:196021 human fecal clone RL179_aah26e02 DQ796

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AY982478.1 gg_id:116264 human sigmoid colon mucosal biopsy clone MM39 AY9824
FJ682393.1 gg_id:528101 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6823
DQ799588.1 gg_id:196948 human fecal clone RL305aal88a06 DQ799
DQ795610.1 gg_id:175007 human fecal clone RL178_aan67a03 DQ795
DQ796306.1 gg_id:183552 human fecal clone RL179_aah25e07 DQ796
AY980794.1 gg_id:126997 human rectum mucosal biopsy clone LO11 AY9807
FJ369908.1 gg_id:364287 feces adult twins and mothers; TS55 clone TS55_a02b08 FJ3699
FJ366270.1 gg_id:370023 feces adult twins and mothers; TS25 clone TS25_a04f10 FJ3662
FJ370213.1 gg_id:368038 feces adult twins and mothers; TS56 clone TS56_a01h01 FJ3702
FJ368827.1 gg_id:365391 feces adult twins and mothers; TS4 clone TS4_a01a12 FJ3688
FJ685443.1 gg_id:529808 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6854
FJ369265.1 gg_id:363127 feces adult twins and mothers; TS50 clone TS50_a02c04 FJ3692
FJ684743.1 gg_id:519921 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6847
DQ796869.1 gg_id:196394 human fecal clone RL179_aao55f11 DQ796
FJ678359.1 gg_id:514400 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6783
FJ370858.1 gg_id:365636 feces adult twins and mothers; TS5 clone TS5_a02a12 FJ3708
FJ365451.1 gg_id:362642 feces adult twins and mothers; TS20 clone TS20_a03a09 FJ3654
DQ800958.1 gg_id:199174 human fecal clone RL387_aao89h08 DQ800
DQ807460.1 gg_id:186561 human fecal clone RL307_aam06h03 DQ807
DQ825285.1 gg_id:174225 human fecal clone RL185_aan87g06 DQ825
DQ809837.1 gg_id:182381 human fecal clone RL184_aao65a01 DQ809
FJ369804.1 gg_id:360862 feces adult twins and mothers; TS55 clone TS55_a01a07 FJ3698
EF402093.1 gg_id:206645 human fecal clone SJTU_B_03_57 EF4020
DQ805865.1 gg_id:198078 human fecal clone RL306aal92a08 DQ805
DQ797393.1 gg_id:195255 human fecal clone RL248_aai98g07 DQ797
DQ326329.1 gg_id:145360 Metagenomic gut microbiome healthy human stool clone C318 DQ326
FJ679248.1 gg_id:528560 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6792
FJ369063.1 gg_id:366153 feces adult twins and mothers; TS4 clone TS4_a03g10 FJ3690
DQ802012.1 gg_id:198227 human fecal clone RL241_aaj01g11 DQ802
FJ369432.1 gg_id:366979 feces adult twins and mothers; TS50 clone TS50_a04d08 FJ3694
DQ798560.1 gg_id:196287 human fecal clone RL181_aan98c07 DQ798
DQ807627.1 gg_id:182679 human fecal clone RL180_aah35b04 DQ807
DQ802564.1 gg_id:179762 human fecal clone RL188_aan93e01 DQ802
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DQ795623.1 gg_id:193991 human fecal clone RL178_aan67c02 DQ795
DQ807694.1 gg_id:195485 human fecal clone RL180_aah36a08 DQ807
AY979910.1 gg_id:127325 human rectum mucosal biopsy clone E224 AY9799
DQ802322.1 gg_id:195976 human fecal clone RL188_aah16a08 DQ802
FJ372011.1 gg_id:367354 feces adult twins and mothers; TS8 clone TS8_a04g04 FJ3720
DQ795329.1 gg_id:192403 human fecal clone RL178_aah53a07 DQ795

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DQ804596.1 gg_id:176409 human fecal clone RL187_aao70b06 DQ804
DQ795087.1 gg_id:183505 human fecal clone RL310_aam40a09 DQ795
DQ325743.1 gg_id:149614 Metagenomic gut microbiome healthy human stool clone B394 DQ325
FJ370065.1 gg_id:369212 feces adult twins and mothers; TS55 clone TS55_a04a08 FJ3700
FJ369870.1 gg_id:365861 feces adult twins and mothers; TS55 clone TS55_a01g03 FJ3698
AY986125.1 gg_id:121971 human stool clone D468 AY986
DQ801863.1 gg_id:178337 human fecal clone RL201_aai47g09 DQ801
DQ807737.1 gg_id:203199 human fecal clone RL180_aah36f02 DQ807
DQ801836.1 gg_id:190239 human fecal clone RL201_aai47e02 DQ801
DQ800317.1 gg_id:192672 human fecal clone RL303_aal71d06 DQ800
FJ364400.1 gg_id:361003 feces adult twins and mothers; TS15 clone TS15_a02e02 FJ3644
DQ325916.1 gg_id:145806 Metagenomic gut microbiome healthy human stool clone B756 DQ325
DQ806845.1 gg_id:183809 human fecal clone RL198_aaj73g08 DQ806
DQ809522.1 gg_id:177501 human fecal clone RL184_aah22c02 DQ809
FJ679540.1 gg_id:519626 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6795
AY983629.1 gg_id:121240 human descending colon mucosal biopsy clone NO71 AY983
DQ801904.1 gg_id:195152 human fecal clone RL201_aai48c10 DQ801
FJ369919.1 gg_id:357017 feces adult twins and mothers; TS55 clone TS55_a02c09 FJ3699
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GQ492513.1 gg_id:576103 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
FJ370081.1 gg_id:361880 feces adult twins and mothers; TS55 clone TS55_a04c01 FJ3700
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DQ806610.1 gg_id:182539 human fecal clone RL186_aao46f10 DQ806
FJ365518.1 gg_id:362419 feces adult twins and mothers; TS20 clone TS20_a03g09 FJ3655
FJ678279.1 gg_id:532113 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6782
DQ802730.1 gg_id:186283 human fecal clone RL188_aan95g12 DQ802
DQ798222.1 gg_id:173959 human fecal clone RL181_aah39a11 DQ798
EU469505.1 gg_id:290281 black lemur feces clone BKLE_a12_3 EU469
EU771816.1 gg_id:310632 African elephant feces clone AFEL2_aao32a11 EU771
DQ807876.1 gg_id:179509 human fecal clone RL180_aah38c10 DQ807
EU761798.1 gg_id:347926 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1 EU761
DQ799845.1 gg_id:195911 human fecal clone RL182_aah34h02 DQ799
DQ809883.1 gg_id:198942 human fecal clone RL184_aao65e03 DQ809
FJ363951.1 gg_id:360540 feces adult twins and mothers; TS150 clone TS150_a01c07 FJ3639
DQ802103.1 gg_id:186515 human fecal clone RL241_aaj03b04 DQ802
GQ897156.1 gg_id:578032 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ897
FJ369904.1 gg_id:362722 feces adult twins and mothers; TS55 clone TS55_a02b04 FJ3699
FJ365750.1 gg_id:368316 feces adult twins and mothers; TS21 clone TS21_a02e10 FJ3657

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FJ673255.1 gg_id:514971 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6732
DQ802337.1 gg_id:185372 human fecal clone RL188_aah16c11 DQ802
DQ795045.1 gg_id:193452 human fecal clone RL310_aam39e06 DQ795
DQ800815.1 gg_id:180261 human fecal clone RL183_aao03g10 DQ800
EU765102.1 gg_id:329212 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2 EU765
FJ672991.1 gg_id:517310 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6729
AJ811983.1 gg_id:187930 human biopsies Human ulcerative colitis biopsy clone UC9-54 AJ8119
EU767603.1 gg_id:307060 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C3 EU767
FJ369453.1 gg_id:365272 feces adult twins and mothers; TS50 clone TS50_a04g01 FJ3694
DQ796031.1 gg_id:185031 human fecal clone RL202_aai50e03 DQ796
EU767247.1 gg_id:339714 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C2 EU767
FJ678499.1 gg_id:511955 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6784
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GQ896598.1 gg_id:584945 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do s GQ896
FJ365768.1 gg_id:367260 feces adult twins and mothers; TS21 clone TS21_a02g06 FJ3657
EU776829.1 gg_id:329520 Mongoose lemur feces clone ML_aaj27g06 EU776
DQ800034.1 gg_id:188008 human fecal clone RL247_aaj23d01 DQ800
FJ369901.1 gg_id:366175 feces adult twins and mothers; TS55 clone TS55_a02b01 FJ3699
DQ810109.1 gg_id:186519 human fecal clone RL184_aao68b09 DQ810
FJ369742.1 gg_id:362935 feces adult twins and mothers; TS51 clone TS51_a04c08 FJ3697
DQ794487.1 gg_id:188965 human fecal clone RL197_aah88e08 DQ794
FJ683151.1 gg_id:520674 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6831
EU763969.1 gg_id:315472 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A5 EU763
DQ807650.1 gg_id:176734 human fecal clone RL180_aah35e01 DQ807
GQ491970.1 gg_id:547083 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
DQ796953.1 gg_id:194935 human fecal clone RL179_aao56h07 DQ796
DQ805288.1 gg_id:188213 human fecal clone RL249_aaj84e10 DQ805
FJ371018.1 gg_id:360947 feces adult twins and mothers; TS5 clone TS5_a04a02 FJ3710
FJ363766.1 gg_id:367562 feces adult twins and mothers; TS14 clone TS14_a03b03 FJ3637
DQ807846.1 gg_id:181642 human fecal clone RL180_aah37h08 DQ807
FJ372359.1 gg_id:367858 feces adult twins and mothers; TS9 clone TS9_a04f09 FJ3723
DQ825288.1 gg_id:188792 human fecal clone RL185_aan87h02 DQ825
FJ365134.1 gg_id:363400 feces adult twins and mothers; TS1 clone TS1_a03c08 FJ3651
EU466767.1 gg_id:287951 African elephant feces clone AFEL2_aao29c01 EU466
FJ684613.1 gg_id:514920 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6846
GQ897903.1 gg_id:547836 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ897
DQ796868.1 gg_id:184057 human fecal clone RL179_aao55f10 DQ796
AY979303.1 gg_id:115974 human transverse colon mucosal biopsy clone Z551 AY9793

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EU461775.1 gg_id:301025 mongoose lemur feces clone ML_aaj28g03 EU461
FJ366421.1 gg_id:364710 feces adult twins and mothers; TS26 clone TS26_a03a02 FJ3664
EU763962.1 gg_id:305501 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A5 EU763
GQ006869.1 gg_id:502796 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu88g06c GQ006
FJ365392.1 gg_id:362829 feces adult twins and mothers; TS20 clone TS20_a02d02 FJ3653
AY978332.1 gg_id:119050 human transverse colon mucosal biopsy clone F237 AY9783
GQ090639.1 gg_id:389523 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw GQ090
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FJ369949.1 gg_id:367658 feces adult twins and mothers; TS55 clone TS55_a02f06 FJ3699
FJ370113.1 gg_id:364878 feces adult twins and mothers; TS55 clone TS55_a04e09 FJ3701
FJ673736.1 gg_id:528127 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6737
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DQ803382.1 gg_id:191172 human fecal clone RL311_aam24h11 DQ803
AY980926.1 gg_id:123426 human rectum mucosal biopsy clone LR38 AY9809
DQ795760.1 gg_id:176845 human fecal clone RL245_aai81h09 DQ795
DQ806962.1 gg_id:194870 human fecal clone RL198_aaj76b10 DQ806
DQ808330.1 gg_id:196701 human fecal clone RL180_aao75d03 DQ808
DQ798132.1 gg_id:180983 human fecal clone RL302_aal95h06 DQ798
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FJ365694.1 gg_id:369815 feces adult twins and mothers; TS21 clone TS21_a01h07 FJ3656
DQ807877.1 gg_id:188165 human fecal clone RL180_aah38c11 DQ807
FJ365904.1 gg_id:358905 feces adult twins and mothers; TS21 clone TS21_a04d08 FJ3659
FJ365475.1 gg_id:358481 feces adult twins and mothers; TS20 clone TS20_a03c12 FJ3654
DQ805397.1 gg_id:188087 human fecal clone RL203_aai62b01 DQ805
FJ364848.1 gg_id:357191 feces adult twins and mothers; TS19 clone TS19_a03h05 FJ3648
DQ804124.1 gg_id:179837 human fecal clone RL187_aah68h11 DQ804
DQ799398.1 gg_id:181828 human fecal clone RL305aal85g07 DQ799
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EU843831.1 gg_id:354158 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8438
EU474950.1 gg_id:292979 red river hog feces clone RRH_aaa03d10 EU4749
AM277070.2 gg_id:232273 fecal microbiota irritable bowel syndrome patients significantly that healthy subject AM277
AB034054.1 gg_id:44311 rumen clone 3C3d-15 AB0340
DQ673542.1 gg_id:163539 rumen fluid clone GRC77 DQ673
EU842352.1 gg_id:308021 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU8423
AB494806.1 gg_id:565292 Fibrobacter succinogenes dominated consortium on hay stems sheep rumen clone A AB4948
AY854287.2 gg_id:110748 herbivore gastrointestinal tract clone CATTLE_25 AY8542
AF202264.1 gg_id:41867 Syntrophococcus sucromutans str. S195 AF2022
EU458753.1 gg_id:288604 Goeldi's marmoset feces clone CAL_d12_2 EU4587

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DQ326866.1 gg_id:149699 Metagenomic gut microbiome healthy human stool clone E348 DQ326
FJ367602.1 gg_id:358858 feces adult twins and mothers; TS2 clone TS2_a01d10 FJ3676
GU304530.1 gg_id:572313 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU304
EU458712.1 gg_id:297942 Goeldi's marmoset feces clone CAL_a12_1 EU458
FJ673087.1 gg_id:525259 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6730
EU844621.1 gg_id:349401 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
DQ804183.1 gg_id:195096 human fecal clone RL187_aah69h07 DQ804
GU304233.1 gg_id:594513 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU304
GU302772.1 gg_id:533877 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU302
EU842324.1 gg_id:356261 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
DQ394607.1 gg_id:151675 -Arctic peninsula Svalbard Norway determined genes and rumen isolates reindeer o DQ394
Y18191.1 gg_id:25317 Syntrophococcus sucromutans str. DSM 3224 Y18191
DQ057372.1 gg_id:136044 chicken ileum/cecum clone cc142 DQ057
AM420242.1 gg_id:235970 Noma subgingival plaque clone 201G01(oral) AM420
FJ976324.1 gg_id:591273 Interindividual healthy human oral microbiota mouth clone 10B859 FJ9763
AF298662.1 gg_id:35683 Lachnobacterium bovis str. LRC 5357 AF298
DQ809911.1 gg_id:182324 human fecal clone RL184_aao65g12 DQ809
EU454692.1 gg_id:313804 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74 EU454
DQ797186.1 gg_id:186096 human fecal clone RL386_aao88b04 DQ797
EF095986.1 gg_id:174276 mouse cecum clone lean2_aaa01d08 EF0959
AF396923.1 gg_id:24050 Eubacterium sp. str. C12b AF3969
DQ810111.1 gg_id:187960 human fecal clone RL184_aao68b11 DQ810
EF404492.1 gg_id:209085 human fecal clone SJTU_C_10_90 EF4044
EU779311.1 gg_id:306866 Visayam Warty Pig feces clone VWP_aaa02f12 EU7793
EU777208.1 gg_id:325580 Okapi feces clone OK1_f05 EU777
FJ365281.1 gg_id:359139 feces adult twins and mothers; TS20 clone TS20_a01a08 FJ3652
EU747905.1 gg_id:328207 neotropical folivorous flying bird adult hoatzin crop clone hoa11_54F07 EU747
DQ015039.1 gg_id:133516 mouse cecum clone M2_c11 DQ015
FJ679958.1 gg_id:521213 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6799
AF202259.1 gg_id:16477 Eubacterium oxidoreducens str. G2-2 AF2022
EF097686.1 gg_id:196519 mouse cecum clone SWPT20_aaa02c09 EF0976
FJ671752.1 gg_id:532247 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface FJ6717
EU450958.1 gg_id:310414 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83 EU450
FJ672619.1 gg_id:515002 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface FJ6726
DQ326964.1 gg_id:147198 Metagenomic gut microbiome healthy human stool clone E457 DQ326
FJ671540.1 gg_id:528645 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface FJ6715
AF202258.1 gg_id:38558 Eubacterium oxidoreducens str. DAS110 AF2022
FJ684882.1 gg_id:526046 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6848
EU504541.1 gg_id:266664 cecal contents Mus musculus strain C57BL/6J; myd1 clone myd1_aaa02b09 EU5045
DQ810115.1 gg_id:180450 human fecal clone RL184_aao68c03 DQ810

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DQ815815.1 gg_id:172307 mouse cecum clone aab22f10 DQ815
DQ825322.1 gg_id:182980 human fecal clone RL185_aan88e06 DQ825
EF603794.1 gg_id:234887 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6037
AF371614.1 gg_id:48120 swine intestine clone p-2184-s959-3 AF3716
EU771470.1 gg_id:320066 Hamadryas Baboon feces clone AFBAB_aai02b09 EU7714
AY992989.1 gg_id:132525 mouse cecum clone C22_n03 AY9929
EU452953.1 gg_id:319558 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75M EU4529
DQ800573.1 gg_id:189216 human fecal clone RL183_aah30b02 DQ800
FJ880786.1 gg_id:421538 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8807
EU503863.1 gg_id:264345 cecal contents Mus musculus strain C57BL/6J; CRWD4 clone CRWD4_aaa01g01 EU5038
EU455016.1 gg_id:341227 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83M EU4550
EU451134.1 gg_id:351978 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83M EU4511
AF396924.1 gg_id:23277 Eubacterium sp. str. C124b AF3969
AB009213.1 gg_id:14027 rumen clone RFN66 bacterium AB0092
EU774428.1 gg_id:343474 mammals their gut microbes Eastern Black and White Colobus feces clone COL_aai1(EU7744
CR933122.1 gg_id:110000 Evry municipal wastewater treatment plant clone 013F01_B_SD_P15 CR9331
EU775845.1 gg_id:347744 Horse feces clone horsem_aai95b05 EU7758
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EU762854.1 gg_id:322408 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A> EU7628
FJ372106.1 gg_id:366903 feces adult twins and mothers; TS9 clone TS9_a01g11 FJ3721
EU774171.1 gg_id:356644 Chimpanzee feces clone CHIMP1_e07 EU7741
FJ368392.1 gg_id:369652 feces adult twins and mothers; TS3 clone TS3_a03h01 FJ3683
DQ797586.1 gg_id:197341 human fecal clone RL206_aaj13d03 DQ797
DQ823650.1 gg_id:178001 human fecal clone RL250_aaj77b04 DQ823
EU765893.1 gg_id:329161 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B4 EU7658
EU774962.1 gg_id:318124 Flying Fox feces clone FF_a06_2 EU7749
FJ369956.1 gg_id:366229 feces adult twins and mothers; TS55 clone TS55_a02g01 FJ3699
DQ806710.1 gg_id:199421 human fecal clone RL186_aao47g12 DQ806
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EU768290.1 gg_id:308000 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C4 EU7682
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DQ777931.1 gg_id:164628 rat feces clone R-1330 DQ777
EU768588.1 gg_id:314431 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C5 EU7685
GQ896729.1 gg_id:555632 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do : GQ896
EU767220.1 gg_id:338700 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C2 EU7672
EU764213.1 gg_id:313911 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A5 EU7642

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DQ809979.1 gg_id:191888 human fecal clone RL184_aao66f05 DQ809
AY985110.1 gg_id:117562 human stool clone BB29 AY9851
AY984128.1 gg_id:127670 human stool clone B006 AY9841
EU764940.1 gg_id:345064 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2 EU7649
FJ364464.1 gg_id:364002 feces adult twins and mothers; TS15 clone TS15_a03c07 FJ3644
EU764204.1 gg_id:306597 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A5 EU7642
EF401947.1 gg_id:210023 human fecal clone SJTU_B_01_68 EF4019
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EU764772.1 gg_id:313876 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2 EU7647
EU762935.1 gg_id:308990 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A9 EU7629
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EF403111.1 gg_id:210835 human fecal clone SJTU_B_09_55 EF4031
FJ372341.1 gg_id:358191 feces adult twins and mothers; TS9 clone TS9_a04e02 FJ3723
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AY977819.1 gg_id:116949 human cecum mucosal biopsy clone LF12 AY9778
EU764742.1 gg_id:317221 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2 EU7647
GU269544.1 gg_id:580185 Lactobacillus rogosae str. ATCC 27753 GU269
FJ364997.1 gg_id:361723 feces adult twins and mothers; TS1 clone TS1_a01f05 FJ3649
AF371643.1 gg_id:46667 swine intestine clone p-268-o5 AF3716
AF371645.1 gg_id:33320 swine intestine clone p-1692-b3 AF3716
EU763400.1 gg_id:306126 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A4 EU7634
GQ079268.1 gg_id:403144 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1230e1 GQ079
EU775973.1 gg_id:350865 Spotted hyena feces clone HY2_d06_1 EU7759
EU763204.1 gg_id:316227 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A9 EU7632
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AY981468.1 gg_id:118941 human sigmoid colon mucosal biopsy clone L567 AY9814
EU763791.1 gg_id:337443 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A5 EU7637
EU763637.1 gg_id:336435 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A4 EU7636
DQ797159.1 gg_id:181148 human fecal clone RL386_aao87f12 DQ797
EF405098.1 gg_id:213526 human fecal clone SJTU_G_07_89 EF4050
EU776399.1 gg_id:323020 Red Kangaroo feces clone KO2_aai17c03 EU7763
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EU764099.1 gg_id:320038 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A5 EU7640

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EU764783.1 gg_id:348687 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2 EU764
EF403988.1 gg_id:216944 human fecal clone SJTU_C_03_25 EF4039
EF098210.1 gg_id:188538 mouse cecum clone SWPT14_aaa03b02 EF0982
EU457079.1 gg_id:315578 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU457
EU006207.1 gg_id:235351 Salmonella enterica serovar typhimurium exploits inflammation compete intestinal r EU006
EF099065.1 gg_id:197605 mouse cecum clone SWPT2_aaa01g04 EF0990
EU503939.1 gg_id:261265 cecal contents Mus musculus strain C57BL/6J; CRWD4 clone CRWD4_aaa03a04 EU5039
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GU304566.1 gg_id:538862 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU304
EU381462.1 gg_id:262031 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid EU381
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GU302622.1 gg_id:533634 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU302
EU843160.1 gg_id:313325 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
GQ000726.1 gg_id:469291 Topographical and Temporal Human Skin Microbiome skin interdigital web space cl GQ000
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NR_029097.1 gg_id:546988 Oribacterium sinus str. AIP 354.02; CIP 107991 NR_02
FJ577249.2 gg_id:571357 Oribacterium sp. oral taxon 078 str. F0262 FJ5772
FJ557800.1 gg_id:524676 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5578
AF481222.1 gg_id:55615 oral endodontic infection clone MCE10_236 AF481
EU557017.1 gg_id:343309 Detection microorganisms involved infectious endocarditis cultivation techniques inf EU557
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FJ557719.1 gg_id:528375 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5577
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AJ428549.1 gg_id:18666 Pseudobutyrivibrio ruminis str. JK 626 AJ4285
U77337.1 gg_id:14054 Butyrivibrio fibrisolvens str. AR27 U7733
AY347530.1 gg_id:92464 Butyrivibrio fibrisolvens str. 0/10 AY3475
AB004910.1 gg_id:14048 Butyrivibrio fibrisolvens str. T63 Bovine rumen AB0049
AF202262.1 gg_id:26725 Pseudobutyrivibrio ruminis str. pC-XS7 AF2022
EU259460.1 gg_id:252825 Rumen yak (Bos grunniens) sequences rumen fluid clone YRC84 EU2594
AB009190.1 gg_id:14062 rumen clone RFN34 bacterium AB0091
EU850527.1 gg_id:314838 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF314 EU8505
AF202260.1 gg_id:19835 Pseudobutyrivibrio ruminis str. pC-XS2 AF2022
AB494819.1 gg_id:532771 Fibrobacter succinogenes dominated consortium on hay stems sheep rumen clone A AB4948
EU381773.1 gg_id:261201 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU381

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DQ326446.1 gg_id:147832 Metagenomic gut microbiome healthy human stool clone C516 DQ326
EU850564.1 gg_id:316947 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF374 EU850
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DQ673524.1 gg_id:164682 rumen fluid clone GRC59 DQ673
AF264034.1 gg_id:36852 Butyrivibrio cf. fibrisolvens EAT6 AF2640
EF400193.1 gg_id:206647 human fecal clone SJTU_E_10_11 EF4001
EU381442.1 gg_id:266929 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid EU3814
AF202261.1 gg_id:74850 Pseudobutyrivibrio ruminis str. pC-XS6 AF2022
AY699284.1 gg_id:102017 Pseudobutyrivibrio ruminis M80 AY6992
AJ428550.1 gg_id:21769 Pseudobutyrivibrio xylanivorans str. JK 23/2 AJ4285
AY699285.1 gg_id:102170 Pseudobutyrivibrio ruminis L4 AY6992
EU381523.1 gg_id:263930 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid EU3815
AY981718.1 gg_id:122818 human sigmoid colon mucosal biopsy clone LA93 AY9817
GQ079203.1 gg_id:440226 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1229g GQ079
EU466812.1 gg_id:301799 African elephant feces clone AFEL2_aao29g08 EU4668
DQ808014.1 gg_id:191640 human fecal clone RL180_aan70f09 DQ808
FJ363716.1 gg_id:366125 feces adult twins and mothers; TS14 clone TS14_a02d10 FJ3637
FJ364199.1 gg_id:364692 feces adult twins and mothers; TS150 clone TS150_a04b04 FJ3641
FJ364099.1 gg_id:364744 feces adult twins and mothers; TS150 clone TS150_a03a03 FJ3640
AY978397.1 gg_id:122629 human transverse colon mucosal biopsy clone F381 AY9783
FJ368518.1 gg_id:361275 feces adult twins and mothers; TS49 clone TS49_a01c08 FJ3685
DQ801440.1 gg_id:187047 human fecal clone RL388_aao95e10 DQ801
DQ795403.1 gg_id:175682 human fecal clone RL178_aah53h10 DQ795
FJ370978.1 gg_id:358935 feces adult twins and mothers; TS5 clone TS5_a03e04 FJ3709
FJ364642.1 gg_id:364428 feces adult twins and mothers; TS19 clone TS19_a01d02 FJ3646
DQ794462.1 gg_id:198095 human fecal clone RL197_aah88b11 DQ794
FJ684267.1 gg_id:524363 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6842
FJ363938.1 gg_id:365290 feces adult twins and mothers; TS150 clone TS150_a01b05 FJ3639
DQ795520.1 gg_id:180861 human fecal clone RL178_aan65f01 DQ795

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FJ679964.1 gg_id:529974 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6799
AY976130.1 gg_id:117542 human ascending colon mucosal biopsy clone LV14 AY976
FJ371875.1 gg_id:357002 feces adult twins and mothers; TS8 clone TS8_a03c02 FJ3718
DQ808157.1 gg_id:187482 human fecal clone RL180_aao73c12 DQ808
AY979857.1 gg_id:122721 human rectum mucosal biopsy clone E057 AY979
DQ794838.1 gg_id:177582 human fecal clone RL310_aam37a02 DQ794
DQ800915.1 gg_id:194884 human fecal clone RL387_aao89c04 DQ800
FJ364158.1 gg_id:362914 feces adult twins and mothers; TS150 clone TS150_a03f08 FJ3641
EU764351.1 gg_id:334650 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1 EU764
DQ805790.1 gg_id:198020 human fecal clone RL306aal91b02 DQ805
FJ371251.1 gg_id:363990 feces adult twins and mothers; TS6 clone TS6_a02g04 FJ3712
FJ369440.1 gg_id:360757 feces adult twins and mothers; TS50 clone TS50_a04e07 FJ3694
FJ371774.1 gg_id:367085 feces adult twins and mothers; TS8 clone TS8_a02a10 FJ3717
FJ364188.1 gg_id:370117 feces adult twins and mothers; TS150 clone TS150_a04a04 FJ3641
EU767090.1 gg_id:327648 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU767
EU767068.1 gg_id:349303 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU767
DQ801829.1 gg_id:190224 human fecal clone RL201_aai47d05 DQ801
DQ798542.1 gg_id:192358 human fecal clone RL181_aan98a06 DQ798
FJ684023.1 gg_id:530357 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6840
DQ802220.1 gg_id:185239 human fecal clone RL241_aaj04f07 DQ802
FJ684345.1 gg_id:522356 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6843
EU764528.1 gg_id:318888 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1 EU764
EU466840.1 gg_id:291245 African elephant feces clone AFEL2_aao30b12 EU466
DQ794811.1 gg_id:181538 human fecal clone RL240_aaj32f08 DQ794
EU763453.1 gg_id:306351 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A4 EU763
FJ365494.1 gg_id:360494 feces adult twins and mothers; TS20 clone TS20_a03e08 FJ3654
EU766711.1 gg_id:322225 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU766
DQ327015.1 gg_id:146118 Metagenomic gut microbiome healthy human stool clone E516 DQ327
DQ802105.1 gg_id:195859 human fecal clone RL241_aaj03b06 DQ802
DQ795257.1 gg_id:196798 human fecal clone RL178_aah52b06 DQ795
DQ824892.1 gg_id:198763 human fecal clone RL185_aao70f03 DQ824
FJ367156.1 gg_id:367005 feces adult twins and mothers; TS28 clone TS28_a04b08 FJ3671
DQ809314.1 gg_id:192285 human fecal clone RL184_aah19b02 DQ809
EU771586.1 gg_id:304401 African elephant feces clone AFEL2_aao31f01 EU771
FJ366967.1 gg_id:368053 feces adult twins and mothers; TS28 clone TS28_a01h06 FJ3669
DQ795483.1 gg_id:193808 human fecal clone RL178_aah54h08 DQ795
EU768273.1 gg_id:328685 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C4 EU768
GQ038693.1 gg_id:399803 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu521f01 GQ038
EU762799.1 gg_id:303965 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A3 EU762
EU767159.1 gg_id:352608 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU767

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FM873062.1 gg_id:369242 occupant source house floor dust clone FC01F07 FM873
FJ685466.1 gg_id:514531 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6854
FJ367319.1 gg_id:366355 feces adult twins and mothers; TS29 clone TS29_a02b03 FJ3673
EU530216.1 gg_id:260086 mucosa adherent and invasive microbes profile adenoma colorectal cancer clone M1 EU530
EU531915.1 gg_id:266916 Predominant role host genetics controlling gut microbiota FMF remission stool clone EU531
EU762836.1 gg_id:325955 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU7628
EU767257.1 gg_id:322662 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C EU767
EU768525.1 gg_id:312541 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C EU7685
AF371600.1 gg_id:73370 swine intestine clone p-1701-b3 AF3716
GQ129843.1 gg_id:462891 Genetic inventory 'JPL-SAF' during MSL mission spacecraft assembly clean room floc GQ129
DQ801833.1 gg_id:175994 human fecal clone RL201_aai47d10 DQ801
FJ370262.1 gg_id:363790 feces adult twins and mothers; TS56 clone TS56_a02e10 FJ3702
DQ806829.1 gg_id:189007 human fecal clone RL198_aaj73e06 DQ806
EU466963.1 gg_id:294109 African elephant feces clone AFEL2_aao31h07 EU466
FJ678204.1 gg_id:522117 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6782
FJ365454.1 gg_id:365282 feces adult twins and mothers; TS20 clone TS20_a03b01 FJ3654
FJ371131.1 gg_id:360819 feces adult twins and mothers; TS6 clone TS6_a01c10 FJ3711
FJ363291.1 gg_id:360701 feces adult twins and mothers; TS149 clone TS149_a01e06 FJ3632
DQ825097.1 gg_id:193400 human fecal clone RL185_aan85d02 DQ825
DQ795533.1 gg_id:187545 human fecal clone RL178_aan65g10 DQ795
DQ802108.1 gg_id:182412 human fecal clone RL241_aaj03b10 DQ802
FJ370203.1 gg_id:365078 feces adult twins and mothers; TS56 clone TS56_a01g02 FJ3702
DQ807826.1 gg_id:183743 human fecal clone RL180_aah37f09 DQ807
AY980662.1 gg_id:126910 human rectum mucosal biopsy clone LL61 AY980
DQ326747.1 gg_id:145280 Metagenomic gut microbiome healthy human stool clone E207 DQ326
FJ364366.1 gg_id:362761 feces adult twins and mothers; TS15 clone TS15_a02b01 FJ3643
DQ808385.1 gg_id:182934 human fecal clone RL180_aao76a03 DQ808
FJ366984.1 gg_id:369024 feces adult twins and mothers; TS28 clone TS28_a02b03 FJ3669
DQ326692.1 gg_id:148261 Metagenomic gut microbiome healthy human stool clone E143 DQ326
DQ905879.1 gg_id:170118 human fecal clone 29c-a2 DQ905
FJ678682.1 gg_id:527684 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6786
DQ795650.1 gg_id:191147 human fecal clone RL178_aan67g05 DQ795
FJ684683.1 gg_id:520217 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6846
DQ805854.1 gg_id:176658 human fecal clone RL306aal91h07 DQ805
FJ369457.1 gg_id:365386 feces adult twins and mothers; TS50 clone TS50_a04g06 FJ3694
EU768472.1 gg_id:309993 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C EU768
DQ825093.1 gg_id:181338 human fecal clone RL185_aan85c09 DQ825
DQ808391.1 gg_id:192447 human fecal clone RL180_aao76a09 DQ808
FJ679037.1 gg_id:516514 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6790
DQ800966.1 gg_id:194840 human fecal clone RL387_aao90a06 DQ800
DQ905661.1 gg_id:168592 human fecal clone 014C-D7 DQ905

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k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

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FJ685051.1 gg_id:524554 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6850
FJ364930.1 gg_id:361763 feces adult twins and mothers; TS19 clone TS19_a04h06 FJ3649
FJ365815.1 gg_id:368017 feces adult twins and mothers; TS21 clone TS21_a03d05 FJ3658
FJ364034.1 gg_id:358949 feces adult twins and mothers; TS150 clone TS150_a02b12 FJ3640
FJ365849.1 gg_id:363597 feces adult twins and mothers; TS21 clone TS21_a03g07 FJ3658
DQ801961.1 gg_id:194918 human fecal clone RL241_aaj01a10 DQ801
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DQ795543.1 gg_id:197014 human fecal clone RL178_aan65h12 DQ795
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DQ795387.1 gg_id:196516 human fecal clone RL178_aah53g02 DQ795
FJ679566.1 gg_id:518807 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6795
EU778355.1 gg_id:352864 feces clone RL388_aao93b11 EU778
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DQ795642.1 gg_id:185901 human fecal clone RL178_aan67f02 DQ795
FJ369224.1 gg_id:366354 feces adult twins and mothers; TS50 clone TS50_a01g03 FJ3692
FJ369777.1 gg_id:358289 feces adult twins and mothers; TS51 clone TS51_a04f10 FJ3697
DQ327557.1 gg_id:146527 Metagenomic gut microbiome healthy human stool clone EB40 DQ327
FJ367937.1 gg_id:359488 feces adult twins and mothers; TS30 clone TS30_a01d07 FJ3679
DQ905520.1 gg_id:173210 human fecal clone 014-f31 DQ905
DQ806541.1 gg_id:179229 human fecal clone RL186_aao45h03 DQ806
FJ369536.1 gg_id:361729 feces adult twins and mothers; TS51 clone TS51_a01g02 FJ3695
DQ802070.1 gg_id:175760 human fecal clone RL241_aaj02f12 DQ802
FJ367978.1 gg_id:359012 feces adult twins and mothers; TS30 clone TS30_a02b01 FJ3679
FJ364903.1 gg_id:364092 feces adult twins and mothers; TS19 clone TS19_a04e11 FJ3649
DQ905882.1 gg_id:168946 human fecal clone 29c-b1 DQ905
FJ368551.1 gg_id:368217 feces adult twins and mothers; TS49 clone TS49_a01f10 FJ3685
EU466961.1 gg_id:296786 African elephant feces clone AFEL2_aao31h05 EU466
AY981367.1 gg_id:119815 human sigmoid colon mucosal biopsy clone G390 AY9813
DQ794832.1 gg_id:177312 human fecal clone RL240_aaj32h08 DQ794
DQ795401.1 gg_id:179074 human fecal clone RL178_aah53h06 DQ795
DQ807853.1 gg_id:198176 human fecal clone RL180_aah38a07 DQ807
EU768747.1 gg_id:352627 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C5 EU768
FJ685239.1 gg_id:517956 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6852
FJ679585.1 gg_id:523170 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6795
DQ326759.1 gg_id:150073 Metagenomic gut microbiome healthy human stool clone E221 DQ326
EU767099.1 gg_id:323352 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU767
DQ905498.1 gg_id:164993 human fecal clone 014-d10 DQ905

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DQ905630.1 gg_id:162644 human fecal clone 014C-A5 DQ905
FJ685450.1 gg_id:521707 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6854
DQ808230.1 gg_id:186955 human fecal clone RL180_aao74b09 DQ808
DQ798354.1 gg_id:194115 human fecal clone RL181_aah41d07 DQ798
FJ364703.1 gg_id:360709 feces adult twins and mothers; TS19 clone TS19_a02a08 FJ3647
DQ825327.1 gg_id:180271 human fecal clone RL185_aan88f05 DQ825
EU762972.1 gg_id:329548 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU762
FJ364641.1 gg_id:367198 feces adult twins and mothers; TS19 clone TS19_a01d01 FJ3646
FJ369275.1 gg_id:369410 feces adult twins and mothers; TS50 clone TS50_a02d04 FJ3692
DQ806442.1 gg_id:175827 human fecal clone RL186_aan92e03 DQ806
FJ372329.1 gg_id:362286 feces adult twins and mothers; TS9 clone TS9_a04d01 FJ3723
FJ673905.1 gg_id:520426 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6739
AY983645.1 gg_id:124589 human descending colon mucosal biopsy clone NP02 AY983
DQ802190.1 gg_id:186848 human fecal clone RL241_aaj04c05 DQ802
DQ794617.1 gg_id:181590 human fecal clone RL240_aaj30c10 DQ794
EU768411.1 gg_id:316275 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C EU768
DQ802179.1 gg_id:177125 human fecal clone RL241_aaj04b03 DQ802
FJ363350.1 gg_id:365129 feces adult twins and mothers; TS149 clone TS149_a02c01 FJ3633
FJ364057.1 gg_id:367480 feces adult twins and mothers; TS150 clone TS150_a02e02 FJ3640
DQ824774.1 gg_id:180624 human fecal clone RL185_aao69b01 DQ824
FJ678132.1 gg_id:509736 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6781
GQ079253.1 gg_id:400680 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1230d GQ079
DQ795352.1 gg_id:186105 human fecal clone RL178_aah53c10 DQ795
AY985878.1 gg_id:116625 human stool clone D156 AY985
DQ805494.1 gg_id:178281 human fecal clone RL203_aai63d06 DQ805
AY976767.1 gg_id:124156 human cecum mucosal biopsy clone K370 AY976
DQ806036.1 gg_id:175467 human fecal clone RL186_aah60c05 DQ806
DQ795457.1 gg_id:180457 human fecal clone RL178_aah54f01 DQ795
DQ801712.1 gg_id:193745 human fecal clone RL201_aai45h04 DQ801
EU762504.1 gg_id:317649 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU762
DQ326990.1 gg_id:146423 Metagenomic gut microbiome healthy human stool clone E487 DQ326
DQ798642.1 gg_id:198695 human fecal clone RL181_aan99d10 DQ798
DQ905512.1 gg_id:170573 human fecal clone 014-e5 DQ905
AY980949.1 gg_id:117339 human rectum mucosal biopsy clone V010 AY980
DQ802310.1 gg_id:189471 human fecal clone RL188_aah15h07 DQ802
DQ795477.1 gg_id:194671 human fecal clone RL178_aah54h01 DQ795
FJ684922.1 gg_id:511827 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6849
DQ800950.1 gg_id:197252 human fecal clone RL387_aao89g11 DQ800
DQ327093.1 gg_id:145310 Metagenomic gut microbiome healthy human stool clone E608 DQ327
FJ368960.1 gg_id:365060 feces adult twins and mothers; TS4 clone TS4_a02f01 FJ3689
DQ905122.1 gg_id:165496 human fecal clone 002C-c11 DQ905

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FJ684593.1 gg_id:510279 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6845
EU466766.1 gg_id:290571 African elephant feces clone AFEL2_aao29b12 EU466
DQ801365.1 gg_id:189974 human fecal clone RL388_aao94e07 DQ801
DQ798551.1 gg_id:187599 human fecal clone RL181_aan98b07 DQ798
FJ367608.1 gg_id:362114 feces adult twins and mothers; TS2 clone TS2_a01e04 FJ3676
FJ365782.1 gg_id:369492 feces adult twins and mothers; TS21 clone TS21_a03a01 FJ3657
FJ680167.1 gg_id:524523 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6801
EU763571.1 gg_id:339729 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A4 EU763
DQ805954.1 gg_id:198934 human fecal clone RL186_aah59b07 DQ805
FJ370172.1 gg_id:357262 feces adult twins and mothers; TS56 clone TS56_a01c07 FJ3701
EU530175.1 gg_id:259373 mucosa adherent and invasive microbes profile adenoma colorectal cancer clone M1 EU530
FJ684449.1 gg_id:525584 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6844
DQ802659.1 gg_id:184827 human fecal clone RL188_aan94g11 DQ802
EU466978.1 gg_id:302677 African elephant feces clone AFEL2_aao32c01 EU466
EU778085.1 gg_id:341146 feces clone RL388_aao93c02 EU778
DQ905692.1 gg_id:162699 human fecal clone 014C-G9 DQ905
DQ798526.1 gg_id:192445 human fecal clone RL181_aan97g10 DQ798
DQ802667.1 gg_id:190315 human fecal clone RL188_aan94h10 DQ802
FJ369582.1 gg_id:359744 feces adult twins and mothers; TS51 clone TS51_a02c06 FJ3695
DQ806738.1 gg_id:197999 human fecal clone RL186_aao48b06 DQ806
FJ364203.1 gg_id:362529 feces adult twins and mothers; TS150 clone TS150_a04b08 FJ3642
FJ676724.1 gg_id:518187 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6767
DQ801645.1 gg_id:195963 human fecal clone RL201_aai45a02 DQ801
DQ807759.1 gg_id:184100 human fecal clone RL180_aah36h04 DQ807
DQ802206.1 gg_id:177793 human fecal clone RL241_aaj04d12 DQ802
FJ370216.1 gg_id:358910 feces adult twins and mothers; TS56 clone TS56_a01h05 FJ3702
GQ042977.1 gg_id:416953 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1011f GQ042
FJ368587.1 gg_id:358837 feces adult twins and mothers; TS49 clone TS49_a02a10 FJ3685
DQ793232.1 gg_id:179396 human fecal clone RL199_aaj41b02 DQ793
DQ802375.1 gg_id:190144 human fecal clone RL188_aah16h03 DQ802
FJ682654.1 gg_id:517334 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6826
DQ801699.1 gg_id:179678 human fecal clone RL201_aai45f09 DQ801
DQ801830.1 gg_id:197323 human fecal clone RL201_aai47d07 DQ801
DQ806212.1 gg_id:199111 human fecal clone RL186_aah62g01 DQ806
DQ806685.1 gg_id:184421 human fecal clone RL186_aao47e09 DQ806
FJ370817.1 gg_id:362130 feces adult twins and mothers; TS5 clone TS5_a01f03 FJ3708
DQ809761.1 gg_id:190930 human fecal clone RL184_aan83g09 DQ809
EU466896.1 gg_id:300009 African elephant feces clone AFEL2_aao31a06 EU466
DQ804763.1 gg_id:187743 human fecal clone RL187_aao72d07 DQ804
FJ365693.1 gg_id:367779 feces adult twins and mothers; TS21 clone TS21_a01h06 FJ3656

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FJ685440.1 gg_id:512889 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6854
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FJ680145.1 gg_id:523776 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6801
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FJ364097.1 gg_id:363592 feces adult twins and mothers; TS150 clone TS150_a03a01 FJ3640
DQ798013.1 gg_id:197372 human fecal clone RL302_aal94e08 DQ798
AY978123.1 gg_id:124624 human cecum mucosal biopsy clone LI93 AY978
DQ808367.1 gg_id:190580 human fecal clone RL180_aao75g07 DQ808
FJ368631.1 gg_id:360078 feces adult twins and mothers; TS49 clone TS49_a02f01 FJ3686
FJ368860.1 gg_id:369361 feces adult twins and mothers; TS4 clone TS4_a01d11 FJ3688
EU466855.1 gg_id:297190 African elephant feces clone AFEL2_aao30d07 EU466
DQ801237.1 gg_id:198348 human fecal clone RL116_aaf02b11 DQ801
FJ363362.1 gg_id:369270 feces adult twins and mothers; TS149 clone TS149_a02d02 FJ3633
DQ810154.1 gg_id:190787 human fecal clone RL184_aao68f08 DQ810
EU762167.1 gg_id:324760 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU762
FJ366995.1 gg_id:363238 feces adult twins and mothers; TS28 clone TS28_a02c02 FJ3669
FJ684040.1 gg_id:512570 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6840
FJ364786.1 gg_id:367532 feces adult twins and mothers; TS19 clone TS19_a03b03 FJ3647
DQ326959.1 gg_id:145511 Metagenomic gut microbiome healthy human stool clone E452 DQ326
DQ804771.1 gg_id:176789 human fecal clone RL187_aao72e04 DQ804
FJ682239.1 gg_id:517986 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6822
DQ794822.1 gg_id:196420 human fecal clone RL240_aaj32g10 DQ794
DQ806119.1 gg_id:198071 human fecal clone RL186_aah61d09 DQ806
FJ367199.1 gg_id:357309 feces adult twins and mothers; TS28 clone TS28_a04f10 FJ3671
GQ079144.1 gg_id:414860 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1229a GQ079
DQ802617.1 gg_id:192223 human fecal clone RL188_aan94b08 DQ802
DQ824777.1 gg_id:197066 human fecal clone RL185_aao69b04 DQ824
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FJ365286.1 gg_id:360736 feces adult twins and mothers; TS20 clone TS20_a01b03 FJ3652
AY977654.1 gg_id:124009 human cecum mucosal biopsy clone LD06 AY977

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s__Eubacterium rectale	17988
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s__Eubacterium rectale	18009
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FJ370282.1 gg_id:367961 feces adult twins and mothers; TS56 clone TS56_a02g11 FJ3702
FJ367008.1 gg_id:369749 feces adult twins and mothers; TS28 clone TS28_a02d05 FJ3670
FJ363179.1 gg_id:359795 feces adult twins and mothers; TS148 clone TS148_a04b01 FJ3631
FJ677840.1 gg_id:526445 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6778
FJ676810.1 gg_id:521922 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6768
DQ798572.1 gg_id:199615 human fecal clone RL181_aan98d10 DQ798
GQ009488.1 gg_id:500178 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw77 GQ009
EU466856.1 gg_id:302746 African elephant feces clone AFEL2_aao30d08 EU466
DQ809092.1 gg_id:178997 human fecal clone RL308_aal81d01 DQ809
EU466947.1 gg_id:294228 African elephant feces clone AFEL2_aao31g01 EU466
FJ371069.1 gg_id:358681 feces adult twins and mothers; TS5 clone TS5_a04e10 FJ3710
FJ369242.1 gg_id:367699 feces adult twins and mothers; TS50 clone TS50_a02a01 FJ3692
FJ370882.1 gg_id:359543 feces adult twins and mothers; TS5 clone TS5_a02d02 FJ3708
DQ806134.1 gg_id:175208 human fecal clone RL186_aah61f08 DQ806
DQ795621.1 gg_id:182233 human fecal clone RL178_aan67b09 DQ795
FJ363075.1 gg_id:358806 feces adult twins and mothers; TS148 clone TS148_a02f09 FJ3630
FJ366916.1 gg_id:365844 feces adult twins and mothers; TS28 clone TS28_a01d01 FJ3669
AY982934.1 gg_id:120934 human descending colon mucosal biopsy clone L134 AY982
DQ805972.1 gg_id:196955 human fecal clone RL186_aah59d07 DQ805
DQ795652.1 gg_id:190044 human fecal clone RL178_aan67g08 DQ795
FJ370353.1 gg_id:368817 feces adult twins and mothers; TS56 clone TS56_a03h02 FJ3703
FJ366299.1 gg_id:365573 feces adult twins and mothers; TS26 clone TS26_a01a07 FJ3662
DQ797907.1 gg_id:194546 human fecal clone RL302_aal93c07 DQ797
FJ370891.1 gg_id:368548 feces adult twins and mothers; TS5 clone TS5_a02d11 FJ3708
DQ804730.1 gg_id:185930 human fecal clone RL187_aao72a03 DQ804
EU762626.1 gg_id:331056 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU762
GQ079168.1 gg_id:409786 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1229d GQ079
DQ806222.1 gg_id:191921 human fecal clone RL186_aah62h03 DQ806
FJ371061.1 gg_id:363317 feces adult twins and mothers; TS5 clone TS5_a04e02 FJ3710
EU467000.1 gg_id:289357 African elephant feces clone AFEL2_aao32e07 EU467
DQ905858.2 gg_id:164028 human fecal clone 29E-g3 DQ905
FJ684372.1 gg_id:522736 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6843
FJ366338.1 gg_id:363459 feces adult twins and mothers; TS26 clone TS26_a01e11 FJ3663
DQ801160.1 gg_id:186450 human fecal clone RL116_aae99d03 DQ801
DQ801269.1 gg_id:184910 human fecal clone RL388_aao93c04 DQ801
DQ798514.1 gg_id:187339 human fecal clone RL181_aan97f09 DQ798
FJ364191.1 gg_id:362123 feces adult twins and mothers; TS150 clone TS150_a04a07 FJ3641
EU763418.1 gg_id:312883 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU763
FJ685507.1 gg_id:515275 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6855
DQ807832.1 gg_id:186292 human fecal clone RL180_aah37g03 DQ807
DQ797700.1 gg_id:198093 human fecal clone RL206_aaj14g09 DQ797

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