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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
FJ815191.2 gg_id:554015 Clostridium sp. str. A6 FJ8151
GU214168.1 gg_id:585365 and biota slimes Canadian paper mills slime mill taken wet section around papermal GU214
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
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EU464172.1 gg_id:289404 reticulated giraffe feces clone gir_aah95e03 EU464
EU473287.1 gg_id:296539 giant panda feces clone GP_1aaa04b12 EU473
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
EU473365.1 gg_id:290438 giant panda feces clone GP_1aaa02b03 EU473
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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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
EU474705.1 gg_id:297093 Indian rhinoceros feces clone IR_aaa03b10 EU474
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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EU463601.1 gg_id:297513 domesticated horse feces clone horsej_aai89e09 EU4636
EU775687.1 gg_id:312729 Hedgehog feces clone HH_aai33b04 EU7756
DQ800651.1 gg_id:179521 human fecal clone RL183_aao01e12 DQ800
FJ682021.1 gg_id:529108 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6820
EU474123.1 gg_id:295402 giant panda feces clone GP_2aaa03d05 EU4741
EU474687.1 gg_id:294960 Indian rhinoceros feces clone IR_aaa04a12 EU4746
FJ683569.1 gg_id:526389 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6835
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 AJ4200
DQ808612.1 gg_id:196359 human fecal clone RL239_aaj10h09 DQ808
FJ678831.1 gg_id:518772 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6788
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EU474011.1 gg_id:298260 giant panda feces clone GP_2aaa03f11 EU4740
EU473282.1 gg_id:294306 giant panda feces clone GP_1aaa02d01 EU4732
EU473204.1 gg_id:288298 giant panda feces clone GP_1aaa04a04 EU4732
EU460605.1 gg_id:296166 polar bear feces clone PB2_aai23c08 EU4606
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 EU4739
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 EU4748
EU773874.1 gg_id:326918 Cheetah feces clone CE3_aai05f04 EU7738
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 EU4708
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 EU4756
EU459347.1 gg_id:296403 hedgehog feces clone HH_aai36h12 EU4593
EU766580.1 gg_id:348914 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU7665
EU468766.1 gg_id:298784 okapi feces clone OK3_c11_1 EU4687
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 EU4607
AB198536.1 gg_id:135311 termite gut wall fraction clone RsW02-061 AB1985
FJ375811.1 gg_id:332200 and prevalence blaTEM genes polar bear feces clone PBF_b42 FJ3758

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EU475640.1 gg_id:302964 babirusa feces clone BARB_aaa01h01 EU475
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EU460503.1 gg_id:287887 polar bear feces clone PB2_aai21g09 EU460
DQ809722.1 gg_id:176126 human fecal clone RL184_aan83c03 DQ809
FJ375922.1 gg_id:309747 and prevalence blaTEM genes polar bear feces clone PBM_b9 FJ3759
AB075771.1 gg_id:46716 Clostridium sordellii str. ATCC 9714 AB075
DQ113681.1 gg_id:130854 dog colon clone C5-09 DQ113
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
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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
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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
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FJ375874.1 gg_id:316634 and prevalence blaTEM genes polar bear feces clone PBF_d11 FJ3758
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EU465318.1 gg_id:299076 lion feces clone LI3_aah75b10 EU4653
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GQ868411.1 gg_id:561998 Fungal and Structure Bioaerosols Pig Stable pig stable bioaerosols clone BBC812 GQ868
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FJ673752.1 gg_id:526864 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6737

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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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EU536029.1 gg_id:287039 profile human microbiota antecubital fossa (inner elbow) skin clone nbt07c07 EU536
DQ196621.2 gg_id:167430 Clostridium sp. str. BL-28 DQ196
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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
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DQ680019.1 gg_id:173147 Clostridium sporogenes str. IBUN 182 DQ680
DQ125892.1 gg_id:134335 uranium contaminated soil clone AKAU4146 DQ125
AJ229230.1 gg_id:35306 anoxic bulk soil flooded rice microcosm clone BSV86 clone AJ2292
AF407686.1 gg_id:60611 Great Artesian Basin clone R10 AF407
AB487192.1 gg_id:572576 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNIRO AB487
AY551086.1 gg_id:102321 Clostridium sp. 17cr1 AY551
AB486869.1 gg_id:558685 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCORC AB486
ABDP01000045.1 gg_id:269119 Clostridium botulinum str. Bf ABDP0
AB487685.1 gg_id:550171 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNSRO AB487
EU537334.1 gg_id:285059 profile human microbiota antecubital fossa (inner elbow) skin clone nbt77a02 EU537
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 AF0925
EF197795.1 gg_id:192526 Clostridium tepidiprofundum str. SG508 EF1977
AF317650.1 gg_id:31985 Clostridium thiosulfatireducens str. Lup21 AF3176
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 AB2183
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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EU468070.1 gg_id:300313 cheetah feces clone CE2_c07_2 EU4680
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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FJ957871.1 gg_id:417891 Clostridium sporogenes str. JPL_17 FJ9578
AB488261.1 gg_id:578160 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSSUR0 AB4882
DQ196626.2 gg_id:167821 Clostridium sp. str. BL-22 DQ196
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EU073771.1 gg_id:248695 Microbial subsurface beds and methanogenic s coal enrichment clone ObedB-8G EU0737
NR_025352.1 gg_id:542995 Clostridium akagii str. CK58; DSM 12554 NR_025
AB239189.1 gg_id:220242 Clone acidigenic anaerobic enriched starch thermophilic methanogenic sludge clone AB2391
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 sediment FJ4559
DQ196619.1 gg_id:168422 Clostridium sp. str. BL-14 DQ196
DQ675453.1 gg_id:172040 Clostridium sp. str. Z-0511 DQ675
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EU878275.1 gg_id:305185 Clostridium sp. Z-0511 str. Z-0511; DSM 18346; VKM B-2402 EU8782
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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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GQ016875.1 gg_id:492792 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw826e0 GQ016
FM872849.1 gg_id:363159 occupant source house floor dust clone FB03F12 FM872
GQ081577.1 gg_id:384208 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1 GQ081
GQ086109.1 gg_id:441795 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ086
GQ044012.1 gg_id:389592 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1017g GQ044
GQ093207.1 gg_id:379387 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw42 GQ093
GQ070149.1 gg_id:449513 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1 GQ070
GQ081583.1 gg_id:383839 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1 GQ081
GQ069472.1 gg_id:463391 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1 GQ069
GQ082189.1 gg_id:457901 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw GQ082
GQ080759.1 gg_id:410475 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1 GQ080
GQ004581.1 gg_id:505083 Topographical and Temporal Human Skin Microbiome skin nare clone nbu60b07c1 GQ004
FJ670693.1 gg_id:514078 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6706
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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NR_026531.1 gg_id:550421 Clostridium ultunense str. BS; DSM 10521 NR_02
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
GQ030213.1 gg_id:446471 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw875a GQ030
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
GQ047161.1 gg_id:393130 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1009d GQ047
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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FJ671406.1 gg_id:522709 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6714
FJ672944.1 gg_id:527947 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6729
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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
FJ960157.1 gg_id:547405 bottlenose dolphin upper respiratory tract blowhole clone D9A4_043 FJ9601
FJ959814.1 gg_id:570444 bottlenose dolphin upper respiratory tract blowhole clone D8A8_165 FJ9598
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
FJ959441.1 gg_id:570348 bottlenose dolphin upper respiratory tract blowhole clone D896_015 FJ9594
FJ960145.1 gg_id:556060 bottlenose dolphin upper respiratory tract blowhole clone D9A4_031 FJ9601
AM176521.1 gg_id:183658 Peptostreptococcus micros gpac022 AM176
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
GQ016336.1 gg_id:493331 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ016
FJ577254.2 gg_id:567933 Peptoniphilus sp. 'Oral Taxon 386' str. F0131 FJ5772
GQ069670.1 gg_id:437159 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw7 GQ069
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GQ004943.1 gg_id:504719 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu65a1 GQ004
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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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
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EU526289.1 gg_id:269603 Peptoniphilus sp. str. WAL 1768N EU5262
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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
FJ825486.1 gg_id:568699 Microbial during start-up mesophilic biogas plant clone 178_BE2_28 FJ8254
AF427155.1 gg_id:34493 Clostridium sp. LTR1 AF4271
AY913838.1 gg_id:136382 fixed-film bioreactor clone MBR283-55 AY9138
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
AY466712.1 gg_id:101098 Clostridiales NS4-1 AY4667
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
GQ461802.1 gg_id:544735 Tissierella praeacuta str. AIP 224.02 GQ461
FN436079.1 gg_id:567822 Molekularbiologische Charakterisierung der bakteriellen Populationsdynamik eines t FN4360
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
FJ672701.1 gg_id:510178 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6727
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
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GQ026805.1 gg_id:447236 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ026
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AM500724.1 gg_id:548585 proof spatial heterogeneity hot composting clone D18 AM500
AB294307.1 gg_id:210515 Microbial structure deep coal seem groundwater clone YWB38 AB2943
EF586050.1 gg_id:240034 Methanol-assimilating anaerobic solid waste digester fed methanol clone M55_D15_ EF5860
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EU289047.1 gg_id:236547 microbiome cloacal openings urogenital and anal tracts tammar wallaby Macropus e EU2890
FJ674639.1 gg_id:526334 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6746
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FM873737.1 gg_id:364028 occupant source house mattress dust clone MA03H02 FM873
GQ004012.1 gg_id:505653 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu67e0 GQ004

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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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AY570635.1 gg_id:108512 biodegraded Canadian oil reservoir clone PL-5B6 AY570
FJ167488.1 gg_id:342752 microbiology granular sludge under autotrophic mixotrophic and heterotrophic denit FJ1674
GQ355042.1 gg_id:583445 structure between two geochemically distinct springs Alum Rock Park spring clone M GQ355
EU662607.1 gg_id:561558 Productivity- Chemolithoautotrophically Based Sulfidic Karst Systems floating microb EU662
AB243990.1 gg_id:245248 Methods Investigate Microbial Niigata oil well clone Niigata-22 AB243
DQ378233.1 gg_id:155716 oil-polluted soil clone M13_Pitesti DQ378
FM205000.1 gg_id:534793 Prokaryote shifts and reductive dehalogenase redundancy response electron donor FM205
GU208315.1 gg_id:584294 Study on Sediment Dongping Lake sediment clone Sef3-12 GU208
AF255644.1 gg_id:41951 EBPR sludge clone Ebpr14 AF255
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 EU794
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 EU234
EU457038.1 gg_id:342368 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU457
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GQ014713.1 gg_id:494953 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw763c GQ014
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EU842915.1 gg_id:335229 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
EU470097.1 gg_id:289968 trancaspain urial feces clone TU1_aaa01h04 EU470
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 EU469
EU462515.1 gg_id:302242 Sumatran orangutan feces clone orang1_aai56b09 EU462
EU468647.1 gg_id:295362 okapi feces clone OK2_d11_1 EU468
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 EU234
EU776276.1 gg_id:319547 Red Kangaroo feces clone KO1_aai42d10 EU776
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 EU344
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 EU463
EU748523.1 gg_id:341085 neotropical folivorous flying bird adult hoatzin crop clone hoa61_11e08 EU748
EU748100.1 gg_id:307485 neotropical folivorous flying bird adult hoatzin crop clone hoa2_42b01 EU748
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
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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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EU775736.1 gg_id:320853 Horse feces clone horsej_aai91a05 EU7757
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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
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FN563391.1 gg_id:572575 Impact changing HRT OLR on prokaryotes involved biomethanizitaion and fuzzy logic FN5633
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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
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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
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EF602919.1 gg_id:228772 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6029
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AB546237.1 gg_id:523930 Acetobacterium carbinolicum str. Mic2c01 AB5462
AB294288.1 gg_id:213453 Microbial structure deep coal seem groundwater clone YWB19 AB2942
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AY185326.1 gg_id:79463 Acetobacterium sp. clone AKS48 AY1853

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X96954.1 gg_id:14237 Acetobacterium woodii str. DSM 1030 X96954
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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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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FJ363787.1 gg_id:364910 feces adult twins and mothers; TS14 clone TS14_a03d01 FJ3637
EU530199.1 gg_id:268713 mucosa adherent and invasive microbes profile adenoma colorectal cancer clone M1 EU530
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
DQ804193.1 gg_id:180310 human fecal clone RL187_aah70b05 DQ804
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 EU762
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 EF404
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 AY976
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 AY982
EU728790.1 gg_id:346709 Ruminococcus sp. str. DJF_VR66 EU728
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 AY978
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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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
DQ807015.1 gg_id:185563 human fecal clone RL244_aaj45b06 DQ807
DQ808195.1 gg_id:183824 human fecal clone RL180_aao73g05 DQ808
DQ810151.1 gg_id:186621 human fecal clone RL184_aao68f05 DQ810
DQ794894.1 gg_id:174093 human fecal clone RL310_aam37f07 DQ794
EU779348.1 gg_id:303897 Somali Wild Ass feces clone WA_aaa02e07 EU779
DQ825110.1 gg_id:197657 human fecal clone RL185_aan85e05 DQ825
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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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
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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
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DQ800660.1 gg_id:185400 human fecal clone RL183_aao01g01 DQ800
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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GQ493873.1 gg_id:571081 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
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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
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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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DQ802572.1 gg_id:182035 human fecal clone RL188_aan93e09 DQ802
DQ803467.1 gg_id:178303 human fecal clone RL251_aaj86b08 DQ803
DQ803488.1 gg_id:194155 human fecal clone RL251_aaj86e01 DQ803
FJ834020.1 gg_id:540096 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P2Q301_49A07 FJ8340
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
DQ804868.1 gg_id:188830 human fecal clone RL385_aao81g08 DQ804
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 AY983
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 EU462
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
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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
DQ810056.1 gg_id:191139 human fecal clone RL184_aao67e12 DQ810
FJ673488.1 gg_id:515386 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6734
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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
DQ808129.1 gg_id:191317 human fecal clone RL180_aao73a06 DQ808
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
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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
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EU776698.1 gg_id:303452 Lion feces clone LI3_aah78h03 EU776

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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
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AY981223.1 gg_id:126425 human sigmoid colon mucosal biopsy clone G186 AY9812
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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
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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
DQ801129.1 gg_id:183212 human fecal clone RL387_aao92f11	DQ801
DQ802249.1 gg_id:189871 human fecal clone RL188_aah15a10	DQ802
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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EU774977.1 gg_id:308504 Flying Fox feces clone FF_-aag84a06 EU774
DQ798974.1 gg_id:198990 human fecal clone RL242_aaj99h04 DQ798
EU466825.1 gg_id:297983 African elephant feces clone AFEL2_aao30a03 EU466
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FJ679697.1 gg_id:516792 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6796
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EU469802.1 gg_id:300479 western lowland gorilla feces clone GOR_aag71c05 EU469
AY442822.1 gg_id:99566 Ruminococcus sp. YE58 AY442
FJ370524.1 gg_id:368808 feces adult twins and mothers; TS57 clone TS57_a02a12 FJ3705
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AM696975.1 gg_id:218995 sequencing libraries indoor dust clone BF0001B001 AM696
FJ363916.1 gg_id:370410 feces adult twins and mothers; TS14 clone TS14_a04h04 FJ3639
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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
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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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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
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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
FJ880700.1 gg_id:420661 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8807
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
FJ370553.1 gg_id:358066 feces adult twins and mothers; TS57 clone TS57_a02d09 FJ3705
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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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
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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
DQ799186.1 gg_id:186828 human fecal clone RL205_aaj18g10 DQ799
DQ805683.1 gg_id:181869 human fecal clone RL306aal89g06 DQ805
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
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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
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AY981581.1 gg_id:126684 human sigmoid colon mucosal biopsy clone L764 AY9815
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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
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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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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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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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FJ680897.1 gg_id:514482 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6808
FJ684208.1 gg_id:521014 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6842
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FJ673417.1 gg_id:521442 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6734
FJ673550.1 gg_id:524819 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6735
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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
DQ810011.1 gg_id:195034 human fecal clone RL184_aao67a08 DQ810
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
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EU844037.1 gg_id:303813 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
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EU842438.1 gg_id:312418 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU8424
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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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FJ172816.1 gg_id:333793 Qinghai Yak Ruminal and Fungi China rumen clone RB-4H4 FJ1728
EU381489.1 gg_id:270511 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid EU3814
FJ833606.1 gg_id:572615 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J1Q401_15G02 FJ8336
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
AB034043.1 gg_id:42145 rumen clone 5C0d-10 AB0340
DQ393009.1 gg_id:154018 on -Arctic peninsula Svalbard Norway determined genes and rumen isolates reindee DQ393
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EU843378.1 gg_id:313437 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8433
EU842593.1 gg_id:317110 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU8425
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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
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DQ393006.1 gg_id:155107 on -Arctic peninsula Svalbard Norway determined genes and rumen isolates reindee DQ393
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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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AF001728.1 gg_id:13939 rumen clone RCP17 AF001
EU748328.1 gg_id:353814 neotropical folivorous flying bird adult hoatzin crop clone hoa5_05b05 EU748
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GU303265.1 gg_id:544781 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU303
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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AJ428552.1 gg_id:29965 Clostridium proteoclasticum str. UC 142 AJ4285
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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GU303019.1 gg_id:556604 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU303
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FJ834274.1 gg_id:584208 Microbial Ecology Crop Folivorous Hoatzin crop contents clone A2Q401_73A10 FJ8342
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FJ833697.1 gg_id:551575 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J2Q101_44D06 FJ8336
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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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DQ806965.1 gg_id:193601 human fecal clone RL198_aaj76c02 DQ806
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
EU455444.1 gg_id:342887 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU455
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
DQ799688.1 gg_id:189413 human fecal clone RL182_aah31c11 DQ799
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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DQ799840.1 gg_id:191687 human fecal clone RL182_aah34g05 DQ799
DQ806982.1 gg_id:179726 human fecal clone RL198_aaj76f07 DQ806
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GQ491160.1 gg_id:544635 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
FJ681675.1 gg_id:513440 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6816
DQ800343.1 gg_id:173900 human fecal clone RL303_aal71h03 DQ800
GQ492164.1 gg_id:534016 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
DQ326040.1 gg_id:202839 Metagenomic distal gut microbiome healthy human stool clone BA08 DQ326
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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FJ681847.1 gg_id:523064 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6818
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
EU459642.1 gg_id:288103 ring-tailed lemur feces clone RT_aai09h02 EU459
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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DQ905410.1 gg_id:163456 human fecal clone 013C-D7 DQ905
GQ016102.1 gg_id:493565 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw GQ016
DQ795830.1 gg_id:189334 human fecal clone RL245_aai83a11 DQ795
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
EF398675.1 gg_id:207959 human fecal clone SJTU_F_05_23 EF3986
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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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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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
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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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EU510719.1 gg_id:269618 cecal contents Mus musculus strain C57BL/6J; WD5 clone WD5_aak39h10 EU5107
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
EF614705.1 gg_id:231146 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o EF6147
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
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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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EF403444.1 gg_id:211174 human fecal clone SJTU_A2_01_30 EF4034
EU508356.1 gg_id:259998 cecal contents Mus musculus strain C57BL/6J; MD27 clone MD27_aaa03f08 EU5083
AY992008.1 gg_id:134549 mouse cecum clone C20_p10 AY9920
EF096052.1 gg_id:180458 mouse cecum clone lean2_aaa03a05 EF0960
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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EU507613.1 gg_id:277365 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_aaa01h09 EU507
GQ867579.1 gg_id:592345 and prevalence blaTEM genes Arctic seals colon content clone CSH88 GQ867
AY978174.1 gg_id:119499 human cecum mucosal biopsy clone LJ63 AY978
DQ507245.1 gg_id:159259 Clostridium sp. str. AIP 321.05 DQ507
EU454693.1 gg_id:329126 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU454
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
FJ363546.1 gg_id:358915 feces adult twins and mothers; TS149 clone TS149_a04e06 FJ3635
EF097971.1 gg_id:176671 mouse cecum clone SWPT12_aaa03b07 EF0979
EU507789.1 gg_id:264568 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_aaa04h05 EU507
EF402492.1 gg_id:213448 human fecal clone SJTU_B_08_62 EF4024
GQ492185.1 gg_id:584906 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
EF099713.1 gg_id:196088 mouse cecum clone SWPT4_aaa03c11 EF0997
GQ493377.1 gg_id:590324 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
EU762698.1 gg_id:307338 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU762
EU504212.1 gg_id:275307 cecal contents Mus musculus strain C57BL/6J; CRWD5 clone CRWD5_aaa04c04 EU504
EU509514.1 gg_id:273179 cecal contents Mus musculus strain C57BL/6J; MD9 clone MD9_aap59g12 EU509
EU509781.1 gg_id:276663 cecal contents Mus musculus strain C57BL/6J; WD10 clone WD10_aak48h05 EU509
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
DQ815462.1 gg_id:162517 mouse cecum clone aab41a11 DQ815
EU939444.1 gg_id:342085 Fecal wild pygmy loris feces clone WF16S_304 EU939
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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EF098230.1 gg_id:193707 mouse cecum clone SWPT14_aaa03d02 EF0982
EU503837.1 gg_id:258710 cecal contents Mus musculus strain C57BL/6J; CRWD4 clone CRWD4_aaa01d01 EU5038
AY991756.1 gg_id:134785 mouse cecum clone C20_c17 AY9917
EF098778.1 gg_id:191205 mouse cecum clone SWPT16_aaa04g08 EF0987
EU510985.1 gg_id:267672 cecal contents Mus musculus strain C57BL/6J; WD6 clone WD6_aak52h01 EU5109
DQ801002.1 gg_id:184794 human fecal clone RL387_aao90g03 DQ801
AY982046.1 gg_id:123136 human sigmoid colon mucosal biopsy clone P435 AY9820
AF371598.1 gg_id:27071 swine intestine clone p-3568-9F3 AF3715
DQ015626.1 gg_id:133410 mouse cecum clone M3_d03_3 DQ015
EU456432.1 gg_id:337754 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H79S EU4564
EU509482.1 gg_id:260401 cecal contents Mus musculus strain C57BL/6J; MD9 clone MD9_aap59a12 EU5094
EU451347.1 gg_id:328290 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H79S EU4513
EU506494.1 gg_id:267348 cecal contents Mus musculus strain C57BL/6J; MD19 clone MD19_aaa02h07 EU5064
AY991972.1 gg_id:133932 mouse cecum clone C20_n14 AY9919
EF098724.1 gg_id:188587 mouse cecum clone SWPT16_aaa04a03 EF0987
GQ867464.1 gg_id:594104 and prevalence blaTEM genes Arctic seals colon content clone CSG33 GQ867
EF098257.1 gg_id:184092 mouse cecum clone SWPT14_aaa03g02 EF0982
EU451916.1 gg_id:351322 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H79S EU4519
GQ867496.1 gg_id:589252 and prevalence blaTEM genes Arctic seals colon content clone CSG68 GQ867
AY976468.1 gg_id:121417 human ascending colon mucosal biopsy clone LZ74 AY9764
EU451067.1 gg_id:333330 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU4510
EU766772.1 gg_id:332005 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU7667
EF096317.1 gg_id:177372 mouse cecum clone obob1_aaa04g09 EF0963
AM932636.1 gg_id:566204 microbiota Toll-like receptor 2 deficient mice exhibits lineage specific modifications AM932
AB075772.1 gg_id:70424 Clostridium sphenoides str. ATCC 19403 AB0757
AM183091.1 gg_id:253465 and its spatial composts compost clone SMC62 AM183
AY305309.1 gg_id:99786 butyrate-producing M62/1 AY3053
DQ905158.1 gg_id:165137 human fecal clone 002C-f12 DQ905
EF096776.1 gg_id:195356 mouse cecum clone SWPT11_aaa04e04 EF0967
EU764399.1 gg_id:321397 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1 EU7643
EF096298.1 gg_id:176380 mouse cecum clone obob1_aaa04d03 EF0962
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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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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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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DQ015254.1 gg_id:132281 mouse cecum clone M2_1b08 DQ015
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
FJ371424.1 gg_id:359347 feces adult twins and mothers; TS6 clone TS6_a04g10 FJ3714
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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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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EU452296.1 gg_id:326031 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU452
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EU455602.1 gg_id:330278 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H79S EU455
EF096300.1 gg_id:198463 mouse cecum clone obob1_aaa04d10 EF0963
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
EU454296.1 gg_id:304917 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU454
EF098140.1 gg_id:174184 mouse cecum clone SWPT14_aaa02b01 EF0981
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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EU503823.1 gg_id:264544 cecal contents Mus musculus strain C57BL/6J; CRWD4 clone CRWD4_aaa01b06 EU503
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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
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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
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AM275397.2 gg_id:231161 fecal microbiota irritable bowel syndrome patients significantly that healthy subject AM275
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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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AB062841.1 gg_id:26279 termite gut homogenate clone BCf8-25 AB0628
AY985062.1 gg_id:126206 human stool clone BA71 AY9850
DQ802414.1 gg_id:180986 human fecal clone RL188_aah17d07 DQ802
DQ799668.1 gg_id:190728 human fecal clone RL305aal88h06 DQ799
FJ676210.1 gg_id:518083 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6762
EF603789.1 gg_id:232266 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6037
AY979358.1 gg_id:127662 human transverse colon mucosal biopsy clone Z695 AY9793
AM943572.1 gg_id:264963 Microbial dolomite formation Lagoa Vermelha Brazil carbonaceous sediments hype AM943
AB192012.1 gg_id:143098 termite gut homogenate clone M2PB4-40 AB1920
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
EF403013.1 gg_id:217103 human fecal clone SJTU_B_15_58 EF4030
AB192210.1 gg_id:141614 termite gut homogenate clone RsTu1-57 AB192
DQ797516.1 gg_id:176077 human fecal clone RL248_aaj00d07 DQ797
FJ678223.1 gg_id:520821 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6782
EU766302.1 gg_id:310536 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU7663
AY571391.1 gg_id:114703 termite gut clone RsaHw471 AY5713
EU511960.1 gg_id:262308 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_aak12a02 EU5119
EU505619.1 gg_id:262012 cecal contents Mus musculus strain C57BL/6J; myd5 clone myd5_aaa03e07 EU5056
DQ905770.2 gg_id:164968 Effect bowel preparation and colonoscopy on post-procedure intestinal microbiota F DQ905
EU344188.1 gg_id:275416 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU3441
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 AB192
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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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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AY981319.1 gg_id:116252 human sigmoid colon mucosal biopsy clone G335 AY9813
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 EU7733
EU466172.1 gg_id:291475 bighorn sheep feces clone BH1_aao27d08 EU4661
EU453188.1 gg_id:328453 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU4531
EU473636.1 gg_id:300295 banteng feces clone BG_aaa02h01.Contig1 EU4736
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 EU5095
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 EU4623
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
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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
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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
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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
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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 EU4670
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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AY981483.1 gg_id:118911 human sigmoid colon mucosal biopsy clone L585 AY9814
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
FJ370085.1 gg_id:369111 feces adult twins and mothers; TS55 clone TS55_a04c05 FJ3700
EU763087.1 gg_id:323066 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A› EU7630
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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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
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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
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FJ370368.1 gg_id:363012 feces adult twins and mothers; TS56 clone TS56_a04a07 FJ3703
DQ795587.1 gg_id:185404 human fecal clone RL178_aan66f07 DQ795
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DQ795236.1 gg_id:179617 human fecal clone RL178_aah51h01 DQ795
DQ806129.1 gg_id:198401 human fecal clone RL186_aah61f03 DQ806
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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DQ327565.1 gg_id:149526 Metagenomic gut microbiome healthy human stool clone EB49 DQ327
DQ795890.1 gg_id:188526 human fecal clone RL245_aai84a10 DQ795
EU763685.1 gg_id:304317 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A4 EU7636
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
FJ368044.1 gg_id:369944 feces adult twins and mothers; TS30 clone TS30_a03c03 FJ3680
DQ824042.1 gg_id:182512 human fecal clone RL204_aaj58e09 DQ824
FJ368850.1 gg_id:358018 feces adult twins and mothers; TS4 clone TS4_a01d01 FJ3688
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
FJ365681.1 gg_id:361061 feces adult twins and mothers; TS21 clone TS21_a01g05 FJ3656
FJ370380.1 gg_id:366297 feces adult twins and mothers; TS56 clone TS56_a04c01 FJ3703
GQ047248.1 gg_id:373386 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1010e GQ047
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
AY981289.1 gg_id:119080 human sigmoid colon mucosal biopsy clone G285 AY9812
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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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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DQ327601.1 gg_id:145551 Metagenomic gut microbiome healthy human stool clone EB91 DQ327
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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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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AY981426.1 gg_id:117920 human sigmoid colon mucosal biopsy clone L493 AY981
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DQ327521.1 gg_id:148085 Metagenomic gut microbiome healthy human stool clone EB01 DQ327
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FJ370968.1 gg_id:365622 feces adult twins and mothers; TS5 clone TS5_a03d05 FJ3709
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DQ809583.1 gg_id:182505 human fecal clone RL184_aan81b10 DQ809
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DQ327280.1 gg_id:145739 Metagenomic gut microbiome healthy human stool clone E824 DQ327
DQ798547.1 gg_id:188522 human fecal clone RL181_aan98b01 DQ798
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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AY981171.1 gg_id:122120 human sigmoid colon mucosal biopsy clone G118 AY981
AY978339.1 gg_id:121348 human transverse colon mucosal biopsy clone F251 AY978
DQ796894.1 gg_id:185065 human fecal clone RL179_aao56a11 DQ796
FJ364707.1 gg_id:360128 feces adult twins and mothers; TS19 clone TS19_a02a12 FJ3647

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EU764211.1 gg_id:327552 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A5 EU764
DQ326455.1 gg_id:150341 Metagenomic gut microbiome healthy human stool clone C530 DQ326
FJ679429.1 gg_id:521644 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6794
DQ807570.1 gg_id:179871 human fecal clone RL307_aam08d05 DQ807
EU762986.1 gg_id:326433 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU762
AY982774.1 gg_id:124418 human descending colon mucosal biopsy clone KZ12 AY982
DQ808101.1 gg_id:175303 human fecal clone RL180_aan72e04 DQ808
FJ367908.1 gg_id:367092 feces adult twins and mothers; TS30 clone TS30_a01a02 FJ3679
AM697416.1 gg_id:222230 sequencing libraries indoor dust clone BF0001D031 AM697
EU766710.1 gg_id:307860 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU766
AY983055.1 gg_id:119891 human descending colon mucosal biopsy clone L291 AY983
GQ897330.1 gg_id:547913 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ897
GQ088675.1 gg_id:404865 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv GQ088
AY978399.1 gg_id:121158 human transverse colon mucosal biopsy clone F383 AY978
FJ682604.1 gg_id:528062 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6826
NZ_ABGC03000041.1 gg_id:469957 Clostridium sp. str. SS2/1 NZ_AB
EU762728.1 gg_id:329976 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU762
DQ807693.1 gg_id:184566 human fecal clone RL180_aah36a07 DQ807
FJ678363.1 gg_id:532186 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6783
DQ795253.1 gg_id:192263 human fecal clone RL178_aah52b02 DQ795
AB486353.1 gg_id:579188 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC AB486
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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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
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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
EU467012.1 gg_id:291448 African elephant feces clone AFEL2_aao32f10 EU467
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
DQ809784.1 gg_id:190984 human fecal clone RL184_aan84b08 DQ809
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
DQ805673.1 gg_id:183956 human fecal clone RL306aal89f08 DQ805
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
EU456777.1 gg_id:351561 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75 EU456

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EU748175.1 gg_id:334172 neotropical folivorous flying bird adult hoatzin crop clone hoa31_49A07.F EU748
FJ364202.1 gg_id:368228 feces adult twins and mothers; TS150 clone TS150_a04b07 FJ3642
GQ896848.1 gg_id:586637 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do GQ896
DQ777934.1 gg_id:167252 rat feces clone R-1199(2) DQ777
EU453406.1 gg_id:354240 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75 EU453
AF371676.1 gg_id:21698 swine intestine clone p-273-o5 AF371
EU765884.1 gg_id:343785 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B EU765
GU302756.1 gg_id:557137 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU302
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EU452252.1 gg_id:319038 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75 EU452
FJ679395.1 gg_id:522077 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6793
EU453604.1 gg_id:353050 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78 EU453
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
AF001721.1 gg_id:14020 rumen clone RC35 AF001
DQ808884.1 gg_id:176257 human fecal clone RL243_aai86e11 DQ808
FJ881245.1 gg_id:430739 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8812
DQ797115.1 gg_id:199013 human fecal clone RL386_aao87b10 DQ797
EF098232.1 gg_id:184535 mouse cecum clone SWPT14_aaa03d04 EF0982
FJ679670.1 gg_id:524122 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6796
FJ681388.1 gg_id:515129 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6813
DQ825335.1 gg_id:178362 human fecal clone RL185_aan88g03 DQ825
EU452326.1 gg_id:333914 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H74 EU452
FJ879304.1 gg_id:411214 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8793
AF371677.1 gg_id:36892 swine intestine clone p-2409-55G5 AF371
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
FJ834237.1 gg_id:567961 Microbial Ecology Crop Folivorous Hoatzin crop contents clone A2Q301_78F10 FJ8342
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
EU462618.1 gg_id:295074 Sumatran orangutan feces clone orang2_aai66b12 EU462
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
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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
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DQ794949.1 gg_id:180449 human fecal clone RL310_aam38c12 DQ794
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DQ824117.1 gg_id:192060 human fecal clone RL204_aaj59e08 DQ824
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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
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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
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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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FJ881307.1 gg_id:430497 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8813
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
AB034069.1 gg_id:23219 rumen clone 5C3d-11 AB0340
DQ794599.1 gg_id:198802 human fecal clone RL240_aaj30b01 DQ794
EU748298.1 gg_id:327252 neotropical folivorous flying bird adult hoatzin crop clone hoa46_69E09 EU7482
EU771329.1 gg_id:346606 Asiatic elephant feces clone AE2_aaa04a09 EU7713
EU766512.1 gg_id:322878 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU7665
EU842325.1 gg_id:341204 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU8423
EU471590.1 gg_id:300123 Asiatic elephant feces clone AE1_aaa03b02 EU4715
EF445162.1 gg_id:209524 rabbit cecum clone NED3B2 EF4451
EU766402.1 gg_id:326396 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU7664
EU748309.1 gg_id:322189 neotropical folivorous flying bird adult hoatzin crop clone hoa46_33A05 EU7483
AY442828.1 gg_id:100506 culturable kangaroo Macropus giganteus Eastern grey Kangaroo forestomach conter AY4428
AY985384.1 gg_id:124285 human stool clone C321 AY9853
AB034025.1 gg_id:25995 rumen clone 4C0d-12 AB0340
EU778254.1 gg_id:354254 feces clone RL387_aao89b04 EU7782
DQ799915.1 gg_id:195196 human fecal clone RL247_aaj21g12 DQ799
EU766173.1 gg_id:324453 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU7661
DQ801370.1 gg_id:182943 human fecal clone RL388_aao94f01 DQ801
DQ801418.1 gg_id:196850 human fecal clone RL388_aao95c06 DQ801
EU764601.1 gg_id:346821 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1 EU7646
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
NZ_AAXA02000006.1 gg_id:270584 Dorea formicigenerans str. ATCC 27755 NZ_AA
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AY976232.1 gg_id:127502 human ascending colon mucosal biopsy clone LW62 AY9762
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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NZ_AAXA02000007.1 gg_id:470229 Dorea formicigenerans str. ATCC 27755 NZ_AA
AY976895.1 gg_id:127343 human cecum mucosal biopsy clone K540 AY9768
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NZ_AAXA02000016.1 gg_id:470230 Dorea formicigenerans str. ATCC 27755 NZ_AA
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AY979418.1 gg_id:118945 human transverse colon mucosal biopsy clone M021 AY9794
EF399958.1 gg_id:215996 human fecal clone SJTU_E_06_56 EF3999
AY979373.1 gg_id:117508 human transverse colon mucosal biopsy clone Z722 AY9793
AY981371.1 gg_id:119304 human sigmoid colon mucosal biopsy clone G395 AY9813
FJ370209.1 gg_id:366476 feces adult twins and mothers; TS56 clone TS56_a01g09 FJ3702
AY983402.1 gg_id:116631 human descending colon mucosal biopsy clone A582 AY9834
AY983685.1 gg_id:118813 human descending colon mucosal biopsy clone NP92 AY9836
AY978285.1 gg_id:127553 human transverse colon mucosal biopsy clone F145 AY9782
FJ362919.1 gg_id:364583 feces adult twins and mothers; TS13 clone TS13_a04g06 FJ3629
AY979732.1 gg_id:118674 human transverse colon mucosal biopsy clone M475 AY9797
AY975739.1 gg_id:115877 human ascending colon mucosal biopsy clone Y189 AY9757
EU530238.1 gg_id:275687 mucosa adherent and invasive microbes adenoma colorectal cancer profile non-ader EU5302
DQ327389.1 gg_id:145925 Metagenomic gut microbiome healthy human stool clone E947 DQ327
AY979917.1 gg_id:123588 human rectum mucosal biopsy clone E239 AY9799
AY983171.1 gg_id:123677 human descending colon mucosal biopsy clone A067 AY9831
AF357564.1 gg_id:70405 mpn-isolate group 16 AF3575
FJ365595.1 gg_id:359355 feces adult twins and mothers; TS20 clone TS20_a04g02 FJ3655
FJ371402.1 gg_id:367855 feces adult twins and mothers; TS6 clone TS6_a04e07 FJ3714
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
AY981721.1 gg_id:120659 human sigmoid colon mucosal biopsy clone LB02 AY9817
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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FJ365317.1 gg_id:366565 feces adult twins and mothers; TS20 clone TS20_a01d12 FJ3653
AY979478.1 gg_id:119402 human transverse colon mucosal biopsy clone M104 AY9794
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
DQ796594.1 gg_id:184918 human fecal clone RL179aan75e08 DQ796
DQ327584.1 gg_id:150493 Metagenomic gut microbiome healthy human stool clone EB69 DQ327
GQ491661.1 gg_id:558736 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
FJ368807.1 gg_id:365239 feces adult twins and mothers; TS49 clone TS49_a04g10 FJ3688
FJ365443.1 gg_id:360796 feces adult twins and mothers; TS20 clone TS20_a02h09 FJ3654
FJ365464.1 gg_id:367576 feces adult twins and mothers; TS20 clone TS20_a03c01 FJ3654
EF401324.1 gg_id:204922 human fecal clone SJTU_D_08_81 EF4013
AY977329.1 gg_id:119218 human cecum mucosal biopsy clone MV44 AY9773
FJ367466.1 gg_id:365137 feces adult twins and mothers; TS29 clone TS29_a03h07 FJ3674
AY981492.1 gg_id:119712 human sigmoid colon mucosal biopsy clone L596 AY9814
AY977315.1 gg_id:116123 human cecum mucosal biopsy clone MV19 AY9773
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AF067413.1 gg_id:14121 Epulopiscium fishelsoni str. Red Sea A1 AF0674
AF067414.1 gg_id:14130 Epulopiscium fishelsoni str. Red Sea A2 AF0674
M99574.1 gg_id:14128 Epulopiscium sp str. morphotype B M9957
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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 EU468
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 EU475
EU470379.1 gg_id:299376 Grevy's zebra feces clone GZ_aaa01c09 EU470
U22332.1 gg_id:14127 "Metabacterium polyspora" U2233
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AB372004.1 gg_id:312201 Eubacterium cellulosolvens str. NE13 AB372
DQ824305.1 gg_id:192536 human fecal clone RL304_aal74c01 DQ824
EU778103.1 gg_id:332313 feces clone RL387_aao89a11.Contig2 EU778
DQ795815.1 gg_id:196272 human fecal clone RL245_aai82g10 DQ795
DQ801788.1 gg_id:197940 human fecal clone RL201_aai46g10 DQ801
DQ805487.1 gg_id:189396 human fecal clone RL203_aai63c09 DQ805

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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
DQ802492.1 gg_id:178191 human fecal clone RL188_aah18d11 DQ802
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
EU771665.1 gg_id:304410 African elephant feces clone AFEL2_aao31f04 EU771
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
DQ794770.1 gg_id:180070 human fecal clone RL240_aaj32b06 DQ794
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
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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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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
DQ807440.1 gg_id:176585 human fecal clone RL307_aam06f06 DQ807
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
DQ904902.1 gg_id:173658 human fecal clone 001C-g7 DQ904
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
DQ802688.1 gg_id:193128 human fecal clone RL188_aan95c02 DQ802
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
FJ369204.1 gg_id:362227 feces adult twins and mothers; TS50 clone TS50_a01e04 FJ3692
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
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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
EU842279.1 gg_id:313296 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
EU843831.1 gg_id:354158 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8438
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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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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
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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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FJ363613.1 gg_id:370350 feces adult twins and mothers; TS14 clone TS14_a01d01 FJ3636
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
AY699277.1 gg_id:106290 Lachnospira pectinoschiza M81 AY6992
EU764725.1 gg_id:331441 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1 EU7647
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
EU762889.1 gg_id:326533 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A> EU7628
EU762896.1 gg_id:346419 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A> EU7628
DQ796214.1 gg_id:181427 human fecal clone RL179_aah23c03 DQ796
EU768290.1 gg_id:308000 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C4 EU7682
EU766675.1 gg_id:324045 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU7666
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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DQ905269.1 gg_id:173712 human fecal clone 013-h10 DQ905
AY984236.1 gg_id:115781 human stool clone B127 AY9842
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
AY985042.1 gg_id:117998 human stool clone BA47 AY9850
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
FJ368313.1 gg_id:368585 feces adult twins and mothers; TS3 clone TS3_a02g09 FJ3683
AY978042.1 gg_id:115457 human cecum mucosal biopsy clone LH86 AY9780
AY985080.1 gg_id:119690 human stool clone BA91 AY9850
DQ809187.1 gg_id:180837 human fecal clone RL308_aal83a10 DQ809
EF402496.1 gg_id:214338 human fecal clone SJTU_B_08_71 EF4024
FJ368843.1 gg_id:367761 feces adult twins and mothers; TS4 clone TS4_a01c05 FJ3688
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
DQ794864.1 gg_id:198909 human fecal clone RL310_aam37c06 DQ794
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
AY984967.1 gg_id:122272 human stool clone B958 AY9849
AY981468.1 gg_id:118941 human sigmoid colon mucosal biopsy clone L567 AY9814
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EU763637.1 gg_id:336435 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A4 EU7636
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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
EF604796.1 gg_id:229388 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6047
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FJ983011.1 gg_id:411796 Aspects Oral Microbiome root canal clone FJ9830
AY278618.1 gg_id:86715 Lachnospiraceae genomosp. C1 AY278
GU304388.1 gg_id:541114 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU304
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
GQ026254.1 gg_id:378008 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl GQ026
GU303144.1 gg_id:560505 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU303
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
FJ557577.1 gg_id:526062 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5575
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
AM697318.1 gg_id:225814 sequencing libraries indoor dust clone BF0002C015 AM697
FJ577261.2 gg_id:566635 Oribacterium sinus str. F0268 FJ5772
FJ557719.1 gg_id:528375 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5577
X95893.1 gg_id:14046 Pseudobutyrivibrio ruminis str. DSM 9787 X95893
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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AY699285.1 gg_id:102170 Pseudobutyrivibrio ruminis L4 AY6992
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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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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
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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
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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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FJ682618.1 gg_id:527893 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6826
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
FJ369277.1 gg_id:360219 feces adult twins and mothers; TS50 clone TS50_a02d06 FJ3692
FJ371240.1 gg_id:367197 feces adult twins and mothers; TS6 clone TS6_a02f02 FJ3712
DQ795543.1 gg_id:197014 human fecal clone RL178_aan65h12 DQ795
FJ369288.1 gg_id:358809 feces adult twins and mothers; TS50 clone TS50_a02e09 FJ3692
FJ678398.1 gg_id:514172 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6783
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
DQ807445.1 gg_id:189908 human fecal clone RL307_aam06f11 DQ807
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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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
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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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DQ794968.1 gg_id:185516 human fecal clone RL310_aam38e10 DQ794
FJ363257.1 gg_id:358710 feces adult twins and mothers; TS149 clone TS149_a01b06 FJ3632
FJ685440.1 gg_id:512889 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6854
DQ904907.1 gg_id:167248 human fecal clone 001C-h12 DQ904
FJ678707.1 gg_id:512903 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6787
FJ680145.1 gg_id:523776 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6801
DQ807568.1 gg_id:181379 human fecal clone RL307_aam08d03 DQ807
FJ676360.1 gg_id:517278 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6763
DQ802464.1 gg_id:188240 human fecal clone RL188_aah18b03 DQ802
DQ806524.1 gg_id:183247 human fecal clone RL186_aao45f09 DQ806
FJ365687.1 gg_id:358679 feces adult twins and mothers; TS21 clone TS21_a01g11 FJ3656
AM697090.1 gg_id:227371 sequencing libraries indoor dust clone BF0002B040 AM697
FJ368351.1 gg_id:357963 feces adult twins and mothers; TS3 clone TS3_a03d01 FJ3683
DQ794647.1 gg_id:186583 human fecal clone RL240_aaj30f05 DQ794
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
DQ801920.1 gg_id:191525 human fecal clone RL201_aai48e03 DQ801
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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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
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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
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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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DQ798746.1 gg_id:182742 human fecal clone RL181_aao00g12 DQ798
FJ371157.1 gg_id:366810 feces adult twins and mothers; TS6 clone TS6_a01f02 FJ3711
FJ365684.1 gg_id:362085 feces adult twins and mothers; TS21 clone TS21_a01g08 FJ3656
DQ806452.1 gg_id:176365 human fecal clone RL186_aan92f10 DQ806
GQ079595.1 gg_id:442940 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1231f0 GQ079
EU768219.1 gg_id:306963 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C4 EU768
DQ327352.1 gg_id:148544 Metagenomic gut microbiome healthy human stool clone E907 DQ327
FJ364209.1 gg_id:369549 feces adult twins and mothers; TS150 clone TS150_a04c03 FJ3642
EU763899.1 gg_id:335439 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A5 EU7638
FJ364351.1 gg_id:358621 feces adult twins and mothers; TS15 clone TS15_a01h08 FJ3643
EU762879.1 gg_id:334484 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A3 EU7628
FJ369459.1 gg_id:370323 feces adult twins and mothers; TS50 clone TS50_a04g08 FJ3694
EU776763.1 gg_id:311423 Mongoose lemur feces clone ML_aaj27a09 EU7767
EU762980.1 gg_id:340350 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A3 EU7629
FJ369896.1 gg_id:360143 feces adult twins and mothers; TS55 clone TS55_a02a07 FJ3698
EU765367.1 gg_id:308641 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B3 EU7653
EU763604.1 gg_id:315672 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A4 EU7636
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FJ369013.1 gg_id:362038 feces adult twins and mothers; TS4 clone TS4_a03c06 FJ3690
FJ364207.1 gg_id:365481 feces adult twins and mothers; TS150 clone TS150_a04c01 FJ3642
FJ368975.1 gg_id:361772 feces adult twins and mothers; TS4 clone TS4_a02g05 FJ3689
FJ371059.1 gg_id:367050 feces adult twins and mothers; TS5 clone TS5_a04d11 FJ3710
DQ808283.1 gg_id:186962 human fecal clone RL180_aao74g07 DQ808
FJ363277.1 gg_id:364103 feces adult twins and mothers; TS149 clone TS149_a01d02 FJ3632
DQ808131.1 gg_id:182892 human fecal clone RL180_aao73a08 DQ808
DQ806615.1 gg_id:197527 human fecal clone RL186_aao46g04 DQ806
DQ325783.1 gg_id:148413 Metagenomic gut microbiome healthy human stool clone B473 DQ325
DQ327426.1 gg_id:148870 Metagenomic gut microbiome healthy human stool clone E985 DQ327
DQ802630.1 gg_id:195582 human fecal clone RL188_aan94c12 DQ802
FJ364463.1 gg_id:368556 feces adult twins and mothers; TS15 clone TS15_a03c06 FJ3644
FJ371335.1 gg_id:364555 feces adult twins and mothers; TS6 clone TS6_a03g03 FJ3713
FJ368262.1 gg_id:364326 feces adult twins and mothers; TS3 clone TS3_a02b08 FJ3682
DQ905146.1 gg_id:161984 human fecal clone 002C-e11 DQ905
DQ806197.1 gg_id:190602 human fecal clone RL186_aah62e05 DQ806
FJ362862.1 gg_id:362903 feces adult twins and mothers; TS13 clone TS13_a04b03 FJ3628
FJ362755.1 gg_id:362203 feces adult twins and mothers; TS13 clone TS13_a02g04 FJ3627
FJ370350.1 gg_id:368308 feces adult twins and mothers; TS56 clone TS56_a03g09 FJ3703
EU763912.1 gg_id:346172 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A5 EU7639
EU766779.1 gg_id:306617 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU7667

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FJ370315.1 gg_id:364928 feces adult twins and mothers; TS56 clone TS56_a03d02 FJ3703
DQ795566.1 gg_id:193977 human fecal clone RL178_aan66d01 DQ795
DQ808026.1 gg_id:193343 human fecal clone RL180_aan70h08 DQ808
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FJ684927.1 gg_id:517856 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6849
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FJ684978.1 gg_id:529927 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6849
FJ369414.1 gg_id:368691 feces adult twins and mothers; TS50 clone TS50_a04b12 FJ3694
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DQ803172.1 gg_id:178123 human fecal clone RL311_aam21e06 DQ803
DQ824944.1 gg_id:176391 human fecal clone RL185_aao71c12 DQ824
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EU466805.1 gg_id:301604 African elephant feces clone AFEL2_aao29g01 EU466
FJ370280.1 gg_id:368376 feces adult twins and mothers; TS56 clone TS56_a02g08 FJ3702
FJ371042.1 gg_id:367397 feces adult twins and mothers; TS5 clone TS5_a04c04 FJ3710
FJ371163.1 gg_id:368473 feces adult twins and mothers; TS6 clone TS6_a01f09 FJ3711
DQ802612.1 gg_id:180645 human fecal clone RL188_aan94b02 DQ802
FJ363008.1 gg_id:365189 feces adult twins and mothers; TS148 clone TS148_a01h01 FJ3630
DQ808019.1 gg_id:190672 human fecal clone RL180_aan70g06 DQ808
DQ809580.1 gg_id:183969 human fecal clone RL184_aan81b05 DQ809
FJ369996.1 gg_id:358126 feces adult twins and mothers; TS55 clone TS55_a03c05 FJ3699
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FJ677317.1 gg_id:519781 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6773
FJ370363.1 gg_id:360803 feces adult twins and mothers; TS56 clone TS56_a03h12 FJ3703
EU466891.1 gg_id:294818 African elephant feces clone AFEL2_aao30h08 EU466
FJ369156.1 gg_id:363988 feces adult twins and mothers; TS4 clone TS4_a04h11 FJ3691
FJ673219.1 gg_id:529666 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6732
FJ678155.1 gg_id:528673 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6781
DQ809907.1 gg_id:187555 human fecal clone RL184_aao65g08 DQ809
FJ684461.1 gg_id:515520 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6844
DQ905807.2 gg_id:164453 human fecal clone 29E-b8 DQ905
DQ804644.1 gg_id:183733 human fecal clone RL187_aao70g09 DQ804
DQ810076.1 gg_id:190298 human fecal clone RL184_aao67g11 DQ810
FJ362918.1 gg_id:358696 feces adult twins and mothers; TS13 clone TS13_a04g05 FJ3629
DQ798438.1 gg_id:193735 human fecal clone RL181_aah42f06 DQ798

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EU768041.1 gg_id:350250 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C4 EU768
DQ794795.1 gg_id:193556 human fecal clone RL240_aaj32d10 DQ794
EU768316.1 gg_id:330961 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C5 EU768
DQ806617.1 gg_id:197873 human fecal clone RL186_aao46g07 DQ806
FJ368207.1 gg_id:368611 feces adult twins and mothers; TS3 clone TS3_a01e03 FJ3682
DQ798454.1 gg_id:189241 human fecal clone RL181_aah42h03 DQ798
DQ798242.1 gg_id:179996 human fecal clone RL181_aah39d05 DQ798
DQ798182.1 gg_id:175518 human fecal clone RL302_aal96e08 DQ798
FJ363366.1 gg_id:360526 feces adult twins and mothers; TS149 clone TS149_a02d06 FJ3633
DQ807352.1 gg_id:178011 human fecal clone RL307_aam05d12 DQ807
DQ805671.1 gg_id:175635 human fecal clone RL306aal89f06 DQ805
DQ801962.1 gg_id:186097 human fecal clone RL241_aaj01a11 DQ801
DQ794835.1 gg_id:176340 human fecal clone RL240_aaj32h11 DQ794
DQ801420.1 gg_id:198605 human fecal clone RL388_aao95c08 DQ801
DQ824792.1 gg_id:197864 human fecal clone RL185_aao69d01 DQ824
DQ825066.1 gg_id:195105 human fecal clone RL185_aao72h10 DQ825
FJ363558.1 gg_id:359682 feces adult twins and mothers; TS149 clone TS149_a04f06 FJ3635
EU728794.1 gg_id:314893 Roseburia sp. str. DJF_VR77 EU728
FJ685213.1 gg_id:516832 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6852
EU531971.1 gg_id:260732 Predominant role host genetics controlling gut microbiota FMF remission stool clone EU531
DQ905089.1 gg_id:166670 human fecal clone 2-002-h1 DQ905
FJ672970.1 gg_id:517938 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6729
DQ797487.1 gg_id:186077 human fecal clone RL248_aaj00a02 DQ797
DQ325547.1 gg_id:145765 Metagenomic gut microbiome healthy human stool clone B003 DQ325
FJ681797.1 gg_id:520892 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6817
DQ825293.1 gg_id:181390 human fecal clone RL185_aan87h10 DQ825
FJ362949.1 gg_id:363026 feces adult twins and mothers; TS148 clone TS148_a01b06 FJ3629
FJ367069.1 gg_id:358597 feces adult twins and mothers; TS28 clone TS28_a03b08 FJ3670
EU768128.1 gg_id:317350 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C4 EU768
EU508660.1 gg_id:261837 cecal contents Mus musculus strain C57BL/6J; MD2 clone MD2_aap36h11 EU508
FJ685484.1 gg_id:514579 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6854
DQ808419.1 gg_id:179885 human fecal clone RL180_aao76d03 DQ808
DQ807601.1 gg_id:177520 human fecal clone RL307_aam08g07 DQ807
FJ685032.1 gg_id:509017 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6850
AF371608.1 gg_id:107098 swine intestine clone p-5-a5 AF371
DQ825299.1 gg_id:177772 human fecal clone RL185_aan88a07 DQ825
AF371610.1 gg_id:26201 swine intestine clone p-969-s962-5 AF371
FJ680909.1 gg_id:514384 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6809
DQ824430.1 gg_id:176014 human fecal clone RL304_aal75h09 DQ824
FJ682651.1 gg_id:512204 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6826

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EU461258.1 gg_id:300235 hamadryas baboon feces clone BAZ_aah91f09 EU461
DQ809931.1 gg_id:182676 human fecal clone RL184_aao66a09 DQ809
FJ679610.1 gg_id:530857 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6796
EU765539.1 gg_id:351850 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B3 EU765
FJ684629.1 gg_id:525474 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6846
FJ679897.1 gg_id:510518 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6798
DQ805120.1 gg_id:193105 human fecal clone RL249_aaj81e02 DQ805
AF371602.1 gg_id:45296 swine intestine clone p-61-a5 AF3716
AY916373.1 gg_id:113909 human stool clone D522 AY9163
EU775400.1 gg_id:313850 Western lowland gorilla feces clone GORSD_2aaa01a04 EU7754
FJ363002.1 gg_id:358798 feces adult twins and mothers; TS148 clone TS148_a01g06 FJ3630
DQ804753.1 gg_id:198208 human fecal clone RL187_aao72c05 DQ804
DQ807158.1 gg_id:196312 human fecal clone RL244_aaj47a03 DQ807
EU762661.1 gg_id:323781 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A3 EU7626
DQ794669.1 gg_id:187633 human fecal clone RL240_aaj30h06 DQ794
DQ532269.1 gg_id:162623 Geographical Variation Microbial Burden and Spacecraft Assembly Johnson Space C DQ532
DQ801408.1 gg_id:197953 human fecal clone RL388_aao95b07 DQ801
DQ808024.1 gg_id:192415 human fecal clone RL180_aan70h06 DQ808
FJ684308.1 gg_id:519190 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6843
FJ681565.1 gg_id:518940 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6815
AM500721.1 gg_id:562038 proof spatial heterogeneity hot composting clone D14 AM500
DQ808441.1 gg_id:195207 human fecal clone RL180_aao76f02 DQ808
GQ448613.1 gg_id:560963 Microbiome neonatal calves: shedding microorganisms fecal clone calf784_6wks_gr GQ448
EU778522.1 gg_id:311704 Red river hog feces clone RRH_aaa04f09 EU7785
FJ371198.1 gg_id:358875 feces adult twins and mothers; TS6 clone TS6_a02a11 FJ3711
EU794281.1 gg_id:316489 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_K16 EU7942
DQ800180.1 gg_id:185651 human fecal clone RL303_aal69c07 DQ800
FJ679371.1 gg_id:526154 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6793
FJ678578.1 gg_id:532316 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6785
DQ803526.1 gg_id:181189 human fecal clone RL251_aaj87a02 DQ803
EU779266.1 gg_id:326170 Trancaspian Urial feces clone TU2_aaa03c05 EU7792
DQ823907.1 gg_id:194053 human fecal clone RL250_aaj80g06 DQ823
FJ685118.1 gg_id:512836 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6851
DQ794531.1 gg_id:195493 human fecal clone RL240_aaj29b12 DQ794
DQ803843.1 gg_id:199643 human fecal clone RL200_aai59a09 DQ803
FJ680496.1 gg_id:522134 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6804
DQ824821.1 gg_id:198616 human fecal clone RL185_aao69f09 DQ824
EU771355.1 gg_id:333279 Asiatic elephant feces clone AE2_aaa01f10 EU7713
GQ448639.1 gg_id:537357 Microbiome neonatal calves: shedding microorganisms fecal clone calf784_6wks_gr GQ448

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DQ794708.1 gg_id:194924 human fecal clone RL240_aaj31d09 DQ794
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FJ679922.1 gg_id:519541 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6799
EU771887.1 gg_id:353124 Southern three-banded armadillo feces clone arma_h05 EU771
AY804148.1 gg_id:109014 Roseburia hominis str. A2-181 AY804
EU761654.1 gg_id:342151 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1 EU761
DQ806172.1 gg_id:187102 human fecal clone RL186_aah62b08 DQ806
EU470290.1 gg_id:290396 Grevy's zebra feces clone GZ_aaa03d08 EU470
FJ683400.1 gg_id:515910 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6834
EU766898.1 gg_id:303749 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU766
FJ365665.1 gg_id:368905 feces adult twins and mothers; TS21 clone TS21_a01e10 FJ3656
EU469042.1 gg_id:302163 Speke's gazelle feces clone SP2_d07_2 EU469
DQ823842.1 gg_id:192656 human fecal clone RL250_aaj79g11 DQ823
DQ824936.1 gg_id:191922 human fecal clone RL185_aao71c02 DQ824
EU776480.1 gg_id:355196 Red Kangaroo feces clone KO1_aai42d01 EU776
FJ679487.1 gg_id:511003 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6794
DQ807467.1 gg_id:190076 human fecal clone RL307_aam06h11 DQ807
EU467554.1 gg_id:303176 southern three-banded armadillo feces clone arma_b02 EU467
FJ683023.1 gg_id:516480 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6830
FJ363524.1 gg_id:369164 feces adult twins and mothers; TS149 clone TS149_a04c03 FJ3635
AF371613.1 gg_id:102506 swine intestine clone p-1590-c5 AF371
FJ678227.1 gg_id:528045 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6782
FJ685493.1 gg_id:524968 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6854
EU475261.1 gg_id:288961 bonobo feces clone BNO_aaa04h02 EU475
DQ810132.1 gg_id:178071 human fecal clone RL184_aao68d09 DQ810
FJ674108.1 gg_id:518613 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6741
FJ676788.1 gg_id:525401 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6767
AF371605.1 gg_id:41673 swine intestine clone p-2176-s959-3 AF371
DQ795660.1 gg_id:198494 human fecal clone RL178_aan67h09 DQ795
FJ684548.1 gg_id:510026 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6845
EU468940.1 gg_id:295804 Speke's gazelle feces clone SP2_f02_1 EU468
FJ369883.1 gg_id:362595 feces adult twins and mothers; TS55 clone TS55_a01h04 FJ3698
DQ904912.1 gg_id:169255 human fecal clone 001C-h7 DQ904
FJ370075.1 gg_id:359007 feces adult twins and mothers; TS55 clone TS55_a04b07 FJ3700
FJ677285.1 gg_id:521162 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6772
AF371616.1 gg_id:50105 swine intestine clone p-2195-s959-3 AF371
FJ684730.1 gg_id:525544 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6847
DQ797220.1 gg_id:185851 human fecal clone RL386_aao88e09 DQ797
FJ371315.1 gg_id:356867 feces adult twins and mothers; TS6 clone TS6_a03e06 FJ3713

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FJ678723.1 gg_id:517172 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6787
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FJ679664.1 gg_id:529516 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6796
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EU764833.1 gg_id:329313 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2 EU7648
FJ678286.1 gg_id:509840 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6782
AM055815.1 gg_id:149843 Roseburia intestinalis str. XB6B4 AM055
FJ684488.1 gg_id:525426 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6844
AF371611.1 gg_id:28914 swine intestine clone p-2418-55G5 AF3716
EU843513.1 gg_id:315537 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8435
AB264068.1 gg_id:187447 Fecal microbial (dugong dugon) determined genes Dugong feces clone dgD-52 AB2640
DQ808335.1 gg_id:184864 human fecal clone RL180_aao75d09 DQ808
EF640148.1 gg_id:254376 pig feces clone lcy29 EF6401
EU775805.1 gg_id:308426 Horse feces clone horsem_aai95b06 EU7758
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FJ675990.1 gg_id:521896 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6759
EU465689.1 gg_id:292399 argali sheep feces clone AS2_aao33e11 EU4656
FJ679322.1 gg_id:524772 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6793
DQ809444.1 gg_id:175532 human fecal clone RL184_aah21a08 DQ809
FJ370372.1 gg_id:359147 feces adult twins and mothers; TS56 clone TS56_a04b02 FJ3703
DQ810104.1 gg_id:194650 human fecal clone RL184_aao68b03 DQ810
FJ365821.1 gg_id:367958 feces adult twins and mothers; TS21 clone TS21_a03d11 FJ3658
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DQ807462.1 gg_id:180878 human fecal clone RL307_aam06h05 DQ807
DQ823759.1 gg_id:179472 human fecal clone RL250_aaj78f11 DQ823
DQ800407.1 gg_id:178751 human fecal clone RL303_aal72g10 DQ800
FJ679215.1 gg_id:509388 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6792
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EU763109.1 gg_id:311820 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A9 EU7631
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EU776429.1 gg_id:347998 Red Kangaroo feces clone KO1_aai41d11 EU7764
FJ364889.1 gg_id:358847 feces adult twins and mothers; TS19 clone TS19_a04d04 FJ3648
FJ679311.1 gg_id:520754 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6793
FJ678871.1 gg_id:513703 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6788
EU765254.1 gg_id:313766 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B3 EU7652
EU469078.1 gg_id:299126 Speke's gazelle feces clone SP3_b01 EU4690
FJ364609.1 gg_id:365492 feces adult twins and mothers; TS19 clone TS19_a01a04 FJ3646

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FJ678840.1 gg_id:518748 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6788
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DQ808114.1 gg_id:197930 human fecal clone RL180_aan72g05 DQ808
DQ808312.1 gg_id:176297 human fecal clone RL180_aao75b06 DQ808
DQ806958.1 gg_id:188023 human fecal clone RL198_aaj76b05 DQ806
DQ804676.1 gg_id:191824 human fecal clone RL187_aao71c03 DQ804
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DQ802458.1 gg_id:178851 human fecal clone RL188_aah18a04 DQ802
DQ799741.1 gg_id:188039 human fecal clone RL182_aah32e04 DQ799
FJ367517.1 gg_id:357232 feces adult twins and mothers; TS29 clone TS29_a04e03 FJ3675
DQ905906.1 gg_id:165146 human fecal clone 29c-e3 DQ905
DQ804408.1 gg_id:190890 human fecal clone RL187_aan79d06 DQ804
EU139255.1 gg_id:245108 Ruminococcus gnavus str. A2 EU139
DQ326730.1 gg_id:146113 Metagenomic gut microbiome healthy human stool clone E185 DQ326
AY976547.1 gg_id:125145 human cecum mucosal biopsy clone K079 AY976
FJ371092.1 gg_id:370360 feces adult twins and mothers; TS5 clone TS5_a04h01 FJ3710
DQ803534.1 gg_id:178103 human fecal clone RL251_aaj87b02 DQ803
FJ370684.1 gg_id:363436 feces adult twins and mothers; TS57 clone TS57_a04a04 FJ3706
FJ978683.1 gg_id:381895 feces clone CL_F_368 FJ9786
FJ370711.1 gg_id:357618 feces adult twins and mothers; TS57 clone TS57_a04c10 FJ3707
FJ371142.1 gg_id:359605 feces adult twins and mothers; TS6 clone TS6_a01d11 FJ3711
GQ001490.1 gg_id:508171 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu173f05 GQ001
GQ492701.1 gg_id:560581 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
GQ492877.1 gg_id:583406 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
EU530390.1 gg_id:264290 mucosa adherent and invasive microbes adenoma colorectal cancer profile non-ader EU530
EU776668.1 gg_id:342397 Lion feces clone LI3_aah76c02 EU776
FJ364832.1 gg_id:358009 feces adult twins and mothers; TS19 clone TS19_a03f10 FJ3648
DQ803563.1 gg_id:198251 human fecal clone RL251_aaj87e03 DQ803
GQ493596.1 gg_id:570712 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
FJ368938.1 gg_id:369562 feces adult twins and mothers; TS4 clone TS4_a02c11 FJ3689
NZ_AAVP02000025.1 gg_id:470974 Ruminococcus torques str. ATCC 27756 NZ_AA
NZ_AAVP02000040.1 gg_id:470983 Ruminococcus torques str. ATCC 27756 NZ_AA
DQ808089.1 gg_id:180432 human fecal clone RL180_aan72c10 DQ808
FJ370299.1 gg_id:363908 feces adult twins and mothers; TS56 clone TS56_a03b03 FJ3702
FJ367673.1 gg_id:358748 feces adult twins and mothers; TS2 clone TS2_a02c03 FJ3676
GQ175509.1 gg_id:592688 Chicken intestinal microbiota modulations various feed supplementations DGGE anc GQ175
DQ327420.1 gg_id:145342 Metagenomic gut microbiome healthy human stool clone E979 DQ327

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AF357572.1 gg_id:71434 mpn-isolate group 24 AF3575
DQ327599.1 gg_id:148987 Metagenomic gut microbiome healthy human stool clone EB87 DQ327
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DQ802435.1 gg_id:175850 human fecal clone RL188_aah17f12 DQ802
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FJ673341.1 gg_id:527086 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6733
FJ372163.1 gg_id:358901 feces adult twins and mothers; TS9 clone TS9_a02d11 FJ3721
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FJ679086.1 gg_id:517721 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6790
EU771983.1 gg_id:332500 Southern three-banded armadillo feces clone arma_aaj55h03 EU7719
GQ493206.1 gg_id:554500 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
FJ366545.1 gg_id:363122 feces adult twins and mothers; TS27 clone TS27_a01a06 FJ3665
FJ367647.1 gg_id:369694 feces adult twins and mothers; TS2 clone TS2_a01h09 FJ3676
DQ803493.1 gg_id:180842 human fecal clone RL251_aaj86e06 DQ803
FJ678322.1 gg_id:517797 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6783
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GQ024140.1 gg_id:485529 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw GQ024
FJ366542.1 gg_id:358321 feces adult twins and mothers; TS27 clone TS27_a01a03 FJ3665
FJ366284.1 gg_id:366435 feces adult twins and mothers; TS25 clone TS25_a04h02 FJ3662
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GQ493221.1 gg_id:547807 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
DQ057412.1 gg_id:136507 chicken ileum/cecum clone oc10 DQ057
FJ364768.1 gg_id:362436 feces adult twins and mothers; TS19 clone TS19_a02h03 FJ3647
AY985538.1 gg_id:123198 human stool clone C514 AY9855
FJ682931.1 gg_id:513285 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6829
GQ491685.1 gg_id:547567 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
AY985811.1 gg_id:120639 human stool clone D066 AY9858

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EU530323.1 gg_id:277190 mucosa adherent and invasive microbes profile adenoma colorectal cancer clone M4 EU5303
FJ366445.1 gg_id:362418 feces adult twins and mothers; TS26 clone TS26_a03d03 FJ3664
EF403738.1 gg_id:216096 human fecal clone SJTU_A2_06_28 EF4037
FJ676553.1 gg_id:519968 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6765
DQ801898.1 gg_id:178400 human fecal clone RL201_aai48c03 DQ801
FJ368926.1 gg_id:369231 feces adult twins and mothers; TS4 clone TS4_a02b11 FJ3689
EU766717.1 gg_id:329034 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU7667
FJ365955.1 gg_id:365845 feces adult twins and mothers; TS25 clone TS25_a01b02 FJ3659
DQ796049.1 gg_id:182889 human fecal clone RL202_aai50g04 DQ796
AY980909.1 gg_id:115735 human rectum mucosal biopsy clone LQ93 AY9809
GQ021410.1 gg_id:488258 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbu27 GQ021
X73443.1 gg_id:14036 Clostridium nexile str. DSM 1787 X73443
DQ327213.1 gg_id:149534 Metagenomic gut microbiome healthy human stool clone E745 DQ327
GQ493793.1 gg_id:551202 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
FJ368206.1 gg_id:369005 feces adult twins and mothers; TS3 clone TS3_a01e02 FJ3682
EU776331.1 gg_id:327642 Red Kangaroo feces clone KO2_aai19a05 EU7763
FJ368881.1 gg_id:358849 feces adult twins and mothers; TS4 clone TS4_a01f08 FJ3688
EU773269.1 gg_id:349002 BigHorn sheep feces clone BH1_aao26g08 EU7732
AY985663.1 gg_id:118706 human stool clone C669 AY9856
DQ798375.1 gg_id:176842 human fecal clone RL181_aah41g02 DQ798
GQ493167.1 gg_id:562750 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
EF398618.1 gg_id:216342 human fecal clone SJTU_F_05_92 EF3986
DQ327425.1 gg_id:145721 Metagenomic gut microbiome healthy human stool clone E984 DQ327
DQ796068.1 gg_id:189296 human fecal clone RL202_aai51a09 DQ796
GQ493326.1 gg_id:542986 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
EU779209.1 gg_id:344114 Trancaspian Urial feces clone TU2_aaa02g10 EU7792
EU467575.1 gg_id:293464 southern three-banded armadillo feces clone arma_a12_1 EU4675
GQ491592.1 gg_id:574834 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
FJ364682.1 gg_id:362668 feces adult twins and mothers; TS19 clone TS19_a01g08 FJ3646
DQ326912.1 gg_id:148744 Metagenomic gut microbiome healthy human stool clone E403 DQ326
EU775324.1 gg_id:310303 Reticulated giraffe feces clone gir_aah93e01 EU7753
GQ493654.1 gg_id:564762 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
DQ808801.1 gg_id:179408 human fecal clone RL243_aai85d10 DQ808
EF025296.1 gg_id:181332 Examination microbial ecology avian vivo bromodeoxyuridine intestine clone B5_N28 EF0252
DQ905636.1 gg_id:162162 human fecal clone 014C-B1 DQ905
DQ905098.1 gg_id:168567 human fecal clone 002C-a10 DQ905
DQ798406.1 gg_id:180049 human fecal clone RL181_aah42b04 DQ798
FJ367447.1 gg_id:365554 feces adult twins and mothers; TS29 clone TS29_a03f09 FJ3674
FJ685477.1 gg_id:527884 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6854

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AY975495.1 gg_id:123346 human ascending colon mucosal biopsy clone N940 AY9754
EU462858.1 gg_id:294353 southern three-banded armadillo feces clone arma_aaj54b02 EU4628
FJ371270.1 gg_id:363882 feces adult twins and mothers; TS6 clone TS6_a03a04 FJ3712
EU460121.1 gg_id:294538 mammals their gut microbes eastern black and white colobus feces clone COL_aai15 EU4601
DQ905700.1 gg_id:165183 human fecal clone 014C-H7 DQ905
DQ327461.1 gg_id:147500 Metagenomic gut microbiome healthy human stool clone EA26 DQ327
FJ366644.1 gg_id:367111 feces adult twins and mothers; TS27 clone TS27_a02b04 FJ3666
AY985305.1 gg_id:121455 human stool clone C209 AY9853
DQ327008.1 gg_id:145570 Metagenomic gut microbiome healthy human stool clone E509 DQ327
AY979201.1 gg_id:115705 human transverse colon mucosal biopsy clone Z319 AY9792
DQ071521.1 gg_id:234309 microbial cecum captive and free-living capercaillies (Tetrao urogallus) clone TuCc28 DQ071
DQ326193.1 gg_id:145742 Metagenomic gut microbiome healthy human stool clone C107 DQ326
DQ809019.1 gg_id:198527 human fecal clone RL243_aai88c09 DQ809
DQ905039.1 gg_id:171469 human fecal clone 2-002-c9 DQ905
FJ366564.1 gg_id:362281 feces adult twins and mothers; TS27 clone TS27_a01c01 FJ3665
FJ371136.1 gg_id:364899 feces adult twins and mothers; TS6 clone TS6_a01d04 FJ3711
DQ801852.1 gg_id:174404 human fecal clone RL201_aai47f07 DQ801
AY982542.1 gg_id:123324 human descending colon mucosal biopsy clone KW06 AY9825
FJ679307.1 gg_id:514046 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6793
DQ905574.1 gg_id:162631 human fecal clone 014B-D5 DQ905
FJ678369.1 gg_id:514646 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6783
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EU461359.1 gg_id:301990 red kangaroo feces clone KO2_aai18f06 EU4613
DQ793683.1 gg_id:199555 human fecal clone RL246_aai75e10 DQ793
EF025237.1 gg_id:197579 Examination microbial ecology avian vivo bromodeoxyuridine intestine clone B5_B29 EF0252
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DQ802748.1 gg_id:180617 human fecal clone RL188_aan96b01 DQ802
FJ368586.1 gg_id:356788 feces adult twins and mothers; TS49 clone TS49_a02a09 FJ3685
L76604.1 gg_id:14012 Ruminococcus torques str. ATCC 27756 L76604
DQ800430.1 gg_id:175474 human fecal clone RL183_aah24c02 DQ800
EU461414.1 gg_id:298557 red kangaroo feces clone KO2_aai20f10 EU4614
AY979054.1 gg_id:120691 human transverse colon mucosal biopsy clone NJ62 AY9790
DQ793576.1 gg_id:182245 human fecal clone RL246_aai73g11 DQ793
DQ327087.1 gg_id:147259 Metagenomic gut microbiome healthy human stool clone E601 DQ327
FJ367828.1 gg_id:369417 feces adult twins and mothers; TS2 clone TS2_a04a09 FJ3678

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DQ794277.1 gg_id:194984 human fecal clone RL176_aan60e06 DQ794
EU462421.1 gg_id:294022 Sumatran orangutan feces clone orang1_aai54c04 EU462
FJ372057.1 gg_id:359245 feces adult twins and mothers; TS9 clone TS9_a01c08 FJ3720
DQ802397.1 gg_id:194364 human fecal clone RL188_aah17b10 DQ802
DQ326751.1 gg_id:145473 Metagenomic gut microbiome healthy human stool clone E211 DQ326
EU776162.1 gg_id:350594 Spotted hyena feces clone HY2_c04 EU776
FJ368890.1 gg_id:366086 feces adult twins and mothers; TS4 clone TS4_a01g06 FJ3688
AY978933.1 gg_id:121792 human transverse colon mucosal biopsy clone NG68 AY9789
EU776398.1 gg_id:352712 Red Kangaroo feces clone KO2_aai17b07 EU776
FJ678828.1 gg_id:525532 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6788
DQ905491.1 gg_id:171386 human fecal clone 014-c3 DQ905
AY684374.2 gg_id:110259 mucosal biopsies human intestine clone HuRC33 AY6843
AY981433.1 gg_id:125763 human sigmoid colon mucosal biopsy clone L513 AY9814
GQ492339.1 gg_id:558380 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
EU772087.1 gg_id:345846 Argali sheep feces clone AS1_aao37b09.Contig1 EU772
FJ677219.1 gg_id:519710 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6772
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DQ801672.1 gg_id:183663 human fecal clone RL201_aai45c08 DQ801
FJ684877.1 gg_id:523542 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6848
DQ326812.1 gg_id:150070 Metagenomic gut microbiome healthy human stool clone E282 DQ326
AY978964.1 gg_id:124012 human transverse colon mucosal biopsy clone NH49 AY9789
GQ492583.1 gg_id:552770 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
DQ326786.1 gg_id:147939 Metagenomic gut microbiome healthy human stool clone E253 DQ326
DQ798077.1 gg_id:189787 human fecal clone RL302_aal95c05 DQ798
DQ326720.1 gg_id:149825 Metagenomic gut microbiome healthy human stool clone E175 DQ326
AY978934.1 gg_id:123993 human transverse colon mucosal biopsy clone NG70 AY9789
AY985948.1 gg_id:121913 human stool clone D246 AY9859
FJ364610.1 gg_id:369632 feces adult twins and mothers; TS19 clone TS19_a01a05 FJ3646
DQ327441.1 gg_id:146930 Metagenomic gut microbiome healthy human stool clone EA04 DQ327
FJ366624.1 gg_id:363033 feces adult twins and mothers; TS27 clone TS27_a01h05 FJ3666
FJ366100.1 gg_id:360703 feces adult twins and mothers; TS25 clone TS25_a02f11 FJ3661
EU774442.1 gg_id:325255 mammals their gut microbes Eastern Black and White Colobus feces clone COL_aai1! EU774
DQ905638.1 gg_id:167163 human fecal clone 014C-B3 DQ905
DQ802606.1 gg_id:179151 human fecal clone RL188_aan94a08 DQ802
FJ680721.1 gg_id:527909 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6807
EU773805.1 gg_id:314832 Cheetah feces clone CE3_aai07d08 EU7738
EU459677.1 gg_id:287645 ring-tailed lemur feces clone RT_aai10g01 EU4596
DQ805533.1 gg_id:184597 human fecal clone RL203_aai63h01 DQ805
EU776169.1 gg_id:333386 Spotted hyena feces clone HY1_f11 EU776

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DQ327068.1 gg_id:145530 Metagenomic gut microbiome healthy human stool clone E576 DQ327
DQ797240.1 gg_id:198105 human fecal clone RL386_aao88g07 DQ797
FJ371212.1 gg_id:360981 feces adult twins and mothers; TS6 clone TS6_a02c03 FJ3712
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FJ370786.1 gg_id:359968 feces adult twins and mothers; TS5 clone TS5_a01c06 FJ3707
EU773988.1 gg_id:333309 Cheetah feces clone CE3_aai06g03 EU773
FJ368092.1 gg_id:370388 feces adult twins and mothers; TS30 clone TS30_a03h07 FJ3680
FJ369085.1 gg_id:359707 feces adult twins and mothers; TS4 clone TS4_a04a09 FJ3690
DQ800102.1 gg_id:185775 human fecal clone RL247_aaj24b10 DQ800
DQ327379.1 gg_id:146834 Metagenomic gut microbiome healthy human stool clone E936 DQ327
DQ071519.1 gg_id:234113 microbial cecum captive and free-living capercaillies (Tetrao urogallus) clone TuCc26 DQ071
DQ905559.1 gg_id:170503 human fecal clone 014B-C2 DQ905
AY977233.1 gg_id:122429 human cecum mucosal biopsy clone MT69 AY977
DQ805113.1 gg_id:184911 human fecal clone RL249_aaj81d05 DQ805
EU462882.1 gg_id:293600 southern three-banded armadillo feces clone arma_aaj54d09 EU462
FJ364879.1 gg_id:360138 feces adult twins and mothers; TS19 clone TS19_a04c04 FJ3648
FJ366558.1 gg_id:359733 feces adult twins and mothers; TS27 clone TS27_a01b07 FJ3665
DQ794475.1 gg_id:193297 human fecal clone RL197_aah88d03 DQ794
FJ678742.1 gg_id:523496 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6787
FJ366836.1 gg_id:366783 feces adult twins and mothers; TS27 clone TS27_a04d10 FJ3668
FJ368994.1 gg_id:367327 feces adult twins and mothers; TS4 clone TS4_a03a06 FJ3689
FJ371218.1 gg_id:362500 feces adult twins and mothers; TS6 clone TS6_a02c09 FJ3712
FJ369934.1 gg_id:359266 feces adult twins and mothers; TS55 clone TS55_a02e01 FJ3699
FJ371690.1 gg_id:359323 feces adult twins and mothers; TS8 clone TS8_a01b07 FJ3716
DQ326814.1 gg_id:146704 Metagenomic gut microbiome healthy human stool clone E285 DQ326
FJ368753.1 gg_id:365790 feces adult twins and mothers; TS49 clone TS49_a04b03 FJ3687
FJ362751.1 gg_id:368009 feces adult twins and mothers; TS13 clone TS13_a02f11 FJ3627

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DQ805425.1 gg_id:174604 human fecal clone RL203_aai62d11 DQ805
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DQ905539.1 gg_id:165398 human fecal clone 014B-A6 DQ905
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FJ678344.1 gg_id:515194 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6783
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GQ493082.1 gg_id:583836 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
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DQ326809.1 gg_id:150159 Metagenomic gut microbiome healthy human stool clone E279 DQ326
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EF399287.1 gg_id:212960 human fecal clone SJTU_F_14_03 EF3992
EU773335.1 gg_id:310492 BigHorn sheep feces clone BH1_aao25f07 EU7733
FJ682187.1 gg_id:522697 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6821
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FJ363264.1 gg_id:362565 feces adult twins and mothers; TS149 clone TS149_a01c01 FJ3632
FJ673945.1 gg_id:512723 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6739
GQ491988.1 gg_id:581922 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
FJ364762.1 gg_id:362461 feces adult twins and mothers; TS19 clone TS19_a02g07 FJ3647
GQ493078.1 gg_id:536373 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
DQ326651.1 gg_id:147001 Metagenomic gut microbiome healthy human stool clone E090 DQ326
DQ801918.1 gg_id:192071 human fecal clone RL201_aai48e01 DQ801
EU460132.1 gg_id:292073 mammals their gut microbes eastern black and white colobus feces clone COL_aai15 EU4601
DQ823822.1 gg_id:191551 human fecal clone RL250_aaj79e10 DQ823
EU776463.1 gg_id:349343 Red Kangaroo feces clone KO1_aai44e01 EU7764
GQ021445.1 gg_id:488223 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbu27 GQ021
EU458416.1 gg_id:300405 spotted hyena feces clone HY1_g09_2 EU4584
GQ493968.1 gg_id:537542 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
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FJ366840.1 gg_id:358475 feces adult twins and mothers; TS27 clone TS27_a04e02 FJ3668
FJ678821.1 gg_id:525885 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6788
FJ675824.1 gg_id:513990 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6758
EF403531.1 gg_id:211175 human fecal clone SJTU_A2_03_09 EF4035

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GQ088713.1 gg_id:433719 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv GQ088
AJ315979.1 gg_id:100067 Ruminococcus sp. str. 14531 AJ3159
DQ808256.1 gg_id:190340 human fecal clone RL180_aao74e01 DQ808
AY981922.1 gg_id:122665 human sigmoid colon mucosal biopsy clone NZ40 AY9819
FJ683488.1 gg_id:516265 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6834
DQ805608.1 gg_id:196505 human fecal clone RL203_aai64h05 DQ805
GQ491205.1 gg_id:578251 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
DQ456364.1 gg_id:157516 pre-adolescent turkey cecum clone CFT212E4 DQ456
EU772704.1 gg_id:341622 Bush dog feces clone bdog1_aai80e08 EU7727
DQ071536.1 gg_id:234421 microbial cecum captive and free-living capercaillies (Tetrao urogallus) clone TuCc23 DQ071
EF399161.1 gg_id:216134 human fecal clone SJTU_F_12_47 EF3991
GQ493957.1 gg_id:582233 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
FJ369466.1 gg_id:367857 feces adult twins and mothers; TS50 clone TS50_a04h04 FJ3694
DQ800183.1 gg_id:195002 human fecal clone RL303_aal69d01 DQ800
DQ796321.1 gg_id:199585 human fecal clone RL179_aah25g04 DQ796
FJ367966.1 gg_id:369900 feces adult twins and mothers; TS30 clone TS30_a01h04 FJ3679
EU530425.1 gg_id:271120 mucosa adherent and invasive microbes profile adenoma colorectal cancer clone M6 EU5304
GQ175466.1 gg_id:593066 Chicken intestinal microbiota modulations various feed supplementations DGGE anc GQ175
DQ905611.1 gg_id:169787 human fecal clone 014B-G8 DQ905
EU475485.1 gg_id:290548 springbok feces clone SBSD_aaa02c06 EU4754
FJ365141.1 gg_id:367587 feces adult twins and mothers; TS1 clone TS1_a03d04 FJ3651
FJ369760.1 gg_id:358260 feces adult twins and mothers; TS51 clone TS51_a04e04 FJ3697
EF403443.1 gg_id:204152 human fecal clone SJTU_A2_01_29 EF4034
DQ796893.1 gg_id:185834 human fecal clone RL179_aao56a10 DQ796
GQ493314.1 gg_id:583398 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
DQ806984.1 gg_id:192413 human fecal clone RL198_aaj76f09 DQ806
EU466859.1 gg_id:291755 African elephant feces clone AFEL2_aao30d11 EU4668
FJ366049.1 gg_id:365527 feces adult twins and mothers; TS25 clone TS25_a02b03 FJ3660
DQ807268.1 gg_id:195172 human fecal clone RL244_aaj48d02 DQ807
AY978903.1 gg_id:118349 human transverse colon mucosal biopsy clone NF82 AY9789
FJ369930.1 gg_id:359000 feces adult twins and mothers; TS55 clone TS55_a02d08 FJ3699
FJ369122.1 gg_id:364608 feces adult twins and mothers; TS4 clone TS4_a04e05 FJ3691
FJ370133.1 gg_id:366858 feces adult twins and mothers; TS55 clone TS55_a04g06 FJ3701
FJ366834.1 gg_id:368301 feces adult twins and mothers; TS27 clone TS27_a04d08 FJ3668
AY981879.1 gg_id:127442 human sigmoid colon mucosal biopsy clone NX61 AY9818
EU530240.1 gg_id:261540 mucosa adherent and invasive microbes adenoma colorectal cancer profile non-aden EU5302
FJ364056.1 gg_id:357671 feces adult twins and mothers; TS150 clone TS150_a02d11 FJ3640
EU530356.1 gg_id:274877 mucosa adherent and invasive microbes profile adenoma colorectal cancer clone M4 EU5303

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DQ800341.1 gg_id:193624 human fecal clone RL303_aal71g11 DQ800
GQ493418.1 gg_id:583336 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
FJ370128.1 gg_id:364901 feces adult twins and mothers; TS55 clone TS55_a04g01 FJ3701
DQ808113.1 gg_id:184492 human fecal clone RL180_aan72g04 DQ808
AY982654.1 gg_id:124568 human descending colon mucosal biopsy clone KX45 AY9826
FJ367173.1 gg_id:359446 feces adult twins and mothers; TS28 clone TS28_a04d05 FJ3671
FJ369758.1 gg_id:361222 feces adult twins and mothers; TS51 clone TS51_a04e02 FJ3697
DQ905477.1 gg_id:164148 human fecal clone 014-b1 DQ905
FJ370411.1 gg_id:368396 feces adult twins and mothers; TS56 clone TS56_a04g05 FJ3704
FJ365992.1 gg_id:360267 feces adult twins and mothers; TS25 clone TS25_a01e03 FJ3659
FJ683878.1 gg_id:525278 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6838
AY980425.1 gg_id:126180 human rectum mucosal biopsy clone N328 AY9804
EU771578.1 gg_id:321693 African elephant feces clone AFEL2_aao32d12 EU7715
FJ371364.1 gg_id:367266 feces adult twins and mothers; TS6 clone TS6_a04b01 FJ3713
FJ680888.1 gg_id:521005 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6808
EU460182.1 gg_id:297182 mammals their gut microbes eastern black and white colobus feces clone COL_aai16 EU4601
DQ798904.1 gg_id:177911 human fecal clone RL242_aaj98h05 DQ798
EU462919.1 gg_id:297641 southern three-banded armadillo feces clone arma_aaj55a04 EU4629
EU776069.1 gg_id:342110 Spotted hyena feces clone HY2_d06 EU7760
AF399956.1 gg_id:44493 Shuttleworthia satelles str. VPI D143K-13 AF3999
AF371623.1 gg_id:39567 swine intestine clone p-986-s962-5 AF3716
AB034118.1 gg_id:34221 rumen clone 2C28d-12 AB0341
EU842536.1 gg_id:348474 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU8425
AB034061.1 gg_id:23832 rumen clone 5C3d-20 AB0340
GQ040708.1 gg_id:384462 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw957g08c GQ040
GQ038576.1 gg_id:467322 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu4 GQ038
GQ044889.1 gg_id:442935 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw GQ044
AY958930.1 gg_id:137153 Microbes on human vaginal epithelium clone rRNA157 AY9589
GQ040803.1 gg_id:464655 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw958g12c GQ040
GQ037634.1 gg_id:392847 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu4 GQ037
GQ036308.1 gg_id:414882 Topographical and Temporal Human Skin Microbiome skin palm clone nbu362f04c1 GQ036
GQ037663.1 gg_id:455181 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu4 GQ037
GQ038522.1 gg_id:455063 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu4 GQ038
GQ040952.1 gg_id:468028 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw960e04c GQ040
AY959202.1 gg_id:134747 Microbes on human vaginal epithelium clone rRNA429 AY9592
GQ042994.1 gg_id:399643 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1011h GQ042
GQ043923.1 gg_id:396628 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw97 GQ043
CR933136.1 gg_id:111355 Evry municipal wastewater treatment plant clone 012F03_B_SD_P15 CR9331
AF001901.2 gg_id:245935 Selenomonas lipolytica str. CF1B AF0019

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EU474631.1 gg_id:290036 Indian rhinoceros feces clone IR_aaa03f07 EU474
FJ676414.1 gg_id:517632 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6764
EU843986.1 gg_id:320857 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
DQ823660.1 gg_id:196625 human fecal clone RL250_aaj77c04 DQ823
EU842482.1 gg_id:355827 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
EU508972.1 gg_id:264231 cecal contents Mus musculus strain C57BL/6J; MD7 clone MD7_aap41a03 EU508
EU764906.1 gg_id:330442 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2 EU764
AF001754.1 gg_id:14043 rumen clone RF22 AF001
DQ807023.1 gg_id:187981 human fecal clone RL244_aaj45c03 DQ807
EU506378.1 gg_id:259787 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aap64e07 EU506
EU767793.1 gg_id:305459 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C3 EU767
AB185510.1 gg_id:107149 rumen clone F23-A07 AB185
EU778970.1 gg_id:306939 Prevost's squirrel feces clone SQ_aah82b05 EU778
EU381472.1 gg_id:259924 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid EU381
AB494831.1 gg_id:588390 Fibrobacter succinogenes dominated consortium on hay stems sheep rumen clone A AB494
EF099443.1 gg_id:182320 mouse cecum clone SWPT3_aaa03c09 EF0994
FJ365654.1 gg_id:358016 feces adult twins and mothers; TS21 clone TS21_a01d11 FJ3656
AJ408980.1 gg_id:36059 human colonic clone HuCA29 AJ4089
FJ370965.1 gg_id:366716 feces adult twins and mothers; TS5 clone TS5_a03d02 FJ3709
EU475072.1 gg_id:297562 visayam warty pig feces clone VWP_aaa03a02 EU475
FJ371068.1 gg_id:364246 feces adult twins and mothers; TS5 clone TS5_a04e09 FJ3710
FJ372184.1 gg_id:357652 feces adult twins and mothers; TS9 clone TS9_a02f11 FJ3721
EU843157.1 gg_id:336336 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
FJ675901.1 gg_id:520529 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6759
EU764581.1 gg_id:328417 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1 EU764
DQ801965.1 gg_id:198450 human fecal clone RL241_aaj01b03 DQ801
EU748359.1 gg_id:344470 neotropical folivorous flying bird adult hoatzin crop clone hoa5_08e06 EU748
EU842506.1 gg_id:327661 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
EU381804.1 gg_id:272076 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU381
EU845648.1 gg_id:322259 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU845
AB494940.1 gg_id:563363 Fibrobacter succinogenes dominated consortium on hay stems sheep rumen clone N AB494
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DQ824783.1 gg_id:176334 human fecal clone RL185_aao69c02 DQ824
EU843223.1 gg_id:324536 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
EF436448.1 gg_id:211900 library-based ruminal water buffalo (Bubalus bubalis) rumen fluid clone BRC162 EF4364
DQ085080.1 gg_id:129331 goat rumen clone A5 DQ085
EU452145.1 gg_id:343630 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU452
FJ364058.1 gg_id:363352 feces adult twins and mothers; TS150 clone TS150_a02e03 FJ3640

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EU475048.1 gg_id:300451 visayam warty pig feces clone VWP_aaa03b10 EU475
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EF099366.1 gg_id:196089 mouse cecum clone SWPT3_aaa02c11 EF0993
EU462315.1 gg_id:292740 chimpanzee feces clone CHIMP1_aaj39h09 EU462
EU511654.1 gg_id:261627 cecal contents Mus musculus strain C57BL/6J; WD9 clone WD9_aak08d01 EU511
EF402928.1 gg_id:215475 human fecal clone SJTU_B_14_32 EF402
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EU764777.1 gg_id:317602 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2 EU764
EU775529.1 gg_id:327067 Western lowland gorilla feces clone GORSD_aaa01c02 EU775
DQ806726.1 gg_id:195865 human fecal clone RL186_aao48a05 DQ806
AY984619.1 gg_id:119853 human stool clone B560 AY984
EF436303.1 gg_id:207063 library-based ruminal water buffalo (Bubalus bubalis) rumen fluid clone BRC17 EF4363
DQ815835.1 gg_id:171399 mouse cecum clone aab22h11 DQ815
AY976863.1 gg_id:116931 human cecum mucosal biopsy clone K494 AY976
EU765422.1 gg_id:329718 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B3 EU765
EF405506.1 gg_id:211212 human fecal clone SJTU_G_03_14 EF4055
AB269957.1 gg_id:165372 Influence temperature and humidity on heifers rumen contents Holstein heifer (Bos AB269
EU778577.1 gg_id:319197 Ring-tailed lemur feces clone RT_aai10h06 EU778
EU844338.1 gg_id:354628 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
FJ364291.1 gg_id:363811 feces adult twins and mothers; TS15 clone TS15_a01c01 FJ3642
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EF098843.1 gg_id:195655 mouse cecum clone SWPT1_aaa01h07 EF0988
EU843456.1 gg_id:313821 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
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EU474961.1 gg_id:288246 red river hog feces clone RRH_aaa03c08 EU474

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DQ796024.1 gg_id:187005 human fecal clone RL202_aai50d07 DQ796
EF614671.1 gg_id:227590 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o EF6146
DQ801769.1 gg_id:177873 human fecal clone RL201_aai46e11 DQ801
FJ362608.1 gg_id:362404 feces adult twins and mothers; TS13 clone TS13_a01a08 FJ3626
DQ673466.1 gg_id:164693 rumen fluid clone GRC01 DQ673
EU474604.1 gg_id:292247 Indian rhinoceros feces clone IR_aaa02b09 EU474
EU462046.1 gg_id:292941 black-handed spider monkey feces clone SPIM_aaj33h05 EU462
DQ796017.1 gg_id:194230 human fecal clone RL202_aai50c10 DQ796
EU506317.1 gg_id:270744 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aap63b07 EU5063
EU778340.1 gg_id:322310 feces clone RL117_aae92f02 EU7783
FJ678071.1 gg_id:521048 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6780
EU779298.1 gg_id:355697 Visayam Warty Pig feces clone VWP_aaa02f06 EU779
DQ796249.1 gg_id:181622 human fecal clone RL179_aah23f09 DQ796
EU844216.1 gg_id:304808 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
EU844334.1 gg_id:303851 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8443
DQ808327.1 gg_id:198696 human fecal clone RL180_aao75c11 DQ808
EU844587.1 gg_id:306615 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8445
EU475295.1 gg_id:299401 rock hyrax feces clone RHSD_aaa03c06 EU475
FJ679775.1 gg_id:511342 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6797
EU777936.1 gg_id:334954 Black rhinoceros feces clone RH_aaj91f07 EU777
EU844336.1 gg_id:343465 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8443
EU504063.1 gg_id:268933 cecal contents Mus musculus strain C57BL/6J; CRWD4 clone CRWD4_aaa04g04 EU5040
EU774295.1 gg_id:322505 Chimpanzee feces clone CHIMP1_aaj37d11 EU774
EU771121.1 gg_id:326860 Asiatic elephant feces clone AE3_aaa02g04 EU771
EU452297.1 gg_id:315880 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77 EU452
EU506324.1 gg_id:269957 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aap63c10 EU5063
EU842673.1 gg_id:338660 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
EU843208.1 gg_id:327837 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
EF614701.1 gg_id:230367 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o EF6147
EU843030.1 gg_id:337355 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
EU765561.1 gg_id:332840 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B EU765
EU509086.1 gg_id:271643 cecal contents Mus musculus strain C57BL/6J; MD7 clone MD7_aap43c12 EU5090
DQ801403.1 gg_id:195792 human fecal clone RL388_aao95a11 DQ801
EF100070.1 gg_id:179793 mouse cecum clone SWPT5_aaa04c05 EF1000
AM932637.1 gg_id:574327 microbiota Toll-like receptor 2 deficient mice exhibits lineage specific modifications AM932
EU468273.1 gg_id:299484 domesticated horse feces clone horsej_a03_1 EU468
GU303565.1 gg_id:578995 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU303
AY452000.1 gg_id:104971 human intestine clone Muc3-3 AY4520
EU471818.1 gg_id:295444 Asiatic elephant feces clone AE2_aaa02h11 EU4718
FJ678005.1 gg_id:516960 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6780

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DQ795469.1 gg_id:193259 human fecal clone RL178_aah54g03 DQ795
AF371587.1 gg_id:68843 swine intestine clone p-393-o3 AF371
FJ363009.1 gg_id:358695 feces adult twins and mothers; TS148 clone TS148_a01h02 FJ3630
EU844524.1 gg_id:335411 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
FJ370373.1 gg_id:367241 feces adult twins and mothers; TS56 clone TS56_a04b03 FJ3703
EU844158.1 gg_id:339661 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
EU764930.1 gg_id:315002 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2 EU764
EU452492.1 gg_id:343968 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83N EU452
EU850566.1 gg_id:328186 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF376 EU850
DQ807313.1 gg_id:190874 human fecal clone RL307_aam05a04 DQ807
EU457580.1 gg_id:312869 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU457
DQ801250.1 gg_id:198511 human fecal clone RL388_aao93a02 DQ801
AF371629.1 gg_id:49854 swine intestine clone p-3848-23G3 AF371
FJ881223.1 gg_id:466102 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8812
AM932616.1 gg_id:564042 microbiota Toll-like receptor 2 deficient mice exhibits lineage specific modifications AM932
DQ800420.1 gg_id:192952 human fecal clone RL183_aah24a07 DQ800
EU508979.1 gg_id:268027 cecal contents Mus musculus strain C57BL/6J; MD7 clone MD7_aap41b12 EU508
AY858542.2 gg_id:109966 gastrointestinal tract eland clone ELAND_95 AY858
DQ810002.1 gg_id:177830 human fecal clone RL184_aao66h08 DQ810
DQ799884.1 gg_id:194960 human fecal clone RL247_aaj21d02 DQ799
EU471607.1 gg_id:296697 Asiatic elephant feces clone AE1_aaa03d11 EU471
EU457025.1 gg_id:306833 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU457
EU456417.1 gg_id:348748 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU456
DQ807358.1 gg_id:192404 human fecal clone RL307_aam05e07 DQ807
EU842275.1 gg_id:353780 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
DQ809266.1 gg_id:197951 human fecal clone RL308_aal84d06 DQ809
EF614892.1 gg_id:233371 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o EF6148
EU509053.1 gg_id:267522 cecal contents Mus musculus strain C57BL/6J; MD7 clone MD7_aap42f10 EU509
EU452320.1 gg_id:307380 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75N EU452
DQ801873.1 gg_id:196540 human fecal clone RL201_aai47h09 DQ801
EU843271.1 gg_id:334890 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
EU842906.1 gg_id:307550 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
EU462328.1 gg_id:296165 chimpanzee feces clone CHIMP1_aaj40c03 EU462
DQ808320.1 gg_id:190565 human fecal clone RL180_aao75c03 DQ808
EU776757.1 gg_id:312291 Mongoose lemur feces clone ML_aae89c03 EU776
EU506267.1 gg_id:267393 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aap61h02 EU506
EU843291.1 gg_id:316384 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
EU844631.1 gg_id:341544 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
EU842443.1 gg_id:303440 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
EU504118.1 gg_id:262724 cecal contents Mus musculus strain C57BL/6J; CRWD5 clone CRWD5_aaa01f05 EU504

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EU775906.1 gg_id:346045 Horse feces clone horsej_aai92b04 EU775
AB494776.1 gg_id:533469 Fibrobacter succinogenes dominated consortium on hay stems sheep rumen clone A AB494
EU779476.1 gg_id:332126 Grevy's Zebra feces clone GZ_aaa03b02 EU779
EU765017.1 gg_id:330857 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2 EU765
FJ370855.1 gg_id:358762 feces adult twins and mothers; TS5 clone TS5_a02a09 FJ3708
EF436398.1 gg_id:203828 library-based ruminal water buffalo (Bubalus bubalis) rumen fluid clone BRC112 EF4363
DQ905416.1 gg_id:171279 human fecal clone 013C-E1 DQ905
DQ327057.1 gg_id:149210 Metagenomic gut microbiome healthy human stool clone E565 DQ327
DQ796618.1 gg_id:176808 human fecal clone RL179aan75h10 DQ796
FJ440065.1 gg_id:543500 Megamonas hypermegale colonization correlates Campylobacter jejuni exclusion pou FJ4400
EU764750.1 gg_id:345111 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2 EU764
FJ677970.1 gg_id:518355 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6779
DQ807812.1 gg_id:178809 human fecal clone RL180_aah37e05 DQ807
EU457826.1 gg_id:334406 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77 EU457
EU844166.1 gg_id:313671 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
DQ797348.1 gg_id:188157 human fecal clone RL248_aai98c03 DQ797
EU764962.1 gg_id:346771 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2 EU764
EU765688.1 gg_id:303913 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B3 EU765
DQ394610.1 gg_id:155943 -Arctic peninsula Svalbard Norway determined genes and rumen isolates reindeer o DQ394
EU767891.1 gg_id:305959 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C3 EU767
DQ796417.1 gg_id:173948 human fecal clone RL179_aah28a05 DQ796
EF100022.1 gg_id:195008 mouse cecum clone SWPT5_aaa03f04 EF1000
EF614690.1 gg_id:229185 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o EF6146
DQ796693.1 gg_id:184508 human fecal clone RL179_aao53c08 DQ796
EU765426.1 gg_id:353963 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B3 EU765
DQ795094.1 gg_id:189624 human fecal clone RL310_aam40b07 DQ795
EU455844.1 gg_id:331471 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H78 EU455
EU771831.1 gg_id:336761 African elephant feces clone AFEL2_aao29a04 EU771
EF399751.1 gg_id:207688 human fecal clone SJTU_E_02_95 EF3997
EF099347.1 gg_id:192378 mouse cecum clone SWPT3_aaa02a09 EF0993
DQ795921.1 gg_id:174251 human fecal clone RL202_aai49a01 DQ795
DQ905702.1 gg_id:173453 human fecal clone 014C-H11 DQ905
DQ799891.1 gg_id:177055 human fecal clone RL247_aaj21d09 DQ799
DQ809456.1 gg_id:196167 human fecal clone RL184_aah21c01 DQ809
EF436294.1 gg_id:217080 library-based ruminal water buffalo (Bubalus bubalis) rumen fluid clone BRC08 EF4362
GU174105.1 gg_id:582627 Microbial Bactrian camel estimated rumen clone XJC73 GU174
EU465612.1 gg_id:289452 argali sheep feces clone AS1_aao39f12.Contig1 EU465
DQ799897.1 gg_id:197545 human fecal clone RL247_aaj21e05 DQ799
EU766081.1 gg_id:352304 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B4 EU766
AY992999.1 gg_id:131132 mouse cecum clone C22_n20 AY992

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EU510165.1 gg_id:274045 cecal contents Mus musculus strain C57BL/6J; WD3 clone WD3_aak02c10 EU510
DQ808203.1 gg_id:191208 human fecal clone RL180_aao73h01 DQ808
DQ806608.1 gg_id:190932 human fecal clone RL186_aao46f08 DQ806
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DQ797022.1 gg_id:178882 human fecal clone RL386_aao85h08 DQ797
DQ796022.1 gg_id:175721 human fecal clone RL202_aai50d05 DQ796
DQ794548.1 gg_id:182451 human fecal clone RL240_aaj29d11 DQ794
EU842898.1 gg_id:328139 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
FJ365859.1 gg_id:365314 feces adult twins and mothers; TS21 clone TS21_a03h06 FJ3658
EU765797.1 gg_id:336866 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B4 EU765
EU506386.1 gg_id:259190 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aap64f09 EU506
EU510847.1 gg_id:276067 cecal contents Mus musculus strain C57BL/6J; WD6 clone WD6_aak50c02 EU510
FJ370807.1 gg_id:370047 feces adult twins and mothers; TS5 clone TS5_a01e05 FJ3708
DQ801853.1 gg_id:195173 human fecal clone RL201_aai47f08 DQ801
EU844476.1 gg_id:306013 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
FJ365832.1 gg_id:363955 feces adult twins and mothers; TS21 clone TS21_a03e11 FJ3658
EU474876.1 gg_id:288437 red river hog feces clone RRH_aaa03c12 EU474
DQ796317.1 gg_id:200365 human fecal clone RL179_aah25f10 DQ796
EU768242.1 gg_id:331476 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C4 EU768
EU474916.1 gg_id:289660 red river hog feces clone RRH_aaa01f06 EU474
EU844386.1 gg_id:334091 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
EU843064.1 gg_id:324476 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
EU778117.1 gg_id:319097 feces clone RL388_aao94b02 EU778
FJ363402.1 gg_id:368090 feces adult twins and mothers; TS149 clone TS149_a02g09 FJ3634
EU778852.1 gg_id:325329 Black-handed Spider Monkey feces clone SPIM_aaj34g06 EU778
EU474666.1 gg_id:296902 Indian rhinoceros feces clone IR_aaa01c12 EU474
EU845645.1 gg_id:338052 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU845
EU765583.1 gg_id:315521 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B3 EU765
DQ823853.1 gg_id:195918 human fecal clone RL250_aaj80a02 DQ823
EU844596.1 gg_id:354870 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
AB185654.1 gg_id:107082 rumen clone F24-H10 AB185
DQ805090.1 gg_id:182927 human fecal clone RL249_aaj81b03 DQ805
DQ798299.1 gg_id:183039 human fecal clone RL181_aah40d02 DQ798
EU344217.1 gg_id:271477 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU344
GU302535.1 gg_id:560114 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU302
EF614553.1 gg_id:233021 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o EF6145
EU842162.1 gg_id:327127 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
AY854275.2 gg_id:110361 herbivore gastrointestinal tract clone CATTLE_13 AY854
DQ794823.1 gg_id:180003 human fecal clone RL240_aaj32g11 DQ794
DQ815758.1 gg_id:171564 mouse cecum clone aab21h09 DQ815

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GU304168.1 gg_id:537874 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU304
EU773362.1 gg_id:325181 BigHorn sheep feces clone BH1_aao27c08 EU773
EU456200.1 gg_id:330064 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU456
FJ363698.1 gg_id:364134 feces adult twins and mothers; TS14 clone TS14_a02c03 FJ3636
DQ795198.1 gg_id:179497 human fecal clone RL178_aah51d08 DQ795
EF098102.1 gg_id:191098 mouse cecum clone SWPT14_aaa01e07 EF0981
EU511649.1 gg_id:264993 cecal contents Mus musculus strain C57BL/6J; WD9 clone WD9_aak08c04 EU511
FJ825526.1 gg_id:570049 Microbial during start-up mesophilic biogas plant clone 68_BS1_3 FJ8255
FJ369018.1 gg_id:369718 feces adult twins and mothers; TS4 clone TS4_a03c11 FJ3690
DQ798894.1 gg_id:189679 human fecal clone RL242_aaj98g06 DQ798
FJ367760.1 gg_id:364753 feces adult twins and mothers; TS2 clone TS2_a03c08 FJ3677
DQ795223.1 gg_id:186212 human fecal clone RL178_aah51f11 DQ795
EU748192.1 gg_id:323465 neotropical folivorous flying bird adult hoatzin crop clone hoa31_70F09.F EU748
EU344216.1 gg_id:270176 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU344
EU467112.1 gg_id:289734 mongoose lemur feces clone ML_aae88e06 EU467
EU456937.1 gg_id:344726 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU456
AY980044.1 gg_id:119655 human rectum mucosal biopsy clone KA62 AY980
AJ576367.1 gg_id:103464 hindgut homogenate Pachnoda ephippiata larva clone PeH54 AJ5763
EU462885.1 gg_id:293078 southern three-banded armadillo feces clone arma_aaj54e01 EU462
EU468602.1 gg_id:299571 okapi feces clone OK1_g12_2 EU468
DQ804842.1 gg_id:180577 human fecal clone RL385_aao81d10 DQ804
FJ880208.1 gg_id:410895 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8802
EF099088.1 gg_id:192491 mouse cecum clone SWPT2_aaa02a12 EF0990
DQ795319.1 gg_id:186286 human fecal clone RL178_aah52h07 DQ795
EF071156.1 gg_id:177665 library survey and quantitative measurement major mucosa- IBD human colonic muc EF0711
EU503880.1 gg_id:264974 cecal contents Mus musculus strain C57BL/6J; CRWD4 clone CRWD4_aaa02a03 EU503
GQ448783.1 gg_id:561027 Microbiome neonatal calves: shedding microorganisms fecal clone calf784_10wks_g GQ448
EU762314.1 gg_id:305841 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU762
DQ015573.1 gg_id:132165 mouse cecum clone M3_f11_2 DQ015
EU465560.1 gg_id:296474 argali sheep feces clone AS1_aao37f12.Contig1 EU465
EU772019.1 gg_id:347774 Argali sheep feces clone AS1_aao40a02.Contig1 EU772
EU474450.1 gg_id:297770 bighorn sheep feces clone BHSD_aaa04a10 EU474
EU474651.1 gg_id:288023 Indian rhinoceros feces clone IR_aaa02d10 EU474
EU771577.1 gg_id:323075 African elephant feces clone AFYEL_aaj65b12 EU771
EU452317.1 gg_id:354783 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU452
GQ448122.1 gg_id:593548 Microbiome neonatal calves: shedding microorganisms fecal clone calf32_6wks_grp GQ448
DQ800565.1 gg_id:191804 human fecal clone RL183_aah29g10 DQ800
EU842210.1 gg_id:332157 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
EU462132.1 gg_id:293232 black-handed spider monkey feces clone SPIM_aaj35e04 EU462
EU470436.1 gg_id:287580 Grevy's zebra feces clone GZ_aaa03a04 EU470

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EU774075.1 gg_id:314104 Chimpanzee feces clone CHIMP12_f09_1 EU774
EU885021.1 gg_id:326380 microbial hindgut chamber Pomacanthus sexstriatus GI tract clone AG6 EU885
EU773057.1 gg_id:352263 Banteng feces clone BG_aaa03g10.Contig1 EU773
FJ364927.1 gg_id:367389 feces adult twins and mothers; TS19 clone TS19_a04h02 FJ3649
EU504389.1 gg_id:268835 cecal contents Mus musculus strain C57BL/6J; CRWD6 clone CRWD6_aaa03e02.Cont EU504
FJ681188.1 gg_id:528390 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6811
FJ879956.1 gg_id:434509 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8799
EF099809.1 gg_id:189189 mouse cecum clone SWPT4_aaa04f05 EF0998
EU766137.1 gg_id:332258 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B EU766
FJ673344.1 gg_id:513208 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6733
EU455182.1 gg_id:305212 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75 EU455
AB189705.1 gg_id:112766 alkaline-enriched termite gut homogenate clone Pl-10e-26 AB189
DQ115999.1 gg_id:130419 bovine teat canal clone D-11 DQ115
AB234461.1 gg_id:150502 termite gut homogenate clone MgMjD-052 AB234
FJ371271.1 gg_id:365753 feces adult twins and mothers; TS6 clone TS6_a03a05 FJ3712
FJ881315.1 gg_id:409738 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8813
GQ491814.1 gg_id:581719 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
DQ815380.1 gg_id:172243 mouse cecum clone aab47c06 DQ815
EU775175.1 gg_id:335003 Francois Langur feces clone FL_1aaa04b03 EU775
DQ014763.1 gg_id:135537 mouse cecum clone M1_d07_2 DQ014
EU506281.1 gg_id:273602 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aap62b09 EU506
EF096045.1 gg_id:182619 mouse cecum clone lean2_aaa02g06 EF096
EU843876.1 gg_id:312849 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
EU772090.1 gg_id:326539 Argali sheep feces clone AS1_aao37e01.Contig1 EU772
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EU505206.1 gg_id:270480 cecal contents Mus musculus strain C57BL/6J; myd3 clone myd3_aaa04e02 EU505
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AF371576.1 gg_id:36647 swine intestine clone p-247-o5 AF371
FJ681025.1 gg_id:515460 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6810
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EU462951.1 gg_id:289874 southern three-banded armadillo feces clone arma_aaj55e12 EU462
FJ535038.1 gg_id:509070 Enhancement protein conversion volatile fatty acids accumulation during addition: ef FJ5350
EF099457.1 gg_id:194292 mouse cecum clone SWPT3_aaa03d12 EF0994
AF371584.1 gg_id:68844 swine intestine clone p-2876-6C5 AF371
EU472103.1 gg_id:292909 francois langur feces clone FL_1aaa02b04 EU472

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EF097936.1 gg_id:198808 mouse cecum clone SWPT12_aaa02d08 EF0979
EU776142.1 gg_id:352869 Spotted hyena feces clone HY2_g07_1 EU776
DQ392993.1 gg_id:154021 -Arctic peninsula Svalbard Norway determined genes and rumen isolates reindeer o DQ392
GQ896946.1 gg_id:583958 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ896
GU304201.1 gg_id:557646 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU304
AB192028.1 gg_id:142325 termite gut homogenate clone M1PT4-46 AB192
EU474658.1 gg_id:296471 Indian rhinoceros feces clone IR_aaa04b03 EU474
GQ448094.1 gg_id:547287 Microbiome neonatal calves: shedding microorganisms fecal clone calf32_6wks_grp GQ448
FJ681179.1 gg_id:510481 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6811
FJ681895.1 gg_id:527278 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6818
EU844275.1 gg_id:356280 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
DQ809132.1 gg_id:187268 human fecal clone RL308_aal82b08 DQ809
EF099847.1 gg_id:190768 mouse cecum clone SWPT5_aaa01c03 EF0998
DQ807837.1 gg_id:197400 human fecal clone RL180_aah37g08 DQ807
EU467569.1 gg_id:290468 southern three-banded armadillo feces clone arma_f11 EU467
AY983157.1 gg_id:121649 human descending colon mucosal biopsy clone A042 AY983
EU505009.1 gg_id:276548 cecal contents Mus musculus strain C57BL/6J; myd3 clone myd3_aaa01e10 EU505
FJ681350.1 gg_id:519742 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6813
DQ804908.1 gg_id:197002 human fecal clone RL385_aao82d06 DQ804
EF097641.1 gg_id:189739 mouse cecum clone SWPT20_aaa01f09 EF0976
EU451955.1 gg_id:320373 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75 EU451
EU472379.1 gg_id:294869 Angola colobus feces clone EAC_1aaa02a01 EU472
FJ880090.1 gg_id:454763 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8800
EU772719.1 gg_id:318651 Bush dog feces clone bdog1_b10_1 EU772
EU466173.1 gg_id:300529 bighorn sheep feces clone BH1_aao27d09 EU466
EU776207.1 gg_id:307217 Spotted hyena feces clone HY2_d02_3 EU776
DQ805004.1 gg_id:192396 human fecal clone RL385_aao83h11 DQ805
EF404593.1 gg_id:209736 human fecal clone SJTU_C_13_24 EF4045
GQ493107.1 gg_id:564188 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
DQ815637.1 gg_id:167512 mouse cecum clone aab44b06 DQ815
AY975277.1 gg_id:118129 human ascending colon mucosal biopsy clone N504 AY975
EU468743.1 gg_id:289743 okapi feces clone OK3_e07 EU468
EU505213.1 gg_id:268085 cecal contents Mus musculus strain C57BL/6J; myd3 clone myd3_aaa04e11 EU505
EU458328.1 gg_id:302494 spotted hyena feces clone HY1_e08 EU458
EU980608.1 gg_id:349074 Eubacterium contortum str. Ala-1 EU980
EU748182.1 gg_id:347442 neotropical folivorous flying bird adult hoatzin crop clone hoa31_71G09.F EU748
EF398528.1 gg_id:217083 human fecal clone SJTU_F_03_04 EF3985
EU775008.1 gg_id:306413 Francois Langur feces clone FL_1aaa01g04 EU775
DQ800395.1 gg_id:181233 human fecal clone RL303_aal72f05 DQ800
GQ897421.1 gg_id:585480 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do GQ897
EU778351.1 gg_id:304327 feces clone RL117_aae92d06 EU778

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FJ673298.1 gg_id:525987 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6732
FJ172888.1 gg_id:335488 Qinghai Yak Ruminal and Fungi China rumen clone RB-12 FJ1728
EU474433.1 gg_id:301633 bighorn sheep feces clone BHSD_aaa04d09 EU474
AJ576351.1 gg_id:106393 hindgut homogenate Pachnoda ephippiata larva clone PeH35 AJ5763
EF100006.1 gg_id:195934 mouse cecum clone SWPT5_aaa03d11 EF1000
EU777278.1 gg_id:331240 Okapi feces clone OK1_f11_3 EU777
EU845293.1 gg_id:335032 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU845
EU768480.1 gg_id:349094 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C5 EU768
DQ815643.1 gg_id:165434 mouse cecum clone aab44c02 DQ815
EF400639.1 gg_id:210200 human fecal clone SJTU_E_16_22 EF4006
EU774752.1 gg_id:309534 Angola Colobus feces clone EAC_2_aaa02h06 EU774
EU466324.1 gg_id:297982 bighorn sheep feces clone BH2_aao21h07 EU466
DQ805037.1 gg_id:190503 human fecal clone RL385_aao84d04 DQ805
DQ793840.1 gg_id:177359 human fecal clone RL176_aah44b09 DQ793
AY685919.1 gg_id:105684 feces clone 2C12 AY685
FJ880101.1 gg_id:467666 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8801
DQ800557.1 gg_id:190849 human fecal clone RL183_aah29f10 DQ800
DQ394642.1 gg_id:151401 -Arctic peninsula Svalbard Norway determined genes and rumen isolates reindeer o DQ394
AY854368.1 gg_id:110858 herbivore gastrointestinal tract clone Thompsons96 AY854
EF605060.1 gg_id:232620 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF605
EU510082.1 gg_id:273594 cecal contents Mus musculus strain C57BL/6J; WD3 clone WD3_aak01a12 EU510
EF100115.1 gg_id:181063 mouse cecum clone SWPT5_aaa04h06 EF1001
EU466107.1 gg_id:302407 bighorn sheep feces clone BH1_aao26a05 EU466
EF402474.1 gg_id:208509 human fecal clone SJTU_B_08_38 EF4024
FJ677261.1 gg_id:530104 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6772
EU775776.1 gg_id:336149 Horse feces clone horsem_aai93d05 EU775
FJ374228.1 gg_id:365377 Inter- and intraspecific humivorous scarab beetle larvae (Pachnoda spp.) larval hindg FJ3742
EF099407.1 gg_id:175432 mouse cecum clone SWPT3_aaa02g12 EF0994
EU454544.1 gg_id:303841 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU454
GQ448134.1 gg_id:508984 Microbiome neonatal calves: shedding microorganisms fecal clone calf32_6wks_grp GQ448
EF603792.1 gg_id:230215 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6037
AY991938.1 gg_id:134424 mouse cecum clone C20_m01 AY991
EU454263.1 gg_id:329122 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H74 EU454
AB189708.1 gg_id:113610 alkaline-enriched termite gut homogenate clone Pl-9.2e-11 AB189
EU776029.1 gg_id:327493 Spotted hyena feces clone HY1_a10 EU776
EU462996.1 gg_id:289304 southern three-banded armadillo feces clone arma_aaj56c08 EU462
FJ364165.1 gg_id:358603 feces adult twins and mothers; TS150 clone TS150_a03g03 FJ3641
EU475432.1 gg_id:299124 springbok feces clone SBSD_aaa03b12 EU475
GQ451207.1 gg_id:553492 Fecal Yunnan snub-nosed monkey feces clone J60 GQ451
EU462878.1 gg_id:296516 southern three-banded armadillo feces clone arma_aaj54d04 EU462

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GQ448108.1 gg_id:511234 Microbiome neonatal calves: shedding microorganisms fecal clone calf32_6wks_grp GQ448
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EU466206.1 gg_id:296103 bighorn sheep feces clone BH1_aao28a06 EU466
EU844598.1 gg_id:339911 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
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FJ681090.1 gg_id:527934 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6810
EU467418.1 gg_id:298916 chimpanzee feces clone CHIMP12_c08_2 EU467
FJ681436.1 gg_id:530379 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6814
EU344395.1 gg_id:276882 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU344
EU455309.1 gg_id:336015 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU455
FJ684450.1 gg_id:529810 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6844
EU764744.1 gg_id:340178 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2 EU764
EU504860.1 gg_id:266418 cecal contents Mus musculus strain C57BL/6J; myd2 clone myd2_aaa03d07 EU5048
FJ676498.1 gg_id:515269 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6764
EU842591.1 gg_id:310078 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
FJ834059.1 gg_id:569871 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P2Q401_57A08 FJ8340
FJ880210.1 gg_id:375678 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8802
EU470158.1 gg_id:294440 trancaspain urial feces clone TU2_aaa02e06 EU470
DQ806761.1 gg_id:178295 human fecal clone RL186_aao48d06 DQ806
EF097997.1 gg_id:183706 mouse cecum clone SWPT12_aaa03g07 EF0979
EU456570.1 gg_id:344418 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H80N EU456
GQ448746.1 gg_id:569582 Microbiome neonatal calves: shedding microorganisms fecal clone calf784_10wks_g GQ448
DQ015243.1 gg_id:135600 mouse cecum clone M2_g05_1 DQ015
EF099755.1 gg_id:194822 mouse cecum clone SWPT4_aaa03h03 EF0997
AY984693.1 gg_id:123923 human stool clone B646 AY984
GU304124.1 gg_id:568828 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU304
DQ327400.1 gg_id:146248 Metagenomic gut microbiome healthy human stool clone E958 DQ327
EU459778.1 gg_id:301110 ring-tailed lemur feces clone RT_aai12f06 EU459
EU344291.1 gg_id:263629 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU344
EU765488.1 gg_id:306345 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B3 EU765
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FJ372006.1 gg_id:360555 feces adult twins and mothers; TS8 clone TS8_a04f09 FJ3720

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EU508357.1 gg_id:262020 cecal contents Mus musculus strain C57BL/6J; MD27 clone MD27_aaa03f09 EU5083
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EF098632.1 gg_id:191109 mouse cecum clone SWPT16_aaa02d10 EF0986
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EU344425.1 gg_id:277063 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU3444
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EU470201.1 gg_id:288049 trancaspain urial feces clone TU2_aaa02a05 EU4702
EU503967.1 gg_id:275366 cecal contents Mus musculus strain C57BL/6J; CRWD4 clone CRWD4_aaa03d06 EU5039
EU778572.1 gg_id:313741 Ring-tailed lemur feces clone RT_aai09b11 EU7785

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EU470427.1 gg_id:289929 Grevy's zebra feces clone GZ_aaa01a02 EU470
EF097990.1 gg_id:178106 mouse cecum clone SWPT12_aaa03f08 EF0979
EF099192.1 gg_id:173850 mouse cecum clone SWPT2_aaa03f07 EF0991
FJ364892.1 gg_id:360165 feces adult twins and mothers; TS19 clone TS19_a04d08 FJ3648
EU509896.1 gg_id:261764 cecal contents Mus musculus strain C57BL/6J; WD11 clone WD11_aak23d01 EU5098
GQ402116.1 gg_id:580171 alpacas and sheep forestomach clone ALP4 GQ402
GQ448593.1 gg_id:541415 Microbiome neonatal calves: shedding microorganisms fecal clone calf784_6wks_gr GQ448
EU844125.1 gg_id:354188 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
GQ448779.1 gg_id:586290 Microbiome neonatal calves: shedding microorganisms fecal clone calf784_10wks_g GQ448
DQ803682.1 gg_id:192159 human fecal clone RL200_aai57b04 DQ803
EU451081.1 gg_id:305919 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H74 EU451
DQ815320.1 gg_id:171333 mouse cecum clone aab45d09 DQ815
FJ366764.1 gg_id:362448 feces adult twins and mothers; TS27 clone TS27_a03f01 FJ3667
EU844936.1 gg_id:350330 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8449
EU456846.1 gg_id:329416 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H80 EU4568
AF371640.1 gg_id:31249 swine intestine clone p-1051-a5 AF3716
EU456659.1 gg_id:334243 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H74 EU4566
EF099478.1 gg_id:178814 mouse cecum clone SWPT3_aaa03f10 EF0994
DQ801377.1 gg_id:181823 human fecal clone RL388_aao94f11 DQ801
EU456554.1 gg_id:323101 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80 EU4565
DQ815728.1 gg_id:162201 mouse cecum clone aab21e06 DQ815
FJ365251.1 gg_id:363014 feces adult twins and mothers; TS1 clone TS1_a04f04 FJ3652
FJ879589.1 gg_id:393167 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8795
FJ369960.1 gg_id:359128 feces adult twins and mothers; TS55 clone TS55_a02g05 FJ3699
DQ800978.1 gg_id:181028 human fecal clone RL387_aao90c04 DQ800
AM237879.1 gg_id:213401 Selective colonization insoluble human faecal faeces clone D1B-6.5-48h-6 AM237
EU468116.1 gg_id:287540 bush dog feces clone bdog3_aad68c08 EU468
EU455153.1 gg_id:334568 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74 EU455
EU469112.1 gg_id:295574 Speke's gazelle feces clone SP3_f08 EU469
EU381677.1 gg_id:259223 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid EU381
EU472185.1 gg_id:291887 francois langur feces clone FL_2aaa03b06 EU472
EU776095.1 gg_id:345340 Spotted hyena feces clone HY1_f07_3 EU776
FJ367192.1 gg_id:363919 feces adult twins and mothers; TS28 clone TS28_a04f02 FJ3671
FJ680926.1 gg_id:519613 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6809
DQ794797.1 gg_id:177828 human fecal clone RL240_aaj32d12 DQ794
FJ879226.1 gg_id:453454 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8792
AY978280.1 gg_id:115403 human transverse colon mucosal biopsy clone F136 AY978
EU454694.1 gg_id:343321 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H79 EU4546
EU764912.1 gg_id:329115 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B EU7649
EU451699.1 gg_id:352956 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80 EU4516

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EU773555.1 gg_id:331026 Goeldi's Marmoset feces clone CAL_b10 EU7735
FJ372060.1 gg_id:359030 feces adult twins and mothers; TS9 clone TS9_a01c11 FJ3720
FJ685170.1 gg_id:514222 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6851
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EU455142.1 gg_id:329968 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU4551
EU776077.1 gg_id:324236 Spotted hyena feces clone HY2_e05_2 EU7760
FJ366998.1 gg_id:360962 feces adult twins and mothers; TS28 clone TS28_a02c05 FJ3669
EF402522.1 gg_id:212503 human fecal clone SJTU_B_09_07 EF4025
DQ809709.1 gg_id:179228 human fecal clone RL184_aan83a07 DQ809
EU842695.1 gg_id:327336 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU8426
EF098880.1 gg_id:180762 mouse cecum clone SWPT1_aaa02e11 EF0988
AY916257.1 gg_id:112783 human rectum biopsy clone E024 AY9162
AY982764.1 gg_id:117348 human descending colon mucosal biopsy clone KY95 AY9827
FJ879404.1 gg_id:393396 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8794
FJ880637.1 gg_id:430724 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8806
EU457036.1 gg_id:347908 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K79S EU4570
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EU474350.1 gg_id:298395 western lowland gorilla feces clone GORSD_aaa03f05 EU4743
EF099720.1 gg_id:178173 mouse cecum clone SWPT4_aaa03d09 EF0997
DQ823850.1 gg_id:182653 human fecal clone RL250_aaj79h07 DQ823
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FJ681380.1 gg_id:532377 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6813
FJ534957.1 gg_id:578649 Enhancement protein conversion volatile fatty acids accumulation during addition: ef FJ5349
EU454243.1 gg_id:325636 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU4542
GQ451310.1 gg_id:584137 Fecal Yunnan snub-nosed monkey feces clone J328 GQ451
EU344239.1 gg_id:271586 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU3442
EU766938.1 gg_id:345367 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU7669
EU503840.1 gg_id:261277 cecal contents Mus musculus strain C57BL/6J; CRWD4 clone CRWD4_aaa01d04 EU5038
AY985158.1 gg_id:123338 human stool clone BB82 AY9851
NZ_AAVL02000015.1 gg_id:470392 Eubacterium ventriosum str. ATCC 27560 NZ_AA
AY977923.1 gg_id:126385 human cecum mucosal biopsy clone LG38 AY9779
EU504089.1 gg_id:268080 cecal contents Mus musculus strain C57BL/6J; CRWD5 clone CRWD5_aaa01b01 EU5040
DQ802226.1 gg_id:184577 human fecal clone RL241_aaj04g04 DQ802
FJ364071.1 gg_id:360291 feces adult twins and mothers; TS150 clone TS150_a02f06 FJ3640
EU467357.1 gg_id:294041 chimpanzee feces clone CHIMP12_c10 EU4673
FJ679672.1 gg_id:530383 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6796

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EU779220.1 gg_id:333341 Trancaspian Urial feces clone TU1_aaa02c09 EU779
AM697093.1 gg_id:222849 sequencing libraries indoor dust clone BF0002B043 AM697
EU462978.1 gg_id:298904 southern three-banded armadillo feces clone arma_aaj56a06 EU462
EU842359.1 gg_id:327905 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
DQ015646.1 gg_id:130175 mouse cecum clone M3_f03_2 DQ015
EU509051.1 gg_id:268982 cecal contents Mus musculus strain C57BL/6J; MD7 clone MD7_aap42f08 EU509
DQ795297.1 gg_id:179333 human fecal clone RL178_aah52f06 DQ795
EU778846.1 gg_id:307536 Black-handed Spider Monkey feces clone SPIM_aaj35e06 EU778
DQ815716.1 gg_id:163512 mouse cecum clone aab21d04 DQ815
EU471878.1 gg_id:300250 Asiatic elephant feces clone AE3_aaa04c05 EU471
AB189704.1 gg_id:113709 alkaline-enriched termite gut homogenate clone Pl-10e-23 AB189
DQ808148.1 gg_id:190954 human fecal clone RL180_aao73c03 DQ808
DQ795170.1 gg_id:177111 human fecal clone RL178_aah51a09 DQ795
FJ879504.1 gg_id:384843 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8795
EU454004.1 gg_id:319241 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83M EU454
DQ796523.1 gg_id:175978 human fecal clone RL179aan74a10 DQ796
EU104043.1 gg_id:330750 Evidence Comamonadaceae determinants settling performance activated sludge clo EU104
FJ680896.1 gg_id:519636 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6808
GQ458226.1 gg_id:570367 Microbial structure co-digestion anaerobic bioreactors treating cassava pulp and pig GQ458
EU461336.1 gg_id:292387 red kangaroo feces clone KO2_aai17g02 EU461
AF371590.1 gg_id:42492 swine intestine clone p-228-o5 AF371
EU468485.1 gg_id:301058 okapi feces clone OK1_g03 EU468
GQ449180.1 gg_id:584396 Microbiome neonatal calves: shedding microorganisms fecal clone calf784_10wks_g GQ449
FJ369574.1 gg_id:360851 feces adult twins and mothers; TS51 clone TS51_a02b09 FJ3695
AY978112.1 gg_id:122693 human cecum mucosal biopsy clone LI81 AY978
AY854367.1 gg_id:110168 herbivore gastrointestinal tract clone Thompsons93 AY854
AF371577.1 gg_id:69988 swine intestine clone p-386-o3 AF371
EU475501.1 gg_id:301156 springbok feces clone SBSD_aaa01f12 EU475
DQ824228.1 gg_id:181843 human fecal clone RL304_aal73b10 DQ824
EU764199.1 gg_id:314290 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A5 EU764
EF405404.1 gg_id:213236 human fecal clone SJTU_G_01_39 EF4054
DQ673494.1 gg_id:169584 rumen fluid clone GRC29 DQ673
AY978565.1 gg_id:116993 human transverse colon mucosal biopsy clone KR31 AY978
EF403815.1 gg_id:215738 human fecal clone SJTU_A2_03_12 EF4038
FJ879683.1 gg_id:397857 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8796
ABOU02000049.1 gg_id:329241 Ruminococcus lactaris str. ATCC 29176 ABOU0
EF614791.1 gg_id:232247 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o EF6147
AY977164.1 gg_id:125656 human cecum mucosal biopsy clone MS39 AY977
DQ796824.1 gg_id:184472 human fecal clone RL179_aao55a08 DQ796
FJ879430.1 gg_id:387084 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8794

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DQ794948.1 gg_id:193833 human fecal clone RL310_aam38c09 DQ794
EU457579.1 gg_id:329555 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K79S EU457
EU456496.1 gg_id:304607 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU456
FJ880297.1 gg_id:409686 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8802
EU474332.1 gg_id:292386 western lowland gorilla feces clone GORSD_aaa03c11 EU474
GQ493316.1 gg_id:545025 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
GQ492842.1 gg_id:568186 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
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DQ796395.1 gg_id:189819 human fecal clone RL179_aah26f09 DQ796
GQ493872.1 gg_id:547852 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
EU460145.1 gg_id:294491 mammals their gut microbes eastern black and white colobus feces clone COL_aai15 EU460
EU775154.1 gg_id:303502 Francois Langur feces clone FL_1aaa03a07 EU775
EU845368.1 gg_id:304394 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU845
EF096845.1 gg_id:197765 mouse cecum clone SWPT13_aaa01f02 EF0968
AY985707.1 gg_id:126405 human stool clone C728 AY985
EF402585.1 gg_id:208154 human fecal clone SJTU_B_09_84 EF4025
GQ897228.1 gg_id:563056 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ897
GQ492934.1 gg_id:535640 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
DQ801473.1 gg_id:175987 human fecal clone RL388_aao96a03 DQ801
GU174117.1 gg_id:567011 Microbial Bactrian camel estimated rumen clone XJC97 GU174
EU764770.1 gg_id:340567 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2 EU764
EU763008.1 gg_id:303930 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A> EU763
FJ372260.1 gg_id:360965 feces adult twins and mothers; TS9 clone TS9_a03e09 FJ3722
EF640147.1 gg_id:248923 pig feces clone lcy22 EF6401
DQ794444.1 gg_id:192127 human fecal clone RL197_aah87g12 DQ794
NZ_ABWN01000012.1 gg_id:469890 Butyrivibrio crossotus str. DSM 2876 NZ_AB
DQ794722.1 gg_id:181041 human fecal clone RL240_aaj31e11 DQ794
DQ238618.1 gg_id:144395 Effect daidzein on piglets piglet gastrointestinal tract clone 1 DQ238
AB270022.1 gg_id:162110 Influence temperature and humidity on heifers rumen contents Holstein heifer (Bos AB270
GQ492433.1 gg_id:571748 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
EU468256.1 gg_id:293542 domesticated horse feces clone horsej_c12_1 EU468
DQ793269.1 gg_id:195777 human fecal clone RL199_aaj41e08 DQ793
EU763093.1 gg_id:343283 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A> EU763
DQ805756.1 gg_id:179905 human fecal clone RL306aal90f08 DQ805
AM696759.1 gg_id:223303 sequencing libraries indoor dust clone BF0001A046 AM696
EU765093.1 gg_id:353263 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2 EU765
EU844548.1 gg_id:340280 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
FJ371396.1 gg_id:359178 feces adult twins and mothers; TS6 clone TS6_a04d11 FJ3713
EF404326.1 gg_id:211540 human fecal clone SJTU_C_08_40 EF4043
DQ794863.1 gg_id:189600 human fecal clone RL310_aam37c05 DQ794

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DQ804158.1 gg_id:191714 human fecal clone RL187_aah69d12 DQ804
DQ795164.1 gg_id:187782 human fecal clone RL310_aam40h12 DQ795
EU762952.1 gg_id:348169 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU762
EU471977.1 gg_id:301388 francois langur feces clone FL_1aaa04a10 EU471
FJ679710.1 gg_id:526071 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6797
AJ409005.1 gg_id:24781 human colonic clone HuCB40 AJ409
EU764765.1 gg_id:327131 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B EU764
DQ806689.1 gg_id:195805 human fecal clone RL186_aao47f01 DQ806
EU504017.1 gg_id:261336 cecal contents Mus musculus strain C57BL/6J; CRWD4 clone CRWD4_aaa04b01 EU504
DQ801110.1 gg_id:193230 human fecal clone RL387_aao92d01 DQ801
EU456575.1 gg_id:332340 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80 EU456
FJ367597.1 gg_id:361213 feces adult twins and mothers; TS2 clone TS2_a01d05 FJ3675
EU530233.1 gg_id:262722 mucosa adherent and invasive microbes adenoma colorectal cancer profile non-ade EU530
DQ800976.1 gg_id:188512 human fecal clone RL387_aao90c01 DQ800
EU765965.1 gg_id:311303 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B EU765
EU462891.1 gg_id:294487 southern three-banded armadillo feces clone arma_aaj54e12 EU462
DQ798871.1 gg_id:190477 human fecal clone RL242_aaj98d11 DQ798
DQ799606.1 gg_id:192915 human fecal clone RL305aal88b12 DQ799
AY985782.1 gg_id:116743 human stool clone D026 AY985
DQ806051.1 gg_id:193217 human fecal clone RL186_aah60e03 DQ806
GQ493445.1 gg_id:546052 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
AB494755.1 gg_id:547665 Fibrobacter succinogenes dominated consortium on hay stems sheep rumen clone A AB494
AB494779.1 gg_id:579311 Fibrobacter succinogenes dominated consortium on hay stems sheep rumen clone A AB494
EF404061.1 gg_id:213816 human fecal clone SJTU_C_04_19 EF404
FJ368330.1 gg_id:361635 feces adult twins and mothers; TS3 clone TS3_a03a08 FJ3683
FJ372168.1 gg_id:367125 feces adult twins and mothers; TS9 clone TS9_a02e06 FJ3721
FJ833467.1 gg_id:510062 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J1Q201_55G07 FJ8334
EU766528.1 gg_id:316083 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B EU766
EF403438.1 gg_id:211181 human fecal clone SJTU_A2_01_21 EF4034
EF402531.1 gg_id:215047 human fecal clone SJTU_B_09_16 EF4025
EU381610.1 gg_id:264313 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid EU381
EU458460.1 gg_id:291414 spotted hyena feces clone HY2_a01 EU458
EU344729.1 gg_id:261203 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU344
EU776091.1 gg_id:305313 Spotted hyena feces clone HY1_g06_1 EU776
DQ801360.1 gg_id:199664 human fecal clone RL388_aao94e02 DQ801
EF403976.1 gg_id:204178 human fecal clone SJTU_C_03_11 EF4039
EU772690.1 gg_id:321253 Bush dog feces clone bdog1_aai79a04 EU772
EU463034.1 gg_id:294961 southern three-banded armadillo feces clone arma_aaj56g08 EU463
FJ672959.1 gg_id:515271 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6729
FJ372102.1 gg_id:366666 feces adult twins and mothers; TS9 clone TS9_a01g07 FJ3721

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DQ807113.1 gg_id:193448 human fecal clone RL244_aaj46d10 DQ807
DQ800347.1 gg_id:194544 human fecal clone RL303_aal71h08 DQ800
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EF686632.1 gg_id:236124 Sequences Manifest Rumen Yunnan Yel Cattle (Bos Taurus) rumen fluid clone YNRC1 EF6866
FJ676668.1 gg_id:517208 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6766
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EU762071.1 gg_id:308387 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1 EU762
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DQ793638.1 gg_id:180227 human fecal clone RL246_aai74h02 DQ793
GQ502571.1 gg_id:590175 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf4- GQ502
EU381592.1 gg_id:275820 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid EU381
FJ676977.1 gg_id:531283 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6769
DQ797151.1 gg_id:196381 human fecal clone RL386_aao87f02 DQ797
FJ368198.1 gg_id:368834 feces adult twins and mothers; TS3 clone TS3_a01d05 FJ3681
EU471825.1 gg_id:290640 Asiatic elephant feces clone AE2_aaa01g09 EU471
EU462992.1 gg_id:294733 southern three-banded armadillo feces clone arma_aaj56c04 EU462
DQ801551.1 gg_id:188196 human fecal clone RL388_aao96h11 DQ801
AF371593.1 gg_id:68842 swine intestine clone p-4575-4Wb3 AF371
DQ326817.1 gg_id:150407 Metagenomic gut microbiome healthy human stool clone E290 DQ326
EU465902.1 gg_id:302429 African elephant feces clone AFEL3_aao13g05 EU465
FJ368441.1 gg_id:364589 feces adult twins and mothers; TS3 clone TS3_a04d05 FJ3684
GQ898745.1 gg_id:565505 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do GQ898
DQ057383.1 gg_id:130103 chicken ileum/cecum clone cc186 DQ057
EU771866.1 gg_id:333067 Southern three-banded armadillo feces clone arma_aaj56e09 EU771
EU381536.1 gg_id:260158 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid EU381
DQ805270.1 gg_id:192488 human fecal clone RL249_aaj84b05 DQ805
EF402051.1 gg_id:203933 human fecal clone SJTU_B_02_93 EF402

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FJ673138.1 gg_id:523606 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6731
EU843729.1 gg_id:327420 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
EU773511.1 gg_id:347200 Bonobo feces clone BNO_aaa02d08 EU773
FJ684021.1 gg_id:522696 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6840
FJ833395.1 gg_id:537491 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J1Q101_45E06 FJ8333
DQ799462.1 gg_id:174709 human fecal clone RL305aal86e11 DQ799
DQ797183.1 gg_id:192513 human fecal clone RL386_aao88a10 DQ797
EF403388.1 gg_id:207390 human fecal clone SJTU_A1_7_6 EF4033
DQ800938.1 gg_id:180562 human fecal clone RL387_aao89f04 DQ800
EU771222.1 gg_id:317818 Asiatic elephant feces clone AE3_aaa01a12 EU771
EU771954.1 gg_id:337465 Southern three-banded armadillo feces clone arma_aaj54f04 EU771
DQ327113.1 gg_id:145966 Metagenomic gut microbiome healthy human stool clone E631 DQ327
EU381587.1 gg_id:268183 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid EU381
EU777129.1 gg_id:324917 Okapi feces clone OK1_g06 EU777
FJ832328.1 gg_id:509226 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P1Q301_31G04 FJ8323
DQ801476.1 gg_id:178774 human fecal clone RL388_aao96a08 DQ801
FJ833622.1 gg_id:594255 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J1Q402_11C02 FJ8336
EU850599.1 gg_id:328553 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF431 EU850
DQ804798.1 gg_id:185925 human fecal clone RL187_aao72g12 DQ804
GQ492365.1 gg_id:536336 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
EU462282.1 gg_id:293511 chimpanzee feces clone CHIMP1_aaj39b12 EU462
DQ673545.1 gg_id:166637 rumen fluid clone GRC80 DQ673
FJ681633.1 gg_id:513474 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6816
EU762110.1 gg_id:323071 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1 EU762
AY984165.1 gg_id:120309 human stool clone B049 AY984
FJ367874.1 gg_id:360592 feces adult twins and mothers; TS2 clone TS2_a04e11 FJ3678
FJ673360.1 gg_id:526301 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6733
DQ805079.1 gg_id:175959 human fecal clone RL385_aao84h09 DQ805
AB494795.1 gg_id:559499 Fibrobacter succinogenes dominated consortium on hay stems sheep rumen clone A AB494
EU844564.1 gg_id:333139 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
AY979556.1 gg_id:124784 human transverse colon mucosal biopsy clone M217 AY979
EU457230.1 gg_id:308224 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU457
DQ803572.1 gg_id:183436 human fecal clone RL251_aaj87f01 DQ803
EU764773.1 gg_id:324574 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2 EU764
FJ672986.1 gg_id:527972 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6729
EU474741.1 gg_id:289636 takin feces clone TAK_aaa01a05 EU474
EU777239.1 gg_id:350732 Okapi feces clone OK3_f07 EU777
DQ326920.1 gg_id:148694 Metagenomic gut microbiome healthy human stool clone E411 DQ326
EU843498.1 gg_id:330352 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
GQ493359.1 gg_id:566623 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493

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AY858459.2 gg_id:110682 gastrointestinal tract zebra clone ZEBRA_20 AY8584
FJ370755.1 gg_id:368416 feces adult twins and mothers; TS57 clone TS57_a04h06 FJ3707
EU748068.1 gg_id:353775 neotropical folivorous flying bird adult hoatzin crop clone hoa2_43g03 EU748
AM697398.1 gg_id:225076 sequencing libraries indoor dust clone BF0001D013 AM697
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EU779344.1 gg_id:334956 Somali Wild Ass feces clone WA_aaa03a06 EU779
DQ796666.1 gg_id:184565 human fecal clone RL179aan76h06 DQ796
AB288925.1 gg_id:202310 termite gut homogenate clone BOf12-06 AB288
EU762975.1 gg_id:316156 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU762
AF371582.1 gg_id:29205 swine intestine clone p-57-a5 AF3715
AY985812.1 gg_id:116723 human stool clone D067 AY9858
DQ057364.1 gg_id:128392 chicken ileum/cecum clone cc110 DQ057
GQ493363.1 gg_id:564583 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
FJ368340.1 gg_id:369404 feces adult twins and mothers; TS3 clone TS3_a03b08 FJ3683
EF403348.1 gg_id:211205 human fecal clone SJTU_A1_6_69 EF4033
EF404635.1 gg_id:214825 human fecal clone SJTU_C_13_82 EF4046
EU459681.1 gg_id:291997 ring-tailed lemur feces clone RT_aai10g06 EU459
FJ367841.1 gg_id:360727 feces adult twins and mothers; TS2 clone TS2_a04c01 FJ3678
DQ794467.1 gg_id:180911 human fecal clone RL197_aah88c06 DQ794
DQ800571.1 gg_id:195449 human fecal clone RL183_aah30a09 DQ800
EU461161.1 gg_id:291713 hamadryas baboon feces clone BAZ_aah89e06 EU461
DQ796881.1 gg_id:195675 human fecal clone RL179_aao55h07 DQ796
EU778721.1 gg_id:327266 Springbok feces clone SBSD_aaa03e05 EU778
EU462798.1 gg_id:289181 southern three-banded armadillo feces clone arma_aaj53c08 EU462
DQ815735.1 gg_id:172857 mouse cecum clone aab21f03 DQ815
DQ326745.1 gg_id:147644 Metagenomic gut microbiome healthy human stool clone E205 DQ326
FJ675975.1 gg_id:530740 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6759
DQ805223.1 gg_id:197121 human fecal clone RL249_aaj83c09 DQ805
EU452521.1 gg_id:320141 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU452
FJ363748.1 gg_id:366612 feces adult twins and mothers; TS14 clone TS14_a02g11 FJ3637
EU748519.1 gg_id:345339 neotropical folivorous flying bird adult hoatzin crop clone hoa61_11d02 EU748
DQ809238.1 gg_id:186237 human fecal clone RL308_aal83g11 DQ809
EU844853.1 gg_id:305726 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
AF371573.1 gg_id:21881 swine intestine clone p-1616-c5 AF3715
GQ493531.1 gg_id:552681 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
EF436378.1 gg_id:207610 library-based ruminal water buffalo (Bubalus bubalis) rumen fluid clone BRC92 EF4363

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GQ491903.1 gg_id:541554 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
GQ175376.1 gg_id:513132 Chicken intestinal microbiota modulations various feed supplementations DGGE anc GQ175
FJ681212.1 gg_id:526436 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6812
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DQ798787.1 gg_id:195294 human fecal clone RL242_aaj97d04 DQ798
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GU302776.1 gg_id:564138 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU302
EU259384.1 gg_id:236097 Rumen yak (Bos grunniens) sequences rumen fluid clone YRC8 EU259
EU766228.1 gg_id:316136 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU766
DQ804133.1 gg_id:186334 human fecal clone RL187_aah69b06 DQ804
GQ493885.1 gg_id:570496 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
EU765927.1 gg_id:320147 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B4 EU765
AF371568.1 gg_id:49141 swine intestine clone p-355-a3 AF371
FJ680379.1 gg_id:530243 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6803
DQ796324.1 gg_id:178474 human fecal clone RL179_aah25g07 DQ796
EU779375.1 gg_id:352840 Somali Wild Ass feces clone WA_aaa01h05 EU779
EU765704.1 gg_id:342929 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B3 EU765
DQ801320.1 gg_id:195032 human fecal clone RL388_aao93h07 DQ801
EU767358.1 gg_id:352792 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C2 EU767
EU472571.1 gg_id:298701 Angola colobus feces clone EAC_2_aaa02h11 EU472
FJ833576.1 gg_id:579126 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J1Q401_47G06 FJ8335
EU778532.1 gg_id:318470 Red river hog feces clone RRH_aaa01c10 EU778
EU464334.1 gg_id:299814 hamadryas baboon feces clone AFBAB_aai02h08 EU464
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AM276768.2 gg_id:230741 fecal microbiota irritable bowel syndrome patients significantly that healthy subject AM276
DQ801456.1 gg_id:190280 human fecal clone RL388_aao95g05 DQ801
EU767534.1 gg_id:339790 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C2 EU767
EU771984.1 gg_id:329662 Southern three-banded armadillo feces clone arma_aaj54g06 EU771
DQ799971.1 gg_id:190961 human fecal clone RL247_aaj22e07 DQ799
EU765750.1 gg_id:322377 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B3 EU765
DQ797780.1 gg_id:195509 human fecal clone RL206_aaj15g06 DQ797
EU767434.1 gg_id:352852 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C2 EU767
AY983070.1 gg_id:119344 human descending colon mucosal biopsy clone L313 AY983
DQ804852.1 gg_id:177986 human fecal clone RL385_aao81f01 DQ804
EU778831.1 gg_id:317041 Black-handed Spider Monkey feces clone SPIM_aaj33f01 EU778
FJ682817.1 gg_id:525948 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6828
FJ370121.1 gg_id:363780 feces adult twins and mothers; TS55 clone TS55_a04f06 FJ3701
DQ798059.1 gg_id:194648 human fecal clone RL302_aal95a11 DQ798

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EU344663.1 gg_id:260855 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU344
FJ679598.1 gg_id:527276 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6795
AY239462.1 gg_id:97679 Clostridium sp. cTPY-17 AY2394
DQ801352.1 gg_id:195793 human fecal clone RL388_aao94d06 DQ801
EU463470.1 gg_id:290514 domesticated horse feces clone horsem_aai94e11 EU463
FJ675753.1 gg_id:519815 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6757
DQ808253.1 gg_id:187425 human fecal clone RL180_aao74d10 DQ808
DQ802555.1 gg_id:196013 human fecal clone RL188_aan93d03 DQ802
FJ367734.1 gg_id:364859 feces adult twins and mothers; TS2 clone TS2_a03a03 FJ3677
FJ880611.1 gg_id:370809 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8806
EU776530.1 gg_id:305881 Lion feces clone LI2_aae49b11 EU776
EU464984.1 gg_id:290079 African elephant feces clone AFYEL_aaj66c03 EU464
EU774288.1 gg_id:356410 Chimpanzee feces clone CHIMP1_b07_1 EU774
DQ795273.1 gg_id:187470 human fecal clone RL178_aah52d02 DQ795
EU467273.1 gg_id:293835 black-handed spider monkey feces clone SPIM_e02_1 EU467
DQ796977.1 gg_id:179115 human fecal clone RL386_aao85c06 DQ796
DQ824427.1 gg_id:199308 human fecal clone RL304_aal75h05 DQ824
AF371554.1 gg_id:22771 swine intestine clone p-214-o5 AF371
EU467600.1 gg_id:302443 southern three-banded armadillo feces clone arma_a10_2 EU467
EU774768.1 gg_id:336539 Angola Colobus feces clone EAC_2_aaa04g07 EU774
DQ327377.1 gg_id:146774 Metagenomic gut microbiome healthy human stool clone E934 DQ327
FJ370482.1 gg_id:363144 feces adult twins and mothers; TS57 clone TS57_a01f02 FJ3704
EU474994.1 gg_id:297271 red river hog feces clone RRH_aaa03a09 EU474
FJ684167.1 gg_id:509948 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6841
EU468918.1 gg_id:288160 Speke's gazelle feces clone SP2_c03_1 EU468
EU771676.1 gg_id:324696 African elephant feces clone AFEL3_aao14d08 EU771
FJ833377.1 gg_id:577323 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J1Q101_06F01 FJ8333
DQ326550.1 gg_id:148288 Metagenomic gut microbiome healthy human stool clone C717 DQ326
FJ678967.1 gg_id:511702 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6789
EU467081.1 gg_id:290467 mongoose lemur feces clone ML_aae87f05 EU467
DQ806352.1 gg_id:183449 human fecal clone RL186_aan91b04 DQ806
DQ803435.1 gg_id:195336 human fecal clone RL251_aaj85g05 DQ803
EU464713.1 gg_id:297440 Hartmann's mountain zebra feces clone AFZEB_aaj69e12 EU464
EU766185.1 gg_id:319374 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU766
FJ673541.1 gg_id:515133 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6735
EU773502.1 gg_id:351880 Bonobo feces clone BNO_aaa03h07 EU773
EU465395.1 gg_id:296257 lion feces clone LI3_aah76f05 EU465
EU344701.1 gg_id:274828 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU344
DQ810001.1 gg_id:177820 human fecal clone RL184_aao66h07 DQ810
FJ366131.1 gg_id:362662 feces adult twins and mothers; TS25 clone TS25_a03b01 FJ3661

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DQ456135.1 gg_id:158566 pre-adolescent turkey cecum clone CFT114G12 DQ456
DQ057374.1 gg_id:130289 chicken ileum/cecum clone cc151 DQ057
FJ683028.1 gg_id:509752 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6830
EU842178.1 gg_id:341449 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
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AF371561.1 gg_id:36330 swine intestine clone p-195-o5 AF371
EU777867.1 gg_id:337551 European rabbit feces clone RA_a03_1 EU777
FJ677862.1 gg_id:527800 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6778
FJ369295.1 gg_id:359255 feces adult twins and mothers; TS50 clone TS50_a02f06 FJ3692
FJ673384.1 gg_id:531690 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6733
DQ326682.1 gg_id:149120 Metagenomic gut microbiome healthy human stool clone E129 DQ326
DQ326355.1 gg_id:146254 Metagenomic gut microbiome healthy human stool clone C358 DQ326
EU469410.1 gg_id:287978 black lemur feces clone BKLE_d05 EU469
EU467214.1 gg_id:291883 black-handed spider monkey feces clone SPIM_c05 EU467
EU771482.1 gg_id:321822 Hamadryas Baboon feces clone AFBAB_aai01h09 EU771
FJ683838.1 gg_id:526575 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6838
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DQ800765.1 gg_id:183368 human fecal clone RL183_aao03b10 DQ800
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FJ673350.1 gg_id:513767 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6733
EU776792.1 gg_id:355905 Mongoose lemur feces clone ML_aaj25h01 EU776
AF371619.1 gg_id:103407 swine intestine clone p-1631-c5 AF371
DQ824461.1 gg_id:195946 human fecal clone RL304_aal76c08 DQ824
FJ679856.1 gg_id:527985 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6798
EU777917.1 gg_id:320009 European rabbit feces clone RA_f07_3 EU777
GQ896703.1 gg_id:593086 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do GQ896
DQ808139.1 gg_id:184983 human fecal clone RL180_aao73b05 DQ808
EU510056.1 gg_id:267797 cecal contents Mus musculus strain C57BL/6J; WD1 clone WD1_aaf11e10 EU510
EU774616.1 gg_id:318760 Angola Colobus feces clone EAC_2_aaa03g04 EU774
FJ370471.1 gg_id:369394 feces adult twins and mothers; TS57 clone TS57_a01e03 FJ3704
DQ801050.1 gg_id:197076 human fecal clone RL387_aao91d10 DQ801
DQ808546.1 gg_id:182513 human fecal clone RL239_aaj10a03 DQ808
DQ806797.1 gg_id:179807 human fecal clone RL186_aao48g11 DQ806
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DQ794523.1 gg_id:182428 human fecal clone RL240_aaj29b04 DQ794

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DQ809906.1 gg_id:190092 human fecal clone RL184_aao65g07 DQ809
GQ896616.1 gg_id:557450 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do GQ896
DQ807661.1 gg_id:178609 human fecal clone RL180_aah35f04 DQ807
DQ796984.1 gg_id:179989 human fecal clone RL386_aao85d04 DQ796
EU778867.1 gg_id:329526 Black-handed Spider Monkey feces clone SPIM_f07_1 EU778
EU775452.1 gg_id:321589 Western lowland gorilla feces clone GORSD_2aaa03d01 EU775
FJ674257.1 gg_id:522727 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6742
FJ682726.1 gg_id:527135 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6827
GQ864252.1 gg_id:592901 microbiota geese cecum lumen clone ML1 GQ864
EU530329.1 gg_id:274745 mucosa adherent and invasive microbes profile adenoma colorectal cancer clone M4 EU530
EU778076.1 gg_id:342933 feces clone RL116_aae99e06 EU778
DQ326564.1 gg_id:147799 Metagenomic gut microbiome healthy human stool clone C746 DQ326
DQ809460.1 gg_id:183866 human fecal clone RL184_aah21c06 DQ809
AY684376.2 gg_id:110457 mucosal biopsies human intestine clone HuRC75 AY6843
FJ673139.1 gg_id:519398 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6731
EU459775.1 gg_id:299302 ring-tailed lemur feces clone RT_aai12e10 EU459
EF403824.1 gg_id:214980 human fecal clone SJTU_C_01_02 EF4038
EU467083.1 gg_id:290922 mongoose lemur feces clone ML_aae87f07 EU467
DQ327356.1 gg_id:149445 Metagenomic gut microbiome healthy human stool clone E911 DQ327
FJ681296.1 gg_id:525329 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6812
FJ673124.1 gg_id:526780 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6731
DQ905375.1 gg_id:164113 human fecal clone 013C-A5 DQ905
EU774799.1 gg_id:311692 Angola Colobus feces clone EAC_2_aaa04g11 EU774
DQ794777.1 gg_id:174078 human fecal clone RL240_aaj32c02 DQ794
EU773433.1 gg_id:325586 Black lemur feces clone BKLE_b02 EU773
DQ777928.1 gg_id:161899 rat feces clone R-1319 DQ777
FJ682390.1 gg_id:520588 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6823
FJ678944.1 gg_id:519149 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6789
FJ678858.1 gg_id:522624 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6788
EU508047.1 gg_id:260800 cecal contents Mus musculus strain C57BL/6J; MD25 clone MD25_aaa02f04 EU508
FJ677197.1 gg_id:514623 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6771
DQ806721.1 gg_id:186869 human fecal clone RL186_aao47h11 DQ806
FJ676370.1 gg_id:528050 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6763
DQ794600.1 gg_id:177977 human fecal clone RL240_aaj30b02 DQ794
FJ364246.1 gg_id:369450 feces adult twins and mothers; TS150 clone TS150_a04f09 FJ3642
DQ797980.1 gg_id:178994 human fecal clone RL302_aal94b03 DQ797
FJ978523.1 gg_id:453756 feces clone CL_F_054 FJ9785
DQ806841.1 gg_id:184514 human fecal clone RL198_aaj73g03 DQ806
FJ363309.1 gg_id:366333 feces adult twins and mothers; TS149 clone TS149_a01f12 FJ3633
FJ679241.1 gg_id:520841 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6792

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EU773219.1 gg_id:352777 BigHorn sheep feces clone BH1_aao26b01 EU773
GQ493996.1 gg_id:557489 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
AY978904.1 gg_id:116192 human transverse colon mucosal biopsy clone NF83 AY978
AJ608222.1 gg_id:145181 human biopsies ulcerative colitis biopsy clone UC7-4 AJ6082
AF371562.1 gg_id:103782 swine intestine clone p-2565-9F5 AF371
DQ804819.1 gg_id:187384 human fecal clone RL385_aao81b03 DQ804
EU774109.1 gg_id:320898 Chimpanzee feces clone CHIMP1_d08 EU774
FJ679838.1 gg_id:527736 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6798
FJ371321.1 gg_id:358483 feces adult twins and mothers; TS6 clone TS6_a03e12 FJ3713
FJ677257.1 gg_id:529683 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6772
DQ797030.1 gg_id:189685 human fecal clone RL386_aao86a10 DQ797
FJ880395.1 gg_id:377385 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8803
EU462840.1 gg_id:299884 southern three-banded armadillo feces clone arma_aaj53h01 EU462
DQ673522.1 gg_id:164569 rumen fluid clone GRC57 DQ673
GQ493042.1 gg_id:578960 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
EU474973.1 gg_id:289074 red river hog feces clone RRH_aaa04d09 EU474
DQ802768.1 gg_id:193704 human fecal clone RL188_aan96d02 DQ802
FJ370555.1 gg_id:361483 feces adult twins and mothers; TS57 clone TS57_a02d11 FJ3705
DQ798027.1 gg_id:178352 human fecal clone RL302_aal94f11 DQ798
EU475035.1 gg_id:297101 visayam warty pig feces clone VWP_aaa02a02 EU475
EU458658.1 gg_id:296606 European rabbit feces clone RA_b11 EU458
EU462117.1 gg_id:298632 black-handed spider monkey feces clone SPIM_aaj35c05 EU462
DQ804840.1 gg_id:185090 human fecal clone RL385_aao81d08 DQ804
FJ672578.1 gg_id:526064 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6725
EU468606.1 gg_id:300581 okapi feces clone OK1_h08_1 EU468
FJ680287.1 gg_id:520937 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6802
EU773244.1 gg_id:316452 BigHorn sheep feces clone BH1_aao28g03 EU773
EU458517.1 gg_id:302666 spotted hyena feces clone HY2_a09 EU458
FJ879040.1 gg_id:391692 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8790
EU765088.1 gg_id:319438 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2 EU765
EU772937.1 gg_id:306431 Bush dog feces clone bdog1_e11_1 EU772
EU765584.1 gg_id:353840 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B3 EU765
EU775824.1 gg_id:333807 Horse feces clone horsem_aai93b02 EU775
DQ803717.1 gg_id:195413 human fecal clone RL200_aai57e06 DQ803
EU461559.1 gg_id:300036 black rhinoceros feces clone RH_aaj92e04 EU461
EU469503.1 gg_id:290696 black lemur feces clone BKLE_a05_2 EU469
EU776796.1 gg_id:303866 Mongoose lemur feces clone ML_aaj26h09 EU776
FJ880217.1 gg_id:455746 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8802
EU466069.1 gg_id:299639 bighorn sheep feces clone BH1_aao25b10 EU466
EU766047.1 gg_id:352733 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B4 EU766

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AY974824.1 gg_id:120145 human ascending colon mucosal biopsy clone KG39 AY974
EU765285.1 gg_id:353980 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B EU765
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AY977050.1 gg_id:125501 human cecum mucosal biopsy clone K737 AY977
DQ057463.1 gg_id:130773 str. ic1311 DQ057
AF349429.1 gg_id:77514 pig feces clone AF349
FJ682459.1 gg_id:531092 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6824
DQ681227.1 gg_id:169077 Clostridium sp. str. CCUG 52336 DQ681
DQ804981.1 gg_id:183879 human fecal clone RL385_aao83e12.Contig2 DQ804
EU765646.1 gg_id:314952 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B EU765
FJ678196.1 gg_id:531800 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6781
EU464411.1 gg_id:294003 hamadryas baboon feces clone AFBAB_aai04e09 EU464
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DQ810086.1 gg_id:173818 human fecal clone RL184_aao67h09 DQ810
FJ683201.1 gg_id:520429 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6832
EU458581.1 gg_id:296062 European rabbit feces clone RA_b10 EU458
DQ806698.1 gg_id:182568 human fecal clone RL186_aao47f11 DQ806
DQ326854.1 gg_id:145816 Metagenomic gut microbiome healthy human stool clone E333 DQ326
EU344424.1 gg_id:274536 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU344
EU764140.1 gg_id:334924 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU764
EU771275.1 gg_id:311521 Asiatic elephant feces clone AE2_aaa01a04 EU771
DQ904671.1 gg_id:166355 human fecal clone 001-c9 DQ904
FJ371836.1 gg_id:368489 feces adult twins and mothers; TS8 clone TS8_a02g04 FJ3718
EU779456.1 gg_id:350041 Grevy's Zebra feces clone GZ_aaa04d07 EU779
FJ677085.1 gg_id:508767 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6770
EU462009.1 gg_id:301062 black-handed spider monkey feces clone SPIM_aaj33c04 EU462
DQ797205.1 gg_id:185589 human fecal clone RL386_aao88d02 DQ797
DQ794958.1 gg_id:174728 human fecal clone RL310_aam38d10 DQ794
EU767041.1 gg_id:308033 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C EU767
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EF686595.1 gg_id:239218 Sequences Manifest Rumen Yunnan Yel Cattle (Bos Taurus) rumen fluid clone YNRC8 EF6865
EU534682.1 gg_id:281927 profile human skin microbiota ear punch biopsy female C57BL/6J mouse clone nbt18 EU534

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EU504979.1 gg_id:268552 cecal contents Mus musculus strain C57BL/6J; myd3 clone myd3_aaa01b03 EU504
EF100032.1 gg_id:175557 mouse cecum clone SWPT5_aaa03g03 EF100
AY993003.1 gg_id:130513 mouse cecum clone C22_n24 AY993
EF099410.1 gg_id:197215 mouse cecum clone SWPT3_aaa02h03 EF0994
EU457313.1 gg_id:344832 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU457
DQ793516.1 gg_id:202709 human fecal clone RL199_aaj44g09 DQ793
EU776954.1 gg_id:304097 Naked mole-rat feces clone molerat_2b12 EU776
EU456999.1 gg_id:324469 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU456
EU451921.1 gg_id:353922 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H78S EU451
EF096326.1 gg_id:185929 mouse cecum clone obob1_aaa04h11 EF0963
EF097332.1 gg_id:199333 mouse cecum clone SWPT19_aaa01c01 EF0973
EU474288.1 gg_id:289866 western lowland gorilla feces clone GORSD_aaa04e11 EU474
EU474220.1 gg_id:303184 western lowland gorilla feces clone GORSD_aaa02a10 EU474
EU453947.1 gg_id:333602 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU453
EU456021.1 gg_id:305896 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75N EU456
EU453094.1 gg_id:313898 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU453
EU505189.1 gg_id:274627 cecal contents Mus musculus strain C57BL/6J; myd3 clone myd3_aaa04b11 EU505
EU452853.1 gg_id:311225 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H74N EU452
EF097330.1 gg_id:191857 mouse cecum clone SWPT19_aaa01b08 EF0973
EU504478.1 gg_id:269893 cecal contents Mus musculus strain C57BL/6J; myd1 clone myd1_aaa01b08 EU504
EU452157.1 gg_id:345604 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H74N EU452
EU510069.1 gg_id:267012 cecal contents Mus musculus strain C57BL/6J; WD1 clone WD1_aaf12b05 EU510
EF099469.1 gg_id:196740 mouse cecum clone SWPT3_aaa03e12 EF0994
EU778263.1 gg_id:352604 feces clone RL388_aao96c11 EU778
DQ014586.1 gg_id:132198 mouse cecum clone M1_d02 DQ014
EU505016.1 gg_id:263685 cecal contents Mus musculus strain C57BL/6J; myd3 clone myd3_aaa01f06 EU505
EU842518.1 gg_id:317517 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
FJ881271.1 gg_id:381030 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8812
EU503982.1 gg_id:268133 cecal contents Mus musculus strain C57BL/6J; CRWD4 clone CRWD4_aaa03f02 EU503
EU468265.1 gg_id:292256 domesticated horse feces clone horsej_f07_2 EU468
EU457124.1 gg_id:331117 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H74N EU457
EU456402.1 gg_id:352955 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU456
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EF097660.1 gg_id:177443 mouse cecum clone SWPT20_aaa01h09 EF0976
FJ833939.1 gg_id:551915 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P2Q201_72H09 FJ8339
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EU458083.1 gg_id:338652 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU458

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EU504954.1 gg_id:265135 cecal contents Mus musculus strain C57BL/6J; myd2 clone myd2_aaa04g05 EU504
EU467414.1 gg_id:296960 chimpanzee feces clone CHIMP12_a09_1 EU467
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EU504093.1 gg_id:263621 cecal contents Mus musculus strain C57BL/6J; CRWD5 clone CRWD5_aaa01b06 EU504
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EU655813.1 gg_id:286236 influence dietary flavonoid-containing extracts on gut microbiota mouse feces clone EU655
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EU451028.1 gg_id:307134 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU451
EU452732.1 gg_id:315731 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU452
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EU778338.1 gg_id:312707 feces clone RL388_aao93g07 EU778
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FJ881252.1 gg_id:372432 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8812
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EF097744.1 gg_id:183649 mouse cecum clone SWPT20_aaa03a10 EF0977
EU474227.1 gg_id:289283 western lowland gorilla feces clone GORSD_aaa02g03 EU474
EU456912.1 gg_id:309335 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H74 EU456
EF097562.1 gg_id:180476 mouse cecum clone SWPT19_aaa04d07 EF0975
EU455509.1 gg_id:313058 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75 EU455
EU467652.1 gg_id:288325 naked mole-rat feces clone molerat_2b01_1 EU467
EU505125.1 gg_id:266288 cecal contents Mus musculus strain C57BL/6J; myd3 clone myd3_aaa03b12 EU505
EF099346.1 gg_id:187648 mouse cecum clone SWPT3_aaa02a07 EF0993
EU503843.1 gg_id:273118 cecal contents Mus musculus strain C57BL/6J; CRWD4 clone CRWD4_aaa01d07 EU503
EU452596.1 gg_id:345936 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74 EU452
EF098890.1 gg_id:196119 mouse cecum clone SWPT1_aaa02g12 EF0988
EU475497.1 gg_id:293085 springbok feces clone SBSD_aaa02d11 EU475
EU778225.1 gg_id:311587 feces clone RL387_aao91b09 EU778
EU773290.1 gg_id:332742 BigHorn sheep feces clone BH1_aao26d03 EU773
DQ805491.1 gg_id:196494 human fecal clone RL203_aai63d02 DQ805
EU461402.1 gg_id:288950 red kangaroo feces clone KO2_aai20c04 EU461
EU778262.1 gg_id:347758 feces clone RL388_aao96h02 EU778
EU503709.1 gg_id:261132 cecal contents Mus musculus strain C57BL/6J; CRWD2 clone CRWD2_aaa03e06 EU503
EU456193.1 gg_id:305753 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77 EU456
EF098371.1 gg_id:202419 mouse cecum clone SWPT15_aaa01g04 EF0983
AB525414.1 gg_id:590169 Eubacterium saburreum str. JCM 11021 AB525
EF096517.1 gg_id:176243 mouse cecum clone obob2_aaa04b10 EF0965
EU451862.1 gg_id:304890 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78 EU451
EU507682.1 gg_id:267982 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_aaa03b04 EU507
EU453519.1 gg_id:325047 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77 EU453
EU455560.1 gg_id:317493 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75 EU455
AJ272036.1 gg_id:30334 Parasporobacterium paucivorans str. SYR1 AJ272
EU504236.1 gg_id:267699 cecal contents Mus musculus strain C57BL/6J; CRWD5 clone CRWD5_aaa04g05 EU504
EU469466.1 gg_id:288134 black lemur feces clone BKLE_d01_2 EU469
FJ677674.1 gg_id:521913 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6776
EU506582.1 gg_id:265839 cecal contents Mus musculus strain C57BL/6J; MD19 clone MD19_aaa04g04 EU506
EU844109.1 gg_id:335527 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
AF287769.1 gg_id:73894 human subgingival plaque clone AH153 AF287
DQ815607.1 gg_id:171088 mouse cecum clone aab43e06 DQ815
GU304514.1 gg_id:539098 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU304
EU843745.1 gg_id:346371 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
EU507725.1 gg_id:261007 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_aaa03g05 EU507
AB185642.1 gg_id:101771 rumen clone F24-G10 AB185
AM420119.1 gg_id:252100 Noma subgingival plaque clone 401E03(oral) AM420
EU465947.1 gg_id:295489 African elephant feces clone AFEL3_aao14f05 EU465

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AF481219.1 gg_id:73120 oral endodontic infection clone MCE9_104 AF481
EU451262.1 gg_id:356504 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU451
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EF686587.1 gg_id:255980 Sequences Manifest Rumen Yunnan Yel Cattle (Bos Taurus) rumen fluid clone YNRC7 EF6865
EU452564.1 gg_id:341005 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K79S EU452
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EU508104.1 gg_id:261114 cecal contents Mus musculus strain C57BL/6J; MD25 clone MD25_aaa04a12 EU508
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FJ976266.1 gg_id:576638 Interindividual healthy human oral microbiota mouth clone 7BB311 FJ9762
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EU461502.1 gg_id:300401 black rhinoceros feces clone RH_aaj91b02 EU461
EF097966.1 gg_id:185707 mouse cecum clone SWPT12_aaa03a11 EF0979
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EU455218.1 gg_id:335042 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H79S EU455
EU455007.1 gg_id:306262 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K77S EU455
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EF096515.1 gg_id:189280 mouse cecum clone obob2_aaa04b08 EF0965
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EU504643.1 gg_id:260192 cecal contents Mus musculus strain C57BL/6J; myd1 clone myd1_aaa03f11 EU504
EU507674.1 gg_id:274979 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_aaa02h10 EU507
EU458018.1 gg_id:313725 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83M EU458
EU510414.1 gg_id:262884 cecal contents Mus musculus strain C57BL/6J; WD4 clone WD4_aal38b12 EU510
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EU503934.1 gg_id:265562 cecal contents Mus musculus strain C57BL/6J; CRWD4 clone CRWD4_aaa02h08 EU503
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GU303201.1 gg_id:555977 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU303
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EU505530.1 gg_id:258177 cecal contents Mus musculus strain C57BL/6J; myd5 clone myd5_aaa02b08 EU505
EU506568.1 gg_id:262414 cecal contents Mus musculus strain C57BL/6J; MD19 clone MD19_aaa04d08 EU506
EF099474.1 gg_id:174030 mouse cecum clone SWPT3_aaa03f05 EF0994
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DQ015489.1 gg_id:129889 mouse cecum clone M3_f10_1 DQ015

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EU455148.1 gg_id:322240 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H78S EU455
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AF287777.1 gg_id:72977 Eubacterium cf. saburreum oral strain str. C27KA AF287
EU511715.1 gg_id:277083 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_aaf07e05 EU511
GU303475.1 gg_id:540405 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU303
FJ834033.1 gg_id:587347 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P2Q301_72H09 FJ8340
DQ825337.1 gg_id:187419 human fecal clone RL185_aan88g05 DQ825
DQ801639.1 gg_id:190464 human fecal clone RL117_aae93c07 DQ801
FJ362624.1 gg_id:368511 feces adult twins and mothers; TS13 clone TS13_a01c01 FJ3626
EU467624.1 gg_id:303028 naked mole-rat feces clone molerat_2c03 EU467
FJ172890.1 gg_id:319578 Qinghai Yak Ruminal and Fungi China rumen clone RB-136 FJ1728
EU451898.1 gg_id:356223 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU451
GQ175482.1 gg_id:548503 Chicken intestinal microbiota modulations various feed supplementations DGGE and GQ175
EU451412.1 gg_id:339546 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU451
EU505103.1 gg_id:264965 cecal contents Mus musculus strain C57BL/6J; myd3 clone myd3_aaa02h08 EU505
EF097313.1 gg_id:182323 mouse cecum clone SWPT18_aaa04h05 EF0973
EU506936.1 gg_id:264987 cecal contents Mus musculus strain C57BL/6J; MD21 clone MD21_aar08f03 EU506
EU475375.1 gg_id:295250 rock hyrax feces clone RHSD_aaa02b09 EU4753
EU505647.1 gg_id:268309 cecal contents Mus musculus strain C57BL/6J; myd5 clone myd5_aaa04a06 EU505
EF098421.1 gg_id:178817 mouse cecum clone SWPT15_aaa02g11 EF0984
EF096464.1 gg_id:192365 mouse cecum clone obob2_aaa03c06 EF0964
EU844657.1 gg_id:346195 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
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EU506457.1 gg_id:258757 cecal contents Mus musculus strain C57BL/6J; MD19 clone MD19_aaa02c02 EU506
EU454280.1 gg_id:331172 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K79S EU454
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AY854354.1 gg_id:110678 herbivore gastrointestinal tract clone Thompsons76 AY8543
DQ795687.1 gg_id:175685 human fecal clone RL178_aan68f01 DQ795
AM420198.1 gg_id:236261 Noma subgingival plaque clone 502G12(oral) AM420
EU504938.1 gg_id:274146 cecal contents Mus musculus strain C57BL/6J; myd2 clone myd2_aaa04e06 EU504
AY991885.1 gg_id:129741 mouse cecum clone C20_j09 AY9918
EF096321.1 gg_id:182712 mouse cecum clone obob1_aaa04h04 EF0963
EF097874.1 gg_id:182950 mouse cecum clone SWPT12_aaa01b07 EF0978
EU843319.1 gg_id:339293 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
EU843771.1 gg_id:333091 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
EU510601.1 gg_id:265569 cecal contents Mus musculus strain C57BL/6J; WD5 clone WD5_aak38a01 EU510

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EU455846.1 gg_id:307194 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU4558
DQ795505.1 gg_id:175704 human fecal clone RL178_aan65c08 DQ795
EU507521.1 gg_id:276702 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_2aaa04e04 EU5075
FJ833056.1 gg_id:557780 Microbial Ecology Crop Folivorous Hoatzin crop contents clone A1Q201_47G06 FJ8330
EU452541.1 gg_id:314032 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83N EU4525
EU504091.1 gg_id:270764 cecal contents Mus musculus strain C57BL/6J; CRWD5 clone CRWD5_aaa01b04 EU5040
EF097896.1 gg_id:177802 mouse cecum clone SWPT12_aaa01e09 EF0978
GU304020.1 gg_id:583584 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU304
EF099869.1 gg_id:190998 mouse cecum clone SWPT5_aaa01e10.Contig2 EF0998
EU454954.1 gg_id:314134 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H80N EU4549
AF287774.1 gg_id:34466 human subgingival plaque clone CK051 AF2877
EU344721.1 gg_id:262716 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU3447
EF100025.1 gg_id:182954 mouse cecum clone SWPT5_aaa03f07 EF1000
EF099731.1 gg_id:191411 mouse cecum clone SWPT4_aaa03e11 EF0997
DQ014709.1 gg_id:135344 mouse cecum clone M1_g06_1 DQ014
EU510229.1 gg_id:266639 cecal contents Mus musculus strain C57BL/6J; WD3 clone WD3_aak03c03 EU5102
EU453164.1 gg_id:324002 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU4531
FJ671909.1 gg_id:515371 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6719
FJ676985.1 gg_id:517545 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6769
EU456100.1 gg_id:332195 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU4561
FJ879691.1 gg_id:456857 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8796
DQ071484.1 gg_id:227682 microbial cecum captive and free-living capercaillies (Tetrao urogallus) clone TuCc9 DQ071
EU622663.1 gg_id:279019 -feed administered sub-therapeutic chlorotetracycline alters structure and but not a EU6226
EF098355.1 gg_id:180944 mouse cecum clone SWPT15_aaa01d09 EF0983
EU510286.1 gg_id:261810 cecal contents Mus musculus strain C57BL/6J; WD3 clone WD3_aak04b06 EU5102
EF097493.1 gg_id:174860 mouse cecum clone SWPT19_aaa03d09 EF0974
EU509521.1 gg_id:276892 cecal contents Mus musculus strain C57BL/6J; MD9 clone MD9_aap60a08 EU5095
EU510230.1 gg_id:265116 cecal contents Mus musculus strain C57BL/6J; WD3 clone WD3_aak03c04 EU5102
EF602978.1 gg_id:231684 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6029
EU508184.1 gg_id:260627 cecal contents Mus musculus strain C57BL/6J; MD26 clone MD26_aaa02g05 EU5081
DQ925472.1 gg_id:251561 Howardella ureilytica str. GPC589 DQ925
EU748032.1 gg_id:342251 neotropical folivorous flying bird adult hoatzin crop clone hoa14_50B07 EU7480
EU775421.1 gg_id:321778 Western lowland gorilla feces clone GOR_aag73a07 EU7754
AF385508.1 gg_id:71387 on Tongue Dorsa Halitosis Healthy Patients healthy and subjects halitosis clone DO008 AF3855
GU303527.1 gg_id:545236 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU303
EU450999.1 gg_id:348518 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU4509
EU451727.1 gg_id:332854 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K77S EU4517
EU747925.1 gg_id:355742 neotropical folivorous flying bird adult hoatzin crop clone hoa11_74B10 EU7479
EU510553.1 gg_id:277176 cecal contents Mus musculus strain C57BL/6J; WD5 clone WD5_aak37a10 EU5105
DQ795656.1 gg_id:199455 human fecal clone RL178_aan67h03 DQ795

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