EU508185.1 gg_id:263902 cecal contents Mus musculus strain C57BL/6J; MD26 clone MD26_aaa02g06 EU508
EU456793.1 gg_id:349351 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU456
DQ015012.1 gg_id:135647 mouse cecum clone M1_1f08_1 DQ015
EF097608.1 gg_id:193114 mouse cecum clone SWPT20_aaa01b10 EF0976
EU509474.1 gg_id:262863 cecal contents Mus musculus strain C57BL/6J; MD9 clone MD9_aap58h11 EU509
EU473647.1 gg_id:295604 banteng feces clone BG_aaa04e01.Contig1 EU473
DQ807928.1 gg_id:196543 human fecal clone RL180_aan69b12 DQ807
DQ394701.1 gg_id:155423 on -Arctic peninsula Svalbard Norway determined genes and rumen isolates reindee DQ394
EU455821.1 gg_id:311513 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H79S EU455
EU456217.1 gg_id:338554 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU456
EU461525.1 gg_id:295410 black rhinoceros feces clone RH_aaj91f05 EU461
EU463215.1 gg_id:295660 naked mole-rat feces clone molerat_aai71g09 EU463
EU455466.1 gg_id:336609 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU455
EU508216.1 gg_id:261925 cecal contents Mus musculus strain C57BL/6J; MD26 clone MD26_aaa03e03 EU508
EU473488.1 gg_id:298870 Somali wild ass feces clone WA_aaa04a09 EU473
EU504009.1 gg_id:260729 cecal contents Mus musculus strain C57BL/6J; CRWD4 clone CRWD4_aaa04a01 EU504
EU454528.1 gg_id:317324 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU454
EU457302.1 gg_id:344723 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU457
EU510167.1 gg_id:275142 cecal contents Mus musculus strain C57BL/6J; WD3 clone WD3_aak02c12 EU510
EU510763.1 gg_id:269872 cecal contents Mus musculus strain C57BL/6J; WD5 clone WD5_aak40h05 EU510
EU509315.1 gg_id:263838 cecal contents Mus musculus strain C57BL/6J; MD8 clone MD8_aap47g07 EU509
EU504767.1 gg_id:265399 cecal contents Mus musculus strain C57BL/6J; myd2 clone myd2_aaa01g10 EU504
AY992587.1 gg_id:130556 mouse cecum clone C23_k07 AY992
EU456389.1 gg_id:318806 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU456
EU453873.1 gg_id:331530 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K79S EU453
DQ015498.1 gg_id:135682 mouse cecum clone M3_g08_1 DQ015
EU469974.1 gg_id:288611 trancaspain urial feces clone TU1_aaa01a01 EU469
EF096162.1 gg_id:186117 mouse cecum clone obob1_aaa01f05 EF0961
EF614468.1 gg_id:228521 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o EF6144
AY992639.1 gg_id:134437 mouse cecum clone C23_m13 AY992
EF614694.1 gg_id:229965 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o EF6146
EU504826.1 gg_id:262976 cecal contents Mus musculus strain C57BL/6J; myd2 clone myd2_aaa02g09 EU504
AF287775.1 gg_id:52106 human subgingival plaque clone CH017 AF287
EU512012.1 gg_id:268423 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_aak12f09 EU512
GU304107.1 gg_id:572067 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU304
EU468937.1 gg_id:292421 Speke's gazelle feces clone SP2_e10_1 EU468
EF099649.1 gg_id:199649 mouse cecum clone SWPT4_aaa02d09 EF0996
EU506486.1 gg_id:276566 cecal contents Mus musculus strain C57BL/6J; MD19 clone MD19_aaa02g03 EU506
EF096836.1 gg_id:181255 mouse cecum clone SWPT13_aaa01d10 EF0968
EU509508.1 gg_id:263860 cecal contents Mus musculus strain C57BL/6J; MD9 clone MD9_aap59f11 EU509
EU466022.1 gg_id:297491 African elephant feces clone AFEL3_aao16a04 EU466

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EU344172.1 gg_id:262696 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU344
EF025286.1 gg_id:189317 Examination microbial ecology avian vivo bromodeoxyuridine intestine clone B5_N17 EF0252
FJ676934.1 gg_id:527024 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6769
EU453854.1 gg_id:320751 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N EU4538
GQ031254.1 gg_id:378428 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor GQ031
EU453250.1 gg_id:341638 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83N EU4532
EU775955.1 gg_id:345806 Rock hyrax feces clone RHSD_aaa01f10 EU7759
EU507097.1 gg_id:262890 cecal contents Mus musculus strain C57BL/6J; MD22 clone MD22_aaa01c09 EU5070
EU842748.1 gg_id:349546 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU8427
DQ353936.1 gg_id:147987 Fecal Wild Gorilla (Gorilla beringei) wild gorilla feces clone Z101 DQ353
DQ825269.1 gg_id:194574 human fecal clone RL185_aan87e08 DQ825
EU509799.1 gg_id:260786 cecal contents Mus musculus strain C57BL/6J; WD11 clone WD11_aak21b11 EU5097
EU508083.1 gg_id:263277 cecal contents Mus musculus strain C57BL/6J; MD25 clone MD25_aaa03e04 EU5080
EU747968.1 gg_id:324173 neotropical folivorous flying bird adult hoatzin crop clone hoa11_93E12 EU7479
FJ834062.1 gg_id:593393 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P2Q401_60D08 FJ8340
EU748508.1 gg_id:334527 neotropical folivorous flying bird adult hoatzin crop clone hoa61_10g04 EU7485
EF686544.1 gg_id:255603 Sequences Manifest Rumen Yunnan Yel Cattle (Bos Taurus) rumen fluid clone YNRC3 EF6865
EU455481.1 gg_id:317698 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K77S EU4554
EU505127.1 gg_id:270077 cecal contents Mus musculus strain C57BL/6J; myd3 clone myd3_aaa03c03 EU5051
EU842663.1 gg_id:335786 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU8426
EF099549.1 gg_id:181865 mouse cecum clone SWPT3_aaa04g08 EF0995
EF098163.1 gg_id:199316 mouse cecum clone SWPT14_aaa02e02 EF0981
EU456278.1 gg_id:338104 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU4562
GU303152.1 gg_id:579509 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU303
EF098202.1 gg_id:174847 mouse cecum clone SWPT14_aaa03a02 EF0982
GU304520.1 gg_id:579045 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU304
EU511987.1 gg_id:268611 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_aak12d02 EU5119
DQ057370.1 gg_id:129783 chicken ileum/cecum clone cc129 DQ057
EF098143.1 gg_id:181392 mouse cecum clone SWPT14_aaa02b07 EF0981
EU771581.1 gg_id:317226 African elephant feces clone AFEL2_aao32f03 EU7715
DQ015472.1 gg_id:131415 mouse cecum clone M3_e03_1 DQ015
EF096536.1 gg_id:192418 mouse cecum clone obob2_aaa04e08 EF0965
EU451224.1 gg_id:329179 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU4512
EU452061.1 gg_id:334921 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K79S EU4520
EU452329.1 gg_id:351175 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N EU4523
EU455127.1 gg_id:339117 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU4551
EF099556.1 gg_id:195421 mouse cecum clone SWPT3_aaa04h12 EF0995
DQ794938.1 gg_id:188844 human fecal clone RL310_aam38b07 DQ794
AY992476.1 gg_id:135367 mouse cecum clone C23_f08 AY9924
EU451826.1 gg_id:322182 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83N EU4518
EU508898.1 gg_id:272770 cecal contents Mus musculus strain C57BL/6J; MD6 clone MD6_aap38a10 EU5088

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EU510991.1 gg_id:268138 cecal contents Mus musculus strain C57BL/6J; WD7 clone WD7_aal01a09 EU510
AY992665.1 gg_id:132681 mouse cecum clone C23_n18 AY992
EF602824.1 gg_id:230748 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF602
AF371669.1 gg_id:50208 swine intestine clone p-2169-s959-3 AF371
FJ881208.1 gg_id:451771 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8812
FJ680992.1 gg_id:515960 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6809
EU748082.1 gg_id:316388 neotropical folivorous flying bird adult hoatzin crop clone hoa2_44b01 EU748
EU508303.1 gg_id:259395 cecal contents Mus musculus strain C57BL/6J; MD27 clone MD27_aaa02b11 EU508
DQ824073.1 gg_id:185705 human fecal clone RL204_aaj59a05 DQ824
EU006427.1 gg_id:241287 Salmonella enterica serovar typhimurium exploits inflammation compete intestinal r EU006
EU452146.1 gg_id:331381 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H79 EU452
EU508800.1 gg_id:262443 cecal contents Mus musculus strain C57BL/6J; MD4 clone MD4_aap51c06 EU508
EU748045.1 gg_id:347653 neotropical folivorous flying bird adult hoatzin crop clone hoa2_43e03 EU748
AY992553.1 gg_id:129913 mouse cecum clone C23_i21 AY992
EU505090.1 gg_id:268244 cecal contents Mus musculus strain C57BL/6J; myd3 clone myd3_aaa02g04 EU505
DQ815411.1 gg_id:167204 mouse cecum clone aab47f11 DQ815
AB185722.1 gg_id:106444 rumen clone U28-G03 AB185
EU452106.1 gg_id:311187 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75 EU452
AY992654.1 gg_id:133327 mouse cecum clone C23_n06 AY992
DQ015332.1 gg_id:129929 mouse cecum clone M2_1h08_2 DQ015
EU453747.1 gg_id:310479 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77 EU453
EU510785.1 gg_id:264159 cecal contents Mus musculus strain C57BL/6J; WD6 clone WD6_aak49c04 EU510
EU508371.1 gg_id:275792 cecal contents Mus musculus strain C57BL/6J; MD27 clone MD27_aaa04b05 EU508
EU451765.1 gg_id:355426 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74 EU451
EU506702.1 gg_id:275914 cecal contents Mus musculus strain C57BL/6J; MD20 clone MD20_aap54g09 EU506
EU454328.1 gg_id:306215 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K77 EU454
EU451491.1 gg_id:335440 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78 EU451
EF096332.1 gg_id:181789 mouse cecum clone obob2_aaa01a09 EF0963
EF604682.1 gg_id:232262 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6046
EU451101.1 gg_id:333207 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74 EU451
EU454602.1 gg_id:314786 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80 EU454
EU843366.1 gg_id:309471 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
EF604679.1 gg_id:228595 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6046
EU454757.1 gg_id:337906 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K77 EU454
DQ015051.1 gg_id:131129 mouse cecum clone M2_d12 DQ015
EU456943.1 gg_id:319388 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75 EU456
EU511944.1 gg_id:266981 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_aak11f07 EU511
EU454080.1 gg_id:329617 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77 EU454
EU779464.1 gg_id:356407 Grevy's Zebra feces clone GZ_aaa01a11 EU779
EU503677.1 gg_id:266790 cecal contents Mus musculus strain C57BL/6J; CRWD2 clone CRWD2_aaa03a02 EU503
EF098940.1 gg_id:184978 mouse cecum clone SWPT1_aaa03e11 EF0989

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EF097752.1 gg_id:193180 mouse cecum clone SWPT20_aaa03b09 EF0977
EU511837.1 gg_id:260533 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_aaf09h02 EU5118
EF098562.1 gg_id:187222 mouse cecum clone SWPT16_aaa01d09 EF0985
EU451150.1 gg_id:339776 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83N EU4511
EU456175.1 gg_id:309702 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU4561
DQ015076.1 gg_id:129833 mouse cecum clone M2_g09 DQ015
EU457597.1 gg_id:347293 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU4575
DQ815590.1 gg_id:162898 mouse cecum clone aab43c10 DQ815
DQ014760.1 gg_id:129394 mouse cecum clone M1_d04_2 DQ014
EF097767.1 gg_id:188496 mouse cecum clone SWPT20_aaa03e01 EF0977
EF602872.1 gg_id:234789 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6028
EF100117.1 gg_id:193034 mouse cecum clone SWPT5_aaa04h10 EF1001
EF097616.1 gg_id:182470 mouse cecum clone SWPT20_aaa01c12 EF0976
EU842777.1 gg_id:312126 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU8427
EU509273.1 gg_id:269277 cecal contents Mus musculus strain C57BL/6J; MD8 clone MD8_aap47a05 EU5092
EF604671.1 gg_id:230102 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6046
EU451155.1 gg_id:306640 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H78S EU4511
EU457089.1 gg_id:346996 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75N EU4570
EU456190.1 gg_id:326286 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H80N EU4561
FJ678423.1 gg_id:523796 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6784
EU456873.1 gg_id:318445 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU4568
EU451180.1 gg_id:316261 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75N EU4511
FJ682440.1 gg_id:526888 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6824
EF436447.1 gg_id:205859 library-based ruminal water buffalo (Bubalus bubalis) rumen fluid clone BRC161 EF4364
EF614812.1 gg_id:232911 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o EF6148
EF097797.1 gg_id:193426 mouse cecum clone SWPT20_aaa03h02 EF0977
EU843542.1 gg_id:326862 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8435
DQ015222.1 gg_id:135715 mouse cecum clone M2_d08_3 DQ015
EU503739.1 gg_id:265374 cecal contents Mus musculus strain C57BL/6J; CRWD2 clone CRWD2_aaa03h05 EU5037
EF096482.1 gg_id:183730 mouse cecum clone obob2_aaa03e11 EF0964
EU452611.1 gg_id:349197 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU4526
EU454775.1 gg_id:309663 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K79S EU4547
EU507387.1 gg_id:271326 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_2aaa02e05 EU5073
EF098491.1 gg_id:182081 mouse cecum clone SWPT15_aaa04b08 EF0984
EU511974.1 gg_id:263834 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_aak12b08 EU5119
EU509198.1 gg_id:275528 cecal contents Mus musculus strain C57BL/6J; MD8 clone MD8_aap45g03 EU5091
DQ326528.1 gg_id:149441 Metagenomic gut microbiome healthy human stool clone C670 DQ326
AY992448.1 gg_id:132937 mouse cecum clone C23_e04 AY9924
EU507630.1 gg_id:264644 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_aaa02b11 EU5076
EU344316.1 gg_id:271681 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU3443

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EU453802.1 gg_id:317167 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU4538
EU463722.1 gg_id:292285 domesticated horse feces clone horsej_aai91f08 EU4637
EF100116.1 gg_id:180818 mouse cecum clone SWPT5_aaa04h07 EF1001
EU509445.1 gg_id:267418 cecal contents Mus musculus strain C57BL/6J; MD9 clone MD9_aap58e04 EU5094
EU451822.1 gg_id:354878 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU4518
EU452341.1 gg_id:307918 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU4523
EF098388.1 gg_id:181733 mouse cecum clone SWPT15_aaa02b05 EF0983
EU509945.1 gg_id:259081 cecal contents Mus musculus strain C57BL/6J; WD11 clone WD11_aak24b07 EU5099
EU457793.1 gg_id:337739 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU4577
EU511827.1 gg_id:275180 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_aaf09g02.Contig3 EU5118
EU456521.1 gg_id:327654 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU4565
EU504059.1 gg_id:258202 cecal contents Mus musculus strain C57BL/6J; CRWD4 clone CRWD4_aaa04f12 EU5040
EU457020.1 gg_id:311520 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75N EU4570
EU655949.1 gg_id:286453 influence dietary flavonoid-containing extracts on gut microbiota mouse feces clone EU6559
EU452489.1 gg_id:308807 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H74N EU4524
EU791075.1 gg_id:436881 Enteric Defensins are Essential Regulators Intestinal Microbial Ecology HD5-- mouse EU7910
EU456820.1 gg_id:331669 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K79S EU4568
EU453751.1 gg_id:345491 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K79S EU4537
EU503966.1 gg_id:261937 cecal contents Mus musculus strain C57BL/6J; CRWD4 clone CRWD4_aaa03d01 EU5039
DQ809100.1 gg_id:190767 human fecal clone RL308_aal81d12 DQ809
DQ815386.1 gg_id:171769 mouse cecum clone aab47d01 DQ815
EU455278.1 gg_id:341516 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75N EU4552
GQ896790.1 gg_id:565987 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do GQ896
DQ014561.1 gg_id:131869 mouse cecum clone M1_a12 DQ014
AY991945.1 gg_id:134421 mouse cecum clone C20_m08 AY9919
EU510036.1 gg_id:273116 cecal contents Mus musculus strain C57BL/6J; WD1 clone WD1_aaf16c05 EU5100
EU455292.1 gg_id:313025 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU4552
EU508993.1 gg_id:265987 cecal contents Mus musculus strain C57BL/6J; MD7 clone MD7_aap41e02 EU5089
EU506679.1 gg_id:266956 cecal contents Mus musculus strain C57BL/6J; MD20 clone MD20_aap54d01 EU5066
EU452961.1 gg_id:308861 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU4529
DQ015060.1 gg_id:131736 mouse cecum clone M2_e09 DQ015
EU452038.1 gg_id:310743 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU4520
EU456424.1 gg_id:321691 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K79S EU4564
DQ015047.1 gg_id:129376 mouse cecum clone M2_d08 DQ015
AY992601.1 gg_id:135442 mouse cecum clone C23_k21 AY9926
FJ881265.1 gg_id:409829 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8812
EF097620.1 gg_id:199574 mouse cecum clone SWPT20_aaa01d07 EF0976
EF603187.1 gg_id:234746 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6031
DQ015465.1 gg_id:134774 mouse cecum clone M3_d08_1 DQ015
EF096423.1 gg_id:191516 mouse cecum clone obob2_aaa02f03 EF0964

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DQ015671.1 gg_id:133649 mouse cecum clone M3_h11_3 DQ015
EF099867.1 gg_id:175731 mouse cecum clone SWPT5_aaa01e07 EF0998
DQ808413.1 gg_id:186008 human fecal clone RL180_aao76c09 DQ808
AB218340.1 gg_id:149327 Fecal microbial (dugong dugon) determined genes Dugong feces clone dgC-100 AB2183
EU504243.1 gg_id:273308 cecal contents Mus musculus strain C57BL/6J; CRWD5 clone CRWD5_aaa04h10 EU504
EU506323.1 gg_id:266017 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aap63c06 EU5063
EU451871.1 gg_id:346750 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU4518
EU762489.1 gg_id:343491 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU7624
EF098532.1 gg_id:181688 mouse cecum clone SWPT16_aaa01a02 EF0985
EF097805.1 gg_id:190057 mouse cecum clone SWPT20_aaa04a01 EF0978
EF099875.1 gg_id:191762 mouse cecum clone SWPT5_aaa01f05 EF0998
EU510827.1 gg_id:261532 cecal contents Mus musculus strain C57BL/6J; WD6 clone WD6_aak49h03 EU5108
FJ833555.1 gg_id:582515 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J1Q401_05E01 FJ8335
EU451866.1 gg_id:307719 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H74N EU4518
EF099337.1 gg_id:179819 mouse cecum clone SWPT3_aaa01h08 EF0993
EF099450.1 gg_id:199453 mouse cecum clone SWPT3_aaa03d05 EF0994
EF434359.1 gg_id:204333 human infant gastrointestinal tract microbiota stool mother babies 13 and 14 7 mont EF4343
EU508086.1 gg_id:270995 cecal contents Mus musculus strain C57BL/6J; MD25 clone MD25_aaa03e08 EU5080
EU510977.1 gg_id:268951 cecal contents Mus musculus strain C57BL/6J; WD6 clone WD6_aak52g03 EU5109
AM932644.1 gg_id:541250 microbiota Toll-like receptor 2 deficient mice exhibits lineage specific modifications AM932
DQ014938.1 gg_id:135493 mouse cecum clone M1_1h06 DQ014
DQ014739.1 gg_id:135448 mouse cecum clone M1_b06_2 DQ014
EF096263.1 gg_id:185989 mouse cecum clone obob1_aaa03f09 EF0962
EU775549.1 gg_id:330417 Western lowland gorilla feces clone GORSD_aaa02h04 EU7755
DQ015321.1 gg_id:129868 mouse cecum clone M2_1g05 DQ015
EF605072.1 gg_id:235136 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6050
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EU459675.1 gg_id:303191 ring-tailed lemur feces clone RT_aai10f10 EU4596
EU457914.1 gg_id:317740 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H79S EU4579
AB192168.1 gg_id:142751 termite gut homogenate clone RsTz-49 AB192
EF614845.1 gg_id:229751 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o EF6148
EF098701.1 gg_id:196922 mouse cecum clone SWPT16_aaa03f07 EF0987
EU504061.1 gg_id:266108 cecal contents Mus musculus strain C57BL/6J; CRWD4 clone CRWD4_aaa04g02 EU5040
DQ015304.1 gg_id:133405 mouse cecum clone M2_1c11 DQ015
EU509118.1 gg_id:274236 cecal contents Mus musculus strain C57BL/6J; MD7 clone MD7_aap44b02 EU5091
AY992677.1 gg_id:135612 mouse cecum clone C23_o08 AY9926

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EU508491.1 gg_id:266933 cecal contents Mus musculus strain C57BL/6J; MD2 clone MD2_aap34c10 EU508
EU471730.1 gg_id:289401 Asiatic elephant feces clone AE2_aaa01c04 EU471
EU748188.1 gg_id:353892 neotropical folivorous flying bird adult hoatzin crop clone hoa33_78F10.F EU748
EF099417.1 gg_id:188786 mouse cecum clone SWPT3_aaa02h10 EF0994
EU457885.1 gg_id:330606 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU457
EU382068.1 gg_id:258566 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU382
EU474422.1 gg_id:293963 western lowland gorilla feces clone GORSD_aaa03h10 EU474
EU509750.1 gg_id:274752 cecal contents Mus musculus strain C57BL/6J; WD10 clone WD10_aak48d02 EU509
EF406641.1 gg_id:209361 mouse colon clone infected_7days-C12 EF406
EU506251.1 gg_id:273127 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aap61d08 EU506
EF097905.1 gg_id:182808 mouse cecum clone SWPT12_aaa01g02 EF0979
EU509001.1 gg_id:274719 cecal contents Mus musculus strain C57BL/6J; MD7 clone MD7_aap41e12 EU509
EU508154.1 gg_id:270273 cecal contents Mus musculus strain C57BL/6J; MD26 clone MD26_aaa01g04 EU508
EU457552.1 gg_id:350089 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU457
EF099531.1 gg_id:176694 mouse cecum clone SWPT3_aaa04e06 EF0995
FJ682372.1 gg_id:525387 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6823
EU503905.1 gg_id:263366 cecal contents Mus musculus strain C57BL/6J; CRWD4 clone CRWD4_aaa02d07 EU503
EU455013.1 gg_id:337002 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83M EU455
EU344186.1 gg_id:265676 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU344
EF097204.1 gg_id:185576 mouse cecum clone SWPT18_aaa03b02 EF0972
EF095984.1 gg_id:194281 mouse cecum clone lean2_aaa01d06 EF0959
EU504772.1 gg_id:261755 cecal contents Mus musculus strain C57BL/6J; myd2 clone myd2_aaa01h07 EU504
EU456684.1 gg_id:333576 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K79S EU456
EU508805.1 gg_id:264439 cecal contents Mus musculus strain C57BL/6J; MD4 clone MD4_aap51d02 EU508
EF096462.1 gg_id:183211 mouse cecum clone obob2_aaa03b12 EF0964
EU506793.1 gg_id:272787 cecal contents Mus musculus strain C57BL/6J; MD20 clone MD20_aap56d07 EU506
DQ801341.1 gg_id:179065 human fecal clone RL388_aao94c03 DQ801
EF096190.1 gg_id:181470 mouse cecum clone obob1_aaa02c05 EF0961
DQ799217.1 gg_id:181170 human fecal clone RL205_aaj19c10 DQ799
EU452204.1 gg_id:342519 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU452
EF603871.1 gg_id:232146 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6038
AY992508.1 gg_id:131139 mouse cecum clone C23_g22 AY9925
EF099749.1 gg_id:182095 mouse cecum clone SWPT4_aaa03g08 EF0997
EF614724.1 gg_id:230719 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o EF6147
EF098157.1 gg_id:193724 mouse cecum clone SWPT14_aaa02d03 EF0981
EU505182.1 gg_id:266389 cecal contents Mus musculus strain C57BL/6J; myd3 clone myd3_aaa04a11 EU505
EF406746.1 gg_id:210149 mouse colon clone infected_14days-D8 EF4067
EF096844.1 gg_id:191951 mouse cecum clone SWPT13_aaa01e11 EF0968
EU457529.1 gg_id:325739 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU457
EF603088.1 gg_id:234218 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6030

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EU472601.1 gg_id:291380 Angola colobus feces clone EAC_2_aaa02e06 EU472
EU381522.1 gg_id:270410 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid EU381
EU457486.1 gg_id:346580 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU457
EU453821.1 gg_id:307296 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU453
EU454911.1 gg_id:310717 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU454
EF097477.1 gg_id:180864 mouse cecum clone SWPT19_aaa03b06 EF097
EU771700.1 gg_id:341089 African elephant feces clone AFEL_aai30b06 EU771
EU507752.1 gg_id:262527 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_aaa04b10 EU507
DQ815934.1 gg_id:166664 mouse cecum clone aab24e02 DQ815
EF614558.1 gg_id:231854 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o EF614
EF096019.1 gg_id:182878 mouse cecum clone lean2_aaa02b08 EF096
EU511067.1 gg_id:272594 cecal contents Mus musculus strain C57BL/6J; WD7 clone WD7_aal02b11 EU511
AF371670.1 gg_id:16766 swine intestine clone p-1807-c3 AF371
EF614648.1 gg_id:229755 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o EF614
EU508931.1 gg_id:262259 cecal contents Mus musculus strain C57BL/6J; MD6 clone MD6_aap39c10 EU508
EF603666.1 gg_id:227933 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF603
EU453485.1 gg_id:308894 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75N EU453
DQ015223.1 gg_id:132697 mouse cecum clone M2_d11_3 DQ015
EU508314.1 gg_id:266562 cecal contents Mus musculus strain C57BL/6J; MD27 clone MD27_aaa02d12 EU508
DQ015366.1 gg_id:130163 mouse cecum clone M3_c01 DQ015
EF098090.1 gg_id:174307 mouse cecum clone SWPT14_aaa01d03 EF098
EU655749.1 gg_id:280818 influence dietary flavonoid-containing extracts on gut microbiota mouse feces clone EU655
EU510201.1 gg_id:266443 cecal contents Mus musculus strain C57BL/6J; WD3 clone WD3_aak02h02 EU510
EU775878.1 gg_id:323189 Horse feces clone horsej_aai91g01 EU775
EU504177.1 gg_id:267302 cecal contents Mus musculus strain C57BL/6J; CRWD5 clone CRWD5_aaa03b05 EU504
EU453237.1 gg_id:344421 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU453
EU504232.1 gg_id:277443 cecal contents Mus musculus strain C57BL/6J; CRWD5 clone CRWD5_aaa04f09 EU504
EU510718.1 gg_id:274056 cecal contents Mus musculus strain C57BL/6J; WD5 clone WD5_aak39h08 EU510
EU508170.1 gg_id:264643 cecal contents Mus musculus strain C57BL/6J; MD26 clone MD26_aaa02d05 EU508
EF614731.1 gg_id:228805 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o EF614
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EU452194.1 gg_id:310089 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU452
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EF603873.1 gg_id:228281 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF603
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DQ015660.1 gg_id:133505 mouse cecum clone M3_g07_3 DQ015
EU454413.1 gg_id:335832 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU454
EU457983.1 gg_id:303510 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75N EU457

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EU511868.1 gg_id:268130 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_aaf10b04 EU511
EU509552.1 gg_id:270545 cecal contents Mus musculus strain C57BL/6J; MD9 clone MD9_aap60f06 EU509
EF099819.1 gg_id:184463 mouse cecum clone SWPT4_aaa04g04 EF099
EF098904.1 gg_id:182079 mouse cecum clone SWPT1_aaa03a09 EF098
EF605077.1 gg_id:228860 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF605
EU455811.1 gg_id:341706 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77 EU455
EU454169.1 gg_id:351220 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H80 EU454
EU503854.1 gg_id:265301 cecal contents Mus musculus strain C57BL/6J; CRWD4 clone CRWD4_aaa01f01 EU503
EU454336.1 gg_id:355053 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75 EU454
EU505201.1 gg_id:267215 cecal contents Mus musculus strain C57BL/6J; myd3 clone myd3_aaa04d07 EU505
DQ673574.1 gg_id:166178 rumen fluid clone GRC109 DQ673
EU507887.1 gg_id:272764 cecal contents Mus musculus strain C57BL/6J; MD24 clone MD24_aaa02g05 EU507
EU506551.1 gg_id:269966 cecal contents Mus musculus strain C57BL/6J; MD19 clone MD19_aaa03g12 EU506
EU455724.1 gg_id:329290 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K79 EU455
DQ815946.1 gg_id:163014 mouse cecum clone aab24f10 DQ815
EU455456.1 gg_id:329010 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K79 EU455
EU761646.1 gg_id:328026 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1 EU761
EU504019.1 gg_id:272454 cecal contents Mus musculus strain C57BL/6J; CRWD4 clone CRWD4_aaa04b04 EU504
EU507347.1 gg_id:268466 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_2aaa01h11 EU507
EU748047.1 gg_id:327000 neotropical folivorous flying bird adult hoatzin crop clone hoa2_44d05 EU748
EU507456.1 gg_id:261848 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_2aaa03e04 EU507
EU454439.1 gg_id:336426 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77 EU454
DQ237938.1 gg_id:142942 influence fumarate disodium on ruminal metabolism goats goat rumen clone M1 DQ237
EF098081.1 gg_id:179438 mouse cecum clone SWPT14_aaa01c03 EF098
EU510103.1 gg_id:264218 cecal contents Mus musculus strain C57BL/6J; WD3 clone WD3_aak01d09 EU510
AY916273.1 gg_id:113572 human rectum biopsy clone N322 AY916
EU506653.1 gg_id:264703 cecal contents Mus musculus strain C57BL/6J; MD20 clone MD20_aap54a02 EU506
EF603185.1 gg_id:231870 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF603
GQ502513.1 gg_id:572072 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf4- GQ502
EU451680.1 gg_id:356109 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H79 EU451
AB088950.1 gg_id:77867 termite gut homogenate clone Rs-B88 bacterium AB088
EU455158.1 gg_id:316064 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75 EU455
EF603953.1 gg_id:230661 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF603
EU457669.1 gg_id:336094 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75 EU457
EU510908.1 gg_id:276935 cecal contents Mus musculus strain C57BL/6J; WD6 clone WD6_aak51d03 EU510
EU510484.1 gg_id:269754 cecal contents Mus musculus strain C57BL/6J; WD4 clone WD4_aal39e07 EU510
EU507594.1 gg_id:259172 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_aaa01e12 EU507
EF603952.1 gg_id:229562 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF603
EU452303.1 gg_id:315527 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H74 EU452
EF098507.1 gg_id:195445 mouse cecum clone SWPT15_aaa04e06 EF098

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EF097774.1 gg_id:174773 mouse cecum clone SWPT20_aaa03e10 EF0977
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EU504879.1 gg_id:273416 cecal contents Mus musculus strain C57BL/6J; myd2 clone myd2_aaa03f11 EU5048
EF098804.1 gg_id:194682 mouse cecum clone SWPT1_aaa01c01 EF0988
EU510206.1 gg_id:262247 cecal contents Mus musculus strain C57BL/6J; WD3 clone WD3_aak02h08 EU510
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EU508068.1 gg_id:263998 cecal contents Mus musculus strain C57BL/6J; MD25 clone MD25_aaa03b04 EU508
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EU452555.1 gg_id:306487 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74 EU452
EU779413.1 gg_id:329742 Hartmann's Mountain Zebra feces clone AFZEB_aaj70d05 EU779
EU771195.1 gg_id:341737 Asiatic elephant feces clone AE3_aaa02d09 EU771
EU505013.1 gg_id:258435 cecal contents Mus musculus strain C57BL/6J; myd3 clone myd3_aaa01f03 EU505
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EU504970.1 gg_id:277068 cecal contents Mus musculus strain C57BL/6J; myd2 clone myd2_aaa04h12 EU504
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EU511903.1 gg_id:268116 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_aak09e11 EU511
DQ815326.1 gg_id:169815 mouse cecum clone aab45e08 DQ815
EU511856.1 gg_id:264239 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_aaf10a06.Contig2 EU511
EF096163.1 gg_id:193879 mouse cecum clone obob1_aaa01f06 EF0961

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EU511605.1 gg_id:277486 cecal contents Mus musculus strain C57BL/6J; WD9 clone WD9_aak07d05 EU511
EU748097.1 gg_id:324079 neotropical folivorous flying bird adult hoatzin crop clone hoa2_42d01 EU748
DQ815446.1 gg_id:162804 mouse cecum clone aab48e08 DQ815
FJ365425.1 gg_id:357471 feces adult twins and mothers; TS20 clone TS20_a02g02 FJ3654
EU455526.1 gg_id:308160 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75N EU455
GQ897103.1 gg_id:545964 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ897
EU452423.1 gg_id:343002 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU452
EF602967.1 gg_id:230212 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF602
EU457703.1 gg_id:339505 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K79S EU457
EU843162.1 gg_id:325894 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
EU465634.1 gg_id:299985 argali sheep feces clone AS1_aao40c12.Contig1 EU465
EU510929.1 gg_id:264556 cecal contents Mus musculus strain C57BL/6J; WD6 clone WD6_aak51g06 EU510
EU457265.1 gg_id:308291 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU457
EF099267.1 gg_id:194520 mouse cecum clone SWPT2_aaa04g10 EF0992
AY992528.1 gg_id:135672 mouse cecum clone C23_h19 AY992
EU453260.1 gg_id:321161 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N EU453
FJ364401.1 gg_id:363280 feces adult twins and mothers; TS15 clone TS15_a02e03 FJ3644
EF614600.1 gg_id:234794 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o EF6146
EU457252.1 gg_id:353188 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU457
EU455732.1 gg_id:337572 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K79S EU455
EF603950.1 gg_id:234179 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF603
EU453621.1 gg_id:333176 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83N EU453
EU451529.1 gg_id:305718 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K79S EU451
EF096968.1 gg_id:175483 mouse cecum clone SWPT13_aaa03e04 EF0969
EU508528.1 gg_id:273169 cecal contents Mus musculus strain C57BL/6J; MD2 clone MD2_aap34h10 EU508
FJ880080.1 gg_id:453405 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8800
EU451060.1 gg_id:316738 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU451
EF097677.1 gg_id:195885 mouse cecum clone SWPT20_aaa02b07 EF0976
EU511942.1 gg_id:271879 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_aak11f04 EU511
AM932615.1 gg_id:575751 microbiota Toll-like receptor 2 deficient mice exhibits lineage specific modifications AM932
DQ015082.1 gg_id:129641 mouse cecum clone M2_h07 DQ015
EU511099.1 gg_id:259148 cecal contents Mus musculus strain C57BL/6J; WD7 clone WD7_aal02f12 EU511
EU775850.1 gg_id:348919 Horse feces clone horsej_a10 EU775
EU454798.1 gg_id:355612 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU454
EU451537.1 gg_id:315395 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU451
EU508286.1 gg_id:259183 cecal contents Mus musculus strain C57BL/6J; MD27 clone MD27_aaa01f05 EU508
EU451665.1 gg_id:332587 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N EU451
EU451748.1 gg_id:322121 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75N EU451
DQ789123.1 gg_id:257328 Isolation Flagellated Crohn's Disease mouse cecum DQ789
DQ815888.1 gg_id:169242 mouse cecum clone aab23g06 DQ815

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GU304203.1 gg_id:585104 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU304
EU506630.1 gg_id:276637 cecal contents Mus musculus strain C57BL/6J; MD20 clone MD20_aap53f06 EU506
EU504958.1 gg_id:272111 cecal contents Mus musculus strain C57BL/6J; myd2 clone myd2_aaa04g10 EU504
EU471846.1 gg_id:293417 Asiatic elephant feces clone AE2_aaa01c10 EU471
EU510054.1 gg_id:276546 cecal contents Mus musculus strain C57BL/6J; WD1 clone WD1_aaf11e08 EU510
EU511233.1 gg_id:265917 cecal contents Mus musculus strain C57BL/6J; WD7 clone WD7_aal04g09 EU511
EU455557.1 gg_id:336092 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU455
DQ815838.1 gg_id:170131 mouse cecum clone aab23a05 DQ815
EU510984.1 gg_id:271528 cecal contents Mus musculus strain C57BL/6J; WD6 clone WD6_aak52g11 EU510
EF097986.1 gg_id:183225 mouse cecum clone SWPT12_aaa03f03 EF097
EU505646.1 gg_id:260752 cecal contents Mus musculus strain C57BL/6J; myd5 clone myd5_aaa04a04 EU505
EU507686.1 gg_id:270439 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_aaa03b11 EU507
DQ015437.1 gg_id:130806 mouse cecum clone M3_a11_1 DQ015
EU454933.1 gg_id:315559 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU454
EU451455.1 gg_id:325386 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU451
FJ880885.1 gg_id:434795 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8808
EU452374.1 gg_id:324596 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N EU452
EU453705.1 gg_id:310281 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K79S EU453
EU451962.1 gg_id:348977 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU451
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EU452895.1 gg_id:303434 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H79S EU452
EU506399.1 gg_id:276681 cecal contents Mus musculus strain C57BL/6J; MD19 clone MD19_aaa01b11 EU506
EU503588.1 gg_id:264252 cecal contents Mus musculus strain C57BL/6J; CRWD2 clone CRWD2_aaa01f04 EU503
EU454860.1 gg_id:343879 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU454
EU506835.1 gg_id:275802 cecal contents Mus musculus strain C57BL/6J; MD21 clone MD21_aar07b02 EU506
EU503936.1 gg_id:275743 cecal contents Mus musculus strain C57BL/6J; CRWD4 clone CRWD4_aaa03a01 EU503
EU511873.1 gg_id:264841 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_10b10.Contig2 EU511
FJ894710.1 gg_id:569581 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota BME; ear p FJ8947
EU510260.1 gg_id:265505 cecal contents Mus musculus strain C57BL/6J; WD3 clone WD3_aak03g01 EU510
EF097133.1 gg_id:177946 mouse cecum clone SWPT18_aaa01h01 EF097
EU451039.1 gg_id:347128 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU451
EU456612.1 gg_id:324754 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H80N EU456
EU454922.1 gg_id:350088 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU454
EU504263.1 gg_id:269057 cecal contents Mus musculus strain C57BL/6J; CRWD6 clone CRWD6_aaa01c10 EU504
EF614840.1 gg_id:230379 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o EF614
EF096403.1 gg_id:193921 mouse cecum clone obob2_aaa02c08 EF096
EF096997.1 gg_id:179928 mouse cecum clone SWPT13_aaa03h09 EF096
EU504310.1 gg_id:269809 cecal contents Mus musculus strain C57BL/6J; CRWD6 clone CRWD6_aaa02b08 EU504
DQ824834.1 gg_id:174571 human fecal clone RL185_aao69g11 DQ824
EU454845.1 gg_id:354667 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU454

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EU504233.1 gg_id:261142 cecal contents Mus musculus strain C57BL/6J; CRWD5 clone CRWD5_aaa04f12 EU504
EF604803.1 gg_id:231563 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6048
EU506340.1 gg_id:265356 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aap63e10 EU5063
EF098095.1 gg_id:189119 mouse cecum clone SWPT14_aaa01d10 EF0980
FJ680678.1 gg_id:527100 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6806
AF371636.1 gg_id:104064 swine intestine clone p-4570-4Wb3 AF3716
EF603797.1 gg_id:233411 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6037
EU450915.1 gg_id:312822 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75M EU4509
EF603872.1 gg_id:227886 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6038
EU455616.1 gg_id:324807 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU4556
EU457421.1 gg_id:347182 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU4574
EF604676.1 gg_id:228048 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6046
EF614887.1 gg_id:230111 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o EF6148
EF096264.1 gg_id:183466 mouse cecum clone obob1_aaa03g03 EF0962
EU622706.1 gg_id:278440 -feed administered sub-therapeutic chlorotetracycline alters structure and but not a EU6227
EU456401.1 gg_id:329421 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75M EU4564
EU453753.1 gg_id:310227 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU4537
EU454376.1 gg_id:322564 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80M EU4543
EU510396.1 gg_id:262556 cecal contents Mus musculus strain C57BL/6J; WD4 clone WD4_aal37h09 EU5103
EF097716.1 gg_id:175859 mouse cecum clone SWPT20_aaa02f11 EF0977
EU622721.1 gg_id:278392 -feed administered sub-therapeutic chlorotetracycline alters structure and but not a EU6227
EU655773.1 gg_id:284761 influence dietary flavonoid-containing extracts on gut microbiota mouse feces clone EU6557
FJ880662.1 gg_id:407782 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8806
EF098059.1 gg_id:186466 mouse cecum clone SWPT12_aaa04h08 EF0980
EU458068.1 gg_id:328433 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75M EU4580
AF371560.1 gg_id:40639 swine intestine clone p-2399-55G5 AF3715
EU452780.1 gg_id:329836 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H74M EU4527
EU344354.1 gg_id:273480 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU3443
EU508661.1 gg_id:272449 cecal contents Mus musculus strain C57BL/6J; MD4 clone MD4_aap49a05 EU5086
EU509421.1 gg_id:271053 cecal contents Mus musculus strain C57BL/6J; MD9 clone MD9_aap57h03 EU5094
EU455225.1 gg_id:319398 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H74M EU4552
EU508200.1 gg_id:265997 cecal contents Mus musculus strain C57BL/6J; MD26 clone MD26_aaa03a06 EU5082
EU503933.1 gg_id:263530 cecal contents Mus musculus strain C57BL/6J; CRWD4 clone CRWD4_aaa02h06 EU5039
EU454836.1 gg_id:339886 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74M EU4548
EU451309.1 gg_id:337174 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75M EU4513
DQ014643.1 gg_id:135643 mouse cecum clone M1_a07_1 DQ014
EU508440.1 gg_id:258344 cecal contents Mus musculus strain C57BL/6J; MD2 clone MD2_aap33e08 EU5084
EU842297.1 gg_id:336994 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU8422
FJ832588.1 gg_id:554490 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P3Q302_04D01 FJ8325
EU507710.1 gg_id:264364 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_aaa03e06 EU5077

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AY992811.1 gg_id:132748 mouse cecum clone C22_c21 AY9928
EU474235.1 gg_id:300219 western lowland gorilla feces clone GORSD_aaa01e06 EU474
EU452309.1 gg_id:349890 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU4523
EU509303.1 gg_id:264933 cecal contents Mus musculus strain C57BL/6J; MD8 clone MD8_aap47e09 EU5093
EU453606.1 gg_id:356353 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83M EU4536
DQ015623.1 gg_id:135607 mouse cecum clone M3_c12_2 DQ015
EU455622.1 gg_id:313634 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU4556
DQ815665.1 gg_id:165845 mouse cecum clone aab44e07 DQ815
EF604806.1 gg_id:229460 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6048
EU508547.1 gg_id:267049 cecal contents Mus musculus strain C57BL/6J; MD2 clone MD2_aap35c01 EU5085
EU748004.1 gg_id:328729 neotropical folivorous flying bird adult hoatzin crop clone hoa14_30F04 EU7480
EF098489.1 gg_id:186151 mouse cecum clone SWPT15_aaa04b06 EF0984
EU505053.1 gg_id:260616 cecal contents Mus musculus strain C57BL/6J; myd3 clone myd3_aaa02c03 EU5050
EU457612.1 gg_id:334547 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83M EU4576
EU455433.1 gg_id:332973 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74M EU4554
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EU511187.1 gg_id:264990 cecal contents Mus musculus strain C57BL/6J; WD7 clone WD7_aal04b02 EU5111
EU509940.1 gg_id:263077 cecal contents Mus musculus strain C57BL/6J; WD11 clone WD11_aak24b01 EU5099
EU457596.1 gg_id:356404 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83M EU4575
DQ015207.1 gg_id:132275 mouse cecum clone M2_b08_3 DQ015
EF605063.1 gg_id:228930 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6050
EF098900.1 gg_id:181344 mouse cecum clone SWPT1_aaa03a05 EF0989
EU504120.1 gg_id:258750 cecal contents Mus musculus strain C57BL/6J; CRWD5 clone CRWD5_aaa01f11 EU5041
EU762169.1 gg_id:323459 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU7621
EU504051.1 gg_id:258546 cecal contents Mus musculus strain C57BL/6J; CRWD4 clone CRWD4_aaa04f01 EU5040
EU507552.1 gg_id:265268 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_aaa01a04 EU5075
EF099992.1 gg_id:173939 mouse cecum clone SWPT5_aaa03c07 EF0999
EF604540.1 gg_id:232969 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6045
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EF096390.1 gg_id:195208 mouse cecum clone obob2_aaa02a09 EF0963
AY991835.1 gg_id:131998 mouse cecum clone C20_g17 AY9918
DQ456362.1 gg_id:158971 pre-adolescent turkey cecum clone CFT212E2 DQ456
EU457498.1 gg_id:315284 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75M EU4574
EU450902.1 gg_id:347778 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H80M EU4509
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EU456745.1 gg_id:303890 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU4567
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EF096673.1 gg_id:175893 mouse cecum clone SWPT11_aaa02h10 EF0966

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EF098091.1 gg_id:191942 mouse cecum clone SWPT14_aaa01d04 EF0980
EU509591.1 gg_id:277550 cecal contents Mus musculus strain C57BL/6J; WD10 clone WD10_aak45d08 EU5095
EF096942.1 gg_id:177095 mouse cecum clone SWPT13_aaa03b02 EF0969
EU508352.1 gg_id:276552 cecal contents Mus musculus strain C57BL/6J; MD27 clone MD27_aaa03e06 EU5083
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EF098359.1 gg_id:178043 mouse cecum clone SWPT15_aaa01e04 EF0983
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EU509455.1 gg_id:270768 cecal contents Mus musculus strain C57BL/6J; MD9 clone MD9_aap58f06 EU5094
EU511589.1 gg_id:271918 cecal contents Mus musculus strain C57BL/6J; WD9 clone WD9_aak07a12 EU5115
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EF099955.1 gg_id:188052 mouse cecum clone SWPT5_aaa02g01 EF0999
AY992695.1 gg_id:135353 mouse cecum clone C23_p02 AY9926
EU457668.1 gg_id:338240 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H78S EU4576
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EU457464.1 gg_id:345956 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU4574
EU509255.1 gg_id:268484 cecal contents Mus musculus strain C57BL/6J; MD8 clone MD8_aap46g02 EU5092
EU451423.1 gg_id:356499 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H79S EU4514
EU453792.1 gg_id:307802 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H74N EU4537
EF098014.1 gg_id:196251 mouse cecum clone SWPT12_aaa04a09 EF0980
EF614834.1 gg_id:229419 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o EF6148
EU457495.1 gg_id:323383 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83N EU4574
EU453160.1 gg_id:304065 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K79S EU4531
EU507400.1 gg_id:258325 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_2aaa02f08 EU5074
DQ015131.1 gg_id:135515 mouse cecum clone M2_g12_1 DQ015
GQ897331.1 gg_id:591724 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ897
FJ682910.1 gg_id:528582 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6829
FJ674029.1 gg_id:521228 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6740
FJ683574.1 gg_id:511181 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6835
EU878317.1 gg_id:547601 Investigation factors influencing production large-scale municipal biogas plant therm EU8783
FJ682798.1 gg_id:522394 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6827
DQ824455.1 gg_id:176312 human fecal clone RL304_aal76c01 DQ824
FJ674105.1 gg_id:530297 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6741
EU458763.1 gg_id:298607 Goeldi's marmoset feces clone CAL_h06_2 EU4587

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EU778295.1 gg_id:351009 feces clone RL117_aae92g08 EU778
EU748229.1 gg_id:325428 neotropical folivorous flying bird adult hoatzin crop clone hoa31_43C06.F EU748
EU776772.1 gg_id:355994 Mongoose lemur feces clone ML_aaj28d07 EU776
FJ683944.1 gg_id:516977 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6839
DQ796840.1 gg_id:193857 human fecal clone RL179_aao55c04 DQ796
DQ801499.1 gg_id:180881 human fecal clone RL388_aao96d01 DQ801
FJ682585.1 gg_id:521919 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6825
EU842502.1 gg_id:318015 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
FJ673100.1 gg_id:509584 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6731
GQ897612.1 gg_id:549435 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ897
FJ673236.1 gg_id:521060 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6732
FJ678637.1 gg_id:527274 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6786
EU765455.1 gg_id:305241 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B3 EU765
FJ673604.1 gg_id:511676 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6736
FJ683547.1 gg_id:523042 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6835
EU766152.1 gg_id:318722 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU766
EF400832.1 gg_id:207360 human fecal clone SJTU_D_02_16 EF4008
EU844606.1 gg_id:310033 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
DQ807203.1 gg_id:199566 human fecal clone RL244_aaj47e06 DQ807
FJ684169.1 gg_id:521869 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6841
EU471640.1 gg_id:293892 Asiatic elephant feces clone AE1_aaa02e03 EU471
GQ897242.1 gg_id:592281 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ897
EU762076.1 gg_id:320832 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1 EU762
EU344634.1 gg_id:267988 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU344
EU461587.1 gg_id:296506 mongoose lemur feces clone ML_aaj25a11 EU461
FJ369987.1 gg_id:362208 feces adult twins and mothers; TS55 clone TS55_a03b06 FJ3699
FJ678935.1 gg_id:526002 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6789
FJ677628.1 gg_id:525254 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6776
FJ678824.1 gg_id:523139 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6788
AF371571.1 gg_id:39350 swine intestine clone p-2168-959-3 AF371
FJ676406.1 gg_id:519924 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6764
FJ365764.1 gg_id:362572 feces adult twins and mothers; TS21 clone TS21_a02g01 FJ3657
FJ365587.1 gg_id:365413 feces adult twins and mothers; TS20 clone TS20_a04f04 FJ3655
FJ673888.1 gg_id:521259 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6738
DQ824009.1 gg_id:174940 human fecal clone RL204_aaj58b02 DQ824
EU768538.1 gg_id:326680 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C5 EU768
GQ493866.1 gg_id:575260 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
GQ896748.1 gg_id:552047 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do s GQ896
FJ678243.1 gg_id:529592 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6782
FJ683038.1 gg_id:525861 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6830

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FJ683628.1 gg_id:518029 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6836
DQ793701.1 gg_id:188799 human fecal clone RL246_aai75h10 DQ793
EU471579.1 gg_id:289088 Asiatic elephant feces clone AE1_aaa02b09 EU471
EU842652.1 gg_id:335926 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
FJ684990.1 gg_id:529224 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6849
EU843303.1 gg_id:333505 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
EU843314.1 gg_id:331449 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
EF402536.1 gg_id:212249 human fecal clone SJTU_B_09_22 EF4025
GQ491740.1 gg_id:539352 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
EU461879.1 gg_id:294773 white-faced saki feces clone Saki_aaj62h02 EU461
GQ493781.1 gg_id:559605 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
DQ798491.1 gg_id:197983 human fecal clone RL181_aan97d06 DQ798
FJ678273.1 gg_id:515680 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6782
DQ797604.1 gg_id:186093 human fecal clone RL206_aaj13e12 DQ797
DQ796765.1 gg_id:197608 human fecal clone RL179_aao54b09 DQ796
EU843910.1 gg_id:342861 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
FJ673106.1 gg_id:518482 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6731
EU467223.1 gg_id:289139 black-handed spider monkey feces clone SPIM_f06 EU467
FJ674067.1 gg_id:514479 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6740
EU766356.1 gg_id:342805 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU7663
EU467254.1 gg_id:294800 black-handed spider monkey feces clone SPIM_b04_1 EU467
EU465864.1 gg_id:298108 African elephant feces clone AFEL3_aao13b07 EU465
DQ801572.1 gg_id:194536 human fecal clone RL117_aae91f06 DQ801
FJ364329.1 gg_id:357050 feces adult twins and mothers; TS15 clone TS15_a01f08 FJ3643
FJ673928.1 gg_id:526343 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6739
EF402856.1 gg_id:205712 human fecal clone SJTU_B_13_37 EF4028
FJ371802.1 gg_id:358665 feces adult twins and mothers; TS8 clone TS8_a02d03 FJ3718
DQ326236.1 gg_id:145868 Metagenomic gut microbiome healthy human stool clone C162 DQ326
FJ679447.1 gg_id:519381 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6794
FJ673719.1 gg_id:519898 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6737
FJ673495.1 gg_id:521206 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6734
FJ371748.1 gg_id:360201 feces adult twins and mothers; TS8 clone TS8_a01g05 FJ3717
DQ824233.1 gg_id:179128 human fecal clone RL304_aal73c09 DQ824
EU530197.1 gg_id:261328 mucosa adherent and invasive microbes profile adenoma colorectal cancer clone M1 EU5301
DQ802278.1 gg_id:175265 human fecal clone RL188_aah15e08 DQ802
GQ897602.1 gg_id:572883 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ897
FJ683310.1 gg_id:528402 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6833
FJ679428.1 gg_id:524599 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6794
DQ796270.1 gg_id:188127 human fecal clone RL179_aah25a02 DQ796
FJ682859.1 gg_id:522528 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6828

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GQ492157.1 gg_id:581415 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
EU471898.1 gg_id:296693 Asiatic elephant feces clone AE3_aaa03a12 EU4718
EU475870.1 gg_id:296283 white-faced saki feces clone Saki_aaj64a08 EU4758
FJ684112.1 gg_id:522879 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6841
AY858455.2 gg_id:110391 gastrointestinal tract zebra clone ZEBRA_16 AY8584
FJ682723.1 gg_id:521317 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6827
EU461713.1 gg_id:293896 mongoose lemur feces clone ML_aaj27e12 EU4617
DQ793365.1 gg_id:188825 human fecal clone RL199_aaj42g08 DQ793
EF403074.1 gg_id:214545 human fecal clone SJTU_B_16_83 EF4030
EU779470.1 gg_id:312217 Grevy's Zebra feces clone GZ_aaa03d11 EU7794
GQ492240.1 gg_id:590750 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
FJ674107.1 gg_id:516460 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6741
DQ905775.2 gg_id:171627 human fecal clone 29A-g6 DQ905
GQ896874.1 gg_id:577529 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do s GQ896
DQ807373.1 gg_id:182026 human fecal clone RL307_aam05f12 DQ807
GQ492743.1 gg_id:587421 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
EU471654.1 gg_id:297144 Asiatic elephant feces clone AE1_aaa02e04 EU4716
GQ897125.1 gg_id:536356 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ897
FJ681997.1 gg_id:522026 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6819
FJ680330.1 gg_id:525458 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6803
FJ679912.1 gg_id:522173 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6799
FJ673906.1 gg_id:525618 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6739
FJ683467.1 gg_id:523977 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6834
FJ673562.1 gg_id:510337 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6735
FJ682168.1 gg_id:516394 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6821
FJ363400.1 gg_id:369471 feces adult twins and mothers; TS149 clone TS149_a02g07 FJ3634
EU775745.1 gg_id:305213 Horse feces clone horsej_f02 EU7757
EU773047.1 gg_id:310136 Banteng feces clone BG_aaa04b11.Contig1 EU7730
FJ367983.1 gg_id:363310 feces adult twins and mothers; TS30 clone TS30_a02b09 FJ3679
GQ492375.1 gg_id:562947 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
EF405447.1 gg_id:203840 human fecal clone SJTU_G_01_94 EF4054
FJ371700.1 gg_id:364251 feces adult twins and mothers; TS8 clone TS8_a01c05 FJ3717
FJ679150.1 gg_id:526934 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6791
FJ681852.1 gg_id:523812 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6818
FJ682435.1 gg_id:519890 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6824
EU344360.1 gg_id:271626 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU3443
AY854317.1 gg_id:109733 herbivore gastrointestinal tract clone Thompsons28 AY8543
EU471699.1 gg_id:296790 Asiatic elephant feces clone AE2_aaa03b02 EU4716
EU767442.1 gg_id:314345 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C2 EU7674
EU344353.1 gg_id:266734 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU3443

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EU775789.1 gg_id:351568 Horse feces clone horsej_f04_1 EU775
AY854266.2 gg_id:109780 herbivore gastrointestinal tract clone CATTLE_4 AY8542
GQ896791.1 gg_id:554178 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do GQ896
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AY993272.1 gg_id:129462 mouse cecum clone C21_l23 AY9932
DQ075205.2 gg_id:138338 caecal flora rats fed diets supplemented mannooligosaccharides caecum clone rcwg DQ075
EU469188.1 gg_id:302376 Speke's gazelle feces clone SP3_g09 EU469
EU504119.1 gg_id:267399 cecal contents Mus musculus strain C57BL/6J; CRWD5 clone CRWD5_aaa01f09 EU504
EU455558.1 gg_id:330269 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77 EU455
EU507225.1 gg_id:269308 cecal contents Mus musculus strain C57BL/6J; MD22 clone MD22_aaa03g11 EU507
FJ366736.1 gg_id:357469 feces adult twins and mothers; TS27 clone TS27_a03c06 FJ3667
EU381648.1 gg_id:274866 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid EU381
FJ832523.1 gg_id:577268 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P3Q201_82B11 FJ8325
EU774277.1 gg_id:303835 Chimpanzee feces clone CHIMP1_aaj38h12 EU774
EF686637.1 gg_id:243317 Sequences Manifest Rumen Yunnan Yel Cattle (Bos Taurus) rumen fluid clone YNRC1 EF6866
EU453282.1 gg_id:335905 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75 EU453
EU454777.1 gg_id:346400 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H80 EU454
EU509987.1 gg_id:272420 cecal contents Mus musculus strain C57BL/6J; WD1 clone WD1_aaf15b07 EU509
AB494893.1 gg_id:567331 Fibrobacter succinogenes dominated consortium on hay stems sheep rumen clone N AB4948
FJ880927.1 gg_id:405192 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8809
EF686527.1 gg_id:257984 Sequences Manifest Rumen Yunnan Yel Cattle (Bos Taurus) rumen fluid clone YNRC1 EF6865
EU779305.1 gg_id:350746 Visayam Warty Pig feces clone VWP_aaa02b08 EU7793
GQ493538.1 gg_id:594376 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
EU776861.1 gg_id:354161 Mongoose lemur feces clone ML_aaj25e03 EU7768
GU112189.1 gg_id:546480 library biogas slurry anaerobic fermentation pig manure clone 69 GU112
CU924224.1 gg_id:535209 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU924
AM697115.1 gg_id:224390 sequencing libraries indoor dust clone BF0002B065 AM697
EU474370.1 gg_id:298797 western lowland gorilla feces clone GORSD_aaa01d01 EU4743
EU773128.1 gg_id:311952 Banteng feces clone BG_aaa03b05.Contig1 EU7731
GQ448782.1 gg_id:570341 Microbiome neonatal calves: shedding microorganisms fecal clone calf784_10wks_g GQ448
AB270049.1 gg_id:165268 Influence temperature and humidity on heifers rumen contents Holstein heifer (Bos AB2700
FJ880641.1 gg_id:370664 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8806
EU472359.1 gg_id:290251 Angola colobus feces clone EAC_1aaa02d07 EU4723
EF603663.1 gg_id:232904 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6036
DQ804773.1 gg_id:186951 human fecal clone RL187_aao72e06 DQ804
DQ796105.1 gg_id:174738 human fecal clone RL202_aai51e12 DQ796
AB270117.1 gg_id:167782 Influence temperature and humidity on heifers rumen contents Holstein heifer (Bos AB2701
AY916358.1 gg_id:114284 human stool clone D145 AY9163
FJ880532.1 gg_id:449325 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8805
EU843442.1 gg_id:328972 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8434

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EU259387.1 gg_id:252823 Rumen yak (Bos grunniens) sequences rumen fluid clone YRC11 EU259
GQ502573.1 gg_id:536185 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf4- GQ502
FJ832542.1 gg_id:571954 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P3Q301_14F02 FJ8325
EF096600.1 gg_id:184966 mouse cecum clone SWPT11_aaa01f11 EF0966
AF371570.1 gg_id:19873 swine intestine clone p-416-o3 AF3715
AF001700.1 gg_id:13936 rumen clone RC7 AF0017
AF371944.1 gg_id:24175 swine intestine clone p-5263-4Wb5 AF3719
EF098533.1 gg_id:190247 mouse cecum clone SWPT16_aaa01a03 EF0985
EU748486.1 gg_id:305869 neotropical folivorous flying bird adult hoatzin crop clone hoa61_12c03 EU7484
DQ801435.1 gg_id:183673 human fecal clone RL388_aao95e04 DQ801
EU466205.1 gg_id:288168 bighorn sheep feces clone BH1_aao28a05 EU4662
AB185603.1 gg_id:99484 rumen clone F24-D03 AB1856
EU504162.1 gg_id:271439 cecal contents Mus musculus strain C57BL/6J; CRWD5 clone CRWD5_aaa02f01 EU5041
FJ880990.1 gg_id:432496 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8809
EU458029.1 gg_id:310878 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU4580
FJ881328.1 gg_id:440840 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8813
EU622678.1 gg_id:277946 -feed administered sub-therapeutic chlorotetracycline alters structure and but not a EU6226
GU455017.1 gg_id:518565 Understanding short-chain fatty acids accumulation enhanced alkaline digestion: kir GU455
DQ802603.1 gg_id:179988 human fecal clone RL188_aan94a02 DQ802
EU842586.1 gg_id:333582 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU8425
EF098948.1 gg_id:196573 mouse cecum clone SWPT1_aaa03f12 EF0989
FJ879499.1 gg_id:451889 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8794
CP001850.1 gg_id:520890 Clostridiales genomosp. BVAB3 str. UPII9-5 CP0018
FJ879178.1 gg_id:396864 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8791
FJ672028.1 gg_id:520726 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6720
AY982878.1 gg_id:117241 human descending colon mucosal biopsy clone L048 AY9828
EU509443.1 gg_id:272879 cecal contents Mus musculus strain C57BL/6J; MD9 clone MD9_aap58e01 EU5094
DQ833493.1 gg_id:172948 detected analyses depth sediment Guanting Reservoir clone 35-56 DQ833
GQ249555.1 gg_id:558397 Microbial anaerobic sediments Bay Cadiz (Spain) marine sediment: 12-14 cm layer cl GQ249
EU467427.1 gg_id:302234 chimpanzee feces clone CHIMP12_f02_1 EU4674
EU778104.1 gg_id:317135 feces clone RL388_aao93g01 EU7781
AB186359.1 gg_id:106370 Clostridium sp. str. EBR-02E-0045 AB1863
EU503570.1 gg_id:258988 cecal contents Mus musculus strain C57BL/6J; CRWD2 clone CRWD2_aaa01d01 EU5035
EF098626.1 gg_id:173837 mouse cecum clone SWPT16_aaa02d03 EF0986
EU460961.1 gg_id:291267 red kangaroo feces clone KO1_aai41b02 EU4609
EU453456.1 gg_id:335267 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU4534
EF099643.1 gg_id:182678 mouse cecum clone SWPT4_aaa02d01 EF0996
EU259405.1 gg_id:256835 Rumen yak (Bos grunniens) sequences rumen fluid clone YRC29 EU2594
AF371823.1 gg_id:26704 swine intestine clone p-2573-9F5 AF3718
AB494758.1 gg_id:579431 Fibrobacter succinogenes dominated consortium on hay stems sheep rumen clone A AB4947
EU358717.1 gg_id:305552 structure archaeal denaturing gel electrophoresis and sequencing mesophilic biogas EU3587

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DQ815566.1 gg_id:162783 mouse cecum clone aab42g10 DQ815
EF614547.1 gg_id:233502 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o EF6145
EU381549.1 gg_id:276508 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid EU381
FJ879935.1 gg_id:417038 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8799
EF096069.1 gg_id:194706 mouse cecum clone lean2_aaa03d06 EF096
EU455610.1 gg_id:307873 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H79 EU455
EU777220.1 gg_id:356580 Okapi feces clone OK3_h11_2 EU777
FJ880235.1 gg_id:399202 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8802
FJ833024.1 gg_id:585251 Microbial Ecology Crop Folivorous Hoatzin crop contents clone A1Q102_11C02 FJ8330
FJ880306.1 gg_id:416879 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8803
DQ815830.1 gg_id:168899 mouse cecum clone aab22h05 DQ815
EU774693.1 gg_id:345658 Angola Colobus feces clone EAC_2_aaa02c07 EU774
AY993138.1 gg_id:133820 mouse cecum clone C21_f19 AY993
EU509852.1 gg_id:273749 cecal contents Mus musculus strain C57BL/6J; WD11 clone WD11_aak22e04 EU5098
DQ801542.1 gg_id:192297 human fecal clone RL388_aao96g12 DQ801
EU452387.1 gg_id:334697 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H79 EU4523
DQ015221.1 gg_id:131501 mouse cecum clone M2_d07_3 DQ015
EU381785.1 gg_id:271614 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU381
EU775015.1 gg_id:350626 Francois Langur feces clone FL_1aaa03a05 EU775
EU777499.1 gg_id:355533 Sumatran orangutan feces clone orang1_aai55a03 EU777
EF604688.1 gg_id:233817 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6046
EU844294.1 gg_id:344664 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8442
EU453075.1 gg_id:326948 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75 EU453
AB034030.1 gg_id:29902 rumen clone 4C0d-17 AB034
EU842983.1 gg_id:333590 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU842
GQ448060.1 gg_id:511006 Microbiome neonatal calves: shedding microorganisms fecal clone calf32_6wks_grp GQ448
EU453313.1 gg_id:329835 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K79S EU4533
EU473462.1 gg_id:295624 Somali wild ass feces clone WA_aaa01b08 EU4734
DQ803288.1 gg_id:180328 human fecal clone RL311_aam23e01 DQ803
EU454107.1 gg_id:333446 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77 EU4541
EU454963.1 gg_id:313345 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77 EU4549
DQ796781.1 gg_id:193538 human fecal clone RL179_aao54d07 DQ796
EU457538.1 gg_id:333351 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K79S EU4575
GQ448690.1 gg_id:551419 Microbiome neonatal calves: shedding microorganisms fecal clone calf784_10wks_g GQ448
FJ959623.1 gg_id:555096 bottlenose dolphin upper respiratory tract blowhole clone D896_223 FJ9596
FJ978619.1 gg_id:454156 feces clone CL_F_263 FJ9786
EU511890.1 gg_id:275096 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_aaf10f08 EU5118
AY992900.1 gg_id:135309 mouse cecum clone C22_h18 AY9929
EU509857.1 gg_id:268700 cecal contents Mus musculus strain C57BL/6J; WD11 clone WD11_aak22f02 EU5098
EU381694.1 gg_id:258928 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid EU3816

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DQ015068.1 gg_id:135391 mouse cecum clone M2_f08 DQ015
EU453173.1 gg_id:339311 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H74 EU453
EU471855.1 gg_id:298374 Asiatic elephant feces clone AE3_aaa02a01 EU471
EF445238.1 gg_id:205432 dairy cow rumen clone NED4B9 EF4452
EU455473.1 gg_id:321694 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74 EU455
EU469156.1 gg_id:297372 Speke's gazelle feces clone SP3_d03_1 EU469
GQ451293.1 gg_id:590914 Fecal Yunnan snub-nosed monkey feces clone J299 GQ451
DQ014873.1 gg_id:130230 mouse cecum clone M1_g01_3 DQ014
EF098503.1 gg_id:187936 mouse cecum clone SWPT15_aaa04d09 EF0985
EU470007.1 gg_id:302616 trancaspain urial feces clone TU1_aaa04b04 EU470
EU510389.1 gg_id:276401 cecal contents Mus musculus strain C57BL/6J; WD4 clone WD4_aal37g10 EU510
GQ492606.1 gg_id:556341 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
EF098574.1 gg_id:196293 mouse cecum clone SWPT16_aaa01e11 EF0985
EU453933.1 gg_id:350274 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75 EU453
EU766029.1 gg_id:352902 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B EU766
EU466367.1 gg_id:301816 bighorn sheep feces clone BH2_aao22f02 EU466
EU465603.1 gg_id:289060 argali sheep feces clone AS1_aao39c01.Contig1 EU465
EF099796.1 gg_id:183784 mouse cecum clone SWPT4_aaa04d11 EF0997
EU510413.1 gg_id:271440 cecal contents Mus musculus strain C57BL/6J; WD4 clone WD4_aal38b10 EU510
EU456729.1 gg_id:327441 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU456
EU344228.1 gg_id:270274 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU344
EU470125.1 gg_id:294416 trancaspain urial feces clone TU2_aaa04a03 EU470
FJ880675.1 gg_id:387743 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8806
EF098685.1 gg_id:192621 mouse cecum clone SWPT16_aaa03d08 EF0986
EU775043.1 gg_id:344285 Francois Langur feces clone FL_2aaa04b01 EU775
EF099416.1 gg_id:190055 mouse cecum clone SWPT3_aaa02h09 EF0994
AY050580.1 gg_id:24626 MCB-contaminated groundwater-treating reactor clone GOUTA8 AY0505
FJ880975.1 gg_id:377946 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8809
DQ809519.1 gg_id:185580 human fecal clone RL184_aah22b10 DQ809
DQ795766.1 gg_id:195312 human fecal clone RL245_aai82a04 DQ795
EU773127.1 gg_id:353983 Banteng feces clone BG_aaa04e08.Contig1 EU773
EF096778.1 gg_id:189709 mouse cecum clone SWPT11_aaa04e06 EF0967
EU463456.1 gg_id:298714 domesticated horse feces clone horsem_aai94c08 EU463
AJ575187.1 gg_id:114854 Fastidiosipila sanguinis str. CCUG 47367 AJ5751
EU509561.1 gg_id:276348 cecal contents Mus musculus strain C57BL/6J; MD9 clone MD9_aap60g10 EU509
EU777987.1 gg_id:353964 Rock hyrax feces clone RHSD_aaa02b05_1 EU777
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DQ815932.1 gg_id:165542 mouse cecum clone aab24d11 DQ815
EU006306.1 gg_id:257792 Salmonella enterica serovar typhimurium exploits inflammation compete intestinal r EU006
AY991787.1 gg_id:129537 mouse cecum clone C20_e11 AY991
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EU455714.1 gg_id:351729 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H74N EU455
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EF686630.1 gg_id:240477 Sequences Manifest Rumen Yunnan Yel Cattle (Bos Taurus) rumen fluid clone YNRC1 EF686
EU469801.1 gg_id:289122 western lowland gorilla feces clone GOR_aag71b10 EU469
EU453544.1 gg_id:322487 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU453
EF100061.1 gg_id:196974 mouse cecum clone SWPT5_aaa04b06 EF100
EU794196.1 gg_id:337495 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_I46 EU794
FJ879948.1 gg_id:380190 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8799
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FJ879202.1 gg_id:427609 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8792
AY991768.1 gg_id:132020 mouse cecum clone C20_d11 AY991
EU622732.1 gg_id:278059 -feed administered sub-therapeutic chlorotetracycline alters structure and but not a EU622
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EU504244.1 gg_id:274137 cecal contents Mus musculus strain C57BL/6J; CRWD5 clone CRWD5_aaa04h12 EU504
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EU381667.1 gg_id:268958 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid p EU381
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GQ491528.1 gg_id:558286 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
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EF099470.1 gg_id:174917 mouse cecum clone SWPT3_aaa03f01 EF0994
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AY992586.1 gg_id:130932 mouse cecum clone C23_k06 AY992
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AF538854.1 gg_id:70302 Clostridiales oral clone P4PB_122 P3 AF538

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GQ493093.1 gg_id:536341 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
FJ880919.1 gg_id:446523 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8809
EU843507.1 gg_id:330879 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8435
EF099589.1 gg_id:176273 mouse cecum clone SWPT4_aaa01e06 EF0995
FJ681169.1 gg_id:516494 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6811
EU462716.1 gg_id:301408 Sumatran orangutan feces clone orang2_aai67h03 EU4627
EF602980.1 gg_id:232570 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6029
FJ880438.1 gg_id:456216 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8804
EU774311.1 gg_id:351200 Chimpanzee feces clone CHIMP12_b09_1 EU7743
EU473712.1 gg_id:291116 banteng feces clone BG_aaa02a09.Contig1 EU4737
EU777158.1 gg_id:325232 Okapi feces clone OK1_h07 EU7771
EU504188.1 gg_id:270908 cecal contents Mus musculus strain C57BL/6J; CRWD5 clone CRWD5_aaa03f05 EU5041
EF098217.1 gg_id:182409 mouse cecum clone SWPT14_aaa03b09 EF0982
EU503870.1 gg_id:267628 cecal contents Mus musculus strain C57BL/6J; CRWD4 clone CRWD4_aaa01h01 EU5038
EU505466.1 gg_id:272919 cecal contents Mus musculus strain C57BL/6J; myd5 clone myd5_aaa01a11 EU5054
EF096588.1 gg_id:186778 mouse cecum clone SWPT11_aaa01e03 EF0965
FM873817.1 gg_id:358712 occupant source house mattress dust clone MB01C04 FM873
GQ448150.1 gg_id:579750 Microbiome neonatal calves: shedding microorganisms fecal clone calf32_6wks_grp GQ448
EU457336.1 gg_id:310420 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU4573
AY991940.1 gg_id:135486 mouse cecum clone C20_m03 AY9919
EU452793.1 gg_id:315390 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K79S EU4527
EU772216.1 gg_id:312422 Argali sheep feces clone AS2_aao34f07 EU7722
AY676481.1 gg_id:99206 bovine teat canal clone B-11 AY6764
GQ406190.1 gg_id:540546 Benthic submerged sinkhole ecosystems sediment clone CS-42-12 GQ406
EU457586.1 gg_id:345796 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU4575
EF559207.1 gg_id:224110 mesophilic anaerobic digester clone A35_D28_L_B_B01 EF5592
AY991815.1 gg_id:130769 mouse cecum clone C20_f21 AY9918
EU450939.1 gg_id:316750 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H78S EU4509
EU511824.1 gg_id:276066 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_aaf09f08.Contig3 EU5118
EU505539.1 gg_id:258581 cecal contents Mus musculus strain C57BL/6J; myd5 clone myd5_aaa02c12 EU5055
EF096655.1 gg_id:197960 mouse cecum clone SWPT11_aaa02f07 EF0966
EF604690.1 gg_id:228124 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6046
EU506611.1 gg_id:269815 cecal contents Mus musculus strain C57BL/6J; MD20 clone MD20_aap53c11 EU5066
AY991778.1 gg_id:129981 mouse cecum clone C20_e02 AY9917
EU381747.1 gg_id:265265 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid EU3817
EU777068.1 gg_id:305262 Okapi feces clone OK3_e03_1 EU7770
EU510134.1 gg_id:270351 cecal contents Mus musculus strain C57BL/6J; WD3 clone WD3_aak01h01 EU5101
AY993642.1 gg_id:129911 mouse cecum clone C15_G11.Contig2 AY9936
EU457228.1 gg_id:310407 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU4572
EU450973.1 gg_id:306066 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H74N EU4509
AY916331.1 gg_id:114115 human stool clone C288 AY9163

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EU381608.1 gg_id:259083 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid p EU3816
FJ880228.1 gg_id:435822 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8802
EU006315.1 gg_id:244824 Salmonella enterica serovar typhimurium exploits inflammation compete intestinal r EU0063
FJ880007.1 gg_id:452844 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8800
EU454879.1 gg_id:307694 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H74N EU4548
EU468759.1 gg_id:291052 okapi feces clone OK3_c03 EU4687
EF031005.1 gg_id:186623 Effect mannan-oligosaccharides on piglets weaning piglet colon digesta clone A151 EF0310
EU472000.1 gg_id:298865 francois langur feces clone FL_1aaa03b01 EU4720
EU775519.1 gg_id:340995 Western lowland gorilla feces clone GOR_aag73h09 EU7755
EU474691.1 gg_id:301072 Indian rhinoceros feces clone IR_aaa03f09 EU4746
EU871348.1 gg_id:331088 Genetic Bovine (Bos taurus) Rumen Thailand clone CF23 EU8713
EU505057.1 gg_id:270831 cecal contents Mus musculus strain C57BL/6J; myd3 clone myd3_aaa02c07 EU5050
GQ448759.1 gg_id:580044 Microbiome neonatal calves: shedding microorganisms fecal clone calf784_10wks_g GQ448
EU812977.1 gg_id:347944 Microbial structure thermophilic reactors biogas reactor fed corn silage clone TUM-M EU8129
EU454557.1 gg_id:341200 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU4545
DQ673537.1 gg_id:166957 rumen fluid clone GRC72 DQ673
EU381845.1 gg_id:270153 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU3818
EU475046.1 gg_id:290853 visayam warty pig feces clone VWP_aaa02d10 EU4750
FJ825529.1 gg_id:551083 Microbial during start-up mesophilic biogas plant clone 93_BS1_8 FJ8255
AM932650.1 gg_id:550224 microbiota Toll-like receptor 2 deficient mice exhibits lineage specific modifications AM932
DQ808639.1 gg_id:180638 human fecal clone RL239_aaj11c07 DQ808
EU510483.1 gg_id:259260 cecal contents Mus musculus strain C57BL/6J; WD4 clone WD4_aal39e03 EU5104
AF286038.1 gg_id:32177 mercury and PCB contaminated saltmarsh sediment clone LCP-84 LCP-84 AF2860
EU772159.1 gg_id:332813 Argali sheep feces clone AS1_aao40g11.Contig1 EU7721
DQ793926.1 gg_id:181849 human fecal clone RL176_aah45d04 DQ793
FJ369326.1 gg_id:367422 feces adult twins and mothers; TS50 clone TS50_a03b05 FJ3693
EU454037.1 gg_id:341084 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K79S EU4540
EU777880.1 gg_id:328083 European rabbit feces clone RA_a03 EU7778
DQ794321.1 gg_id:176038 human fecal clone RL197_aah85c11 DQ794
EU467126.1 gg_id:296137 mongoose lemur feces clone ML_aae88h03 EU4671
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EU457497.1 gg_id:327959 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU4574
DQ105659.1 gg_id:132400 pig feces clone DGGE band K9 DQ105
AY953213.1 gg_id:114814 anaerobic swine lagoon clone A-2BS AY9532
DQ799703.1 gg_id:196632 human fecal clone RL182_aah31g02 DQ799
EU475420.1 gg_id:294302 springbok feces clone SBSD_aaa02e07 EU4754
EU509679.1 gg_id:259477 cecal contents Mus musculus strain C57BL/6J; WD10 clone WD10_aak47a07 EU5096
EU773209.1 gg_id:346587 BigHorn sheep feces clone BH1_aao25b06 EU7732
EF096101.1 gg_id:195849 mouse cecum clone lean2_aaa04b08 EF0961

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FJ881204.1 gg_id:437135 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8812
AF001734.1 gg_id:13969 rumen clone RF1 AF0017
EF602963.1 gg_id:231048 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6029
EU381560.1 gg_id:261251 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid EU3815
DQ815533.1 gg_id:163997 mouse cecum clone aab42d04 DQ815
EU454751.1 gg_id:336211 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU4547
EU511976.1 gg_id:265151 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_aak12b10 EU5119
AY993340.1 gg_id:131512 mouse cecum clone C21_p09 AY9933
DQ455918.1 gg_id:157957 pre-adolescent turkey cecum clone CFT111B7 DQ455
DQ327275.1 gg_id:146153 Metagenomic gut microbiome healthy human stool clone E819 DQ327
EU456344.1 gg_id:352378 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83N EU4563
EF098266.1 gg_id:197596 mouse cecum clone SWPT14_aaa03h05 EF0982
DQ815575.1 gg_id:161940 mouse cecum clone aab43b04 DQ815
EU455996.1 gg_id:321938 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N EU4559
FJ680504.1 gg_id:514124 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6805
EF096296.1 gg_id:182906 mouse cecum clone obob1_aaa04c11 EF0962
EU505095.1 gg_id:259218 cecal contents Mus musculus strain C57BL/6J; myd3 clone myd3_aaa02g10 EU5050
EF096762.1 gg_id:180115 mouse cecum clone SWPT11_aaa04c06 EF0967
DQ805630.1 gg_id:181224 human fecal clone RL306aal89b10 DQ805
FJ366193.1 gg_id:368787 feces adult twins and mothers; TS25 clone TS25_a03g08 FJ3661
GQ449028.1 gg_id:575261 Microbiome neonatal calves: shedding microorganisms fecal clone calf783_6wks_gr GQ449
FJ880777.1 gg_id:377763 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8807
EF603798.1 gg_id:231568 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6037
EU771265.1 gg_id:313106 Asiatic elephant feces clone AE2_aaa03g01 EU7712
EU622725.1 gg_id:279340 -feed administered sub-therapeutic chlorotetracycline alters structure and but not a EU6227
AY992440.1 gg_id:135500 mouse cecum clone C23_d20 AY9924
EU459615.1 gg_id:302902 ring-tailed lemur feces clone RT_aai09c08 EU4596
FJ880454.1 gg_id:429481 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8804
AB494799.1 gg_id:569774 Fibrobacter succinogenes dominated consortium on hay stems sheep rumen clone A AB4947
EU457718.1 gg_id:353820 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75N EU4577
FJ880595.1 gg_id:436138 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8805
EU776749.1 gg_id:317127 Mongoose lemur feces clone ML_aae89h02 EU7767
AB185617.1 gg_id:105179 rumen clone F24-E05 AB1856
EU504656.1 gg_id:270170 cecal contents Mus musculus strain C57BL/6J; myd1 clone myd1_aaa04a05 EU5046
EU505379.1 gg_id:262055 cecal contents Mus musculus strain C57BL/6J; myd4 clone myd4_aaa03e09 EU5053
EU474329.1 gg_id:300780 western lowland gorilla feces clone GORSD_aaa03f04 EU4743
EU451975.1 gg_id:352125 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83N EU4519
EU760447.1 gg_id:336277 Mouse fecal microbiota feces clone 3B9 EU7604
FJ880686.1 gg_id:419637 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8806
DQ777889.1 gg_id:171674 rat feces clone R-1167 DQ777
EU451287.1 gg_id:339718 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83N EU4512

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EF099176.1 gg_id:176740 mouse cecum clone SWPT2_aaa03d09 EF0991
DQ800492.1 gg_id:199335 human fecal clone RL183_aah27d07 DQ800
AJ249104.1 gg_id:74679 SHA-33 clone AJ2491
GQ448666.1 gg_id:570554 Microbiome neonatal calves: shedding microorganisms fecal clone calf784_10wks_g GQ448
FJ879613.1 gg_id:456061 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8796
FJ368324.1 gg_id:360562 feces adult twins and mothers; TS3 clone TS3_a03a01 FJ3683
EU452598.1 gg_id:308400 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU4525
EU844761.1 gg_id:346496 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8447
EU381802.1 gg_id:264507 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU3818
EU475309.1 gg_id:300568 rock hyrax feces clone RHSD_aaa01c02 EU4753
EU344529.1 gg_id:264444 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU3445
EF098822.1 gg_id:175293 mouse cecum clone SWPT1_aaa01e01 EF0988
FJ880618.1 gg_id:399241 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8806
AY991839.1 gg_id:135320 mouse cecum clone C20_g21 AY9918
AY991747.1 gg_id:134555 mouse cecum clone C20_c05 AY9917
AY916380.1 gg_id:112852 human stool clone D692 AY9163
EU472520.1 gg_id:288931 Angola colobus feces clone EAC_2_aaa04f09 EU4725
DQ815359.1 gg_id:162963 mouse cecum clone aab46e08 DQ815
FJ371057.1 gg_id:369145 feces adult twins and mothers; TS5 clone TS5_a04d09 FJ3710
FJ365220.1 gg_id:357560 feces adult twins and mothers; TS1 clone TS1_a04c06 FJ3652
EU452553.1 gg_id:354736 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU4525
EU451399.1 gg_id:345802 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU4513
EF614465.1 gg_id:232814 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o EF6144
FJ672016.1 gg_id:519103 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6720
EF098796.1 gg_id:175435 mouse cecum clone SWPT1_aaa01a10 EF0987
AF001769.1 gg_id:13959 rumen clone RF38 AF0017
EU381678.1 gg_id:274151 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid p EU3816
EU475068.1 gg_id:292585 visayam warty pig feces clone VWP_aaa04c11 EU4750
EF098038.1 gg_id:192598 mouse cecum clone SWPT12_aaa04e02 EF0980
EF436360.1 gg_id:211744 library-based ruminal water buffalo (Bubalus bubalis) rumen fluid clone BRC74 EF4363
EF098379.1 gg_id:182840 mouse cecum clone SWPT15_aaa01h08 EF0983
EU451092.1 gg_id:329830 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N EU4510
DQ799437.1 gg_id:184190 human fecal clone RL305aal86c06 DQ799
AY993078.1 gg_id:129832 mouse cecum clone C21_c22 AY9930
EU509028.1 gg_id:267478 cecal contents Mus musculus strain C57BL/6J; MD7 clone MD7_aap42c02 EU5090
EU455579.1 gg_id:333837 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83N EU4555
EF097847.1 gg_id:176322 mouse cecum clone SWPT20_aaa04f12 EF0978
EF098579.1 gg_id:178378 mouse cecum clone SWPT16_aaa01f07 EF0985
EU775500.1 gg_id:317892 Western lowland gorilla feces clone GOR_aag71f08 EU7755
EF099953.1 gg_id:184851 mouse cecum clone SWPT5_aaa02f11 EF0999

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EU510410.1 gg_id:275352 cecal contents Mus musculus strain C57BL/6J; WD4 clone WD4_aal38b07 EU510
EU507862.1 gg_id:273518 cecal contents Mus musculus strain C57BL/6J; MD24 clone MD24_aaa02c08 EU507
EU774696.1 gg_id:355197 Angola Colobus feces clone EAC_2_aaa01a03 EU774
EU452019.1 gg_id:342872 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H74 EU452
AY994025.1 gg_id:136722 Abundant and fungal microbiota murine intestine clone 31-1 AY994
EU458660.1 gg_id:302600 European rabbit feces clone RA_c05_1 EU458
EF098087.1 gg_id:183553 mouse cecum clone SWPT14_aaa01c10 EF098
AY992716.1 gg_id:135235 mouse cecum clone C23_p24 AY992
EU457950.1 gg_id:333133 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU457
FJ881075.1 gg_id:440302 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8810
EU511923.1 gg_id:266657 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_aak11c11 EU511
GQ492378.1 gg_id:563252 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
EU772166.1 gg_id:355615 Argali sheep feces clone AS1_aao38g10.Contig1 EU772
EU508392.1 gg_id:266059 cecal contents Mus musculus strain C57BL/6J; MD27 clone MD27_aaa04g10 EU508
EF409958.1 gg_id:215507 Isolation equol-producing fecal clone QE8 EF409
EU471999.1 gg_id:297009 francois langur feces clone FL_1aaa02e08 EU471
EU451066.1 gg_id:316021 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77 EU451
EU511755.1 gg_id:269211 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_aaf08h08 EU511
EU771407.1 gg_id:305787 Asiatic elephant feces clone AE1_aaa04e05 EU771
FJ879257.1 gg_id:406987 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8792
EU778096.1 gg_id:304663 feces clone RL388_aao94c12 EU778
EU454432.1 gg_id:356288 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77 EU454
EU773120.1 gg_id:325945 Banteng feces clone BG_aaa01c08.Contig1 EU773
EF099617.1 gg_id:174061 mouse cecum clone SWPT4_aaa01h08 EF099
AJ278163.1 gg_id:65412 G+C gram-positive clone SHD-209 AJ2781
EU463338.1 gg_id:291644 bush dog feces clone bdog1_aai79a02 EU463
EU381866.1 gg_id:272871 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU381
DQ815961.1 gg_id:173218 mouse cecum clone aab24h05 DQ815
EU844581.1 gg_id:316964 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
EU775062.1 gg_id:340111 Francois Langur feces clone FL_1aaa03g08 EU775
EU469766.1 gg_id:296900 flying fox feces clone FF_e04_2 EU469
EU457875.1 gg_id:332496 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77 EU457
EU457395.1 gg_id:354536 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77 EU457
EF604623.1 gg_id:227635 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6046
EU456346.1 gg_id:320048 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75 EU456
DQ673521.1 gg_id:165839 rumen fluid clone GRC56 DQ673
EU455843.1 gg_id:317867 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75 EU455
DQ815543.1 gg_id:161927 mouse cecum clone aab42e06 DQ815
EU778561.1 gg_id:320354 Ring-tailed lemur feces clone RT_aai09b08 EU778
EU474327.1 gg_id:296966 western lowland gorilla feces clone GORSD_aaa02a12 EU474

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GQ897162.1 gg_id:585939 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ897
AB009229.1 gg_id:13970 rumen clone RFN81 bacterium AB009
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EU774485.1 gg_id:333426 mammals their gut microbes Eastern Black and White Colobus feces clone COL_aai1 EU774
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EU843138.1 gg_id:343455 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
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EU454417.1 gg_id:338552 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75 EU454
DQ327522.1 gg_id:147285 Metagenomic gut microbiome healthy human stool clone EB02 DQ327
AB185607.1 gg_id:100110 rumen clone F24-D07 AB185
EU509524.1 gg_id:267219 cecal contents Mus musculus strain C57BL/6J; MD9 clone MD9_aap60b06 EU509
DQ824652.1 gg_id:175240 human fecal clone RL185_aaj71b06 DQ824
FJ172894.1 gg_id:313603 Qinghai Yak Ruminal and Fungi China rumen clone RB-53 FJ1728
EU505188.1 gg_id:276312 cecal contents Mus musculus strain C57BL/6J; myd3 clone myd3_aaa04b10 EU505
FJ363611.1 gg_id:368015 feces adult twins and mothers; TS14 clone TS14_a01c11 FJ3636
EU457930.1 gg_id:323131 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77 EU457
EU773116.1 gg_id:321078 Banteng feces clone BG_aaa02c11.Contig1 EU773
EF603861.1 gg_id:234912 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6038
EF608548.1 gg_id:234586 predatory Poecilus chalcites their response lab rearing and antibiotic treatment diges EF6085
EF559219.1 gg_id:218576 mesophilic anaerobic digester clone A35_D28_L_B_H03 EF5592
FJ959475.1 gg_id:589021 bottlenose dolphin upper respiratory tract blowhole clone D896_055 FJ9594
EU778309.1 gg_id:305086 feces clone RL388_aao93d02 EU778
AY992700.1 gg_id:130265 mouse cecum clone C23_p07 AY992
EU453798.1 gg_id:317210 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75 EU453
EU457478.1 gg_id:306446 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H74 EU457
AB009220.1 gg_id:15975 rumen clone RFN72 bacterium AB009
EF604668.1 gg_id:229386 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6046
FJ881318.1 gg_id:375892 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8813
EU456058.1 gg_id:341671 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77 EU456
EU454052.1 gg_id:311779 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77 EU454
EU452368.1 gg_id:306599 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75 EU452
AB185775.1 gg_id:105358 rumen clone U29-D04 AB185
EU511880.1 gg_id:260953 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_aaf10d05 EU511
EU471860.1 gg_id:298446 Asiatic elephant feces clone AE3_aaa02c04 EU471
EU454220.1 gg_id:306865 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K77 EU454
DQ809170.1 gg_id:179557 human fecal clone RL308_aal82g02 DQ809

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FJ172796.1 gg_id:327925 Qinghai Yak Ruminal and Fungi China rumen clone RB-3G1 FJ1727
DQ014691.1 gg_id:131938 mouse cecum clone M1_e09_1 DQ014
EU542497.1 gg_id:271116 Effects chemical structure concentration on pathways microbial during dechlorinatio EU542
DQ326577.1 gg_id:146579 Metagenomic gut microbiome healthy human stool clone E010 DQ326
FJ880324.1 gg_id:450047 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8803
EU464099.1 gg_id:297396 reticulated giraffe feces clone gir_aah93f07 EU464
FJ365218.1 gg_id:364080 feces adult twins and mothers; TS1 clone TS1_a04c04 FJ3652
FJ880951.1 gg_id:425779 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8809
AY949857.1 gg_id:114488 Clostridium sp. strain str. P6 AY9498
EU511842.1 gg_id:270244 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_aaf09h07.Contig2 EU511
GQ448173.1 gg_id:569073 Microbiome neonatal calves: shedding microorganisms fecal clone calf32_6wks_grp GQ448
DQ795747.1 gg_id:198826 human fecal clone RL245_aai81g02 DQ795
EU509463.1 gg_id:266261 cecal contents Mus musculus strain C57BL/6J; MD9 clone MD9_aap58g10 EU509
EF436456.1 gg_id:205296 library-based ruminal water buffalo (Bubalus bubalis) rumen fluid clone BRC170 EF4364
AM176886.1 gg_id:159709 Recovery mangrove sediment clone SZB25 AM176
AF481208.1 gg_id:69664 oral endodontic infection clone MCE3_9 AF481
AY991809.1 gg_id:132201 mouse cecum clone C20_f15 AY991
DQ801570.1 gg_id:199522 human fecal clone RL117_aae91f03 DQ801
EU456301.1 gg_id:327792 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83 EU456
DQ793297.1 gg_id:195191 human fecal clone RL199_aaj41h08 DQ793
EF098483.1 gg_id:174380 mouse cecum clone SWPT15_aaa04a07 EF0984
EU451728.1 gg_id:325518 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74 EU451
DQ815397.1 gg_id:171547 mouse cecum clone aab47e07 DQ815
EU503956.1 gg_id:266413 cecal contents Mus musculus strain C57BL/6J; CRWD4 clone CRWD4_aaa03c01 EU503
EU474661.1 gg_id:288965 Indian rhinoceros feces clone IR_aaa03a01 EU474
DQ801415.1 gg_id:192187 human fecal clone RL388_aao95c03 DQ801
EF096155.1 gg_id:190763 mouse cecum clone obob1_aaa01e01 EF0961
DQ905376.1 gg_id:168318 human fecal clone 013C-A6 DQ905
AY993086.1 gg_id:131034 mouse cecum clone C21_d09 AY993
AF371588.1 gg_id:53640 swine intestine clone p-2592-9F5 AF371
EU845442.1 gg_id:319597 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU845
EU511169.1 gg_id:271815 cecal contents Mus musculus strain C57BL/6J; WD7 clone WD7_aal03g08 EU511
EU453919.1 gg_id:314110 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78 EU453
DQ799133.1 gg_id:183994 human fecal clone RL205_aaj18a09 DQ799
EU844615.1 gg_id:328318 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
FN397806.1 gg_id:406604 geomicrobiological investigation sediments Gulf Cadiz GeoB 9072-1 anoxic sub-surfa FN3978
EU508822.1 gg_id:269845 cecal contents Mus musculus strain C57BL/6J; MD4 clone MD4_aap51g02 EU508
EU452455.1 gg_id:327632 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80 EU452
DQ809698.1 gg_id:175552 human fecal clone RL184_aan82h02 DQ809
DQ799363.1 gg_id:195677 human fecal clone RL305aal85d05 DQ799

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DQ905439.1 gg_id:167609 human fecal clone 013C-G1 DQ905
EF434365.1 gg_id:207897 human infant gastrointestinal tract microbiota stool mother babies 13 and 14 7 mont EF4343
EU344195.1 gg_id:259265 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU344
DQ394680.1 gg_id:155461 on -Arctic peninsula Svalbard Norway determined genes and rumen isolates reindee DQ394
DQ456150.1 gg_id:158082 pre-adolescent turkey cecum clone CFT29A4 DQ456
AB270012.1 gg_id:165855 Influence temperature and humidity on heifers rumen contents Holstein heifer (Bos AB270
DQ326202.1 gg_id:146564 Metagenomic gut microbiome healthy human stool clone C117 DQ326
AB034077.1 gg_id:17384 rumen clone 5C3d-17 AB034
FJ680716.1 gg_id:519408 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6807
FJ680945.1 gg_id:532188 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6809
DQ394665.1 gg_id:155763 on -Arctic peninsula Svalbard Norway determined genes and rumen isolates reindee DQ394
EU773804.1 gg_id:336979 Cheetah feces clone CE3_aai05g02 EU773
EF445156.1 gg_id:210895 rabbit cecum clone NED3A9 EF4451
DQ071471.1 gg_id:230618 microbial cecum captive and free-living capercaillies (Tetrao urogallus) clone TuCw3 DQ071
EF398626.1 gg_id:204351 human fecal clone SJTU_F_05_82 EF3986
GQ042974.1 gg_id:419365 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1011f GQ042
AY985745.1 gg_id:124662 human stool clone C776 AY985
EU459375.1 gg_id:303222 cheetah feces clone CE3_aai06c09 EU459
FJ680706.1 gg_id:519088 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6807
DQ905348.1 gg_id:164129 human fecal clone 013B-G1 DQ905
EU475249.1 gg_id:297219 bonobo feces clone BNO_aaa04f02 EU475
FJ680586.1 gg_id:516316 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6805
EU464455.1 gg_id:296649 African elephant feces clone AFEL_aai29d09 EU464
FJ679113.1 gg_id:512391 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6791
FJ366090.1 gg_id:358312 feces adult twins and mothers; TS25 clone TS25_a02e11 FJ3660
EU774998.1 gg_id:346253 Francois Langur feces clone FL_1aaa02g02 EU774
DQ455897.1 gg_id:157282 pre-adolescent turkey cecum clone CFT19H10 DQ455
EU747939.1 gg_id:321027 neotropical folivorous flying bird adult hoatzin crop clone hoa14_31G04 EU747
FJ681240.1 gg_id:518967 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6812
EU844442.1 gg_id:345337 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
DQ905430.1 gg_id:162057 human fecal clone 013C-F3 DQ905
AF018562.1 gg_id:16003 rumen fluid clone 12-110 AF018
AB185671.1 gg_id:107768 rumen clone U28-B05 AB185
DQ456202.1 gg_id:158293 pre-adolescent turkey cecum clone CFT29E12 DQ456
EU850513.1 gg_id:304381 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF288 EU850
EU381446.1 gg_id:260323 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid EU381
EF445244.1 gg_id:208300 dairy cow rumen clone NED4C2 EF4452
DQ905280.1 gg_id:169515 human fecal clone 013-h9 DQ905
AM275445.2 gg_id:230437 fecal microbiota irritable bowel syndrome patients significantly that healthy subject AM275
DQ905419.1 gg_id:168661 human fecal clone 013C-E4 DQ905

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EU381976.1 gg_id:275429 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU381
AY992012.1 gg_id:135387 mouse cecum clone C20_p15 AY992
DQ394601.1 gg_id:153187 -Arctic peninsula Svalbard Norway determined genes and rumen isolates reindeer o DQ394
FJ677334.1 gg_id:514315 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6773
EU468486.1 gg_id:302171 okapi feces clone OK1_g04 EU468
FJ683863.1 gg_id:525747 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6838
DQ905300.1 gg_id:162453 human fecal clone 013B-B9 DQ905
DQ905386.1 gg_id:170086 human fecal clone 013C-B5 DQ905
GU174115.1 gg_id:591032 Microbial Bactrian camel estimated rumen clone XJC92 GU174
EU509379.1 gg_id:273428 cecal contents Mus musculus strain C57BL/6J; MD8 clone MD8_aap48h09 EU509
GQ448528.1 gg_id:562369 Microbiome neonatal calves: shedding microorganisms fecal clone calf784_6wks_gr GQ448
DQ394677.1 gg_id:152381 on -Arctic peninsula Svalbard Norway determined genes and rumen isolates reindee DQ394
FJ681824.1 gg_id:529341 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6818
FJ681732.1 gg_id:529192 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6817
FJ681326.1 gg_id:518019 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6813
EU844329.1 gg_id:313037 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
GQ448446.1 gg_id:544734 Microbiome neonatal calves: shedding microorganisms fecal clone calf783_10wks_g GQ448
FJ371714.1 gg_id:361344 feces adult twins and mothers; TS8 clone TS8_a01d07 FJ3717
DQ327134.1 gg_id:156306 Metagenomic gut microbiome healthy human stool clone E653 DQ327
DQ327191.1 gg_id:146348 Metagenomic gut microbiome healthy human stool clone E721 DQ327
AY992864.1 gg_id:129944 mouse cecum clone C22_g02 AY992
EF445172.1 gg_id:214214 rabbit cecum clone NED2B8 EF4451
DQ796500.1 gg_id:179429 human fecal clone RL179aan73d10 DQ796
DQ115994.1 gg_id:132122 bovine teat canal clone B-75 DQ115
AY854312.1 gg_id:109792 herbivore gastrointestinal tract clone Thompsons22 AY854
DQ015052.1 gg_id:130049 mouse cecum clone M2_e01 DQ015
EU507039.1 gg_id:271602 cecal contents Mus musculus strain C57BL/6J; MD21 clone MD21_aar10c06 EU507
EU842723.1 gg_id:307789 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
EF436444.1 gg_id:205594 library-based ruminal water buffalo (Bubalus bubalis) rumen fluid clone BRC158 EF4364
DQ815745.1 gg_id:162816 mouse cecum clone aab21g06 DQ815
DQ455840.1 gg_id:157193 pre-adolescent turkey cecum clone CFT19B10 DQ455
EU845662.1 gg_id:305717 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU845
FJ684114.1 gg_id:520033 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6841
EU474476.1 gg_id:298486 bighorn sheep feces clone BHSD_aaa03a11 EU474
GQ896678.1 gg_id:580809 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do GQ896
DQ394663.1 gg_id:155156 on -Arctic peninsula Svalbard Norway determined genes and rumen isolates reindee DQ394
AY570605.1 gg_id:108481 biodegraded Canadian oil reservoir clone PL-22B3 AY570
AY570606.1 gg_id:108482 biodegraded Canadian oil reservoir clone PL-22B5 AY570
EU766863.1 gg_id:327800 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU766
CU920499.1 gg_id:559940 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU920

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DQ394605.1 gg_id:152014 -Arctic peninsula Svalbard Norway determined genes and rumen isolates reindeer o DQ394
DQ455839.1 gg_id:157804 pre-adolescent turkey cecum clone CFT19B9 DQ455
FJ172778.1 gg_id:338971 Qinghai Yak Ruminal and Fungi China rumen clone RB-3D4 FJ1727
DQ057401.1 gg_id:134365 chicken ileum/cecum clone cc376 DQ057
EU509847.1 gg_id:260454 cecal contents Mus musculus strain C57BL/6J; WD11 clone WD11_aak22d05 EU5098
AY991724.1 gg_id:130890 mouse cecum clone C20_a22 AY9917
FJ674739.1 gg_id:516321 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6747
EU469866.1 gg_id:295651 western lowland gorilla feces clone GOR_aag72h05 EU4698
EU381605.1 gg_id:265306 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid p EU3816
DQ394597.1 gg_id:155616 -Arctic peninsula Svalbard Norway determined genes and rumen isolates reindeer o DQ394
EU842968.1 gg_id:304526 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8429
FJ677534.1 gg_id:522041 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6775
EU459381.1 gg_id:294178 cheetah feces clone CE3_aai06e03 EU4593
EU009808.1 gg_id:254600 intestinal microbiota domestic and wild turkeys turkey cecum clone WTB_D44 EU0098
AF371822.1 gg_id:17822 swine intestine clone p-1014-a5 AF3718
DQ905450.2 gg_id:162592 human fecal clone 013C-G12 DQ905
EU344691.1 gg_id:263796 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU3446
AB355062.1 gg_id:249776 Monitoring and archaeal two heavy polluted areas lake Egypt based on sediment Ma AB3550
FJ680233.1 gg_id:532067 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6802
AY854353.1 gg_id:109787 herbivore gastrointestinal tract clone Thompsons74 AY8543
AY992826.1 gg_id:132145 mouse cecum clone C22_e01 AY9928
EU474740.1 gg_id:287827 takin feces clone TAK_aaa03c08 EU4747
DQ456160.1 gg_id:157744 pre-adolescent turkey cecum clone CFT29B3 DQ456
EU844570.1 gg_id:309973 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8445
EU507073.1 gg_id:277498 cecal contents Mus musculus strain C57BL/6J; MD21 clone MD21_aar10g05 EU5070
AY993189.1 gg_id:133439 mouse cecum clone C21_i05 AY9931
FJ675513.1 gg_id:510671 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6755
EU009766.1 gg_id:237063 intestinal microbiota domestic and wild turkeys turkey cecum clone DTB_AD46 EU0097
DQ673509.1 gg_id:165623 rumen fluid clone GRC44 DQ673
EU381964.1 gg_id:272169 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU3819
FJ366113.1 gg_id:363430 feces adult twins and mothers; TS25 clone TS25_a02h02 FJ3661
EU458475.1 gg_id:300102 spotted hyena feces clone HY2_d11 EU4584
EU773919.1 gg_id:308652 Cheetah feces clone CE3_aai06c12 EU7739
DQ456423.1 gg_id:157818 pre-adolescent turkey cecum clone CFT214F6 DQ456
FJ676362.1 gg_id:525102 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6763
FJ678094.1 gg_id:529559 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6780
FJ676053.1 gg_id:517448 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6760
FJ679869.1 gg_id:529035 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6798
EF404664.1 gg_id:209153 human fecal clone SJTU_C_14_24 EF4046
FJ681148.1 gg_id:510114 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6811

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DQ777937.2 gg_id:168060 rat feces clone R-1334 DQ777
DQ325974.1 gg_id:148500 Metagenomic gut microbiome healthy human stool clone B869 DQ325
AB270076.1 gg_id:168698 Influence temperature and humidity on heifers rumen contents Holstein heifer (Bos AB270
AF371809.1 gg_id:70137 swine intestine clone p-656-a5 AF3718
FJ684733.1 gg_id:523289 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6847
FJ366015.1 gg_id:367674 feces adult twins and mothers; TS25 clone TS25_a01g03 FJ3660
EU344335.1 gg_id:269956 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU3443
FJ371694.1 gg_id:368399 feces adult twins and mothers; TS8 clone TS8_a01b11 FJ3716
DQ905260.1 gg_id:161946 human fecal clone 013-g1 DQ905
AY985388.1 gg_id:119418 human stool clone C326 AY9853
DQ673484.1 gg_id:164940 rumen fluid clone GRC19 DQ673
GQ898082.1 gg_id:588534 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ898
EU843078.1 gg_id:355687 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
FJ680520.1 gg_id:524781 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6805
AY993113.1 gg_id:130628 mouse cecum clone C21_e16 AY9931
AY571402.1 gg_id:114670 termite gut clone RsaHf437 AY5714
FJ679178.1 gg_id:520330 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6791
EF445206.1 gg_id:214651 rabbit cecum clone NED3H5 EF4452
FJ675782.1 gg_id:524758 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6757
FJ976346.1 gg_id:585819 Interindividual healthy human oral microbiota mouth clone 12B940 FJ9763
FJ684559.1 gg_id:520651 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6845
AF385563.1 gg_id:17517 on or epthelial purified crevicular epithelial cells clone BU014 AF3855
AF018564.1 gg_id:16004 rumen fluid clone 12-124 AF0185
DQ673496.1 gg_id:170496 rumen fluid clone GRC31 DQ673
AB185778.1 gg_id:105813 rumen clone U29-D08 AB1857
EU843837.1 gg_id:335004 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8438
AB034045.1 gg_id:42029 rumen clone 5C0d-12 AB0340
GU174095.1 gg_id:574394 Microbial Bactrian camel estimated rumen clone XJC60 GU174
AM277551.2 gg_id:229088 fecal microbiota irritable bowel syndrome patients significantly that healthy subject AM277
EU766064.1 gg_id:331187 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B4 EU7660
AY854286.1 gg_id:110924 herbivore gastrointestinal tract clone CATTLE_24 AY8542
FJ679911.1 gg_id:530129 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6799
FJ673267.1 gg_id:523440 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6732
EU009792.1 gg_id:238056 intestinal microbiota domestic and wild turkeys turkey cecum clone WTB_AA12 EU0097
AY916239.1 gg_id:113676 human descending colon biopsy clone MF35 AY9162
EU843660.1 gg_id:350056 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8436
EU844249.1 gg_id:314703 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8442
FJ675915.1 gg_id:522124 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6759
FJ677125.1 gg_id:511272 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6771
FJ677384.1 gg_id:528095 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6773

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EU461903.1 gg_id:295617 white-faced saki feces clone Saki_aaj63e01 EU461
DQ394678.1 gg_id:151406 on -Arctic peninsula Svalbard Norway determined genes and rumen isolates reindee DQ394
EU773937.1 gg_id:340833 Cheetah feces clone CE3_aai06f11 EU773
FJ676661.1 gg_id:522924 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6766
EU259413.1 gg_id:242512 Rumen yak (Bos grunniens) sequences rumen fluid clone YRC37 EU259
EU344349.1 gg_id:267638 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU3443
EF686560.1 gg_id:240691 Sequences Manifest Rumen Yunnan Yel Cattle (Bos Taurus) rumen fluid clone YNRC4 EF6865
DQ394661.1 gg_id:153075 on -Arctic peninsula Svalbard Norway determined genes and rumen isolates reindee DQ394
EU794208.1 gg_id:333352 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_O12 EU794
EU764137.1 gg_id:343371 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU7641
FJ681295.1 gg_id:522514 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6812
AY916340.1 gg_id:114041 human stool clone C627 AY9163
FJ673199.1 gg_id:514445 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6731
EU259397.1 gg_id:239427 Rumen yak (Bos grunniens) sequences rumen fluid clone YRC21 EU2593
EU531934.1 gg_id:258829 Predominant role host genetics controlling gut microbiota FMF remission stool clone EU531
EU381808.1 gg_id:276563 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU3818
EU464093.1 gg_id:293092 reticulated giraffe feces clone gir_aah93e04 EU4640
GQ175439.1 gg_id:509971 Chicken intestinal microbiota modulations various feed supplementations DGGE anc GQ175
DQ394637.1 gg_id:152278 -Arctic peninsula Svalbard Norway determined genes and rumen isolates reindeer o DQ394
DQ327572.1 gg_id:146754 Metagenomic gut microbiome healthy human stool clone EB56 DQ327
FJ677229.1 gg_id:529582 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6772
AB185546.1 gg_id:105349 rumen clone F23-E06 AB1855
FJ677274.1 gg_id:532372 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6772
AB487981.1 gg_id:584682 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSSUR AB4879
AY916150.1 gg_id:114270 human transverse colon biopsy clone M220 AY9161
EF445284.1 gg_id:207718 dairy cow rumen clone NED5G11 EF4452
EU871342.1 gg_id:314152 Genetic Bovine (Bos taurus) Rumen Thailand clone CF11 EU8713
FJ366276.1 gg_id:362403 feces adult twins and mothers; TS25 clone TS25_a04g05 FJ3662
EU850451.1 gg_id:338243 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF18 EU8504
FJ680532.1 gg_id:523645 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6805
EU773256.1 gg_id:330287 BigHorn sheep feces clone BH1_aao27h04 EU7732
FJ685072.1 gg_id:519741 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6850
FJ680782.1 gg_id:517071 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6807
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AB269956.1 gg_id:173608 Influence temperature and humidity on heifers rumen contents Holstein heifer (Bos AB2699
AB270018.1 gg_id:168096 Influence temperature and humidity on heifers rumen contents Holstein heifer (Bos AB2700

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EU773847.1 gg_id:346063 Cheetah feces clone CE3_aai08f04 EU773
FJ676116.1 gg_id:515219 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6761
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AB185678.1 gg_id:99888 rumen clone U28-B12 AB185
EU381739.1 gg_id:260948 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid EU381
AB185701.1 gg_id:105109 rumen clone U28-E03 AB185
EU469811.1 gg_id:293570 western lowland gorilla feces clone GOR_aag71e02 EU469
FJ365006.1 gg_id:365319 feces adult twins and mothers; TS1 clone TS1_a01g03 FJ3650
AB426234.1 gg_id:260909 -situ identification study benzene-degrading s under methanogenic condition anaerc AB426
AM947517.1 gg_id:267608 Minor changes detected microbial structure and after three week thermophilic dige AM947
EU878346.1 gg_id:583047 Investigation factors influencing production large-scale municipal biogas plant therm EU878
DQ256297.1 gg_id:144471 subsurface water clone EV818BHEB6102702SAFF7 DQ256
FJ825480.1 gg_id:553823 Microbial during start-up mesophilic biogas plant clone 166_BE1_21 FJ8254
AF280848.1 gg_id:29289 bioreactor clone mle1-9 AF280
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DQ887927.1 gg_id:169056 thermophilic anaerobic solid waste bioreactor clone GHB3C09 DQ887
AB476673.1 gg_id:545286 SSU sequences prokaryotes inside emergency Gotthard road tunnel Switzerland sulf AB476
AB186884.1 gg_id:105619 polychlorinated dioxin dechlorinating microcosm clone TSAF09 AB186
AB487319.1 gg_id:574748 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNIR0 AB487
DQ251789.1 gg_id:141271 subsurface water clone EV818BHEB6111502SAGG22 DQ251
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FJ825509.1 gg_id:570957 Microbial during start-up mesophilic biogas plant clone 16_BS3_30 FJ8255
FJ269100.1 gg_id:314041 dissimilatory ferric iron reducers arsenic contaminated Hunan south China paddy soil FJ2691
GU455260.1 gg_id:523387 Understanding short-chain fatty acids accumulation enhanced alkaline digestion: kir GU455
AM947537.1 gg_id:270478 Minor changes detected microbial structure and after three week thermophilic dige AM947
AM778023.1 gg_id:248504 nonsaline . Influence pore-size filters determination structure alkaline groundwater AM778
AB237710.1 gg_id:139607 microorganisms deep subsurface groundwater sedimentary rock milieu clone HDBW AB237
DQ088770.1 gg_id:130916 subsurface clone BE325FW032701CTS_hole1-5 DQ088
AB487422.1 gg_id:579422 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNIR0 AB487
AB232808.1 gg_id:138579 Microbial mesophilic chemostat cultivation propionate-degrading methanogenic con AB2328
DQ801312.1 gg_id:188238 human fecal clone RL388_aao93g10 DQ801
EU465913.1 gg_id:289424 African elephant feces clone AFEL3_aao14a02 EU465
EU771501.1 gg_id:342688 Hamadryas Baboon feces clone AFBAB_aai02b06 EU771
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EU289058.1 gg_id:236283 microbiome cloacal openings urogenital and anal tracts tammar wallaby Macropus e EU289
EU245382.1 gg_id:252441 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M1-A0 EU245
EU869412.1 gg_id:336463 Microbial hypersaline Sidi Ameur water Himalatt Salt Lake Algerian Sahara clone ARD EU869
EU246061.1 gg_id:240732 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-P2-F02 EU246

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EU246114.1 gg_id:252431 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-P3-F08 EU246
FN436094.1 gg_id:538857 Molekularbiologische Charakterisierung der bakteriellen Populationsdynamik eines t FN436
EU245798.1 gg_id:253481 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M6-E0 EU245
AY176772.1 gg_id:99126 Garciella nitratireducens str. Met 79; DSM 15102; CIP 107615 AY176
EU358718.1 gg_id:307463 structure archaeal denaturing gel electrophoresis and sequencing mesophilic biogas EU358
AY272039.1 gg_id:85846 Guggenheimia bovis str. OMZ913 AY272
EU245221.1 gg_id:257609 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-H4-C10 EU245
EU245533.1 gg_id:236398 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M2-G0 EU245
EF116488.1 gg_id:176096 Proteolyticum ethanoligenes str. GW EF116
AM943575.1 gg_id:266069 Microbial dolomite formation Lagoa Vermelha Brazil carbonaceous sediments hype AM943
GU083681.1 gg_id:589048 Microorganism Xiarinur soda lake sediment clone x124 GU083
GU455082.1 gg_id:529217 Understanding short-chain fatty acids accumulation enhanced alkaline digestion: kir GU455
EU246326.1 gg_id:247641 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-P6-H10 EU246
FJ672228.1 gg_id:518452 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6722
AM982554.2 gg_id:278979 microbial and slurry pig saw dust spent bedding clone PISD-AJC08 AM982
AY542206.1 gg_id:113661 Gulf Mexico seafloor sediments clone GoM HDB-21 AY542
FJ269087.1 gg_id:338939 dissimilatory ferric iron reducers arsenic contaminated Hunan south China paddy soil FJ2690
AF371683.1 gg_id:33133 swine intestine clone p-3212-42A2 AF371
EU885003.1 gg_id:343949 microbial hindgut chamber Pomacanthus sexstriatus GI tract clone AD7 EU885
EU772218.1 gg_id:343551 Argali sheep feces clone AS1_aao38b12.Contig1 EU772
EU842821.1 gg_id:323417 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
EU773185.1 gg_id:315831 BigHorn sheep feces clone BH2_aao21e05 EU773
EU567322.1 gg_id:275937 Clostridiisalibacter sp. SOL3f37 str. SOL3F37 EU567
EU871405.1 gg_id:336747 Genetic Bovine (Bos taurus) Rumen Thailand clone CF357 EU871
EU850582.1 gg_id:329788 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF398 EU850
EU843088.1 gg_id:323155 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
DQ806377.1 gg_id:174033 human fecal clone RL186_aan91d11 DQ806
FJ202295.1 gg_id:341289 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2022
AB185803.1 gg_id:102459 rumen clone U29-G05 AB185
FJ202473.1 gg_id:352772 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2024
EU843322.1 gg_id:327368 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
FJ202134.1 gg_id:308089 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2021
EU475352.1 gg_id:297242 rock hyrax feces clone RHSD_aaa01c01 EU475
EF401863.1 gg_id:208565 human fecal clone SJTU_D_16_65 EF401
EU842456.1 gg_id:329258 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
AB192034.1 gg_id:141366 termite gut homogenate clone M2PB4-24 AB192
FJ880869.1 gg_id:374478 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8808
EU468721.1 gg_id:302410 okapi feces clone OK2_f09_1 EU468
EU461084.1 gg_id:295935 red kangaroo feces clone KO1_aai43h03 EU461
EU778074.1 gg_id:331417 feces clone RL387_aao92e05 EU778

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EU842889.1 gg_id:348906 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
DQ116004.1 gg_id:133222 bovine teat canal clone D-45 DQ116
FJ202794.1 gg_id:318487 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2027
AY244961.1 gg_id:83170 cow rumen clone BS7 AY244
EU472329.1 gg_id:287808 Angola colobus feces clone EAC_1aaa02f06 EU472
AB192167.1 gg_id:144213 termite gut homogenate clone RsTz-70 AB192
EU466117.1 gg_id:299745 bighorn sheep feces clone BH1_aao26c07 EU466
FJ203029.1 gg_id:307377 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c FJ2030
EU842351.1 gg_id:319333 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
EU774694.1 gg_id:317515 Angola Colobus feces clone EAC_1aaa02f10 EU774
FN356255.1 gg_id:577649 Prokaryotic structure sulfate reducer activity -temperature reservoirs and without ni FN356
EU842717.1 gg_id:354533 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
EU458450.1 gg_id:299730 spotted hyena feces clone HY1_f09_1 EU458
DQ809339.1 gg_id:185339 human fecal clone RL184_aah19d09 DQ809
EU748157.1 gg_id:353984 neotropical folivorous flying bird adult hoatzin crop clone hoa32_04D01.F EU748
EU842775.1 gg_id:320068 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
DQ824525.1 gg_id:191866 human fecal clone RL185_aaj69c03 DQ824
AB062845.1 gg_id:41514 termite gut homogenate clone BCf9-13 AB062
EF559146.1 gg_id:227245 mesophilic anaerobic digester clone G35_D8_L_B_D10 EF559
DQ794082.1 gg_id:175110 human fecal clone RL176_aan57g06 DQ794
EU458499.1 gg_id:303129 spotted hyena feces clone HY2_d09_1 EU458
AB089013.2 gg_id:77906 termite gut homogenate clone Rs-D61 bacterium AB089
EU458529.1 gg_id:287954 spotted hyena feces clone HY2_d05_1 EU458
EU474437.1 gg_id:293164 bighorn sheep feces clone BHSD_aaa01a11 EU474
EU234161.1 gg_id:246299 receiving river and un techniques effluent WWTP treating penicillin G production wa EU234
EF099902.1 gg_id:184543 mouse cecum clone SWPT5_aaa02a01 EF099
EU844065.1 gg_id:336674 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
FJ202657.1 gg_id:304514 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2026
FJ833810.1 gg_id:590193 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J2Q401_59C08 FJ8338
DQ326171.1 gg_id:148992 Metagenomic gut microbiome healthy human stool clone C070 DQ326
AB494884.1 gg_id:583213 Fibrobacter succinogenes dominated consortium on hay stems sheep rumen clone N AB494
DQ797460.1 gg_id:186606 human fecal clone RL248_aai99f02 DQ797
EU844527.1 gg_id:310757 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
AJ306757.1 gg_id:102610 DCP-dechlorinating consortium clone SHA-88 AJ3067
EU465832.1 gg_id:287880 argali sheep feces clone AS2_aao36e01 EU465
EU775730.1 gg_id:312520 Horse feces clone horsej_aai92f05 EU775
EU842760.1 gg_id:334353 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
EU469665.1 gg_id:287595 flying fox feces clone FF_-aag84g01 EU469
DQ018793.1 gg_id:135436 Unique Microbial Anaerobic Swine Lagoons anaerobic swine lagoon clone C-27 DQ018
FJ645701.1 gg_id:546684 Microbial dynamics during -temperature biotreatment PCP-contaminated wastestrea FJ6457

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DQ353918.1 gg_id:145887 Fecal Wild Gorilla (Gorilla beringei) wild gorilla feces clone Z40 DQ353
GU303518.1 gg_id:589662 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU303
AB185628.1 gg_id:101491 rumen clone F24-F07 AB185
FJ712620.1 gg_id:516702 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) k FJ7126
FJ202337.1 gg_id:329006 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2023
FJ833451.1 gg_id:537503 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J1Q201_27C04 FJ8334
FJ202205.1 gg_id:341505 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2022
GQ502518.1 gg_id:583465 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf4- GQ502
EU471736.1 gg_id:303248 Asiatic elephant feces clone AE2_aaa04c06 EU471
FJ202656.1 gg_id:344298 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2026
FJ202847.1 gg_id:317519 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2028
EU474444.1 gg_id:299306 bighorn sheep feces clone BHSD_aaa02d03 EU474
AM500722.1 gg_id:552988 proof spatial heterogeneity hot composting clone D15 AM500
EU467383.1 gg_id:289639 chimpanzee feces clone CHIMP12_e11_1 EU467
AB198491.1 gg_id:135781 termite gut wall fraction clone RsW01-063 AB198
EU842745.1 gg_id:335962 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
DQ125504.1 gg_id:134310 uranium contaminated soil clone AKAU3463 DQ125
FJ202532.1 gg_id:318462 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2025
AY858433.2 gg_id:112234 gastrointestinal tract Grant's gazelle clone GRANT14 AY858
EU510643.1 gg_id:273453 cecal contents Mus musculus strain C57BL/6J; WD5 clone WD5_aak38f06 EU510
EU774305.1 gg_id:318385 Chimpanzee feces clone CHIMP1_aaj39b06 EU774
GQ016326.1 gg_id:493341 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ016
FJ202869.1 gg_id:309864 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2028
AB185663.1 gg_id:103085 rumen clone U28-A08 AB185
GQ897425.1 gg_id:545462 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do s GQ897
EU843540.1 gg_id:310192 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
EU842540.1 gg_id:324834 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
GQ079312.1 gg_id:376610 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1231c1 GQ079
DQ796776.1 gg_id:177039 human fecal clone RL179_aao54c12 DQ796
AY985323.1 gg_id:124331 human stool clone C233 AY985
EU779164.1 gg_id:317992 Trancaspian Urial feces clone TU2_aaa03c06 EU779
EU842677.1 gg_id:306050 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
AY858395.3 gg_id:112201 gastrointestinal tract Grant's gazelle clone GRANT29 AY858
FJ832792.1 gg_id:566105 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J3Q201_14F02 FJ8327
AB486866.1 gg_id:582846 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCORC AB486
AB088978.1 gg_id:104874 termite gut homogenate clone Rs-N60 AB088
EU468858.1 gg_id:291601 Speke's gazelle feces clone SP2_b04 EU468
FJ202192.1 gg_id:347602 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2021
AB185658.1 gg_id:107668 rumen clone U28-A03 AB185
FJ362914.1 gg_id:366873 feces adult twins and mothers; TS13 clone TS13_a04f11 FJ3629

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AY570608.1 gg_id:108483 biodegraded Canadian oil reservoir clone PL-23B11 AY570
FJ367867.1 gg_id:365631 feces adult twins and mothers; TS2 clone TS2_a04e04 FJ3678
FJ202131.1 gg_id:330835 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2021
EU748027.1 gg_id:344227 neotropical folivorous flying bird adult hoatzin crop clone hoa11_52D07 EU748
AJ408962.1 gg_id:44983 human colonic clone HuCA6 AJ4089
AB491857.1 gg_id:562002 affiliation (Litopenaeus vannamei) Banyuwangi East Java microbial flocs floating brac AB491
EU776002.1 gg_id:337327 Spotted hyena feces clone HY2_c11 EU776
EU844091.1 gg_id:304930 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
EU771111.1 gg_id:316977 Asiatic elephant feces clone AE1_aaa04g06 EU771
EU467372.1 gg_id:289867 chimpanzee feces clone CHIMP12_h10 EU467
DQ816804.1 gg_id:165602 mouse cecum clone aaa99f09 DQ816
EU843202.1 gg_id:339638 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
GQ079246.1 gg_id:452620 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1230c1 GQ079
FJ374201.1 gg_id:363631 Inter- and intraspecific humivorous scarab beetle larvae (Pachnoda spp.) larval hindgı FJ3742
EU531917.1 gg_id:270505 Predominant role host genetics controlling gut microbiota FMF remission stool clone EU531
FJ202833.1 gg_id:348838 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2028
EU748350.1 gg_id:346326 neotropical folivorous flying bird adult hoatzin crop clone hoa5_05f08 EU748
FJ202630.1 gg_id:333126 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2026
FJ202826.1 gg_id:306847 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2028
FJ202211.1 gg_id:308897 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2022
FJ202232.1 gg_id:324044 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2022
CU919783.1 gg_id:555678 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU919
EU458485.1 gg_id:302584 spotted hyena feces clone HY2_g12 EU458
AB034035.1 gg_id:29646 rumen clone 3C0d-20 AB034
FJ792421.1 gg_id:513460 Unexpectedly archaeal species shift between rare and dominant over thousand year FJ7924
AB232817.1 gg_id:138569 Microbial mesophilic chemostat cultivation propionate-degrading methanogenic con AB2328
EU462765.1 gg_id:288426 Sumatran orangutan feces clone orang2_aai68f11 EU462
AF371682.1 gg_id:101981 swine intestine clone p-2405-55G5 AF3716
FJ202592.1 gg_id:327300 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2025
AB546246.1 gg_id:529003 Tindallia sp. str. Mic8c12 AB546
EU774299.1 gg_id:313590 Chimpanzee feces clone CHIMP1_aaj40g03 EU774
EU845191.1 gg_id:315173 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU845
EU472631.1 gg_id:292205 Angola colobus feces clone EAC_2_aaa02d12 EU472
EU466188.1 gg_id:302105 bighorn sheep feces clone BH1_aao27f07 EU466
AY592141.1 gg_id:105499 marine ANAMMOX sediment clone AY592141 AY592
FJ380149.1 gg_id:359400 ornithogenic Ross Sea region Antarctica AB1 soil clone 9/1/11H FJ3801
FJ678598.1 gg_id:513299 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6785
FJ680976.1 gg_id:524935 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6809
EU487893.1 gg_id:567760 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU487

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AB198494.1 gg_id:135738 termite gut wall fraction clone RsW01-067 AB198
DQ270635.1 gg_id:202645 Methane- and Sulfur-Metabolizing Microbial Dominate Ecosystem carbonate chimn DQ270
FJ202190.1 gg_id:334481 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2021
AB186360.1 gg_id:101117 Clostridium sp. str. EBR-02E-0046 AB186
AY985595.1 gg_id:126254 human stool clone C584 AY985
EU774747.1 gg_id:330496 Angola Colobus feces clone EAC_2_aaa02g08 EU774
AJ488067.1 gg_id:66196 chlorobenzene-degrading consortium clone IA-10 AJ488
AB198476.1 gg_id:135425 termite gut wall fraction clone RsW01-043 AB198
FJ202845.1 gg_id:353563 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2028
AB486752.1 gg_id:585277 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCOR AB486
EU283548.1 gg_id:278481 Model Early Earth Harbors Deeply Divergent Divisions Anderson Lake clone A1675 EU283
FJ202381.1 gg_id:325562 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2023
EU381476.1 gg_id:267510 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid EU381
EU471529.1 gg_id:299073 Asiatic elephant feces clone AE1_aaa02d07 EU471
AB185728.1 gg_id:107369 rumen clone U28-G09 AB185
DQ117467.1 gg_id:170514 gen. sp. nov. anaerobic thermotolerant wetland receiving acid sulfate water Gracilib DQ117
EU843200.1 gg_id:337726 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
AB288889.1 gg_id:202115 termite gut homogenate clone BOf2-18 AB288
EU142044.1 gg_id:255423 Methyl sulfides intermediates anaerobic oxidation methane seep sediment clone SR EU142
EF063612.1 gg_id:180400 Microbial ecology autotrophic denitrifying anaerobic methanogenic UASB reactor clo EF0636
EU844835.1 gg_id:309501 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8448
EU507965.1 gg_id:268582 cecal contents Mus musculus strain C57BL/6J; MD24 clone MD24_aaa04f02 EU507
AB248638.1 gg_id:146312 mesophilic anaerobic butyrate-degrading reactor clone BHB09 AB248
AY491543.1 gg_id:105229 microbial fuel cell enriched with acetate clone 45#2 AY491
DQ809863.1 gg_id:179910 human fecal clone RL184_aao65c04 DQ809
GU118586.1 gg_id:591565 Threatened Corals Provide Microbial Habitats clone Mfav_O07 GU118
EU885002.1 gg_id:326523 microbial hindgut chamber Pomacanthus sexstriatus GI tract clone A3H6 EU885
EF026082.1 gg_id:180011 Clostridium sp. str. 37HS60 EF026
AB088961.2 gg_id:77744 termite gut homogenate clone Rs-B74 bacterium AB088
EU775509.1 gg_id:306730 Western lowland gorilla feces clone GOR_aag73e05 EU775
AJ012604.1 gg_id:14147 isolate dentoalveolar abscess clone PUS9.170 PUS9.170 AJ0126
EU466131.1 gg_id:287904 bighorn sheep feces clone BH1_aao26f01 EU466
EU844360.1 gg_id:351498 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
AJ229190.1 gg_id:20289 anoxic bulk soil flooded rice microcosm clone BSV28 clone AJ2291
EU845497.1 gg_id:315749 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU845
FJ681155.1 gg_id:520505 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6811
EU775231.1 gg_id:303417 Reticulated giraffe feces clone gir_aah93c01 EU775
EU844616.1 gg_id:321163 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
EU843765.1 gg_id:333231 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
AB189701.1 gg_id:113972 termite gut homogenate clone Tc-71 AB189

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EU842890.1 gg_id:344940 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
EU764530.1 gg_id:350480 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1 EU764
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EU844486.1 gg_id:328183 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
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GQ079660.1 gg_id:394828 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1232h(GQ079
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EU842594.1 gg_id:348243 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
AY854299.1 gg_id:111024 herbivore gastrointestinal tract clone Thompsons101 AY854
GQ356941.1 gg_id:557019 Metal Dependent Marine Methane Oxidation methane seep sediment clone Fe_B_1 GQ356
EU777123.1 gg_id:308849 Okapi feces clone OK3_e09_1 EU777
EU382037.1 gg_id:271320 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU382
EU843321.1 gg_id:318414 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
AB062842.1 gg_id:51211 termite gut homogenate clone BCf9-05 AB062
AB248624.1 gg_id:148942 mesophilic anaerobic butyrate-degrading reactor clone BLB02 AB248
EU469900.1 gg_id:297878 western lowland gorilla feces clone GOR_aag73g11 EU469
FN356268.1 gg_id:582966 Prokaryotic structure sulfate reducer activity -temperature reservoirs and without ni FN356
EU747953.1 gg_id:319999 neotropical folivorous flying bird adult hoatzin crop clone hoa12_65A09 EU747
EU772107.1 gg_id:317656 Argali sheep feces clone AS2_aao33c04 EU772
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FJ203156.1 gg_id:349191 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c FJ2031
AM696804.1 gg_id:218710 sequencing libraries indoor dust clone BF0001A091 AM696
DQ905299.1 gg_id:165846 human fecal clone 013B-B8 DQ905
EU472472.1 gg_id:300300 Angola colobus feces clone EAC_2_aaa02h08 EU472
AB270003.1 gg_id:164436 Influence temperature and humidity on heifers rumen contents Holstein heifer (Bos AB270
FJ983022.1 gg_id:444822 Aspects Oral Microbiome root canal clone FJ9830
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AB185569.1 gg_id:106984 rumen clone F23-H07 AB185
FJ202303.1 gg_id:348533 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2023
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GQ502532.1 gg_id:583216 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf4- GQ502

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AJ576325.1 gg_id:100766 hindgut homogenate Pachnoda ephippiata larva clone PeH05 AJ5763
AY854296.1 gg_id:110551 herbivore gastrointestinal tract clone Thompsons8 AY8542
FJ202930.1 gg_id:317077 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2029
DQ327075.1 gg_id:147680 Metagenomic gut microbiome healthy human stool clone E583 DQ327
EU460959.1 gg_id:291686 red kangaroo feces clone KO1_aai41a12 EU460
GQ175404.1 gg_id:570930 Chicken intestinal microbiota modulations various feed supplementations DGGE anc GQ175
DQ816463.1 gg_id:162397 mouse cecum clone aab18d06 DQ816
U65987.1 gg_id:14149 Eubacterium saphenum str. ATCC 49989 U6598
EU772012.1 gg_id:339656 Argali sheep feces clone AS1_aao40b04.Contig1 EU772
FJ879407.1 gg_id:393699 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8794
AB185599.1 gg_id:104268 rumen clone F24-C10 AB185
EU843182.1 gg_id:305640 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
EF208712.1 gg_id:199886 Vertical and horizontal structure microbial sandy carbonate sediment clone CI75cm.2 EF2087
FJ202107.1 gg_id:324552 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2021
DQ798198.1 gg_id:175649 human fecal clone RL302_aal96g03 DQ798
AY858448.2 gg_id:110327 gastrointestinal tract zebra clone ZEBRA_9 AY858
EU776163.1 gg_id:349251 Spotted hyena feces clone HY1_b08 EU776
EU474679.1 gg_id:302881 Indian rhinoceros feces clone IR_aaa04g06 EU474
GQ502544.1 gg_id:591372 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf4- GQ502
FJ792387.1 gg_id:562958 Unexpectedly archaeal species shift between rare and dominant over thousand year FJ7923
DQ795882.1 gg_id:177446 human fecal clone RL245_aai83h11 DQ795
EU470137.1 gg_id:292215 trancaspain urial feces clone TU2_aaa02d04 EU470
FJ202163.1 gg_id:349988 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2021
FJ202628.1 gg_id:332785 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2026
DQ815756.1 gg_id:173597 mouse cecum clone aab21h07 DQ815
AJ306755.1 gg_id:66939 DCP-dechlorinating consortium clone SHA-74 AJ3067
DQ115987.1 gg_id:131845 bovine teat canal clone B-25 DQ115
EU843854.1 gg_id:331183 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
AY854303.1 gg_id:110359 herbivore gastrointestinal tract clone Thompsons105 AY8543
EU844826.1 gg_id:344489 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8448
EU748139.1 gg_id:343079 neotropical folivorous flying bird adult hoatzin crop clone hoa31_26B04.F EU748
AB062775.1 gg_id:23926 termite gut homogenate clone BCf10-04 AB062
EU474932.1 gg_id:289855 red river hog feces clone RRH_aaa03e05 EU474
FJ202222.1 gg_id:327787 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2022
EU381471.1 gg_id:260907 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid EU381
AJ408959.1 gg_id:21985 human colonic clone HuCA3 AJ4089
EF436355.1 gg_id:213337 library-based ruminal water buffalo (Bubalus bubalis) rumen fluid clone BRC69 EF4363
EU844018.1 gg_id:356078 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
FJ365219.1 gg_id:362283 feces adult twins and mothers; TS1 clone TS1_a04c05 FJ3652
AB231069.1 gg_id:149597 termite gut wall clone NkW01-043 AB231
GQ356994.1 gg_id:547804 Metal Dependent Marine Methane Oxidation methane seep sediment clone FeLive GQ356

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EU844741.1 gg_id:314505 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
AJ229189.1 gg_id:112263 anoxic bulk soil flooded rice microcosm clone BSV27 AJ2291
FJ202445.1 gg_id:311816 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2024
DQ353919.1 gg_id:146485 Fecal Wild Gorilla (Gorilla beringei) wild gorilla feces clone Z41 DQ353
DQ809616.1 gg_id:198173 human fecal clone RL184_aan81f03 DQ809
EU474587.1 gg_id:301486 bighorn sheep feces clone BHSD_aaa04d11 EU474
AY160817.1 gg_id:102595 termite intestinal tract clone COB P1-16 AY160
GQ356944.1 gg_id:591869 Metal Dependent Marine Methane Oxidation methane seep sediment clone Fe_B_1 GQ356
FJ374203.1 gg_id:358826 Inter- and intraspecific humivorous scarab beetle larvae (Pachnoda spp.) larval hindgu FJ3742
FJ202883.1 gg_id:341689 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2028
FJ202854.1 gg_id:329364 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2028
EU843155.1 gg_id:352100 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
FJ202138.1 gg_id:313395 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2021
FJ202666.1 gg_id:354799 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2026
FJ833538.1 gg_id:510387 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J1Q301_70F09 FJ8335
FJ202546.1 gg_id:351892 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2025
FJ202754.1 gg_id:316242 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2027
AY134903.1 gg_id:59564 Necrotizing Ulcerative Periodontitis HIV-Positive Subjects Eubacterium oral clone FX02 AY1349
EF686517.1 gg_id:242873 Sequences Manifest Rumen Yunnan Yel Cattle (Bos Taurus) rumen fluid clone YNRC6 EF6865
DQ125852.1 gg_id:131000 uranium contaminated soil clone AKAU4083 DQ125
DQ809461.1 gg_id:181788 human fecal clone RL184_aah21c08 DQ809
EU844330.1 gg_id:356192 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
AY207065.1 gg_id:83830 human mouth clone P4PA_66 AY207
FJ833537.1 gg_id:573551 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J1Q301_68D09 FJ8335
EU468451.1 gg_id:299957 black rhinoceros feces clone RH_aad13d09 EU468
AM745203.1 gg_id:293386 Impact oil er hydrocarbons on microbial and activity Gulf Mexico cold seep marine s AM745
EF688241.1 gg_id:311772 Detection microbial sludge anaerobic wastewater treatment system clone 6B5_cons EF6882
DQ905434.1 gg_id:166928 human fecal clone 013C-F8 DQ905
GQ458222.1 gg_id:536955 Microbial structure co-digestion anaerobic bioreactors treating cassava pulp and pig GQ458
AB088987.2 gg_id:78236 termite gut homogenate clone Rs-E61 bacterium AB088
FJ879883.1 gg_id:371416 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8798
AJ969455.1 gg_id:157625 Microbial black smoker s Mid Atlantic Ridge ecological implications rock fragments ch AJ9694
EU142060.1 gg_id:245992 Methyl sulfides intermediates anaerobic oxidation methane seep sediment clone SR EU142
FJ374205.1 gg_id:360186 Inter- and intraspecific humivorous scarab beetle larvae (Pachnoda spp.) larval hindgu FJ3742
AY349373.1 gg_id:92717 human oral cavity clone JH012 AY3493
AB185679.1 gg_id:100045 rumen clone U28-C01 AB185
EU475269.1 gg_id:299810 rock hyrax feces clone RHSD_aaa04b09 EU475
FJ202769.1 gg_id:306175 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2027
AB488208.1 gg_id:590807 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSSUR0 AB488
FJ366048.1 gg_id:362955 feces adult twins and mothers; TS25 clone TS25_a02b02 FJ3660
EU748410.1 gg_id:326674 neotropical folivorous flying bird adult hoatzin crop clone hoa5_05g10 EU748

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EF436322.1 gg_id:206909 library-based ruminal water buffalo (Bubalus bubalis) rumen fluid clone BRC36 EF4363
GU119002.1 gg_id:590570 Threatened Corals Provide Microbial Habitats clone Past_G15 GU119
EU773230.1 gg_id:341717 BigHorn sheep feces clone BH1_aao28e09 EU773
EU843731.1 gg_id:309157 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
AY349378.1 gg_id:92043 human oral cavity clone JS001 AY3493
EU843425.1 gg_id:336199 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8434
AB486148.1 gg_id:538464 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC AB486
AB231067.1 gg_id:150434 termite gut wall clone NkW01-032 AB2310
AB009218.1 gg_id:15994 rumen clone RFN70 bacterium AB009
EU469793.1 gg_id:299525 western lowland gorilla feces clone GOR_aag71a08 EU469
FJ366878.1 gg_id:365297 feces adult twins and mothers; TS27 clone TS27_a04h09 FJ3668
AY442821.1 gg_id:99414 culturable kangaroo Macropus giganteus Eastern grey Kangaroo forestomach content AY4428
EF436353.1 gg_id:209059 library-based ruminal water buffalo (Bubalus bubalis) rumen fluid clone BRC67 EF4363
EU842327.1 gg_id:319862 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU8423
EU844283.1 gg_id:322100 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8442
EU474565.1 gg_id:300285 bighorn sheep feces clone BHSD_aaa04c01 EU4745
EU776476.1 gg_id:331014 Red Kangaroo feces clone KO1_aai43a01 EU7764
GU302736.1 gg_id:542417 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU302
FJ833556.1 gg_id:584340 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J1Q401_08H01 FJ8335
FJ202951.1 gg_id:342341 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2029
DQ353927.1 gg_id:148368 Fecal Wild Gorilla (Gorilla beringei) wild gorilla feces clone Z67 DQ353
EU344373.1 gg_id:258791 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU3443
EU772259.1 gg_id:327560 Argali sheep feces clone AS1_aao37d09.Contig1 EU772
AB185640.1 gg_id:101427 rumen clone F24-G08 AB1856
EU771420.1 gg_id:347636 Asiatic elephant feces clone AE1_aaa01d12 EU7714
FJ202506.1 gg_id:350204 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2025
EU843472.1 gg_id:325246 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8434
EU344337.1 gg_id:259158 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU3443
EU772071.1 gg_id:326804 Argali sheep feces clone AS1_aao37e11.Contig1 EU7720
EU771699.1 gg_id:323118 African elephant feces clone AFEL3_aao13f07 EU7716
EU772345.1 gg_id:355003 Argali sheep feces clone AS2_aao36c12 EU7723
EU845143.1 gg_id:344950 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8451
EU459464.1 gg_id:290585 capybara feces clone CAP_aah97f05 EU4594
EU775239.1 gg_id:333033 Reticulated giraffe feces clone gir_aah95f12 EU7752
GQ502539.1 gg_id:538259 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf4- GQ502
AJ229251.1 gg_id:16084 Clostridium sp. str. FCB90-3 AJ2292
AB185675.1 gg_id:99422 rumen clone U28-B09 AB1856
EU844859.1 gg_id:339851 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8448
GU303511.1 gg_id:568051 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU303
EU381806.1 gg_id:265281 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU3818

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EU747957.1 gg_id:303546 neotropical folivorous flying bird adult hoatzin crop clone hoa11_63G08 EU747
AF113543.1 gg_id:33448 Thermohalobacter berrensis str. CTT3 AF113
EU842587.1 gg_id:348804 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
AB192215.1 gg_id:142575 termite gut homogenate clone RsTu1-67 AB192
GU303282.1 gg_id:581109 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU303
FJ202538.1 gg_id:319554 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2025
EU764620.1 gg_id:308595 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1 EU764
EU469106.1 gg_id:301218 Speke's gazelle feces clone SP3_e11 EU469
AJ576359.1 gg_id:107607 hindgut homogenate Pachnoda ephippiata larva clone PeH45 AJ5763
EU774684.1 gg_id:346374 Angola Colobus feces clone EAC_2_aaa04d04 EU774
AJ229231.1 gg_id:43679 anoxic bulk soil flooded rice microcosm clone BSV87 clone AJ2292
FN396778.1 gg_id:562532 constant flux thermophilic cold seabed Arctic marine surface sediment clone s5_8_I_ FN396
EU842257.1 gg_id:335015 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
GU303696.1 gg_id:586039 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU303
FJ202265.1 gg_id:309316 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2022
FJ202104.1 gg_id:324384 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2021
AY548990.2 gg_id:103172 marine bone clone boneC3C9 AY548
EF603658.1 gg_id:229659 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6036
EU843093.1 gg_id:310811 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
FJ202602.1 gg_id:327128 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2026
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EU842996.1 gg_id:345307 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU842
AB264073.1 gg_id:183822 Fecal microbial (dugong dugon) determined genes Dugong feces clone dgD-113 AB264
FJ202587.1 gg_id:338369 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2025
EU778539.1 gg_id:313089 Red river hog feces clone RRH_aaa01d04 EU778
GQ897435.1 gg_id:560873 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do GQ897
EU777042.1 gg_id:317655 Naked mole-rat feces clone molerat_2b10 EU777
EU777099.1 gg_id:352847 Okapi feces clone OK3_f02_1 EU777
FJ462083.1 gg_id:577684 Microbial ecology industrial digestor mesophilic anaerobic reactor fed effluent chemi FJ4620
EU842916.1 gg_id:318804 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
EU470283.1 gg_id:294860 Grevy's zebra feces clone GZ_aaa04a01 EU470
AB486501.1 gg_id:539216 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC AB486
AB244003.1 gg_id:246964 Methods Investigate Microbial Niigata oil well clone Niigata-01 AB244
FJ172885.1 gg_id:305371 Qinghai Yak Ruminal and Fungi China rumen clone RB-2H1 FJ1728
GU303804.1 gg_id:564617 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU303
FJ792303.1 gg_id:535751 Unexpectedly archaeal species shift between rare and dominant over thousand year FJ7923
EU037308.2 gg_id:263172 structure landfill sediments receiving long-term augmentations wastes chromium co EU037
EU471539.1 gg_id:297730 Asiatic elephant feces clone AE1_aaa02c03 EU471
FJ792320.1 gg_id:533932 Unexpectedly archaeal species shift between rare and dominant over thousand year FJ7923
EU771240.1 gg_id:339673 Asiatic elephant feces clone AE3_aaa04f12 EU771

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AJ608236.1 gg_id:149841 human biopsies ulcerative colitis biopsy clone UC7-27 AJ6082
AB185703.1 gg_id:105420 rumen clone U28-E05 AB185
FJ202755.1 gg_id:334367 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2027
AY704384.1 gg_id:112091 Gram-positive thermophile ODP159-02 AY7043
EU467076.1 gg_id:292648 mongoose lemur feces clone ML_aae87d04 EU467
EU772164.1 gg_id:339693 Argali sheep feces clone AS2_aao33b04 EU772
U13038.1 gg_id:14158 Eubacterium brachy str. ATCC 33089 U13038
EU844516.1 gg_id:350648 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8445
FJ901004.1 gg_id:562763 Polymorphism microbial reservoirs water cut stage oil field clone G-28 FJ9010
FJ202481.1 gg_id:333926 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2024
FJ202308.1 gg_id:343324 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2023
EU775115.1 gg_id:348609 Francois Langur feces clone FL_1aaa03c07 EU775
DQ326136.1 gg_id:148804 Metagenomic gut microbiome healthy human stool clone C022 DQ326
GQ502582.1 gg_id:579712 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf4- GQ502
AJ240981.1 gg_id:16087 Norway:(Svalbard)Hornsund clone Sva0855 AJ2409
CU921201.1 gg_id:571666 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU921
EU469143.1 gg_id:296709 Speke's gazelle feces clone SP3_b09_1 EU469
AB185711.1 gg_id:101249 rumen clone U28-F01 AB185
EU617877.1 gg_id:338399 Seasonal variation microbial Yel Sea sediment clone A13S-96 EU6178
DQ796528.1 gg_id:191842 human fecal clone RL179aan74b10 DQ796
EU245251.1 gg_id:256125 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-H4-G11 EU2452
EU763133.1 gg_id:316040 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A› EU763
EU842645.1 gg_id:331305 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU8426
AY854366.1 gg_id:110428 herbivore gastrointestinal tract clone Thompsons91 AY8543
AB185543.1 gg_id:104895 rumen clone F23-D12 AB1855
EU844127.1 gg_id:338099 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8441
AF450134.1 gg_id:51973 Frigovirgula patagoniensis str. PPP2 AF4501
FJ682273.1 gg_id:523453 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6822
EU509548.1 gg_id:266930 cecal contents Mus musculus strain C57BL/6J; MD9 clone MD9_aap60f02 EU5095
AY682207.1 gg_id:99507 Clostridium mesophilicum str. ZLJ115 AY6822
AY570631.1 gg_id:108507 biodegraded Canadian oil reservoir clone PL-3B11 AY5706
EU475596.1 gg_id:294159 babirusa feces clone BARB_aaa01f08 EU4755
EU773174.1 gg_id:316897 BigHorn sheep feces clone BH1_aao28d12 EU7731
DQ809373.1 gg_id:187115 human fecal clone RL184_aah20a03 DQ809
EF688361.1 gg_id:239670 soil clone F5-01 EF6883
EU508724.1 gg_id:275345 cecal contents Mus musculus strain C57BL/6J; MD4 clone MD4_aap50a04 EU5087
EU506556.1 gg_id:273198 cecal contents Mus musculus strain C57BL/6J; MD19 clone MD19_aaa04b01 EU5065
EU771449.1 gg_id:325608 Hamadryas Baboon feces clone AFBAB_aai02e01 EU7714
EU089965.1 gg_id:344394 Clostridium maritimum str. G12 EU0899
EU511168.1 gg_id:270382 cecal contents Mus musculus strain C57BL/6J; WD7 clone WD7_aal03g07 EU5111

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GU180173.1 gg_id:533896 Impact coplanar PCBs on microbial activity anaerobic estuarine sediments sediment GU180
GQ898114.1 gg_id:548163 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do s GQ898
EU507984.1 gg_id:266315 cecal contents Mus musculus strain C57BL/6J; MD25 clone MD25_aaa01c06 EU5079
EU506197.1 gg_id:277213 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aaa03d05 EU5061
EU460644.1 gg_id:293064 polar bear feces clone PB2_aai23g11 EU4606
EU507055.1 gg_id:267879 cecal contents Mus musculus strain C57BL/6J; MD21 clone MD21_aar10e06 EU5070
EU506204.1 gg_id:275338 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aaa03f09 EU5062
FJ371865.1 gg_id:368561 feces adult twins and mothers; TS8 clone TS8_a03b03 FJ3718
AM697593.1 gg_id:224573 sequencing libraries indoor dust clone BF0002D104 AM697
DQ815910.1 gg_id:166779 mouse cecum clone aab24b07 DQ815
EU887828.1 gg_id:350385 Clostridium lituseburense str. H17 EU8878
EU763559.1 gg_id:342099 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A4 EU7635
GQ897786.1 gg_id:580529 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ897
DQ327022.1 gg_id:150427 Metagenomic gut microbiome healthy human stool clone E526 DQ327
GU293195.1 gg_id:542859 Microbial contents and mucus yel catfish (Pelteobagrus fulvidraco) stomach content GU293
FJ365988.1 gg_id:357507 feces adult twins and mothers; TS25 clone TS25_a01d11 FJ3659
EU772547.1 gg_id:353871 Hamadryas Baboon feces clone BAZ_d05 EU7725
FJ879777.1 gg_id:448519 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8797
EU508666.1 gg_id:275043 cecal contents Mus musculus strain C57BL/6J; MD4 clone MD4_aap49a11 EU5086
EU472508.1 gg_id:303273 Angola colobus feces clone EAC_2_aaa02a08 EU4725
DQ809395.1 gg_id:197479 human fecal clone RL184_aah20c09 DQ809
EU775225.1 gg_id:332025 Reticulated giraffe feces clone gir_aah93h12 EU7752
FJ684275.1 gg_id:529717 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6842
EU475704.1 gg_id:301650 babirusa feces clone BARB_aaa04h03 EU4757
EU507766.1 gg_id:261333 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_aaa04d08 EU5077
DQ800770.1 gg_id:188281 human fecal clone RL183_aao03c03 DQ800
DQ801143.1 gg_id:173883 human fecal clone RL387_aao92h05 DQ801
FJ484698.1 gg_id:557428 microbial autonomous rover world's deepest phreatic sinkhole wall biomat El Zacator FJ4846
DQ801584.1 gg_id:185221 human fecal clone RL117_aae92a06 DQ801
EU506436.1 gg_id:261590 cecal contents Mus musculus strain C57BL/6J; MD19 clone MD19_aaa01g02 EU5064
EU475590.1 gg_id:290893 babirusa feces clone BARB_aaa01b11 EU4755
GQ491609.1 gg_id:533578 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
EU509534.1 gg_id:263072 cecal contents Mus musculus strain C57BL/6J; MD9 clone MD9_aap60c11 EU5095
EU508634.1 gg_id:261667 cecal contents Mus musculus strain C57BL/6J; MD2 clone MD2_aap36f01 EU5086
EU774784.1 gg_id:349055 Angola Colobus feces clone EAC_1aaa02f11 EU7747
FJ685114.1 gg_id:527948 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6851
EU459252.1 gg_id:301971 hedgehog feces clone HH_aai34h03 EU4592
FJ658881.1 gg_id:508840 Metalworking Fluids and Aerosols Metallurgy Plant metalworking aerosol clone Sumn FJ6588
DQ015428.1 gg_id:129748 mouse cecum clone M3_a02_1 DQ015
FJ363275.1 gg_id:357739 feces adult twins and mothers; TS149 clone TS149_a01c12 FJ3632
EU472347.1 gg_id:296215 Angola colobus feces clone EAC_1aaa03d05 EU4723

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EF446226.1 gg_id:214221 Prokaryotic and Ecology Floating Macroscopic Filaments Extreme Acidic River Rio Tin EF4462
EU468617.1 gg_id:294213 okapi feces clone OK2_c05 EU468
FJ879803.1 gg_id:442805 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8798
EU885014.1 gg_id:324246 microbial hindgut chamber Pomacanthus sexstriatus GI tract clone A3E11 EU885
AM697550.1 gg_id:221701 sequencing libraries indoor dust clone BF0002D061 AM697
EU507344.1 gg_id:276478 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_2aaa01h07 EU507
EU509286.1 gg_id:263973 cecal contents Mus musculus strain C57BL/6J; MD8 clone MD8_aap47b11 EU509
EU509170.1 gg_id:275277 cecal contents Mus musculus strain C57BL/6J; MD8 clone MD8_aap45c12 EU509
EU506393.1 gg_id:269174 cecal contents Mus musculus strain C57BL/6J; MD19 clone MD19_aaa01b03 EU506
GU455178.1 gg_id:532325 Understanding short-chain fatty acids accumulation enhanced alkaline digestion: kir GU455
DQ809724.1 gg_id:178698 human fecal clone RL184_aan83c06 DQ809
FJ682922.1 gg_id:526070 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6829
EU510064.1 gg_id:273677 cecal contents Mus musculus strain C57BL/6J; WD1 clone WD1_aaf11h06 EU510
EU531942.1 gg_id:268758 Predominant role host genetics controlling gut microbiota FMF remission stool clone EU531
DQ129557.1 gg_id:138368 microarray level air two cities Texas urban aerosol clone AKIW850 DQ129
AB294941.1 gg_id:227058 -dependent & analyses hydrothermal system off Taketomi Island Japan microbial ma AB294
EU509279.1 gg_id:263015 cecal contents Mus musculus strain C57BL/6J; MD8 clone MD8_aap47b04 EU509
EU037362.2 gg_id:259404 structure landfill sediments receiving long-term augmentations wastes chromium co EU037
AM933653.1 gg_id:271027 Enrichment dioxin-dehalogenating two-liquid phase s anaerobic enrichment clone M AM933
EU507204.1 gg_id:273775 cecal contents Mus musculus strain C57BL/6J; MD22 clone MD22_aaa03d10 EU507
DQ809337.1 gg_id:196217 human fecal clone RL184_aah19d07 DQ809
EU508701.1 gg_id:272404 cecal contents Mus musculus strain C57BL/6J; MD4 clone MD4_aap49f04 EU508
GU083683.1 gg_id:575278 Microorganism Xiarinur soda lake sediment clone x171 GU083
EU506379.1 gg_id:269641 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aap64e09 EU506
EU506687.1 gg_id:269977 cecal contents Mus musculus strain C57BL/6J; MD20 clone MD20_aap54e04 EU506
EU775300.1 gg_id:316093 Reticulated giraffe feces clone gir_aah93c08 EU775
AF071416.1 gg_id:14182 Eubacterium acidaminophilum str. DSM 3953 AF071
DQ532227.1 gg_id:168307 Geographical Variation Microbial Burden and Spacecraft Assembly Johnson Space Ce DQ532
DQ804419.1 gg_id:175724 human fecal clone RL187_aan79e10 DQ804
DQ810032.1 gg_id:178724 human fecal clone RL184_aao67c07 DQ810
DQ809594.1 gg_id:192509 human fecal clone RL184_aan81c11 DQ809
EU475667.1 gg_id:293475 babirusa feces clone BARB_aaa01c09 EU475
EU464080.1 gg_id:297143 reticulated giraffe feces clone gir_aah93b09 EU464
EU538381.1 gg_id:280850 profile human microbiota antecubital fossa (inner elbow) skin clone nbt87a06 EU538
DQ325905.1 gg_id:149477 Metagenomic gut microbiome healthy human stool clone B727 DQ325
EU508007.1 gg_id:271552 cecal contents Mus musculus strain C57BL/6J; MD25 clone MD25_aaa01g07 EU508
FM995176.1 gg_id:538182 digestive gland QX infected and naive Sydney rock oysters Saccostrea glomerata Clo FM995
EU460720.1 gg_id:290150 polar bear feces clone PB2_aai24h11 EU460
FJ683014.1 gg_id:520795 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6830
AY493973.1 gg_id:136314 Fingerprinting aggregates soil clone 397 AY493

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EU508509.1 gg_id:265169 cecal contents Mus musculus strain C57BL/6J; MD2 clone MD2_aap34e11 EU508
DQ800967.1 gg_id:181377 human fecal clone RL387_aao90a09 DQ800
AM500797.1 gg_id:561500 proof spatial heterogeneity hot composting clone E118 AM500
FJ880267.1 gg_id:396393 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8802
FJ684177.1 gg_id:518480 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6841
EF025231.1 gg_id:188167 Examination microbial ecology avian vivo bromodeoxyuridine intestine clone B5_B22 EF0252
EU507395.1 gg_id:258167 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_2aaa02f02 EU507
EU763466.1 gg_id:340154 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU763
FM873937.1 gg_id:357984 occupant source house mattress dust clone MB03G05 FM873
FJ685045.1 gg_id:522767 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6850
DQ800778.1 gg_id:190283 human fecal clone RL183_aao03d02 DQ800
EU777126.1 gg_id:332131 Okapi feces clone OK2_g11 EU777
X77845.1 gg_id:14180 Clostridium litorale str. DSM 5388 X77845
EU506220.1 gg_id:258904 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aaa04e06 EU506
EU507335.1 gg_id:267494 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_2aaa01g07 EU507
FJ881142.1 gg_id:426452 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8811
EU762773.1 gg_id:332626 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU762
EU511619.1 gg_id:273357 cecal contents Mus musculus strain C57BL/6J; WD9 clone WD9_aak07f08 EU511
EU775226.1 gg_id:339254 Reticulated giraffe feces clone gir_aah96e03 EU775
EU775251.1 gg_id:312461 Reticulated giraffe feces clone gir_aah94d10 EU775
DQ824044.1 gg_id:191957 human fecal clone RL204_aaj58e11 DQ824
EU506214.1 gg_id:270918 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aaa04a08 EU506
AM697479.1 gg_id:226881 sequencing libraries indoor dust clone BF0001D094 AM697
DQ809820.1 gg_id:177546 human fecal clone RL184_aan84f11 DQ809
EU507305.1 gg_id:272351 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_2aaa01d07 EU507
EU475564.1 gg_id:290375 babirusa feces clone BARB_aaa03d10 EU475
EU506563.1 gg_id:259523 cecal contents Mus musculus strain C57BL/6J; MD19 clone MD19_aaa04d02 EU506
DQ796115.1 gg_id:194767 human fecal clone RL202_aai51f12 DQ796
AM275438.2 gg_id:231824 fecal microbiota irritable bowel syndrome patients significantly that healthy subject AM275
FJ375921.1 gg_id:322118 and prevalence blaTEM genes polar bear feces clone PBM_b7 FJ3759
DQ798228.1 gg_id:187484 human fecal clone RL181_aah39b06 DQ798
EU507754.1 gg_id:259527 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_aaa04c01 EU507
FJ675978.1 gg_id:513564 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6759
FJ167487.1 gg_id:331482 microbiology granular sludge under autotrophic mixotrophic and heterotrophic denit FJ1674
FJ715987.1 gg_id:565776 Diet- gut microbiota Lumbricus rubellus fingerprinting technique and cloning intestin FJ7159
EU508677.1 gg_id:260869 cecal contents Mus musculus strain C57BL/6J; MD4 clone MD4_aap49c08 EU508
GQ175565.1 gg_id:588840 Chicken intestinal microbiota modulations various feed supplementations DGGE an GQ175
EU775185.1 gg_id:308895 Reticulated giraffe feces clone gir_aah94g04 EU775
EU509429.1 gg_id:275291 cecal contents Mus musculus strain C57BL/6J; MD9 clone MD9_aap58a04 EU509
EU763392.1 gg_id:308791 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU763

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EU466147.1 gg_id:290249 bighorn sheep feces clone BH1_aao26h06 EU466
EU475135.1 gg_id:296746 visayam warty pig feces clone VWP_aaa01e04 EU475
GQ898484.1 gg_id:584271 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ898
EU509012.1 gg_id:273287 cecal contents Mus musculus strain C57BL/6J; MD7 clone MD7_aap41g07 EU509
EU506217.1 gg_id:265899 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aaa04c04 EU506
EU464129.1 gg_id:295947 reticulated giraffe feces clone gir_aah94d09 EU464
FJ683046.1 gg_id:526895 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6830
FJ879833.1 gg_id:376716 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8798
DQ815891.1 gg_id:162177 mouse cecum clone aab23g10 DQ815
GQ111279.1 gg_id:410501 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ111
EU468472.1 gg_id:301484 okapi feces clone OK1_d08 EU468
EU509609.1 gg_id:267447 cecal contents Mus musculus strain C57BL/6J; WD10 clone WD10_aak45f12 EU509
FJ684800.1 gg_id:526955 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6848
EU089964.1 gg_id:347553 Clostridium ruminantium str. LA1 EU089
EF404526.1 gg_id:209535 human fecal clone SJTU_C_11_71 EF4045
DQ809953.1 gg_id:193374 human fecal clone RL184_aao66c12 DQ809
DQ663785.1 gg_id:165071 Dehalobacter sp. MS DQ663
U84497.2 gg_id:13898 Dehalobacter restrictus str. PER-K23 U8449
AB294743.1 gg_id:213971 Dechlorination biphenyl polychlorinated dibenzo-p-dioxin species genus Dehalobact AB294
GU139293.1 gg_id:557393 lactate formate propionate hydrogen donors reductive dehalogenation trichloroeth GU139
GU139338.1 gg_id:573280 lactate formate propionate hydrogen donors reductive dehalogenation trichloroeth GU139
AY548779.1 gg_id:100438 Desulfitobacterium sp. str. RPf35Ei AY548
AB486840.1 gg_id:535804 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCOR AB486
AF297871.1 gg_id:28888 Desulfitobacterium metallireducens AF297
AB299029.1 gg_id:222688 Description sp. strain anaerobic tetrachloroethene reductive dechlorinating Desulfit AB299
AB486627.1 gg_id:561685 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCOR AB486
DQ125569.1 gg_id:137396 uranium contaminated soil clone AKAU3562 DQ125
X81032.1 gg_id:13900 Desulfitobacterium sp str. PCE1 X81032
AF357919.1 gg_id:50658 Desulfitobacterium sp. str. Viet-1 AF357
AJ565938.1 gg_id:94154 Desulfitobacterium dichloroeliminans str. LMG P-21439 AJ5659
AJ493052.1 gg_id:63748 Desulfosporosinus orientis str. DSMZ 7493 AJ4930
AJ582757.1 gg_id:96132 Desulfosporosinus limneticum str. STP12 AJ5827
AJ302078.1 gg_id:70866 Desulfosporosinus sp. LauIII AJ3020
AF414575.1 gg_id:74312 uranium mine sediment clone P3IB-3 AF414
DQ117470.1 gg_id:164901 Desulfosporosinus youngii str. JW/YJL-B18 DQ117
AF050590.1 gg_id:13872 contaminated aquifer clone WCHB1-77 AF0505
AF414568.1 gg_id:26036 uranium mine sediment clone P3IB-51 AF414
FN429795.1 gg_id:567684 Biogeochemistry -activity cold seep Larsen B area western Weddell Sea Antarctica m FN429
AY214183.1 gg_id:81849 benzene-contaminated groundwater clone ZZ12C8 AY214
EF200116.1 gg_id:200918 mine sulfur-cycling assemblage subpermafrost fracture waters Arctic gold mines clon EF2001
AF076248.1 gg_id:13889 Desulfosporosinus meridiei str. S5 AF0762

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CP001720.1 gg_id:521696 Desulfotomaculum acetoxidans str. DSM 771 CP001
CP001720.1 gg_id:521695 Desulfotomaculum acetoxidans str. DSM 771 CP001
AY742958.1 gg_id:100724 Desulfotomaculum nigrificans str. CW-01 AY742
EU999019.1 gg_id:317841 Predominance Methanolobus and Methanoculleus spp. Archaeal Saline Gas Field Fo EU999
Y11567.1 gg_id:13652 Desulfotomaculum geothermicum str. DSM 3669 Y11567
AJ294433.1 gg_id:51740 Desulfotomaculum gibsoniae str. DSM 7213 AJ2944
EF081293.1 gg_id:183856 Desulfotomaculum sp. str. LamD5 EF0812
AF053933.1 gg_id:13918 Desulfotomaculum putei str. SMCC W463 AF053
Y11579.1 gg_id:13912 Desulfotomaculum sp. str. DSM 7440 Y11579
CP000612.1 gg_id:204695 Desulfotomaculum reducens str. MI-1 CP000
NC_009253.1 gg_id:207678 Desulfotomaculum reducens str. MI-1 NC_00
Y11577.1 gg_id:30024 Desulfotomaculum sp. str. DSM 7474 Y11577
Y11574.1 gg_id:13671 Desulfotomaculum thermobenzoicum str. DSM 6193 Y11574
FJ792276.1 gg_id:535456 Unexpectedly archaeal species shift between rare and dominant over thousand year FJ7922
AF295656.1 gg_id:71619 Desulfotomaculum sp. str. 175 AF295
FN396784.1 gg_id:554125 constant flux thermophilic cold seabed Arctic marine surface sediment clone s5_8_I_ FN396
NR_026061.1 gg_id:548913 Desulfotomaculum halophilum str. SEBR 3139; DSM 11559 NR_02
FJ791924.1 gg_id:574637 Unexpectedly archaeal species shift between rare and dominant over thousand year FJ7919
M96665.1 gg_id:13657 Desulfotomaculum australicum str. AB33 M9666
AM184185.1 gg_id:146933 Desulfotomaculum indicum A5LFS102 AM184
AB237717.1 gg_id:139691 microorganisms deep subsurface groundwater sedimentary rock milieu clone HDBW AB237
EU651884.1 gg_id:541860 Anaerobic degradation aromatic hydrocarbon biphenyl biphenyl-degrading sulfate-r EU651
GQ921389.1 gg_id:577360 Worms hell: presence Nematoda terrestrial deep subsurface (0.9-3.6 km) fracture w GQ921
AF407206.1 gg_id:43356 CB-contaminated groundwater clone GIF17 AF407
GQ921451.1 gg_id:588472 Worms hell: presence Nematoda terrestrial deep subsurface (0.9-3.6 km) fracture w GQ921
AY604051.1 gg_id:104769 Chuniespoort group dolomite at 896 meters depth clone DR9IPCB16SCT7 AY604
FJ638572.1 gg_id:513053 Temperature dependent succession sulfate reducing muddy southwestern Taiwan hc FJ6385
FJ792415.1 gg_id:572534 Unexpectedly archaeal species shift between rare and dominant over thousand year FJ7924
FJ202905.1 gg_id:333130 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2029
EU522656.1 gg_id:273540 hydrocarbon-degrading methanogenic microbial consortia settling basin Northern Al EU522
FJ792042.1 gg_id:532958 Unexpectedly archaeal species shift between rare and dominant over thousand year FJ7920
FJ791886.1 gg_id:545567 Unexpectedly archaeal species shift between rare and dominant over thousand year FJ7918
FJ792123.1 gg_id:575922 Unexpectedly archaeal species shift between rare and dominant over thousand year FJ7921
FJ792287.1 gg_id:513089 Unexpectedly archaeal species shift between rare and dominant over thousand year FJ7922
AB026550.1 gg_id:13911 Desulfotomaculum nigrificans AB026
DQ270651.1 gg_id:143189 hydrothermal carbonate chimney clone LC1228B-98 DQ270
AF069293.1 gg_id:13654 Desulfotomaculum luciae str. SLT AF069
GQ921447.1 gg_id:574986 Worms hell: presence Nematoda terrestrial deep subsurface (0.9-3.6 km) fracture w GQ921
AB237718.1 gg_id:140022 microorganisms deep subsurface groundwater sedimentary rock milieu clone HDBW AB237
Y14845.1 gg_id:13667 Sporotomaculum hydroxybenzoicum str. BT DSM 5475 Y14845
GQ921388.1 gg_id:562429 Worms hell: presence Nematoda terrestrial deep subsurface (0.9-3.6 km) fracture w GQ921

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DQ129296.1 gg_id:137544 urban aerosol clone AKIW847 DQ129
AJ294427.1 gg_id:29438 Desulfotomaculum kuznetsovii str. DSM 6115 AJ2944
GQ921427.1 gg_id:587786 Worms hell: presence Nematoda terrestrial deep subsurface (0.9-3.6 km) fracture w GQ921
AF295657.1 gg_id:73391 Desulfotomaculum sp. str. 176 AF2956
FJ792335.1 gg_id:571754 Unexpectedly archaeal species shift between rare and dominant over thousand year FJ7923
AB294140.1 gg_id:208871 Desulfotomaculum ruminis str. DSM 2154 AB2941
U95951.1 gg_id:13914 Desulfotomaculum reducens str. MI-1 U95951
DQ129327.1 gg_id:138472 microarray level air two cities Texas urban aerosol clone AKIW597 DQ129
Z26315.1 gg_id:13681 Desulfotomaculum thermosapovorans str. MLF Z26315
DQ148942.1 gg_id:151851 Desulfotomaculum arcticum str. 15 DQ148
AY796046.1 gg_id:108765 gold mine bore hole clone 47mm6 AY7960
Y11575.1 gg_id:13664 Desulfotomaculum thermosapovorans str. DSM 6562 Y11575
NC_009454.1 gg_id:335682 Pelotomaculum thermopropionicum str. SI NC_009
AB091328.1 gg_id:60012 UASB granular sludge clone UT-2 AB0913
EF198039.1 gg_id:183266 Microbial structures mesophilic and methanogenic consortia anaerobic thermophilic EF1980
DQ129561.1 gg_id:138436 microarray level air two cities Texas urban aerosol clone AKIW964 DQ129
FN436066.1 gg_id:567349 Molekularbiologische Charakterisierung der bakteriellen Populationsdynamik eines t FN4360
EU307089.1 gg_id:246858 Changes microbial metabolic and along hydrogeochemically variable profile unsatura EU3070
DQ080182.1 gg_id:132576 sediment clone A8 DQ080
AB154390.1 gg_id:100060 Pelotomaculum sp. str. MGP AB1543
AB091323.1 gg_id:60009 Pelotomaculum sp. str. JT AB0913
EU523090.1 gg_id:560194 Anaerobic benzene degradation sulfate-reducing benzene-degrading enrichment clo EU5230
FN436047.1 gg_id:574137 Molekularbiologische Charakterisierung der bakteriellen Populationsdynamik eines t FN4360
EU523084.1 gg_id:553277 Anaerobic benzene degradation sulfate-reducing benzene-degrading enrichment clo EU5230
AF050588.1 gg_id:13674 contaminated aquifer clone WCHB1-89 AF0505
AB232816.1 gg_id:139284 Microbial mesophilic chemostat cultivation propionate-degrading methanogenic con AB2328
AB300074.1 gg_id:225576 Wide ancient microbial DNAs Quaternary sediments holocene mud sediment clone S AB3000
AY327251.1 gg_id:89131 Cryptanaerobacter phenolicus str. LR7.2 AY3272
EU651870.1 gg_id:576570 Anaerobic degradation aromatic hydrocarbon biphenyl biphenyl-degrading sulfate-re EU6518
AY741713.1 gg_id:105289 borehole water gold mine clone TTMF122 AY7417
EU651879.1 gg_id:592307 Anaerobic degradation aromatic hydrocarbon biphenyl biphenyl-degrading sulfate-re EU6518
AJ306756.1 gg_id:66938 DCP-dechlorinating consortium clone SHA-86 AJ3067
NR_029221.1 gg_id:540915 Peptococcus niger str. DSM 20475 NR_029
EU462414.1 gg_id:292842 Sumatran orangutan feces clone orang1_aai54b05 EU4624
EU459377.1 gg_id:287968 cheetah feces clone CE3_aai06d05 EU4593
DQ325836.1 gg_id:149814 Metagenomic gut microbiome healthy human stool clone B583 DQ325
DQ800782.1 gg_id:194763 human fecal clone RL183_aao03d06 DQ800
EU459373.1 gg_id:292581 cheetah feces clone CE3_aai06b08 EU4593
FJ368683.1 gg_id:362540 feces adult twins and mothers; TS49 clone TS49_a03c07 FJ3686
EU467504.1 gg_id:294049 Sumatran orangutan feces clone orang1_c08_1 EU4675
AM278590.2 gg_id:231310 fecal microbiota irritable bowel syndrome patients significantly that healthy subject AM278

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AM420144.1 gg_id:249899 Noma subgingival plaque clone 402D01(oral) AM420
AF371709.1 gg_id:29453 swine intestine clone p-2785-24E5 AF3717
FJ976236.1 gg_id:571035 Interindividual healthy human oral microbiota mouth clone 3A79 FJ9762
EU459357.1 gg_id:300587 cheetah feces clone CE3_aai05d05 EU4593
EU289049.1 gg_id:255053 microbiome cloacal openings urogenital and anal tracts tammar wallaby Macropus e EU2890
AB486907.1 gg_id:540653 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCOR(AB4869
AJ249098.1 gg_id:33138 SHA-15 clone AJ2490
AY631277.1 gg_id:107179 Thermoincola ferriacetica str. Z-0001 AY6312
DQ088773.1 gg_id:131994 subsurface clone BE16FW031601GDW_hole1-26 DQ088
AJ229187.1 gg_id:40595 anoxic bulk soil flooded rice microcosm clone BSV24 clone AJ2291
GQ502576.1 gg_id:546369 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf4- GQ502
EU776389.1 gg_id:335519 Red Kangaroo feces clone KO1_aai41h02 EU7763
AB486622.1 gg_id:585355 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCOR(AB4866
EU466065.1 gg_id:296726 bighorn sheep feces clone BH1_aao25a03 EU4660
Y18214.1 gg_id:33780 Desulfonispora thiosulfatigenes str. DSM 11270 Y18214
AY780555.1 gg_id:110610 ethene-dechlorinating enrichment clone KB-1 1 AY7805
EF464635.1 gg_id:217190 Identification sulfate reducing methylmercury contaminated SSU genes ethanol enric EF4646
AY050581.1 gg_id:50913 MCB-contaminated groundwater-treating reactor clone GOUTA9 AY0505
EU508106.1 gg_id:275248 cecal contents Mus musculus strain C57BL/6J; MD25 clone MD25_aaa04b03 EU5081
AB436739.1 gg_id:281469 Desulfonosporus sp. str. AAN04 AB4367
DQ537526.1 gg_id:165741 manganese oxidation soil clone JH-WH22 DQ537
DQ351908.1 gg_id:168489 manganese oxidation soil clone JH-WH13 DQ351
FJ672118.1 gg_id:514927 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6721
AB487134.1 gg_id:560863 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNIR0 AB4871
EU156143.1 gg_id:247631 thermal spring microbial and functional genes Coffee Pots Hot Spring clone pCOF_65 EU1561
FJ672140.1 gg_id:530374 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6721
X99706.1 gg_id:13894 Syntrophobotulus glycolicus str. SlGlym X99706
DQ537527.1 gg_id:164972 manganese oxidation soil clone JH-WH28 DQ537
EU509828.1 gg_id:263705 cecal contents Mus musculus strain C57BL/6J; WD11 clone WD11_aak21f11 EU5098
AF050591.1 gg_id:13873 contaminated aquifer clone WCHB1-84 AF0505
EF492899.1 gg_id:249156 Iron-manganese Nodule and Its Surrounding Soil soil around iron-manganese nodule EF4928
FN356261.1 gg_id:556351 Prokaryotic structure sulfate reducer activity -temperature reservoirs and without ni FN3562
EU507221.1 gg_id:261076 cecal contents Mus musculus strain C57BL/6J; MD22 clone MD22_aaa03g06 EU5072
FJ880663.1 gg_id:458154 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8806
FJ879275.1 gg_id:468179 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8792
FN356252.1 gg_id:553279 Prokaryotic structure sulfate reducer activity -temperature reservoirs and without ni FN3562
AB487787.1 gg_id:553152 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNSR0 AB4877
AB243993.1 gg_id:254109 Methods Investigate Microbial Niigata oil well clone Niigata-25 AB2439
FJ671684.1 gg_id:527817 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6716
AY862394.1 gg_id:110317 human intestinal tract clone HuDI10 AY8623
EU777207.1 gg_id:335045 Okapi feces clone OK3_f11 EU7772

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AY326462.1 gg_id:89770 Peptostreptococcus anaerobius str. NCTC 11460 AY3264
AY581818.1 gg_id:107080 feces clone 1E3 AY5818
EU681991.1 gg_id:294715 microflora imbalances intestine dogs inflammatory bowel disease duodenum health EU6819
DQ160208.1 gg_id:146581 Peptostreptococcus stomatis str. W2278 DQ160
AY581819.1 gg_id:107233 feces clone 2B6 AY5818
AY729956.1 gg_id:105998 Peptostreptococcus sp. C27 AY7299
AF044947.1 gg_id:14228 Peptostreptococcus sp. str. D1 AF0449
NR_029081.1 gg_id:576230 Tepidibacter formicigenes str. DV1184; DSM 15518 NR_029
AB470957.1 gg_id:550312 Tepidibacter sp. str. r60 AB4709
AY158079.1 gg_id:76251 Tepidibacter thalassicus str. SC 562 AY1580
AJ810557.1 gg_id:104867 superficial sediments clone AJ8105
L35515.1 gg_id:15999 Acetivibrio cellulolyticus L35515
AB240338.1 gg_id:142890 microbial structure Phragmites rhizosphere biofilm reed bed reactor laboratory clone AB2403
NR_026099.2 gg_id:538328 Clostridium aldrichii str. P-1; DSM 6159 NR_026
DQ011251.1 gg_id:129433 stratum sewage clone 4 DQ011
X98011.1 gg_id:16058 Anaerofilum agile str. F; DSM 4272 X98011
DQ011252.1 gg_id:130679 stratum sewage clone 5 DQ011
NZ_ABGD02000032.1 gg_id:469662 Anaerotruncus colihominis str. DSM 17241 NZ_AB
EU815226.1 gg_id:315223 Anaerotruncus sp. str. NML 070203 EU8152
FJ366425.1 gg_id:367814 feces adult twins and mothers; TS26 clone TS26_a03a06 FJ3664
NZ_AAXG02000037.1 gg_id:469742 Bacteroides capillosus str. ATCC 29799 NZ_AA
NZ_ABCB02000019.1 gg_id:470116 Clostridium leptum str. DSM 753 NZ_AB
NR_029355.1 gg_id:585848 Clostridium methylpentosum str. R2; DSM 5476 NR_029
EU761907.1 gg_id:352133 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1 EU7619
GQ493291.1 gg_id:585132 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
EU767704.1 gg_id:314107 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C3 EU7677
GQ492826.1 gg_id:564717 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
EU767580.1 gg_id:337051 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C3 EU7675
EU763019.1 gg_id:319661 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A3 EU7630
EU762625.1 gg_id:322493 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A3 EU7626
DQ799271.1 gg_id:194128 human fecal clone RL205_aaj20a05 DQ799
EU541438.1 gg_id:292685 Clostridium orbiscindens str. AIP204.04 EU5414
FJ370821.1 gg_id:358732 feces adult twins and mothers; TS5 clone TS5_a01f07 FJ3708
GQ493730.1 gg_id:581079 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
FJ370641.1 gg_id:366959 feces adult twins and mothers; TS57 clone TS57_a03e02 FJ3706
DQ797542.1 gg_id:182100 human fecal clone RL248_aaj00g06 DQ797
EU767539.1 gg_id:341820 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C3 EU7675
NR_029356.1 gg_id:594203 Clostridium orbiscindens str. 265; DSM 6740 NR_029
FJ369713.1 gg_id:368781 feces adult twins and mothers; TS51 clone TS51_a03h07 FJ3697
EU767763.1 gg_id:309355 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C3 EU7677

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EU766943.1 gg_id:344062 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU766
EU768379.1 gg_id:332921 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C5 EU768
EU767001.1 gg_id:333134 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU767
EU763709.1 gg_id:340410 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A4 EU763
EU541436.1 gg_id:300808 Clostridium orbiscindens str. AIP165.06 EU541
EU768104.1 gg_id:337445 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C4 EU768
EU767624.1 gg_id:350155 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C3 EU767
GQ491837.1 gg_id:589198 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
DQ456395.1 gg_id:158160 pre-adolescent turkey cecum clone CFT212H8 DQ456
GQ492531.1 gg_id:566065 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
EU764382.1 gg_id:342921 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1 EU764
AB269990.1 gg_id:166206 Influence temperature and humidity on heifers rumen contents Holstein heifer (Bos AB269
EU887962.1 gg_id:345568 Microbial structure hydrolytic stage two-stage anaerobic digestion grass silage leach EU887
AM277367.2 gg_id:228080 fecal microbiota irritable bowel syndrome patients significantly that healthy subject AM277
EU842642.1 gg_id:307476 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
GQ505064.1 gg_id:555524 55 degree C kitchen-waste-hydrogen fermentor clone TKW-HPB-11 GQ505
DQ794006.1 gg_id:182439 human fecal clone RL176_aah46e08 DQ794
FJ364302.1 gg_id:361844 feces adult twins and mothers; TS15 clone TS15_a01d02 FJ3643
AJ404681.1 gg_id:45135 anaerobic dechlorinating enrichment clone ZF3 ZF3 AJ4046
EF400570.1 gg_id:205435 human fecal clone SJTU_E_15_18 EF4005
FJ367252.1 gg_id:363845 feces adult twins and mothers; TS29 clone TS29_a01d02 FJ3672
GQ492466.1 gg_id:590106 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
DQ015186.1 gg_id:133905 mouse cecum clone M2_f10_1 DQ015
EU771946.1 gg_id:328302 Southern three-banded armadillo feces clone arma_aaj53f08 EU771
FJ364578.1 gg_id:358345 feces adult twins and mothers; TS15 clone TS15_a04f04 FJ3645
AY949858.1 gg_id:114730 Clostridium sp. strain str. S6 AY9498
EF405280.1 gg_id:203788 human fecal clone SJTU_G_03_48 EF4052
EU887966.1 gg_id:347421 Microbial structure hydrolytic stage two-stage anaerobic digestion grass silage leach EU887
DQ905296.1 gg_id:162952 human fecal clone 013B-B5 DQ905
EU768158.1 gg_id:304598 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C4 EU768
AF376228.1 gg_id:24921 ckncm324-B6-45 clone AF3762
EU887965.1 gg_id:342390 Microbial structure hydrolytic stage two-stage anaerobic digestion grass silage leach EU887
DQ905581.1 gg_id:169961 human fecal clone 014B-D12 DQ905
EF099895.1 gg_id:183270 mouse cecum clone SWPT5_aaa01h06 EF0998
EU381961.1 gg_id:265386 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU381
EU844591.1 gg_id:306523 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
AY295777.2 gg_id:139189 Ethanologenbacterium harbinese str. YUAN-3 AY2957
EU219958.1 gg_id:243384 study prokaryotic approach landfill soil 5.5 ft. depth clone C120B EU219
L09177.1 gg_id:16059 Clostridium cellulosi L09177
EU887969.1 gg_id:314629 Microbial structure hydrolytic stage two-stage anaerobic digestion grass silage leach EU887

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EU266550.1 gg_id:341811 Eubacterium siraeum str. 70/3 EU2665
DQ808693.1 gg_id:181882 human fecal clone RL239_aaj11h11 DQ808
EU778187.1 gg_id:319411 feces clone RL388_aao95c07 EU7781
DQ793394.1 gg_id:181016 human fecal clone RL199_aaj43b09 DQ793
EU469704.1 gg_id:301678 flying fox feces clone FF_c12_1 EU4697
EU762757.1 gg_id:329717 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A> EU7627
DQ815544.1 gg_id:163232 mouse cecum clone aab42e07 DQ815
EU767472.1 gg_id:321239 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C2 EU7674
EF602866.1 gg_id:229922 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6028
EU778907.1 gg_id:342487 Black-handed Spider Monkey feces clone SPIM_a11 EU7789
EF602941.1 gg_id:234652 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6029
AB494836.1 gg_id:549330 Fibrobacter succinogenes dominated consortium on hay stems sheep rumen clone A AB4948
DQ806020.1 gg_id:193348 human fecal clone RL186_aah60a08 DQ806
EU509850.1 gg_id:259499 cecal contents Mus musculus strain C57BL/6J; WD11 clone WD11_aak22e01 EU5098
EU850555.1 gg_id:325103 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF359 EU8505
EU451219.1 gg_id:331604 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU4512
EF604817.1 gg_id:233939 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6048
AY244949.1 gg_id:84779 cow rumen clone BE33 AY2449
EF603072.1 gg_id:232036 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6030
AF371737.1 gg_id:43051 swine intestine clone p-810-a5 AF3717
DQ793694.1 gg_id:187181 human fecal clone RL246_aai75g05 DQ793
EU475566.1 gg_id:295339 babirusa feces clone BARB_aaa03f06 EU4755
AB192029.1 gg_id:143859 termite gut homogenate clone M1PT4-77 AB1920
EU767356.1 gg_id:314146 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C2 EU7673
EF404885.1 gg_id:212130 human fecal clone SJTU_G_09_71 EF4048
EU006202.1 gg_id:236392 Salmonella enterica serovar typhimurium exploits inflammation compete intestinal r EU0062
EF605049.1 gg_id:231992 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6050
EU762054.1 gg_id:307886 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1 EU7620
EF603180.1 gg_id:227740 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6031
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DQ796974.1 gg_id:188022 human fecal clone RL386_aao85b12 DQ796
AB192171.1 gg_id:141809 termite gut homogenate clone RsTz-42 AB1921
AB192211.1 gg_id:144676 termite gut homogenate clone RsTu1-33 AB1922
DQ824869.1 gg_id:197459 human fecal clone RL185_aao70c07 DQ824
DQ805295.1 gg_id:182098 human fecal clone RL249_aaj84f11 DQ805
FJ362806.1 gg_id:367743 feces adult twins and mothers; TS13 clone TS13_a03d08 FJ3628
FJ367146.1 gg_id:363979 feces adult twins and mothers; TS28 clone TS28_a04a08 FJ3671
FJ677070.1 gg_id:518546 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6770
AY986249.1 gg_id:127846 human stool clone D624 AY9862

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DQ806291.1 gg_id:183895 human fecal clone RL186_aan90a02 DQ806
FJ372178.1 gg_id:366585 feces adult twins and mothers; TS9 clone TS9_a02f05 FJ3721
DQ806570.1 gg_id:197639 human fecal clone RL186_aao46c01 DQ806
FJ362917.1 gg_id:369466 feces adult twins and mothers; TS13 clone TS13_a04g04 FJ3629
DQ777883.1 gg_id:162423 rat feces clone R-1152 DQ777
DQ808624.1 gg_id:174050 human fecal clone RL239_aaj11b01 DQ808
DQ808593.1 gg_id:192872 human fecal clone RL239_aaj10e12 DQ808
AY979460.1 gg_id:126958 human transverse colon mucosal biopsy clone M075 AY979
DQ805106.1 gg_id:187530 human fecal clone RL249_aaj81c10 DQ805
FJ676705.1 gg_id:509914 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6767
DQ326521.1 gg_id:147761 Metagenomic gut microbiome healthy human stool clone C660 DQ326
FJ368366.1 gg_id:360141 feces adult twins and mothers; TS3 clone TS3_a03e05 FJ3683
AY976711.1 gg_id:121279 human cecum mucosal biopsy clone K293 AY976
FJ367117.1 gg_id:364030 feces adult twins and mothers; TS28 clone TS28_a03f12 FJ3671
EF402060.1 gg_id:216252 human fecal clone SJTU_B_03_07 EF402
DQ795919.1 gg_id:182156 human fecal clone RL245_aai84h09 DQ795
FJ365238.1 gg_id:366761 feces adult twins and mothers; TS1 clone TS1_a04e03 FJ3652
DQ798178.1 gg_id:183655 human fecal clone RL302_aal96d12 DQ798
FJ679861.1 gg_id:514245 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6798
FJ677390.1 gg_id:524414 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6773
FJ371718.1 gg_id:365749 feces adult twins and mothers; TS8 clone TS8_a01d11 FJ3717
DQ801056.1 gg_id:186986 human fecal clone RL387_aao91e05 DQ801
GQ079666.1 gg_id:409613 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1232h GQ079
FJ673858.1 gg_id:520067 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6738
FJ683700.1 gg_id:530124 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6837
DQ809290.1 gg_id:188326 human fecal clone RL308_aal84g02 DQ809
FJ371170.1 gg_id:367157 feces adult twins and mothers; TS6 clone TS6_a01g05 FJ3711
GQ079267.1 gg_id:386197 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1230e GQ079
FJ672383.1 gg_id:515835 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface FJ6723
DQ801536.1 gg_id:183679 human fecal clone RL388_aao96g06 DQ801
DQ797803.1 gg_id:180672 human fecal clone RL206_aaj16a08 DQ797
FJ675708.1 gg_id:527624 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6757
DQ806371.1 gg_id:184697 human fecal clone RL186_aan91d03 DQ806
FJ363178.1 gg_id:356734 feces adult twins and mothers; TS148 clone TS148_a04a12 FJ3631
FJ362817.1 gg_id:360446 feces adult twins and mothers; TS13 clone TS13_a03e08 FJ3628
FJ673085.1 gg_id:515366 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6730
DQ797076.1 gg_id:193759 human fecal clone RL386_aao86f09 DQ797
FJ368341.1 gg_id:358640 feces adult twins and mothers; TS3 clone TS3_a03b09 FJ3683
FJ366039.1 gg_id:358261 feces adult twins and mothers; TS25 clone TS25_a02a05 FJ3660
FJ363519.1 gg_id:359595 feces adult twins and mothers; TS149 clone TS149_a04b10 FJ3635

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DQ799978.1 gg_id:186662 human fecal clone RL247_aaj22f03 DQ799
FJ677420.1 gg_id:515988 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6774
FJ363461.1 gg_id:362313 feces adult twins and mothers; TS149 clone TS149_a03e05 FJ3634
DQ801112.1 gg_id:177915 human fecal clone RL387_aao92d05 DQ801
FJ680563.1 gg_id:509205 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6805
AY981895.1 gg_id:126792 human sigmoid colon mucosal biopsy clone NY21 AY9818
FJ673099.1 gg_id:527224 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6730
DQ806448.1 gg_id:196829 human fecal clone RL186_aan92f04 DQ806
FJ675770.1 gg_id:519140 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6757
AY978231.1 gg_id:119111 human transverse colon mucosal biopsy clone F042 AY9782
FJ363272.1 gg_id:362223 feces adult twins and mothers; TS149 clone TS149_a01c09 FJ3632
EU764166.1 gg_id:317470 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A5 EU7641
DQ805150.1 gg_id:195803 human fecal clone RL249_aaj82a09 DQ805
FJ678815.1 gg_id:532216 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6788
DQ807006.1 gg_id:179496 human fecal clone RL244_aaj45a09 DQ807
FJ367155.1 gg_id:362755 feces adult twins and mothers; TS28 clone TS28_a04b07 FJ3671
DQ798149.1 gg_id:181186 human fecal clone RL302_aal96b04 DQ798
FJ368390.1 gg_id:363470 feces adult twins and mothers; TS3 clone TS3_a03g10 FJ3683
AY976559.1 gg_id:117805 human cecum mucosal biopsy clone K091 AY9765
FJ366101.1 gg_id:361581 feces adult twins and mothers; TS25 clone TS25_a02g01 FJ3661
FJ364535.1 gg_id:369621 feces adult twins and mothers; TS15 clone TS15_a04b03 FJ3645
DQ797719.1 gg_id:190450 human fecal clone RL206_aaj15a09 DQ797
DQ801057.1 gg_id:192213 human fecal clone RL387_aao91e06 DQ801
FJ674114.1 gg_id:526444 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6741
FJ371794.1 gg_id:361302 feces adult twins and mothers; TS8 clone TS8_a02c07 FJ3717
FJ372326.1 gg_id:359353 feces adult twins and mothers; TS9 clone TS9_a04c09 FJ3723
AY983735.1 gg_id:127543 human descending colon mucosal biopsy clone NQ90 AY9837
DQ796668.1 gg_id:190349 human fecal clone RL179aan76h09 DQ796
FJ372377.1 gg_id:358978 feces adult twins and mothers; TS9 clone TS9_a04h07 FJ3723
DQ802763.1 gg_id:173925 human fecal clone RL188_aan96c04 DQ802
AY980091.1 gg_id:126990 human rectum mucosal biopsy clone KB76 AY9800
DQ807487.1 gg_id:184511 human fecal clone RL307_aam07b12 DQ807
DQ797771.1 gg_id:182099 human fecal clone RL206_aaj15f08 DQ797
FJ676704.1 gg_id:511201 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6767
GQ896765.1 gg_id:593775 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do s GQ896
DQ807022.1 gg_id:187683 human fecal clone RL244_aaj45c02 DQ807
FJ368404.1 gg_id:360454 feces adult twins and mothers; TS3 clone TS3_a04a02 FJ3684
EU768433.1 gg_id:327174 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C5 EU7684
DQ808853.1 gg_id:193692 human fecal clone RL243_aai86b09 DQ808
FJ684635.1 gg_id:515604 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6846

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FJ683444.1 gg_id:524301 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6834
FJ679335.1 gg_id:516420 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6793
FJ676481.1 gg_id:509521 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6764
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DQ805695.1 gg_id:177693 human fecal clone RL306aal89h08 DQ805
DQ802522.1 gg_id:179153 human fecal clone RL188_aah18h08 DQ802
AY980001.1 gg_id:118473 human rectum mucosal biopsy clone K947 AY980
FJ364444.1 gg_id:362881 feces adult twins and mothers; TS15 clone TS15_a03a07 FJ3644
FJ363446.1 gg_id:365421 feces adult twins and mothers; TS149 clone TS149_a03d02 FJ3634
FJ364498.1 gg_id:369805 feces adult twins and mothers; TS15 clone TS15_a03f07 FJ3644
FJ677909.1 gg_id:525340 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6779
DQ798615.1 gg_id:192312 human fecal clone RL181_aan99a08 DQ798
FJ677130.1 gg_id:529423 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6771
AY977231.1 gg_id:121190 human cecum mucosal biopsy clone MT65 AY977
DQ797686.1 gg_id:188637 human fecal clone RL206_aaj14f05 DQ797
FJ678087.1 gg_id:512637 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6780
DQ797124.1 gg_id:179993 human fecal clone RL386_aao87c08 DQ797
FJ367178.1 gg_id:366211 feces adult twins and mothers; TS28 clone TS28_a04d10 FJ3671
FJ682718.1 gg_id:528518 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6827
DQ806579.1 gg_id:181428 human fecal clone RL186_aao46c10 DQ806
FJ362808.1 gg_id:366046 feces adult twins and mothers; TS13 clone TS13_a03d10 FJ3628
DQ825089.1 gg_id:186293 human fecal clone RL185_aan85c05 DQ825
FJ683660.1 gg_id:526565 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6836
FJ363540.1 gg_id:367305 feces adult twins and mothers; TS149 clone TS149_a04d09 FJ3635
DQ904859.1 gg_id:165658 human fecal clone 001C-d10 DQ904
AY981706.1 gg_id:116922 human sigmoid colon mucosal biopsy clone LA73 AY981
DQ801787.1 gg_id:198699 human fecal clone RL201_aai46g08 DQ801
DQ802307.1 gg_id:176501 human fecal clone RL188_aah15h04 DQ802
FJ368368.1 gg_id:361238 feces adult twins and mothers; TS3 clone TS3_a03e07 FJ3683
FJ682091.1 gg_id:518619 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6820
FJ679998.1 gg_id:517625 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6799
DQ802430.1 gg_id:174750 human fecal clone RL188_aah17f04 DQ802
FJ367036.1 gg_id:359356 feces adult twins and mothers; TS28 clone TS28_a02g03 FJ3670
AY981892.1 gg_id:120988 human sigmoid colon mucosal biopsy clone NY16 AY981
FJ681394.1 gg_id:524729 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6813
DQ825282.1 gg_id:176478 human fecal clone RL185_aan87g03 DQ825
DQ796042.1 gg_id:198500 human fecal clone RL202_aai50f07 DQ796
FJ676008.1 gg_id:517634 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6760
DQ808788.1 gg_id:190619 human fecal clone RL243_aai85c06 DQ808
FJ366198.1 gg_id:361897 feces adult twins and mothers; TS25 clone TS25_a03h03 FJ3661

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GQ079657.1 gg_id:379338 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1232g(GQ079
DQ802160.1 gg_id:175200 human fecal clone RL241_aaj03g12 DQ802
FJ370737.1 gg_id:357325 feces adult twins and mothers; TS57 clone TS57_a04f06 FJ3707
FJ682975.1 gg_id:510844 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6829
FJ368223.1 gg_id:357049 feces adult twins and mothers; TS3 clone TS3_a01f10 FJ3682
FJ362734.1 gg_id:365698 feces adult twins and mothers; TS13 clone TS13_a02e04 FJ3627
X85022.1 gg_id:16080 Faecalibacterium prausnitzii str. ATCC 27766 X85022
FJ683322.1 gg_id:520036 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6833
DQ805109.1 gg_id:186615 human fecal clone RL249_aaj81d01 DQ805
FJ368210.1 gg_id:358511 feces adult twins and mothers; TS3 clone TS3_a01e06 FJ3682
DQ802304.1 gg_id:197773 human fecal clone RL188_aah15g12 DQ802
DQ800745.1 gg_id:175486 human fecal clone RL183_aao02h05 DQ800
FJ677381.1 gg_id:512684 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6773
GQ016214.1 gg_id:493453 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw GQ016
DQ808935.1 gg_id:195949 human fecal clone RL243_aai87b10 DQ808
FJ366204.1 gg_id:358031 feces adult twins and mothers; TS25 clone TS25_a03h09 FJ3662
AY984534.1 gg_id:121004 human stool clone B467 AY9845
DQ823651.1 gg_id:186746 human fecal clone RL250_aaj77b05 DQ823
FJ368396.1 gg_id:367252 feces adult twins and mothers; TS3 clone TS3_a03h05 FJ3683
DQ808676.1 gg_id:197151 human fecal clone RL239_aaj11g03 DQ808
DQ823860.1 gg_id:182792 human fecal clone RL250_aaj80a10 DQ823
FJ676940.1 gg_id:526806 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6769
FJ682765.1 gg_id:516967 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6827
DQ807193.1 gg_id:196274 human fecal clone RL244_aaj47d07 DQ807
FJ368279.1 gg_id:368720 feces adult twins and mothers; TS3 clone TS3_a02d04 FJ3682
DQ798653.1 gg_id:175327 human fecal clone RL181_aan99f02 DQ798
DQ808739.1 gg_id:183992 human fecal clone RL239_aaj12f03 DQ808
FJ676367.1 gg_id:525215 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6763
FJ371732.1 gg_id:359892 feces adult twins and mothers; TS8 clone TS8_a01f01 FJ3717
AY981970.1 gg_id:125704 human sigmoid colon mucosal biopsy clone P116 AY9819
FJ681947.1 gg_id:516458 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6819
GQ898221.1 gg_id:573850 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do GQ898
FJ372279.1 gg_id:363371 feces adult twins and mothers; TS9 clone TS9_a03g05 FJ3722
FJ362819.1 gg_id:369719 feces adult twins and mothers; TS13 clone TS13_a03e10 FJ3628
DQ797578.1 gg_id:188572 human fecal clone RL206_aaj13c07 DQ797
DQ797050.1 gg_id:189061 human fecal clone RL386_aao86c10 DQ797
FJ676962.1 gg_id:520940 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6769
EU762767.1 gg_id:334218 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU762
DQ325773.1 gg_id:145129 Metagenomic gut microbiome healthy human stool clone B456 DQ325
DQ807292.1 gg_id:190132 human fecal clone RL244_aaj48f11 DQ807

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FJ367026.1 gg_id:368897 feces adult twins and mothers; TS28 clone TS28_a02f04 FJ3670
FJ366977.1 gg_id:358050 feces adult twins and mothers; TS28 clone TS28_a02a08 FJ3669
FJ367852.1 gg_id:357060 feces adult twins and mothers; TS2 clone TS2_a04d01 FJ3678
DQ797406.1 gg_id:196536 human fecal clone RL248_aai98h09 DQ797
FJ371731.1 gg_id:365987 feces adult twins and mothers; TS8 clone TS8_a01e12 FJ3717
AY975989.1 gg_id:122299 human ascending colon mucosal biopsy clone LT21 AY975
DQ801706.1 gg_id:177293 human fecal clone RL201_aai45g09 DQ801
GQ079667.1 gg_id:378231 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1232h GQ079
DQ824797.1 gg_id:173874 human fecal clone RL185_aao69d06 DQ824
DQ824200.1 gg_id:175829 human fecal clone RL204_aaj60g06 DQ824
FJ371997.1 gg_id:359519 feces adult twins and mothers; TS8 clone TS8_a04e11 FJ3719
EU762904.1 gg_id:334000 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU762
FJ678360.1 gg_id:531016 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6783
FJ677247.1 gg_id:530453 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6772
FJ679411.1 gg_id:532050 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6794
DQ808630.1 gg_id:194943 human fecal clone RL239_aaj11b07 DQ808
FJ679099.1 gg_id:515418 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6790
DQ805736.1 gg_id:191097 human fecal clone RL306aal90d08 DQ805
DQ797455.1 gg_id:189565 human fecal clone RL248_aai99e09 DQ797
GQ898309.1 gg_id:561072 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ898
FJ363853.1 gg_id:362076 feces adult twins and mothers; TS14 clone TS14_a04b06 FJ3638
GQ448799.1 gg_id:563000 Microbiome neonatal calves: shedding microorganisms fecal clone calf32_2wks_grp GQ448
AY976039.1 gg_id:127495 human ascending colon mucosal biopsy clone LT85 AY976
EU768031.1 gg_id:337270 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C EU768
FJ672952.1 gg_id:532368 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6729
FJ683091.1 gg_id:525598 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6830
DQ824097.1 gg_id:194295 human fecal clone RL204_aaj59c08 DQ824
FJ683320.1 gg_id:520100 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6833
AY980035.1 gg_id:118025 human rectum mucosal biopsy clone KA46 AY980
AY975993.1 gg_id:126037 human ascending colon mucosal biopsy clone LT26 AY975
DQ805145.1 gg_id:192670 human fecal clone RL249_aaj82a02 DQ805
FJ682300.1 gg_id:511438 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6823
FJ682808.1 gg_id:521352 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6828
FJ363520.1 gg_id:357653 feces adult twins and mothers; TS149 clone TS149_a04b11 FJ3635
FJ680182.1 gg_id:517702 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6801
AY979304.1 gg_id:116818 human transverse colon mucosal biopsy clone Z552 AY979
FJ371792.1 gg_id:360409 feces adult twins and mothers; TS8 clone TS8_a02c05 FJ3717
EU762928.1 gg_id:312909 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU762

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FJ371762.1 gg_id:357116 feces adult twins and mothers; TS8 clone TS8_a01h08 FJ3717
FJ368421.1 gg_id:368885 feces adult twins and mothers; TS3 clone TS3_a04b07 FJ3684
FJ683649.1 gg_id:511146 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6836
FJ675765.1 gg_id:516596 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6757
FJ365059.1 gg_id:359429 feces adult twins and mothers; TS1 clone TS1_a02d02 FJ3650
FJ363233.1 gg_id:360875 feces adult twins and mothers; TS148 clone TS148_a04g09 FJ3632
FJ678462.1 gg_id:525424 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6784
FJ681572.1 gg_id:525266 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6815
FJ371015.1 gg_id:358551 feces adult twins and mothers; TS5 clone TS5_a03h11 FJ3710
EU766741.1 gg_id:310266 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU766
DQ824365.1 gg_id:193027 human fecal clone RL304_aal75b02 DQ824
FJ676223.1 gg_id:532364 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6762
FJ678820.1 gg_id:530122 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6788
GQ079592.1 gg_id:396769 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1231f0 GQ079
DQ825084.1 gg_id:196335 human fecal clone RL185_aan85b10 DQ825
FJ368328.1 gg_id:369628 feces adult twins and mothers; TS3 clone TS3_a03a05 FJ3683
FJ371966.1 gg_id:369890 feces adult twins and mothers; TS8 clone TS8_a04c03 FJ3719
AY984008.1 gg_id:117564 human descending colon mucosal biopsy clone MD39 AY984
FJ677419.1 gg_id:528411 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6774
FJ366584.1 gg_id:369402 feces adult twins and mothers; TS27 clone TS27_a01d09 FJ3665
AY976645.1 gg_id:116370 human cecum mucosal biopsy clone K209 AY976
FJ683355.1 gg_id:530874 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6833
EU766087.1 gg_id:318761 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B4 EU766
AY981955.1 gg_id:117906 human sigmoid colon mucosal biopsy clone P066 AY981
FJ362977.1 gg_id:361017 feces adult twins and mothers; TS148 clone TS148_a01e01 FJ3629
FJ678798.1 gg_id:509230 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6787
DQ797565.1 gg_id:189766 human fecal clone RL206_aaj13b04 DQ797
FJ677300.1 gg_id:524186 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6773
DQ807504.1 gg_id:190383 human fecal clone RL307_aam07d10 DQ807
FJ682049.1 gg_id:520324 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6820
FJ368391.1 gg_id:360575 feces adult twins and mothers; TS3 clone TS3_a03g11 FJ3683
FJ673618.1 gg_id:521759 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6736
FJ682690.1 gg_id:530116 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6826
FJ362861.1 gg_id:358726 feces adult twins and mothers; TS13 clone TS13_a04b02 FJ3628
AF371733.1 gg_id:53461 swine intestine clone p-1749-b3 AF371
AY978922.1 gg_id:116985 human transverse colon mucosal biopsy clone NG46 AY978
DQ824173.1 gg_id:194654 human fecal clone RL204_aaj60d03 DQ824
FJ364960.1 gg_id:361692 feces adult twins and mothers; TS1 clone TS1_a01c03 FJ3649
FJ366957.1 gg_id:362748 feces adult twins and mothers; TS28 clone TS28_a01g06 FJ3669
FJ673049.1 gg_id:531814 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6730

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DQ797086.1 gg_id:196032 human fecal clone RL386_aao86g10 DQ797
FJ682856.1 gg_id:532075 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6828
FJ372330.1 gg_id:368391 feces adult twins and mothers; TS9 clone TS9_a04d02 FJ3723
FJ363529.1 gg_id:361893 feces adult twins and mothers; TS149 clone TS149_a04c08 FJ3635
DQ810047.1 gg_id:186399 human fecal clone RL184_aao67e01 DQ810
DQ797285.1 gg_id:199747 human fecal clone RL248_aai97d02 DQ797
FJ674151.1 gg_id:531913 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6741
DQ797142.1 gg_id:199675 human fecal clone RL386_aao87e05 DQ797
DQ805166.1 gg_id:184769 human fecal clone RL249_aaj82d03 DQ805
FJ678884.1 gg_id:516808 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6788
AY981760.1 gg_id:119353 human sigmoid colon mucosal biopsy clone NS18 AY981
FJ363485.1 gg_id:364316 feces adult twins and mothers; TS149 clone TS149_a03g08 FJ3634
DQ804716.1 gg_id:191008 human fecal clone RL187_aao71g07 DQ804
DQ796571.1 gg_id:192277 human fecal clone RL179aan75a10 DQ796
FJ677086.1 gg_id:531356 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6770
FJ677159.1 gg_id:524005 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6771
FJ363429.1 gg_id:360503 feces adult twins and mothers; TS149 clone TS149_a03b08 FJ3634
FJ364952.1 gg_id:365904 feces adult twins and mothers; TS1 clone TS1_a01b07 FJ3649
DQ806522.1 gg_id:183548 human fecal clone RL186_aao45f07 DQ806
DQ825246.1 gg_id:196043 human fecal clone RL185_aan87c05 DQ825
DQ825332.1 gg_id:175009 human fecal clone RL185_aan88f10 DQ825
FJ675699.1 gg_id:532420 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6756
FJ371790.1 gg_id:367433 feces adult twins and mothers; TS8 clone TS8_a02c03 FJ3717
DQ797607.1 gg_id:179098 human fecal clone RL206_aaj13f06 DQ797
EU767489.1 gg_id:348947 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C2 EU767
FJ684923.1 gg_id:519030 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6849
FJ363574.1 gg_id:363425 feces adult twins and mothers; TS149 clone TS149_a04h05 FJ3635
AY985869.1 gg_id:117448 human stool clone D146 AY985
EU763276.1 gg_id:331791 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A4 EU763
AY976537.1 gg_id:125456 human cecum mucosal biopsy clone K068 AY976
FJ365026.1 gg_id:362229 feces adult twins and mothers; TS1 clone TS1_a02a02 FJ3650
FJ673737.1 gg_id:517362 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6737
DQ797238.1 gg_id:196576 human fecal clone RL386_aao88g05 DQ797
DQ825022.1 gg_id:182247 human fecal clone RL185_aao72d05 DQ825
DQ805284.1 gg_id:180071 human fecal clone RL249_aaj84d08 DQ805
DQ800902.1 gg_id:176255 human fecal clone RL387_aao89a10 DQ800
EU768078.1 gg_id:319777 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C4 EU768
EU766703.1 gg_id:336041 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU766
FJ371389.1 gg_id:360139 feces adult twins and mothers; TS6 clone TS6_a04d03 FJ3713
FJ368265.1 gg_id:360406 feces adult twins and mothers; TS3 clone TS3_a02b11 FJ3682

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FJ363256.1 gg_id:370290 feces adult twins and mothers; TS149 clone TS149_a01b05 FJ3632
FJ363311.1 gg_id:366678 feces adult twins and mothers; TS149 clone TS149_a01g02 FJ3633
FJ673284.1 gg_id:515583 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6732
AY974989.1 gg_id:120171 human ascending colon mucosal biopsy clone KJ67 AY974
FJ676846.1 gg_id:518075 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6768
FJ364541.1 gg_id:359242 feces adult twins and mothers; TS15 clone TS15_a04b09 FJ3645
FJ677273.1 gg_id:525333 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6772
DQ809074.1 gg_id:187923 human fecal clone RL308_aal81b02 DQ809
DQ803755.1 gg_id:174064 human fecal clone RL200_aai58a06 DQ803
FJ675906.1 gg_id:518491 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6759
FJ676247.1 gg_id:519214 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6762
DQ825233.1 gg_id:182153 human fecal clone RL185_aan87a07 DQ825
FJ673948.1 gg_id:531698 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6739
AY977259.1 gg_id:117767 human cecum mucosal biopsy clone MU17 AY977
FJ682626.1 gg_id:527192 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6826
DQ795927.1 gg_id:175982 human fecal clone RL202_aai49a11 DQ795
DQ805916.1 gg_id:182290 human fecal clone RL306aal92f04 DQ805
FJ368355.1 gg_id:368447 feces adult twins and mothers; TS3 clone TS3_a03d05 FJ3683
NZ_ABED02000023.1 gg_id:470396 Faecalibacterium prausnitzii str. M21/2 NZ_AB
FJ683231.1 gg_id:512652 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6832
FJ682434.1 gg_id:531492 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6824
DQ801870.1 gg_id:190725 human fecal clone RL201_aai47h06 DQ801
FJ362727.1 gg_id:366508 feces adult twins and mothers; TS13 clone TS13_a02d08 FJ3627
DQ798709.1 gg_id:176959 human fecal clone RL181_aao00d07 DQ798
DQ805730.1 gg_id:182977 human fecal clone RL306aal90d02 DQ805
AY975201.1 gg_id:117940 human ascending colon mucosal biopsy clone KN33 AY975
DQ825294.1 gg_id:178414 human fecal clone RL185_aan87h11 DQ825
DQ325830.1 gg_id:148853 Metagenomic gut microbiome healthy human stool clone B575 DQ325
DQ802743.1 gg_id:199018 human fecal clone RL188_aan96a08 DQ802
EF402055.1 gg_id:208163 human fecal clone SJTU_B_03_01 EF402
FJ366865.1 gg_id:368718 feces adult twins and mothers; TS27 clone TS27_a04g05 FJ3668
FJ676063.1 gg_id:525944 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6760
FJ371912.1 gg_id:370384 feces adult twins and mothers; TS8 clone TS8_a03f05 FJ3719
FJ363490.1 gg_id:361225 feces adult twins and mothers; TS149 clone TS149_a03h02 FJ3634
DQ797128.1 gg_id:183253 human fecal clone RL386_aao87d02 DQ797
DQ797747.1 gg_id:175431 human fecal clone RL206_aaj15d08 DQ797
FJ365164.1 gg_id:362669 feces adult twins and mothers; TS1 clone TS1_a03f05 FJ3651
DQ809102.1 gg_id:176892 human fecal clone RL308_aal81e07 DQ809
FJ683832.1 gg_id:530482 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6838
DQ800052.1 gg_id:189132 human fecal clone RL247_aaj23e12 DQ800

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FJ363310.1 gg_id:365361 feces adult twins and mothers; TS149 clone TS149_a01g01 FJ3633
FJ683439.1 gg_id:523054 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6834
AY976930.1 gg_id:126260 human cecum mucosal biopsy clone K583 AY976
FJ372125.1 gg_id:364515 feces adult twins and mothers; TS9 clone TS9_a02a07 FJ3721
FJ365117.1 gg_id:356850 feces adult twins and mothers; TS1 clone TS1_a03a10 FJ3651
AY984472.1 gg_id:119651 human stool clone B385 AY984
EF403544.1 gg_id:214690 human fecal clone SJTU_A2_03_29 EF4035
DQ796787.1 gg_id:193058 human fecal clone RL179_aao54e02 DQ796
DQ800105.1 gg_id:199166 human fecal clone RL247_aaj24c02 DQ800
DQ806550.1 gg_id:177636 human fecal clone RL186_aao46a01 DQ806
FJ676416.1 gg_id:514349 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6764
DQ808762.1 gg_id:193515 human fecal clone RL239_aaj12h12 DQ808
DQ808860.1 gg_id:177557 human fecal clone RL243_aai86c04 DQ808
DQ797831.1 gg_id:175317 human fecal clone RL206_aaj16d02 DQ797
AY979261.1 gg_id:127242 human transverse colon mucosal biopsy clone Z454 AY979
FJ368209.1 gg_id:356839 feces adult twins and mothers; TS3 clone TS3_a01e05 FJ3682
DQ801033.1 gg_id:189405 human fecal clone RL387_aao91b11 DQ801
DQ806501.1 gg_id:174551 human fecal clone RL186_aao45d07 DQ806
DQ795954.1 gg_id:191184 human fecal clone RL202_aai49d06 DQ795
FJ368473.1 gg_id:366463 feces adult twins and mothers; TS3 clone TS3_a04g09 FJ3684
FJ363414.1 gg_id:369631 feces adult twins and mothers; TS149 clone TS149_a03a02 FJ3634
FJ683870.1 gg_id:527654 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6838
FJ679967.1 gg_id:515363 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6799
DQ806783.1 gg_id:196261 human fecal clone RL186_aao48f07 DQ806
FJ371915.1 gg_id:361722 feces adult twins and mothers; TS8 clone TS8_a03f08 FJ3719
FJ683272.1 gg_id:524095 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6832
DQ805812.1 gg_id:190533 human fecal clone RL306aal91d03 DQ805
DQ798647.1 gg_id:191168 human fecal clone RL181_aan99e06 DQ798
DQ797657.1 gg_id:199518 human fecal clone RL206_aaj14c10 DQ797
FJ368246.1 gg_id:363949 feces adult twins and mothers; TS3 clone TS3_a02a02 FJ3682
AY979276.1 gg_id:123222 human transverse colon mucosal biopsy clone Z478 AY979
FJ363427.1 gg_id:370001 feces adult twins and mothers; TS149 clone TS149_a03b06 FJ3634
FJ683442.1 gg_id:526004 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6834
AY978195.1 gg_id:117979 human cecum mucosal biopsy clone LJ88 AY978
AY978386.1 gg_id:126895 human transverse colon mucosal biopsy clone F361 AY978
FJ368293.1 gg_id:366116 feces adult twins and mothers; TS3 clone TS3_a02e09 FJ3682
DQ797764.1 gg_id:186892 human fecal clone RL206_aaj15f01 DQ797
FJ371968.1 gg_id:363824 feces adult twins and mothers; TS8 clone TS8_a04c05 FJ3719
FJ372247.1 gg_id:361689 feces adult twins and mothers; TS9 clone TS9_a03d07 FJ3722
GQ448805.1 gg_id:512975 Microbiome neonatal calves: shedding microorganisms fecal clone calf32_2wks_grp GQ448

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FJ683114.1 gg_id:518707 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6831
EU762212.1 gg_id:320919 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU762
FJ363216.1 gg_id:363830 feces adult twins and mothers; TS148 clone TS148_a04f02 FJ3632
DQ806450.1 gg_id:193849 human fecal clone RL186_aan92f06 DQ806
FJ363395.1 gg_id:362850 feces adult twins and mothers; TS149 clone TS149_a02g01 FJ3633
DQ797730.1 gg_id:186927 human fecal clone RL206_aaj15b11 DQ797
GQ492289.1 gg_id:585294 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
FJ371832.1 gg_id:364644 feces adult twins and mothers; TS8 clone TS8_a02f11 FJ3718
DQ807605.1 gg_id:180431 human fecal clone RL307_aam08g11 DQ807
DQ825248.1 gg_id:194165 human fecal clone RL185_aan87c07 DQ825
FJ363358.1 gg_id:367817 feces adult twins and mothers; TS149 clone TS149_a02c10 FJ3633
FJ675716.1 gg_id:520165 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6757
FJ678964.1 gg_id:513926 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6789
DQ824098.1 gg_id:189092 human fecal clone RL204_aaj59c09 DQ824
FJ683764.1 gg_id:520147 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6837
EU462900.1 gg_id:290260 southern three-banded armadillo feces clone arma_aaj54f12 EU462
FJ675941.1 gg_id:522302 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6759
AY986127.1 gg_id:116066 human stool clone D470 AY986
FJ677162.1 gg_id:509732 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6771
AY978645.1 gg_id:122335 human transverse colon mucosal biopsy clone KS69 AY978
EU767465.1 gg_id:334169 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C EU767
FJ683090.1 gg_id:509794 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6830
FJ364531.1 gg_id:365618 feces adult twins and mothers; TS15 clone TS15_a04a09 FJ3645
AY976087.1 gg_id:120790 human ascending colon mucosal biopsy clone LU53 AY976
FJ372155.1 gg_id:360307 feces adult twins and mothers; TS9 clone TS9_a02d03 FJ3721
DQ798510.1 gg_id:198985 human fecal clone RL181_aan97f04 DQ798
AY979116.1 gg_id:119029 human transverse colon mucosal biopsy clone Z106 AY979
DQ825001.1 gg_id:199365 human fecal clone RL185_aao72b02 DQ825
DQ799860.1 gg_id:177835 human fecal clone RL247_aaj21a09 DQ799
FJ365130.1 gg_id:365847 feces adult twins and mothers; TS1 clone TS1_a03c03 FJ3651
DQ797750.1 gg_id:197588 human fecal clone RL206_aaj15d11 DQ797
EU766518.1 gg_id:329204 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B EU766
AY980264.1 gg_id:122590 human rectum mucosal biopsy clone MX02 AY980
FJ675845.1 gg_id:531756 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6758
FJ678348.1 gg_id:514528 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6783
DQ808489.1 gg_id:178182 human fecal clone RL239_aaj09c01 DQ808
DQ805871.1 gg_id:193568 human fecal clone RL306aal92b02 DQ805
FJ362780.1 gg_id:359489 feces adult twins and mothers; TS13 clone TS13_a03b02 FJ3627
AY977263.1 gg_id:119827 human cecum mucosal biopsy clone MU25 AY977

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FJ364542.1 gg_id:360700 feces adult twins and mothers; TS15 clone TS15_a04b10 FJ3645
FJ677797.1 gg_id:524520 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6777
FJ677397.1 gg_id:508946 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6773
FJ676031.1 gg_id:525774 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6760
FJ676037.1 gg_id:517253 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6760
DQ800296.1 gg_id:185734 human fecal clone RL303_aal71a10 DQ800
FJ367860.1 gg_id:365095 feces adult twins and mothers; TS2 clone TS2_a04d09 FJ3678
FJ368453.1 gg_id:369565 feces adult twins and mothers; TS3 clone TS3_a04e08 FJ3684
AY977188.1 gg_id:122726 human cecum mucosal biopsy clone MS75 AY977
DQ798517.1 gg_id:197692 human fecal clone RL181_aan97f12 DQ798
AY983849.1 gg_id:116710 human descending colon mucosal biopsy clone M958 AY9838
AY978863.1 gg_id:119743 human transverse colon mucosal biopsy clone NE21 AY9788
DQ797475.1 gg_id:180665 human fecal clone RL248_aai99g10 DQ797
DQ806951.1 gg_id:180304 human fecal clone RL198_aaj76a06 DQ806
EU768089.1 gg_id:309417 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C4 EU768
FJ368256.1 gg_id:362528 feces adult twins and mothers; TS3 clone TS3_a02b02 FJ3682
FJ366006.1 gg_id:368013 feces adult twins and mothers; TS25 clone TS25_a01f05 FJ3660
FJ366953.1 gg_id:360356 feces adult twins and mothers; TS28 clone TS28_a01g02 FJ3669
EU766649.1 gg_id:343703 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU766
AY975796.1 gg_id:122273 human ascending colon mucosal biopsy clone Y282 AY9757
AY978859.1 gg_id:122231 human transverse colon mucosal biopsy clone NE10 AY9788
DQ057476.1 gg_id:132991 str. ic1379 DQ057
GQ079221.1 gg_id:380701 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1229h GQ079
DQ808789.1 gg_id:182311 human fecal clone RL243_aai85c07 DQ808
FJ368259.1 gg_id:369725 feces adult twins and mothers; TS3 clone TS3_a02b05 FJ3682
DQ800929.1 gg_id:181459 human fecal clone RL387_aao89d11 DQ800
EF402790.1 gg_id:216642 human fecal clone SJTU_B_12_54 EF4027
FJ362717.1 gg_id:361654 feces adult twins and mothers; TS13 clone TS13_a02c07 FJ3627
AY976344.1 gg_id:123881 human ascending colon mucosal biopsy clone LY20 AY9763
FJ683181.1 gg_id:524386 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6831
DQ796660.1 gg_id:176153 human fecal clone RL179aan76g09 DQ796
FJ675796.1 gg_id:528915 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6757
DQ805171.1 gg_id:189368 human fecal clone RL249_aaj82e01 DQ805
FJ684556.1 gg_id:518669 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6845
FJ678769.1 gg_id:529017 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6787
AJ413954.1 gg_id:27866 Faecalibacterium prausnitzii str. ATCC 27768 AJ4139
AY978779.1 gg_id:126514 human transverse colon mucosal biopsy clone KV58 AY9787
AY982315.1 gg_id:118123 human sigmoid colon mucosal biopsy clone MI93 AY9823
FJ363392.1 gg_id:368116 feces adult twins and mothers; TS149 clone TS149_a02f10 FJ3633
FJ677277.1 gg_id:520176 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6772

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FJ677143.1 gg_id:531846 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6771
AY980222.1 gg_id:121082 human rectum mucosal biopsy clone KF57 AY9802
GQ898254.1 gg_id:580699 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do GQ898
FJ366936.1 gg_id:361935 feces adult twins and mothers; TS28 clone TS28_a01e09 FJ3669
FJ681202.1 gg_id:521577 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6812
FJ677631.1 gg_id:529962 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6776
FJ371203.1 gg_id:370371 feces adult twins and mothers; TS6 clone TS6_a02b04 FJ3712
FJ677001.1 gg_id:515558 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6770
DQ807434.1 gg_id:198323 human fecal clone RL307_aam06e11 DQ807
FJ362670.1 gg_id:368410 feces adult twins and mothers; TS13 clone TS13_a01g04 FJ3626
AY975435.1 gg_id:117722 human ascending colon mucosal biopsy clone N810 AY9754
DQ801588.1 gg_id:177348 human fecal clone RL117_aae92b03 DQ801
FJ673090.1 gg_id:527183 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6730
AY984427.1 gg_id:119554 human stool clone B337 AY9844
FJ364270.1 gg_id:360741 feces adult twins and mothers; TS15 clone TS15_a01a02 FJ3642
FJ677462.1 gg_id:530601 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6774
EU761801.1 gg_id:354500 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1 EU7618
FJ363015.1 gg_id:362968 feces adult twins and mothers; TS148 clone TS148_a01h09 FJ3630
FJ676412.1 gg_id:523534 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6764
FJ673029.1 gg_id:512771 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6730
AY978657.1 gg_id:116927 human transverse colon mucosal biopsy clone KS92 AY9786
AY975875.1 gg_id:118366 human ascending colon mucosal biopsy clone Y431 AY9758
DQ810166.1 gg_id:187387 human fecal clone RL184_aao68g09 DQ810
FJ363312.1 gg_id:368581 feces adult twins and mothers; TS149 clone TS149_a01g03 FJ3633
FJ677073.1 gg_id:517736 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6770
AY975709.1 gg_id:122537 human ascending colon mucosal biopsy clone Y139 AY9757
DQ825196.1 gg_id:189477 human fecal clone RL185_aan86e09 DQ825
FJ677264.1 gg_id:518031 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6772
FJ677780.1 gg_id:514577 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6777
DQ802252.1 gg_id:187307 human fecal clone RL188_aah15b05 DQ802
FJ371780.1 gg_id:369584 feces adult twins and mothers; TS8 clone TS8_a02b04 FJ3717
EU763004.1 gg_id:352406 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A> EU7630
DQ824290.1 gg_id:195125 human fecal clone RL304_aal74a05 DQ824
AY976691.1 gg_id:124150 human cecum mucosal biopsy clone K266 AY9766
FJ371813.1 gg_id:362246 feces adult twins and mothers; TS8 clone TS8_a02e02 FJ3718
FJ371429.1 gg_id:365427 feces adult twins and mothers; TS6 clone TS6_a04h03 FJ3714
FJ677912.1 gg_id:519045 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6779
DQ824156.1 gg_id:188822 human fecal clone RL204_aaj60b01 DQ824

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DQ824007.1 gg_id:190675 human fecal clone RL204_aaj58a12 DQ824
FJ363426.1 gg_id:366306 feces adult twins and mothers; TS149 clone TS149_a03b05 FJ3634
FJ676070.1 gg_id:516297 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6760
DQ797557.1 gg_id:193090 human fecal clone RL206_aaj13a06 DQ797
FJ362934.1 gg_id:356892 feces adult twins and mothers; TS13 clone TS13_a04h10 FJ3629
DQ904721.1 gg_id:161730 human fecal clone 001-h11 DQ904
FJ676590.1 gg_id:519312 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6765
DQ325893.1 gg_id:147702 Metagenomic gut microbiome healthy human stool clone B707 DQ325
AY985082.1 gg_id:120978 human stool clone BA93 AY985
AY982259.1 gg_id:121043 human sigmoid colon mucosal biopsy clone MH88 AY982
FJ682388.1 gg_id:514957 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6823
DQ797107.1 gg_id:185781 human fecal clone RL386_aao87a10 DQ797
FJ363314.1 gg_id:364280 feces adult twins and mothers; TS149 clone TS149_a01g05 FJ3633
AY976301.1 gg_id:117575 human ascending colon mucosal biopsy clone LX56 AY976
FJ363063.1 gg_id:357077 feces adult twins and mothers; TS148 clone TS148_a02e08 FJ3630
FJ368438.1 gg_id:364732 feces adult twins and mothers; TS3 clone TS3_a04d02 FJ3684
AY975301.1 gg_id:119040 human ascending colon mucosal biopsy clone N543 AY975
FJ369154.1 gg_id:367936 feces adult twins and mothers; TS4 clone TS4_a04h08 FJ3691
DQ798258.1 gg_id:176134 human fecal clone RL181_aah39f09 DQ798
DQ802139.1 gg_id:181599 human fecal clone RL241_aaj03e11 DQ802
FJ682924.1 gg_id:515542 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6829
DQ823721.1 gg_id:175507 human fecal clone RL250_aaj78b08 DQ823
DQ799344.1 gg_id:183199 human fecal clone RL305aal85b08 DQ799
FJ673013.1 gg_id:519728 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6730
DQ797160.1 gg_id:178415 human fecal clone RL386_aao87g03 DQ797
DQ795925.1 gg_id:196355 human fecal clone RL202_aai49a07 DQ795
FJ680048.1 gg_id:509868 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6800
FJ682123.1 gg_id:517664 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6821
DQ809683.1 gg_id:190160 human fecal clone RL184_aan82e10 DQ809
FJ673930.1 gg_id:527068 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6739
EU778899.1 gg_id:312048 Black-handed Spider Monkey feces clone SPIM_aaj34c01 EU778
FJ368385.1 gg_id:359648 feces adult twins and mothers; TS3 clone TS3_a03g03 FJ3683
FJ673582.1 gg_id:516105 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6735
FJ368730.1 gg_id:367876 feces adult twins and mothers; TS49 clone TS49_a03g09 FJ3687
DQ805164.1 gg_id:176115 human fecal clone RL249_aaj82d01 DQ805
FJ365243.1 gg_id:369949 feces adult twins and mothers; TS1 clone TS1_a04e08 FJ3652
DQ797216.1 gg_id:179154 human fecal clone RL386_aao88e03 DQ797
DQ806821.1 gg_id:184353 human fecal clone RL198_aaj73c11 DQ806
DQ795862.1 gg_id:181839 human fecal clone RL245_aai83e10 DQ795
FJ366968.1 gg_id:362324 feces adult twins and mothers; TS28 clone TS28_a01h07 FJ3669

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DQ796890.1 gg_id:186384 human fecal clone RL179_aao56a07 DQ796
EU137427.1 gg_id:274356 Bartonella-positive fleas: and assembly patterns Oropsylla hirsuta (prairie dog flea) C EU137
DQ824425.1 gg_id:180298 human fecal clone RL304_aal75h03 DQ824
FJ365608.1 gg_id:360246 feces adult twins and mothers; TS20 clone TS20_a04h06 FJ3656
FJ364313.1 gg_id:358850 feces adult twins and mothers; TS15 clone TS15_a01e03 FJ3643
DQ824052.1 gg_id:185390 human fecal clone RL204_aaj58f07 DQ824
FJ681716.1 gg_id:522178 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6817
DQ797720.1 gg_id:194473 human fecal clone RL206_aaj15a10 DQ797
FJ363829.1 gg_id:360685 feces adult twins and mothers; TS14 clone TS14_a03h03 FJ3638
FJ674061.1 gg_id:528652 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6740
FJ372221.1 gg_id:364955 feces adult twins and mothers; TS9 clone TS9_a03b04 FJ3722
FJ683526.1 gg_id:528460 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6835
DQ904725.1 gg_id:163923 human fecal clone 001-h3 DQ904
EF399784.1 gg_id:211230 human fecal clone SJTU_E_03_35 EF3997
FJ677024.1 gg_id:527090 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6770
FJ679261.1 gg_id:527410 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6792
FJ682135.1 gg_id:530792 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6821
FJ366934.1 gg_id:368952 feces adult twins and mothers; TS28 clone TS28_a01e07 FJ3669
FJ364397.1 gg_id:358114 feces adult twins and mothers; TS15 clone TS15_a02d09 FJ3643
DQ824258.1 gg_id:188630 human fecal clone RL304_aal73f05 DQ824
FJ682920.1 gg_id:515163 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6829
FJ370948.1 gg_id:365717 feces adult twins and mothers; TS5 clone TS5_a03b06 FJ3709
DQ905120.1 gg_id:170059 human fecal clone 002C-b9 DQ905
FJ684239.1 gg_id:519857 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6842
EF403960.1 gg_id:214401 human fecal clone SJTU_C_02_87 EF4039
AY975137.1 gg_id:124838 human ascending colon mucosal biopsy clone KM32 AY9751
DQ824456.1 gg_id:193985 human fecal clone RL304_aal76c03 DQ824
DQ796110.1 gg_id:183916 human fecal clone RL202_aai51f06 DQ796
FJ364947.1 gg_id:364154 feces adult twins and mothers; TS1 clone TS1_a01b02 FJ3649
FJ676519.1 gg_id:511985 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6765
FJ685192.1 gg_id:527560 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6851
DQ801628.1 gg_id:174618 human fecal clone RL117_aae93a06 DQ801
FJ683339.1 gg_id:531419 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6833
AY982207.1 gg_id:121572 human sigmoid colon mucosal biopsy clone MH04 AY982
FJ684175.1 gg_id:529507 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6841
FJ673554.1 gg_id:515086 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6735
FJ684184.1 gg_id:518792 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6841
AF376201.1 gg_id:26738 ckncm297-B1-1 clone AF376
FJ683263.1 gg_id:514730 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6832
FJ677043.1 gg_id:519585 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6770

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FJ679195.1 gg_id:521174 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6791
FJ682077.1 gg_id:523004 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6820
FJ679008.1 gg_id:517327 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6790
AY981330.1 gg_id:119373 human sigmoid colon mucosal biopsy clone G348 AY9813
DQ824177.1 gg_id:179618 human fecal clone RL204_aaj60d08 DQ824
DQ455894.1 gg_id:157039 pre-adolescent turkey cecum clone CFT19H5 DQ455
FJ363424.1 gg_id:362434 feces adult twins and mothers; TS149 clone TS149_a03b03 FJ3634
EU765882.1 gg_id:343729 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B4 EU7658
FJ673757.1 gg_id:531957 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6737
DQ824273.1 gg_id:182474 human fecal clone RL304_aal73g10 DQ824
FJ673321.1 gg_id:525934 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6733
DQ904869.1 gg_id:165924 human fecal clone 001C-d8 DQ904
DQ326102.1 gg_id:147918 Metagenomic gut microbiome healthy human stool clone BB48 DQ326
FJ673706.1 gg_id:515571 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6737
FJ365373.1 gg_id:360869 feces adult twins and mothers; TS20 clone TS20_a02b07 FJ3653
FJ682702.1 gg_id:511628 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6827
EF404926.1 gg_id:208689 human fecal clone SJTU_G_08_51 EF4049
AY982292.1 gg_id:120787 human sigmoid colon mucosal biopsy clone MI44 AY9822
FJ365144.1 gg_id:364153 feces adult twins and mothers; TS1 clone TS1_a03d07 FJ3651
FJ363150.1 gg_id:366680 feces adult twins and mothers; TS148 clone TS148_a03f10 FJ3631
FJ673221.1 gg_id:519426 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6732
DQ825336.1 gg_id:180951 human fecal clone RL185_aan88g04 DQ825
FJ362937.1 gg_id:366344 feces adult twins and mothers; TS148 clone TS148_a01a05 FJ3629
FJ365109.1 gg_id:369337 feces adult twins and mothers; TS1 clone TS1_a03a02 FJ3651
EF403511.1 gg_id:209544 human fecal clone SJTU_A2_02_43 EF4035
FJ676561.1 gg_id:529243 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6765
FJ367175.1 gg_id:363148 feces adult twins and mothers; TS28 clone TS28_a04d07 FJ3671
DQ794121.1 gg_id:187979 human fecal clone RL176_aan58c09 DQ794
FJ677399.1 gg_id:513641 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6773
FJ680807.1 gg_id:514436 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6808
FJ678672.1 gg_id:513184 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6786
DQ325805.1 gg_id:149722 Metagenomic gut microbiome healthy human stool clone B526 DQ325
FJ372166.1 gg_id:369577 feces adult twins and mothers; TS9 clone TS9_a02e04 FJ3721
FJ367110.1 gg_id:362343 feces adult twins and mothers; TS28 clone TS28_a03f05 FJ3671
FJ680954.1 gg_id:525656 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6809
FJ677126.1 gg_id:528180 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6771
FJ369848.1 gg_id:364242 feces adult twins and mothers; TS55 clone TS55_a01e03 FJ3698
FJ370300.1 gg_id:363387 feces adult twins and mothers; TS56 clone TS56_a03b04 FJ3703
DQ825190.1 gg_id:190661 human fecal clone RL185_aan86e02 DQ825

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FJ367563.1 gg_id:365091 feces adult twins and mothers; TS2 clone TS2_a01a07 FJ3675
DQ797833.1 gg_id:176515 human fecal clone RL206_aaj16d04 DQ797
FJ673732.1 gg_id:530736 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6737
DQ796920.1 gg_id:184733 human fecal clone RL179_aao56d09 DQ796
EF404253.1 gg_id:207136 human fecal clone SJTU_C_07_11 EF4042
EF071181.1 gg_id:197944 library survey and quantitative measurement major mucosa- IBD human colonic muc EF0711
FJ371801.1 gg_id:370194 feces adult twins and mothers; TS8 clone TS8_a02d02 FJ3718
FJ673783.1 gg_id:516446 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6737
DQ905052.1 gg_id:164808 human fecal clone 2-002-e10 DQ905
EF403326.1 gg_id:204360 human fecal clone SJTU_A1_2_67 EF4033
FJ673815.1 gg_id:528588 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6738
FJ673046.1 gg_id:526346 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6730
DQ796290.1 gg_id:198873 human fecal clone RL179_aah25c10 DQ796
FJ362905.1 gg_id:366390 feces adult twins and mothers; TS13 clone TS13_a04f02 FJ3629
DQ801422.1 gg_id:178266 human fecal clone RL388_aao95c10 DQ801
FJ365496.1 gg_id:357223 feces adult twins and mothers; TS20 clone TS20_a03e10 FJ3654
FJ370818.1 gg_id:364588 feces adult twins and mothers; TS5 clone TS5_a01f04 FJ3708
FJ367962.1 gg_id:358593 feces adult twins and mothers; TS30 clone TS30_a01g09 FJ3679
FJ372239.1 gg_id:362043 feces adult twins and mothers; TS9 clone TS9_a03c11 FJ3722
FJ679571.1 gg_id:515141 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6795
FJ363627.1 gg_id:366946 feces adult twins and mothers; TS14 clone TS14_a01e03 FJ3636
FJ677044.1 gg_id:511855 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6770
DQ802010.1 gg_id:184270 human fecal clone RL241_aaj01g09 DQ802
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DQ797810.1 gg_id:186215 human fecal clone RL206_aaj16b03 DQ797
DQ795974.1 gg_id:198529 human fecal clone RL202_aai49f11 DQ795
FJ363086.1 gg_id:361639 feces adult twins and mothers; TS148 clone TS148_a02g10 FJ3630
FJ678576.1 gg_id:520430 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6785
EU768009.1 gg_id:310054 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C4 EU768
FJ678764.1 gg_id:510485 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6787
EU766847.1 gg_id:337990 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU766
FJ676734.1 gg_id:528844 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6767
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DQ809728.1 gg_id:183171 human fecal clone RL184_aan83c11 DQ809
FJ365578.1 gg_id:367683 feces adult twins and mothers; TS20 clone TS20_a04e06 FJ3655
DQ805660.1 gg_id:192800 human fecal clone RL306aal89e05 DQ805
DQ793292.1 gg_id:187426 human fecal clone RL199_aaj41h01 DQ793

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FJ367544.1 gg_id:363659 feces adult twins and mothers; TS29 clone TS29_a04g10 FJ3675
FJ674048.1 gg_id:516845 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6740
FJ683190.1 gg_id:512718 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6831
DQ325841.1 gg_id:147654 Metagenomic gut microbiome healthy human stool clone B594 DQ325
FJ679786.1 gg_id:518929 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6797
FJ372209.1 gg_id:359305 feces adult twins and mothers; TS9 clone TS9_a03a04 FJ3722
DQ801133.1 gg_id:183347 human fecal clone RL387_aao92g04 DQ801
FJ673763.1 gg_id:526469 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6737
FJ682837.1 gg_id:517363 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6828
EU766860.1 gg_id:316816 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU766
DQ796611.1 gg_id:181620 human fecal clone RL179aan75g10 DQ796
FJ677314.1 gg_id:522498 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6773
DQ456290.1 gg_id:157756 pre-adolescent turkey cecum clone CFT211E12 DQ456
DQ904670.1 gg_id:169786 human fecal clone 001-c8 DQ904
EF402606.1 gg_id:215013 human fecal clone SJTU_B_10_14 EF4026
FJ370336.1 gg_id:368289 feces adult twins and mothers; TS56 clone TS56_a03f05 FJ3703
FJ368299.1 gg_id:364051 feces adult twins and mothers; TS3 clone TS3_a02f05 FJ3682
FJ366958.1 gg_id:358048 feces adult twins and mothers; TS28 clone TS28_a01g07 FJ3669
FJ683641.1 gg_id:524114 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6836
DQ800981.1 gg_id:191715 human fecal clone RL387_aao90c08 DQ800
GQ898224.1 gg_id:589684 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do GQ898
FJ683130.1 gg_id:529709 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6831
FJ679304.1 gg_id:523216 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6793
EU774255.1 gg_id:315391 Chimpanzee feces clone CHIMP1_aaj37h05 EU774
DQ326396.1 gg_id:147155 Metagenomic gut microbiome healthy human stool clone C433 DQ326
FJ372294.1 gg_id:367632 feces adult twins and mothers; TS9 clone TS9_a03h12 FJ3722
EU767087.1 gg_id:327918 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU767
DQ905091.1 gg_id:169975 human fecal clone 2-002-h3 DQ905
FJ678239.1 gg_id:524423 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6782
FJ370406.1 gg_id:366038 feces adult twins and mothers; TS56 clone TS56_a04f04 FJ3704
DQ804705.1 gg_id:192118 human fecal clone RL187_aao71f07 DQ804
EU777395.1 gg_id:314971 Sumatran orangutan feces clone orang2_aai68f02 EU777
DQ824046.1 gg_id:191356 human fecal clone RL204_aaj58f01 DQ824
DQ456182.1 gg_id:157426 pre-adolescent turkey cecum clone CFT29D1 DQ456
AY980880.1 gg_id:127786 human rectum mucosal biopsy clone LQ10 AY980
DQ798620.1 gg_id:175207 human fecal clone RL181_aan99b03 DQ798
EU766848.1 gg_id:320759 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU766
DQ798754.1 gg_id:198057 human fecal clone RL181_aao00h10 DQ798
FJ684971.1 gg_id:529824 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6849
FJ679193.1 gg_id:521326 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6791

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EU762682.1 gg_id:325461 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU762
GQ175486.1 gg_id:588729 Chicken intestinal microbiota modulations various feed supplementations DGGE an GQ175
DQ806469.1 gg_id:191959 human fecal clone RL186_aao45a09 DQ806
DQ801687.1 gg_id:197415 human fecal clone RL201_aai45e06 DQ801
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FJ682094.1 gg_id:528585 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6820
FJ365268.1 gg_id:366317 feces adult twins and mothers; TS1 clone TS1_a04h02 FJ3652
FJ677326.1 gg_id:521282 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6773
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FJ678720.1 gg_id:517184 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6787
FJ673068.1 gg_id:520389 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6730
FJ368316.1 gg_id:364708 feces adult twins and mothers; TS3 clone TS3_a02h02 FJ3683
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FJ676954.1 gg_id:525735 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6769
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FJ363363.1 gg_id:363925 feces adult twins and mothers; TS149 clone TS149_a02d03 FJ3633
FJ365444.1 gg_id:360470 feces adult twins and mothers; TS20 clone TS20_a03a01 FJ3654
FJ673804.1 gg_id:523203 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6738
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DQ794142.1 gg_id:184788 human fecal clone RL176_aan58f02 DQ794
FJ676193.1 gg_id:522012 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6761
FJ371133.1 gg_id:367892 feces adult twins and mothers; TS6 clone TS6_a01d01 FJ3711
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DQ797644.1 gg_id:194905 human fecal clone RL206_aaj14b08 DQ797
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FJ365576.1 gg_id:361467 feces adult twins and mothers; TS20 clone TS20_a04e04 FJ3655
FJ673788.1 gg_id:523374 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6737
FJ370164.1 gg_id:359647 feces adult twins and mothers; TS56 clone TS56_a01b09 FJ3701
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AY981009.1 gg_id:119750 human rectum mucosal biopsy clone V165 AY981
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DQ806386.1 gg_id:199397 human fecal clone RL186_aan91f02 DQ806
AY979366.1 gg_id:119372 human transverse colon mucosal biopsy clone Z711 AY9793
FJ372236.1 gg_id:367540 feces adult twins and mothers; TS9 clone TS9_a03c08 FJ3722
AY976211.1 gg_id:116392 human ascending colon mucosal biopsy clone LW36 AY9762
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DQ801227.1 gg_id:188144 human fecal clone RL116_aaf01h01 DQ801
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FJ370097.1 gg_id:369940 feces adult twins and mothers; TS55 clone TS55_a04d05 FJ3700
FJ673826.1 gg_id:520993 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6738
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FJ673324.1 gg_id:515481 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6733
FJ367239.1 gg_id:368259 feces adult twins and mothers; TS29 clone TS29_a01b10 FJ3672

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DQ904732.1 gg_id:163467 human fecal clone 001B-a10 DQ904
FJ675779.1 gg_id:515438 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6757
FJ365643.1 gg_id:369286 feces adult twins and mothers; TS21 clone TS21_a01c10 FJ3656
DQ796604.1 gg_id:178339 human fecal clone RL179aan75f11 DQ796
DQ797136.1 gg_id:194708 human fecal clone RL386_aao87d10 DQ797
EF400902.1 gg_id:208457 human fecal clone SJTU_D_03_19 EF4009
EF404984.1 gg_id:209911 human fecal clone SJTU_G_05_50 EF4049
FJ683493.1 gg_id:521773 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6834
FJ682763.1 gg_id:522043 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6827
EU763863.1 gg_id:346867 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A5 EU7638
EF405285.1 gg_id:209137 human fecal clone SJTU_G_03_59 EF4052
DQ796999.1 gg_id:192936 human fecal clone RL386_aao85e11 DQ796
DQ793280.1 gg_id:177721 human fecal clone RL199_aaj41f11 DQ793
EF403278.1 gg_id:205028 human fecal clone SJTU_A1_3_53 EF4032
FJ367046.1 gg_id:357836 feces adult twins and mothers; TS28 clone TS28_a02h02 FJ3670
FJ682297.1 gg_id:524726 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6822
EU763421.1 gg_id:337991 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A4 EU7634
FJ683916.1 gg_id:517515 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6839
EF402319.1 gg_id:215061 human fecal clone SJTU_B_06_36 EF4023
DQ806205.1 gg_id:186576 human fecal clone RL186_aah62f05 DQ806
FJ682383.1 gg_id:522784 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6823
FJ363715.1 gg_id:367988 feces adult twins and mothers; TS14 clone TS14_a02d09 FJ3637
EF404396.1 gg_id:209672 human fecal clone SJTU_C_09_42 EF4043
AY976064.1 gg_id:120976 human ascending colon mucosal biopsy clone LU21 AY9760
FJ673310.1 gg_id:516016 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6733
DQ824877.1 gg_id:189055 human fecal clone RL185_aao70d10 DQ824
FJ371414.1 gg_id:363722 feces adult twins and mothers; TS6 clone TS6_a04f09 FJ3714
DQ797226.1 gg_id:177587 human fecal clone RL386_aao88f04 DQ797
FJ673952.1 gg_id:517339 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6739
DQ904701.1 gg_id:169896 human fecal clone 001-f3 DQ904
EF400765.1 gg_id:207334 human fecal clone SJTU_D_01_26 EF4007
DQ797659.1 gg_id:173956 human fecal clone RL206_aaj14c12 DQ797
EF402703.1 gg_id:209510 human fecal clone SJTU_B_11_38 EF4027
FJ677098.1 gg_id:531403 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6770
FJ672949.1 gg_id:509934 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6729
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FJ682721.1 gg_id:530545 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6827
EU765972.1 gg_id:333253 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B4 EU765
DQ455837.1 gg_id:158377 pre-adolescent turkey cecum clone CFT19B6 DQ455
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EF402831.1 gg_id:215016 human fecal clone SJTU_B_13_09 EF4028
DQ801723.1 gg_id:186002 human fecal clone RL201_aai46a09 DQ801
FJ675872.1 gg_id:526506 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6758
FJ683292.1 gg_id:516858 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6832
EU764935.1 gg_id:353272 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2 EU764
DQ905093.1 gg_id:167659 human fecal clone 2-002-h5 DQ905
EU530424.1 gg_id:274738 mucosa adherent and invasive microbes profile adenoma colorectal cancer clone M6 EU530
EU766146.1 gg_id:313430 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU766
EF405024.1 gg_id:206629 human fecal clone SJTU_G_07_03 EF4050
FJ673782.1 gg_id:519219 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6737
FJ676929.1 gg_id:530715 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6769
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EF403393.1 gg_id:211843 human fecal clone SJTU_A1_7_65 EF4033
AY982915.1 gg_id:121762 human descending colon mucosal biopsy clone L106 AY982
EU467322.1 gg_id:301906 chimpanzee feces clone CHIMP1_f05 EU467
DQ809123.1 gg_id:177872 human fecal clone RL308_aal81g11 DQ809
DQ802345.1 gg_id:180178 human fecal clone RL188_aah16d10 DQ802
DQ800008.1 gg_id:179287 human fecal clone RL247_aaj23a08 DQ800
DQ905156.1 gg_id:170981 human fecal clone 002C-f10 DQ905
FJ673481.1 gg_id:515674 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6734
DQ797371.1 gg_id:193574 human fecal clone RL248_aai98e03 DQ797
DQ803312.1 gg_id:190701 human fecal clone RL311_aam23h03 DQ803
FJ363156.1 gg_id:364468 feces adult twins and mothers; TS148 clone TS148_a03g05 FJ3631
FJ366455.1 gg_id:359333 feces adult twins and mothers; TS26 clone TS26_a03e03 FJ3664
DQ798245.1 gg_id:180281 human fecal clone RL181_aah39d09 DQ798
FJ683213.1 gg_id:525431 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6832
FJ683412.1 gg_id:527951 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6834
AY978428.1 gg_id:127100 human transverse colon mucosal biopsy clone KO36 AY978
FJ679905.1 gg_id:529329 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6799
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DQ807554.1 gg_id:198606 human fecal clone RL307_aam08b06 DQ807
DQ804568.1 gg_id:176437 human fecal clone RL187_aao69g06 DQ804
FJ675851.1 gg_id:519831 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6758
DQ801530.1 gg_id:183361 human fecal clone RL388_aao96f11 DQ801

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FJ363601.1 gg_id:366068 feces adult twins and mothers; TS14 clone TS14_a01c01 FJ3636
FJ371005.1 gg_id:359467 feces adult twins and mothers; TS5 clone TS5_a03h01 FJ3710
AY979529.1 gg_id:123479 human transverse colon mucosal biopsy clone M180 AY9795
FJ370804.1 gg_id:366916 feces adult twins and mothers; TS5 clone TS5_a01e02 FJ3708
FJ673658.1 gg_id:515075 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6736
EF399941.1 gg_id:210404 human fecal clone SJTU_E_05_96 EF3999
FJ371804.1 gg_id:365075 feces adult twins and mothers; TS8 clone TS8_a02d05 FJ3718
FJ682112.1 gg_id:525703 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6821
DQ797519.1 gg_id:191286 human fecal clone RL248_aaj00d12 DQ797
FJ364478.1 gg_id:368957 feces adult twins and mothers; TS15 clone TS15_a03d10 FJ3644
DQ794259.1 gg_id:191088 human fecal clone RL176_aan60c06 DQ794
AY978866.1 gg_id:117362 human transverse colon mucosal biopsy clone NE31 AY9788
FJ371736.1 gg_id:363136 feces adult twins and mothers; TS8 clone TS8_a01f05 FJ3717
FJ679943.1 gg_id:523123 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6799
FJ367279.1 gg_id:367728 feces adult twins and mothers; TS29 clone TS29_a01f05 FJ3672
FJ371386.1 gg_id:364979 feces adult twins and mothers; TS6 clone TS6_a04c11 FJ3713
GQ896640.1 gg_id:533914 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do GQ896
FJ364337.1 gg_id:369540 feces adult twins and mothers; TS15 clone TS15_a01g04 FJ3643
FJ368388.1 gg_id:368518 feces adult twins and mothers; TS3 clone TS3_a03g08 FJ3683
FM873463.1 gg_id:365347 occupant source house floor dust clone FD04A09 FM873
DQ796425.1 gg_id:180981 human fecal clone RL179_aah28b06 DQ796
AY977092.1 gg_id:119801 human cecum mucosal biopsy clone K782 AY977
EF403170.1 gg_id:208332 human fecal clone SJTU_A1_1_05 EF4031
DQ325722.1 gg_id:147313 Metagenomic gut microbiome healthy human stool clone B363 DQ325
DQ801372.1 gg_id:187382 human fecal clone RL388_aao94f04 DQ801
DQ800359.1 gg_id:175653 human fecal clone RL303_aal72b02 DQ800
GQ038488.1 gg_id:461772 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu4 GQ038
FJ678822.1 gg_id:528715 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6788
FJ368086.1 gg_id:359840 feces adult twins and mothers; TS30 clone TS30_a03h01 FJ3680
FJ371394.1 gg_id:365787 feces adult twins and mothers; TS6 clone TS6_a04d09 FJ3713
FJ672996.1 gg_id:519087 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6729
FJ680690.1 gg_id:517251 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6806
FJ370369.1 gg_id:357768 feces adult twins and mothers; TS56 clone TS56_a04a09 FJ3703
EF402269.1 gg_id:211130 human fecal clone SJTU_B_05_74 EF4022
FJ364321.1 gg_id:364093 feces adult twins and mothers; TS15 clone TS15_a01e11 FJ3643
FJ367945.1 gg_id:361901 feces adult twins and mothers; TS30 clone TS30_a01e06 FJ3679
DQ796342.1 gg_id:192023 human fecal clone RL179_aah26a05 DQ796
FJ682336.1 gg_id:526850 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6823
EU766815.1 gg_id:342863 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU766

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FJ680071.1 gg_id:524461 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6800
EU761635.1 gg_id:329509 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1 EU761
EF403807.1 gg_id:214604 human fecal clone SJTU_A3_11_28 EF4038
EU774128.1 gg_id:310301 Chimpanzee feces clone CHIMP1_aaj38b03 EU774
FJ683496.1 gg_id:527743 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6834
FJ370925.1 gg_id:361734 feces adult twins and mothers; TS5 clone TS5_a02h04 FJ3709
FJ677019.1 gg_id:517142 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6770
FJ364613.1 gg_id:358324 feces adult twins and mothers; TS19 clone TS19_a01a08 FJ3646
FJ362730.1 gg_id:369611 feces adult twins and mothers; TS13 clone TS13_a02d11 FJ3627
DQ796897.1 gg_id:179291 human fecal clone RL179_aao56b02 DQ796
FJ680023.1 gg_id:522639 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6800
EU761995.1 gg_id:334919 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1 EU761
FJ679977.1 gg_id:517083 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6799
FJ677857.1 gg_id:521195 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6778
FJ681949.1 gg_id:513569 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6819
EF400356.1 gg_id:210432 human fecal clone SJTU_E_12_09 EF4003
EF405201.1 gg_id:217164 human fecal clone SJTU_G_04_21 EF4052
FJ680077.1 gg_id:516044 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6800
AY984867.1 gg_id:127621 human stool clone B841 AY984
EU763157.1 gg_id:309611 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU763
FJ371159.1 gg_id:365400 feces adult twins and mothers; TS6 clone TS6_a01f05 FJ3711
FJ683410.1 gg_id:531453 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6834
DQ794046.1 gg_id:185772 human fecal clone RL176_aan57b11 DQ794
FJ682245.1 gg_id:521193 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6822
FJ673477.1 gg_id:520316 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6734
DQ905741.2 gg_id:164241 human fecal clone 29A-d7 DQ905
FJ372190.1 gg_id:359880 feces adult twins and mothers; TS9 clone TS9_a02g06 FJ3721
FJ685342.1 gg_id:515553 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6853
FJ368347.1 gg_id:366580 feces adult twins and mothers; TS3 clone TS3_a03c08 FJ3683
FJ365095.1 gg_id:368089 feces adult twins and mothers; TS1 clone TS1_a02g06 FJ3650
FJ366277.1 gg_id:358995 feces adult twins and mothers; TS25 clone TS25_a04g06 FJ3662
FJ371104.1 gg_id:365661 feces adult twins and mothers; TS6 clone TS6_a01a03 FJ3711
AY985216.1 gg_id:119095 human stool clone C080 AY985
FJ369891.1 gg_id:359736 feces adult twins and mothers; TS55 clone TS55_a02a02 FJ3698
FJ684085.1 gg_id:517705 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6840
DQ325670.1 gg_id:145519 Metagenomic gut microbiome healthy human stool clone B262 DQ325
EU766758.1 gg_id:322883 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU766
DQ806563.1 gg_id:195758 human fecal clone RL186_aao46b05 DQ806
FJ362646.1 gg_id:365822 feces adult twins and mothers; TS13 clone TS13_a01d12 FJ3626

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FJ370204.1 gg_id:362927 feces adult twins and mothers; TS56 clone TS56_a01g03 FJ3702
DQ802480.1 gg_id:193583 human fecal clone RL188_aah18c11 DQ802
FJ683617.1 gg_id:524643 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6836
FJ678572.1 gg_id:527621 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6785
DQ801657.1 gg_id:178139 human fecal clone RL201_aai45b04 DQ801
FJ673415.1 gg_id:532467 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6734
FJ372244.1 gg_id:366729 feces adult twins and mothers; TS9 clone TS9_a03d04 FJ3722
FJ678365.1 gg_id:528634 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6783
FJ368893.1 gg_id:356750 feces adult twins and mothers; TS4 clone TS4_a01g09 FJ3688
EF405023.1 gg_id:215838 human fecal clone SJTU_G_07_02 EF405
FJ363642.1 gg_id:361321 feces adult twins and mothers; TS14 clone TS14_a01f07 FJ3636
DQ797286.1 gg_id:183033 human fecal clone RL248_aai97d04 DQ797
FJ684341.1 gg_id:508990 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6843
DQ800968.1 gg_id:197811 human fecal clone RL387_aao90a10 DQ800
DQ795769.1 gg_id:191005 human fecal clone RL245_aai82a11 DQ795
FJ684460.1 gg_id:512202 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6844
EU778065.1 gg_id:332745 feces clone RL117_aae93c03 EU778
FJ679157.1 gg_id:525268 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6791
EU761901.1 gg_id:336184 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1 EU761
FJ676393.1 gg_id:520110 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6763
AY985777.1 gg_id:122394 human stool clone D020 AY985
AY978413.1 gg_id:118037 human transverse colon mucosal biopsy clone KO12 AY978
DQ797125.1 gg_id:194262 human fecal clone RL386_aao87c10 DQ797
FJ366217.1 gg_id:364840 feces adult twins and mothers; TS25 clone TS25_a04b02 FJ3662
FJ684396.1 gg_id:531731 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6843
FJ676113.1 gg_id:527838 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6761
DQ800942.1 gg_id:184549 human fecal clone RL387_aao89f11 DQ800
FJ363122.1 gg_id:360347 feces adult twins and mothers; TS148 clone TS148_a03d04 FJ3631
DQ797806.1 gg_id:184609 human fecal clone RL206_aaj16a11 DQ797
FJ368088.1 gg_id:359308 feces adult twins and mothers; TS30 clone TS30_a03h03 FJ3680
FJ364489.1 gg_id:363784 feces adult twins and mothers; TS15 clone TS15_a03e10 FJ3644
AY982071.1 gg_id:127146 human sigmoid colon mucosal biopsy clone P522 AY982
FJ680054.1 gg_id:519260 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6800
FJ678075.1 gg_id:529865 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6780
FJ371741.1 gg_id:370050 feces adult twins and mothers; TS8 clone TS8_a01f10 FJ3717
AY977065.1 gg_id:124585 human cecum mucosal biopsy clone K753 AY977
EU764123.1 gg_id:312088 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A5 EU764
FJ371415.1 gg_id:365951 feces adult twins and mothers; TS6 clone TS6_a04f10 FJ3714

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EF071157.1 gg_id:199708 library survey and quantitative measurement major mucosa- IBD human colonic muc EF0711
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FJ362639.1 gg_id:368154 feces adult twins and mothers; TS13 clone TS13_a01d04 FJ3626
FJ679858.1 gg_id:527207 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6798
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FJ683435.1 gg_id:529645 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6834
FJ675792.1 gg_id:518214 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6757
EU767181.1 gg_id:305562 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C2 EU767
FJ372286.1 gg_id:359224 feces adult twins and mothers; TS9 clone TS9_a03h02 FJ3722
EF402118.1 gg_id:204479 human fecal clone SJTU_B_03_85 EF4021
FJ685348.1 gg_id:529021 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6853
DQ326221.1 gg_id:150345 Metagenomic gut microbiome healthy human stool clone C143 DQ326
FJ366949.1 gg_id:368858 feces adult twins and mothers; TS28 clone TS28_a01f10 FJ3669
DQ325799.1 gg_id:150495 Metagenomic gut microbiome healthy human stool clone B514 DQ325
DQ798719.1 gg_id:198812 human fecal clone RL181_aao00e05 DQ798
AY978564.1 gg_id:116677 human transverse colon mucosal biopsy clone KR30 AY978
FJ678164.1 gg_id:520304 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6781
FJ370309.1 gg_id:365868 feces adult twins and mothers; TS56 clone TS56_a03c05 FJ3703
EF405227.1 gg_id:212715 human fecal clone SJTU_G_04_56 EF4052
FJ678642.1 gg_id:516541 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6786
FJ683970.1 gg_id:516455 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6839
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GQ898076.1 gg_id:543631 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ898
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FJ371649.1 gg_id:370248 feces adult twins and mothers; TS7 clone TS7_a04f04 FJ3716
DQ808981.1 gg_id:180285 human fecal clone RL243_aai87g06 DQ808
GQ898670.1 gg_id:564850 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do GQ898
FJ680944.1 gg_id:527158 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6809
DQ798679.1 gg_id:180255 human fecal clone RL181_aao00a05 DQ798
FJ673821.1 gg_id:517670 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6738
DQ798530.1 gg_id:189377 human fecal clone RL181_aan97h03 DQ798
EF402819.1 gg_id:212119 human fecal clone SJTU_B_12_91 EF4028
DQ799487.1 gg_id:186154 human fecal clone RL305aal86h04 DQ799

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FJ682451.1 gg_id:526673 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6824
FJ673483.1 gg_id:527767 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6734
FJ362814.1 gg_id:364795 feces adult twins and mothers; TS13 clone TS13_a03e05 FJ3628
FJ372156.1 gg_id:359874 feces adult twins and mothers; TS9 clone TS9_a02d04 FJ3721
DQ326201.1 gg_id:145226 Metagenomic gut microbiome healthy human stool clone C116 DQ326
FJ680188.1 gg_id:528166 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6801
DQ804764.1 gg_id:181116 human fecal clone RL187_aao72d08 DQ804
FJ369823.1 gg_id:364058 feces adult twins and mothers; TS55 clone TS55_a01c02 FJ3698
FJ684742.1 gg_id:520441 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6847
FJ370273.1 gg_id:362326 feces adult twins and mothers; TS56 clone TS56_a02f11 FJ3702
EU765118.1 gg_id:309167 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2 EU765
FJ362692.1 gg_id:366820 feces adult twins and mothers; TS13 clone TS13_a02a04 FJ3626
FJ367260.1 gg_id:369708 feces adult twins and mothers; TS29 clone TS29_a01d10 FJ3672
FJ363053.1 gg_id:370232 feces adult twins and mothers; TS148 clone TS148_a02d07 FJ3630
FJ371283.1 gg_id:360702 feces adult twins and mothers; TS6 clone TS6_a03b05 FJ3712
FJ365677.1 gg_id:367205 feces adult twins and mothers; TS21 clone TS21_a01g01 FJ3656
DQ799510.1 gg_id:186884 human fecal clone RL305aal87b07 DQ799
GQ175373.1 gg_id:584966 Chicken intestinal microbiota modulations various feed supplementations DGGE anc GQ175
EF402512.1 gg_id:203664 human fecal clone SJTU_B_08_92 EF4025
FJ673240.1 gg_id:516744 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6732
FJ371180.1 gg_id:365540 feces adult twins and mothers; TS6 clone TS6_a01h03 FJ3711
FJ683865.1 gg_id:523118 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6838
EF401959.1 gg_id:212271 human fecal clone SJTU_B_01_85 EF4019
FJ673944.1 gg_id:523733 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6739
FJ364604.1 gg_id:365932 feces adult twins and mothers; TS15 clone TS15_a04h10 FJ3646
AY983235.1 gg_id:122065 human descending colon mucosal biopsy clone A192 AY983
DQ804507.1 gg_id:186014 human fecal clone RL187_aao69a03 DQ804
DQ808734.1 gg_id:199447 human fecal clone RL239_aaj12e07 DQ808
FJ680784.1 gg_id:530524 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6807
FJ679029.1 gg_id:513799 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6790
DQ808691.1 gg_id:190119 human fecal clone RL239_aaj11h08 DQ808
FJ367381.1 gg_id:365214 feces adult twins and mothers; TS29 clone TS29_a02g09 FJ3673
EF402416.1 gg_id:206779 human fecal clone SJTU_B_07_64 EF4024
FJ371107.1 gg_id:364493 feces adult twins and mothers; TS6 clone TS6_a01a08 FJ3711
DQ802576.1 gg_id:188600 human fecal clone RL188_aan93f02 DQ802
FJ679591.1 gg_id:522278 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6795
FJ679377.1 gg_id:516690 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6793
DQ825338.1 gg_id:192202 human fecal clone RL185_aan88g06 DQ825
EF400945.1 gg_id:208336 human fecal clone SJTU_D_03_77 EF4009

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FJ673301.1 gg_id:525513 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6733
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DQ798521.1 gg_id:192503 human fecal clone RL181_aan97g05 DQ798
GQ897282.1 gg_id:558123 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ897
EF402700.1 gg_id:214090 human fecal clone SJTU_B_11_34 EF4027
DQ825176.1 gg_id:178234 human fecal clone RL185_aan86c10 DQ825
DQ801178.1 gg_id:188051 human fecal clone RL116_aaf00a03 DQ801
FJ370149.1 gg_id:360416 feces adult twins and mothers; TS56 clone TS56_a01a04 FJ3701
FJ367847.1 gg_id:364381 feces adult twins and mothers; TS2 clone TS2_a04c07 FJ3678
DQ469229.1 gg_id:158909 Microbial and ecology water Zhong Tiaoshan mine Shanxi province China AMD clone DQ469
FJ683359.1 gg_id:523960 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6833
EF403721.1 gg_id:212755 human fecal clone SJTU_A2_05_86 EF4037
DQ797650.1 gg_id:192042 human fecal clone RL206_aaj14c03 DQ797
DQ798554.1 gg_id:194392 human fecal clone RL181_aan98b11 DQ798
FJ367121.1 gg_id:360386 feces adult twins and mothers; TS28 clone TS28_a03g04 FJ3671
EU766034.1 gg_id:352547 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B4 EU766
EU778232.1 gg_id:308969 feces clone RL388_aao95a03 EU778
FJ365927.1 gg_id:366110 feces adult twins and mothers; TS21 clone TS21_a04g04 FJ3659
DQ796459.1 gg_id:188277 human fecal clone RL179_aah28f11 DQ796
FJ362745.1 gg_id:369094 feces adult twins and mothers; TS13 clone TS13_a02f05 FJ3627
FJ371672.1 gg_id:358662 feces adult twins and mothers; TS7 clone TS7_a04h10 FJ3716
FJ675980.1 gg_id:511246 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6759
EU766901.1 gg_id:306887 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU766
DQ823998.1 gg_id:184400 human fecal clone RL204_aaj57h10 DQ823
FJ370290.1 gg_id:362757 feces adult twins and mothers; TS56 clone TS56_a03a01 FJ3702
FJ681145.1 gg_id:530484 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6811
EF400967.1 gg_id:204553 human fecal clone SJTU_D_04_90 EF4009
EU764451.1 gg_id:323792 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1 EU764
FJ675800.1 gg_id:531629 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6758
FJ682966.1 gg_id:522398 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6829
FJ369910.1 gg_id:359256 feces adult twins and mothers; TS55 clone TS55_a02b11 FJ3699
DQ905116.1 gg_id:161788 human fecal clone 002C-b5 DQ905
DQ793377.1 gg_id:197159 human fecal clone RL199_aaj43a01 DQ793
EU766025.1 gg_id:304228 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B4 EU766
FJ673225.1 gg_id:521732 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6732
FJ682288.1 gg_id:519606 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6822
FJ673158.1 gg_id:522957 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6731
FJ682107.1 gg_id:516615 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6821
FJ370322.1 gg_id:367382 feces adult twins and mothers; TS56 clone TS56_a03e02 FJ3703

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FJ682406.1 gg_id:531662 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6824
DQ798507.1 gg_id:183096 human fecal clone RL181_aan97e12 DQ798
FJ677575.1 gg_id:515083 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6775
AY983422.1 gg_id:123823 human descending colon mucosal biopsy clone NK14 AY983
FJ683598.1 gg_id:522106 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6835
DQ798678.1 gg_id:198469 human fecal clone RL181_aao00a04 DQ798
EF402454.1 gg_id:203687 human fecal clone SJTU_B_08_14 EF4024
FJ683257.1 gg_id:528148 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6832
AY981461.1 gg_id:118731 human sigmoid colon mucosal biopsy clone L558 AY981
EU767939.1 gg_id:341514 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C EU767
FJ362628.1 gg_id:367786 feces adult twins and mothers; TS13 clone TS13_a01c05 FJ3626
FJ673672.1 gg_id:524310 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6736
EU767080.1 gg_id:340311 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU767
FJ368434.1 gg_id:359625 feces adult twins and mothers; TS3 clone TS3_a04c09 FJ3684
FJ364880.1 gg_id:365919 feces adult twins and mothers; TS19 clone TS19_a04c05 FJ3648
FJ367215.1 gg_id:366962 feces adult twins and mothers; TS28 clone TS28_a04h05 FJ3672
FJ678145.1 gg_id:518849 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6781
DQ799361.1 gg_id:186348 human fecal clone RL305aal85d03 DQ799
FJ683668.1 gg_id:520472 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6836
FJ364280.1 gg_id:364565 feces adult twins and mothers; TS15 clone TS15_a01a12 FJ3642
FJ366929.1 gg_id:361813 feces adult twins and mothers; TS28 clone TS28_a01e02 FJ3669
FJ363897.1 gg_id:366974 feces adult twins and mothers; TS14 clone TS14_a04f07 FJ3638
FJ367152.1 gg_id:364498 feces adult twins and mothers; TS28 clone TS28_a04b04 FJ3671
GQ492964.1 gg_id:591625 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
DQ797761.1 gg_id:184060 human fecal clone RL206_aaj15e10 DQ797
FJ679711.1 gg_id:530337 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6797
FJ676397.1 gg_id:526989 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6763
FJ673113.1 gg_id:512268 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6731
DQ801294.1 gg_id:176684 human fecal clone RL388_aao93e09 DQ801
EF399852.1 gg_id:206460 human fecal clone SJTU_E_04_61 EF3998
FJ371178.1 gg_id:362345 feces adult twins and mothers; TS6 clone TS6_a01h01 FJ3711
GQ448356.1 gg_id:580587 Microbiome neonatal calves: shedding microorganisms fecal clone calf783_2wks_gr GQ448
FJ676463.1 gg_id:521552 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6764
FJ677694.1 gg_id:513781 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6776
FJ681996.1 gg_id:516655 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6819
FJ368879.1 gg_id:366263 feces adult twins and mothers; TS4 clone TS4_a01f06 FJ3688
EF401378.1 gg_id:210066 human fecal clone SJTU_D_09_55 EF4013
DQ805727.1 gg_id:184345 human fecal clone RL306aal90c11 DQ805
DQ796525.1 gg_id:197708 human fecal clone RL179aan74b04 DQ796
DQ809575.1 gg_id:194381 human fecal clone RL184_aan81a10 DQ809

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FJ367002.1 gg_id:367845 feces adult twins and mothers; TS28 clone TS28_a02c09 FJ3670
AY983882.1 gg_id:121178 human descending colon mucosal biopsy clone MA45 AY9838
DQ797931.1 gg_id:190417 human fecal clone RL302_aal93e09 DQ797
DQ797343.1 gg_id:183574 human fecal clone RL248_aai98b05 DQ797
FJ364420.1 gg_id:361296 feces adult twins and mothers; TS15 clone TS15_a02g03 FJ3644
FJ371744.1 gg_id:370012 feces adult twins and mothers; TS8 clone TS8_a01g01 FJ3717
GQ898023.1 gg_id:593129 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ898
DQ798241.1 gg_id:187941 human fecal clone RL181_aah39d04 DQ798
DQ824074.1 gg_id:193147 human fecal clone RL204_aaj59a06 DQ824
FJ677745.1 gg_id:519105 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6777
EU767143.1 gg_id:354400 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU767
EF399615.1 gg_id:204783 human fecal clone SJTU_E_01_19 EF3996
DQ797984.1 gg_id:173930 human fecal clone RL302_aal94b07 DQ797
FJ367273.1 gg_id:367414 feces adult twins and mothers; TS29 clone TS29_a01e11 FJ3672
DQ801207.1 gg_id:176772 human fecal clone RL116_aaf01b03 DQ801
FJ680161.1 gg_id:509641 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6801
EU467468.1 gg_id:292663 Sumatran orangutan feces clone orang1_b07_1 EU467
EF404759.1 gg_id:207172 human fecal clone SJTU_C_16_02 EF4047
AY978993.1 gg_id:117865 human transverse colon mucosal biopsy clone NI25 AY9789
FJ371951.1 gg_id:365814 feces adult twins and mothers; TS8 clone TS8_a04a11 FJ3719
EU765841.1 gg_id:311856 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B4 EU7658
AY984598.1 gg_id:117840 human stool clone B538 AY9845
DQ823889.1 gg_id:197321 human fecal clone RL250_aaj80e04 DQ823
DQ805135.1 gg_id:176841 human fecal clone RL249_aaj81g07 DQ805
EF402826.1 gg_id:213151 human fecal clone SJTU_B_13_04 EF4028
DQ794060.1 gg_id:181139 human fecal clone RL176_aan57d12 DQ794
FJ363917.1 gg_id:361782 feces adult twins and mothers; TS14 clone TS14_a04h05 FJ3639
EU764825.1 gg_id:304968 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2 EU7648
FJ674170.1 gg_id:517053 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6741
FJ681616.1 gg_id:514621 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6816
DQ806320.1 gg_id:175470 human fecal clone RL186_aan90e10 DQ806
FJ672977.1 gg_id:514264 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6729
DQ806282.1 gg_id:192267 human fecal clone RL186_aan89g11 DQ806
EU766845.1 gg_id:308323 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU7668
GQ897146.1 gg_id:579284 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ897
FJ677737.1 gg_id:514226 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6777
FJ365873.1 gg_id:365362 feces adult twins and mothers; TS21 clone TS21_a04a11 FJ3658
DQ905134.1 gg_id:166310 human fecal clone 002C-d11 DQ905
DQ824337.1 gg_id:198459 human fecal clone RL304_aal74f10 DQ824

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DQ805302.1 gg_id:181045 human fecal clone RL249_aaj84g09 DQ805
EU765096.1 gg_id:329822 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2 EU765
FJ371751.1 gg_id:356933 feces adult twins and mothers; TS8 clone TS8_a01g08 FJ3717
FJ371913.1 gg_id:365185 feces adult twins and mothers; TS8 clone TS8_a03f06 FJ3719
FJ673425.1 gg_id:531791 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6734
FJ673914.1 gg_id:522500 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6739
FJ365029.1 gg_id:364449 feces adult twins and mothers; TS1 clone TS1_a02a05 FJ3650
FJ365142.1 gg_id:358772 feces adult twins and mothers; TS1 clone TS1_a03d05 FJ3651
FJ362744.1 gg_id:365960 feces adult twins and mothers; TS13 clone TS13_a02f04 FJ3627
FJ683387.1 gg_id:517313 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6833
EU764113.1 gg_id:341093 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A5 EU764
DQ797772.1 gg_id:187746 human fecal clone RL206_aaj15f09 DQ797
DQ797534.1 gg_id:183136 human fecal clone RL248_aaj00f10 DQ797
EU764195.1 gg_id:348580 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A5 EU764
FJ673014.1 gg_id:511426 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6730
EU761607.1 gg_id:348796 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1 EU761
FJ677915.1 gg_id:529462 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6779
EF405259.1 gg_id:208204 human fecal clone SJTU_G_03_12 EF4052
FJ676446.1 gg_id:530143 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6764
DQ796680.1 gg_id:196638 human fecal clone RL179_aao53b02 DQ796
DQ801683.1 gg_id:178701 human fecal clone RL201_aai45d10 DQ801
DQ806770.1 gg_id:181056 human fecal clone RL186_aao48e04 DQ806
DQ808834.1 gg_id:192290 human fecal clone RL243_aai85h09 DQ808
AY976679.1 gg_id:116489 human cecum mucosal biopsy clone K250 AY976
GQ175391.1 gg_id:558789 Chicken intestinal microbiota modulations various feed supplementations DGGE anc GQ175
FJ674228.1 gg_id:516246 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6742
DQ801519.1 gg_id:199423 human fecal clone RL388_aao96e10 DQ801
DQ809610.1 gg_id:180497 human fecal clone RL184_aan81e09 DQ809
DQ801990.1 gg_id:193716 human fecal clone RL241_aaj01e07 DQ801
FJ366675.1 gg_id:367013 feces adult twins and mothers; TS27 clone TS27_a02e04 FJ3666
FJ372098.1 gg_id:363190 feces adult twins and mothers; TS9 clone TS9_a01g03 FJ3720
FJ369985.1 gg_id:363252 feces adult twins and mothers; TS55 clone TS55_a03b04 FJ3699
EU766632.1 gg_id:355409 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU766
DQ798390.1 gg_id:179266 human fecal clone RL181_aah41h08 DQ798
FJ367658.1 gg_id:361552 feces adult twins and mothers; TS2 clone TS2_a02a10 FJ3676
FJ682429.1 gg_id:519971 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6824
DQ797383.1 gg_id:198948 human fecal clone RL248_aai98f08 DQ797
EU765795.1 gg_id:347325 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B4 EU765
DQ801446.1 gg_id:197808 human fecal clone RL388_aao95f06 DQ801

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AY984022.1 gg_id:126113 human descending colon mucosal biopsy clone MD70 AY984(
GQ896716.1 gg_id:542108 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do : GQ896
FJ678508.1 gg_id:520211 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6785
FJ676564.1 gg_id:528965 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6765
DQ794660.1 gg_id:192639 human fecal clone RL240_aaj30g09 DQ794
DQ796603.1 gg_id:180806 human fecal clone RL179aan75f08 DQ796
GQ898587.1 gg_id:581146 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ898
FJ367324.1 gg_id:367882 feces adult twins and mothers; TS29 clone TS29_a02b08 FJ3673
EU530324.1 gg_id:266565 mucosa adherent and invasive microbes profile adenoma colorectal cancer clone M4 EU5303
DQ797997.1 gg_id:183690 human fecal clone RL302_aal94c12 DQ797
FJ365543.1 gg_id:357034 feces adult twins and mothers; TS20 clone TS20_a04b04 FJ3655
FJ682343.1 gg_id:532151 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6823
FJ369100.1 gg_id:368378 feces adult twins and mothers; TS4 clone TS4_a04c02 FJ3691
DQ800205.1 gg_id:193761 human fecal clone RL303_aal69f05 DQ800
EF404910.1 gg_id:212246 human fecal clone SJTU_G_08_82 EF4049
DQ823816.1 gg_id:183130 human fecal clone RL250_aaj79e01 DQ823
DQ825130.1 gg_id:179990 human fecal clone RL185_aan85g01 DQ825
FJ673886.1 gg_id:529617 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6738
DQ798665.1 gg_id:199278 human fecal clone RL181_aan99g06 DQ798
FJ371302.1 gg_id:361142 feces adult twins and mothers; TS6 clone TS6_a03d05 FJ3713
EU762609.1 gg_id:331713 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A› EU762(
AY981634.1 gg_id:120836 human sigmoid colon mucosal biopsy clone L882 AY9816
FJ685245.1 gg_id:520987 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6852
DQ796422.1 gg_id:199691 human fecal clone RL179_aah28b03 DQ796
EU762758.1 gg_id:309246 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A› EU762
FJ683417.1 gg_id:522721 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6834
FJ677548.1 gg_id:512140 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6775
FJ677427.1 gg_id:522865 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6774
DQ798435.1 gg_id:177901 human fecal clone RL181_aah42f03 DQ798
DQ808929.1 gg_id:194039 human fecal clone RL243_aai87b03 DQ808
FJ370405.1 gg_id:366787 feces adult twins and mothers; TS56 clone TS56_a04f03 FJ3704
FJ674086.1 gg_id:518723 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6740
AY980789.1 gg_id:115448 human rectum mucosal biopsy clone LN96 AY9807
DQ905151.1 gg_id:165073 human fecal clone 002C-e4 DQ905
FJ363345.1 gg_id:362865 feces adult twins and mothers; TS149 clone TS149_a02b06 FJ3633
DQ793304.1 gg_id:189470 human fecal clone RL199_aaj42a04 DQ793
DQ798518.1 gg_id:182532 human fecal clone RL181_aan97g01 DQ798
FJ371667.1 gg_id:364017 feces adult twins and mothers; TS7 clone TS7_a04h05 FJ3716
DQ805129.1 gg_id:198350 human fecal clone RL249_aaj81f06 DQ805
DQ799479.1 gg_id:178024 human fecal clone RL305aal86g06 DQ799
DQ801480.1 gg_id:194565 human fecal clone RL388_aao96b02 DQ801

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GQ896629.1 gg_id:586659 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do : GQ896
DQ809292.1 gg_id:183138 human fecal clone RL308_aal84g06 DQ809
FJ681165.1 gg_id:522292 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6811
FJ364574.1 gg_id:368806 feces adult twins and mothers; TS15 clone TS15_a04e10 FJ3645
FJ371121.1 gg_id:361332 feces adult twins and mothers; TS6 clone TS6_a01b10 FJ3711
FJ366966.1 gg_id:367186 feces adult twins and mothers; TS28 clone TS28_a01h04 FJ3669
FJ365772.1 gg_id:364220 feces adult twins and mothers; TS21 clone TS21_a02g10 FJ3657
FJ371239.1 gg_id:360105 feces adult twins and mothers; TS6 clone TS6_a02f01 FJ3712
EF401978.1 gg_id:213059 human fecal clone SJTU_B_02_07 EF4019
FJ370385.1 gg_id:361908 feces adult twins and mothers; TS56 clone TS56_a04c07 FJ3703
FJ371972.1 gg_id:359377 feces adult twins and mothers; TS8 clone TS8_a04c09 FJ3719
FJ682937.1 gg_id:524620 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6829
DQ804722.1 gg_id:177290 human fecal clone RL187_aao71h01 DQ804
FJ674211.1 gg_id:521267 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6742
FJ674262.1 gg_id:509902 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6742
FJ366994.1 gg_id:365372 feces adult twins and mothers; TS28 clone TS28_a02c01 FJ3669
DQ797057.1 gg_id:199702 human fecal clone RL386_aao86d06 DQ797
EF401918.1 gg_id:211569 human fecal clone SJTU_B_01_36 EF4019
FJ677730.1 gg_id:529525 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6777
FJ682261.1 gg_id:515263 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6822
FJ676043.1 gg_id:523341 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6760
FJ684204.1 gg_id:528631 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6842
FJ372174.1 gg_id:364920 feces adult twins and mothers; TS9 clone TS9_a02f01 FJ3721
EU763635.1 gg_id:346744 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A4 EU763
FJ678787.1 gg_id:518372 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6787
FJ370357.1 gg_id:369735 feces adult twins and mothers; TS56 clone TS56_a03h06 FJ3703
DQ801136.1 gg_id:176406 human fecal clone RL387_aao92g07 DQ801
EF403779.1 gg_id:211449 human fecal clone SJTU_A2_01_87 EF4037
FJ684659.1 gg_id:522195 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6846
FJ673761.1 gg_id:523868 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6737
FJ673351.1 gg_id:528895 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6733
FJ677040.1 gg_id:524573 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6770
DQ326036.1 gg_id:145325 Metagenomic gut microbiome healthy human stool clone B995 DQ326
EU763234.1 gg_id:308821 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU763
DQ823731.1 gg_id:186747 human fecal clone RL250_aaj78c08 DQ823
FJ673135.1 gg_id:524901 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6731
AY984095.1 gg_id:125128 human descending colon mucosal biopsy clone MF44 AY984
FJ681597.1 gg_id:524607 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6815
FJ673131.1 gg_id:524709 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6731
GQ175392.1 gg_id:513594 Chicken intestinal microbiota modulations various feed supplementations DGGE anc GQ175
FJ677929.1 gg_id:514388 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6779

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EU763835.1 gg_id:336251 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A5 EU763
DQ808548.1 gg_id:182564 human fecal clone RL239_aaj10a05 DQ808
FJ673880.1 gg_id:509345 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6738
FJ372054.1 gg_id:367381 feces adult twins and mothers; TS9 clone TS9_a01c04 FJ3720
EF403391.1 gg_id:205407 human fecal clone SJTU_A1_7_63 EF4033
EU762875.1 gg_id:339857 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU762
DQ823947.1 gg_id:188746 human fecal clone RL204_aaj57c11 DQ823
FJ676061.1 gg_id:514351 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6760
EF399739.1 gg_id:206680 human fecal clone SJTU_E_02_77 EF3997
FJ683906.1 gg_id:531564 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6839
FM872976.1 gg_id:368070 occupant source house floor dust clone FB02D07 FM872
AY977987.1 gg_id:124878 human cecum mucosal biopsy clone LH20 AY977
DQ809400.1 gg_id:195007 human fecal clone RL184_aah20d03 DQ809
FJ673167.1 gg_id:526881 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6731
FJ681199.1 gg_id:530877 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6811
FJ673280.1 gg_id:530737 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6732
FJ371430.1 gg_id:362768 feces adult twins and mothers; TS6 clone TS6_a04h04 FJ3714
FJ363908.1 gg_id:367938 feces adult twins and mothers; TS14 clone TS14_a04g06 FJ3639
FJ364309.1 gg_id:364689 feces adult twins and mothers; TS15 clone TS15_a01d10 FJ3643
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FJ368050.1 gg_id:363378 feces adult twins and mothers; TS30 clone TS30_a03d03 FJ3680
FJ364919.1 gg_id:356959 feces adult twins and mothers; TS19 clone TS19_a04g04 FJ3649
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DQ797572.1 gg_id:193525 human fecal clone RL206_aaj13b11 DQ797
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DQ798824.1 gg_id:191107 human fecal clone RL242_aaj97g11 DQ798
EU767214.1 gg_id:346411 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C2 EU767
DQ801929.1 gg_id:189446 human fecal clone RL201_aai48f03 DQ801
FJ364480.1 gg_id:363456 feces adult twins and mothers; TS15 clone TS15_a03e01 FJ3644
DQ797715.1 gg_id:192366 human fecal clone RL206_aaj15a03 DQ797
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FJ363596.1 gg_id:363155 feces adult twins and mothers; TS14 clone TS14_a01b08 FJ3635
FJ678584.1 gg_id:517247 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6785
FJ364312.1 gg_id:367840 feces adult twins and mothers; TS15 clone TS15_a01e02 FJ3643
AY980741.1 gg_id:127355 human rectum mucosal biopsy clone LN11 AY980
DQ825253.1 gg_id:181977 human fecal clone RL185_aan87d01 DQ825
DQ904946.1 gg_id:168940 human fecal clone 002-c5 DQ904
EU767293.1 gg_id:318264 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C2 EU767
DQ795812.1 gg_id:185120 human fecal clone RL245_aai82g07 DQ795

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EU763991.1 gg_id:347489 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A5 EU7639
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FJ368449.1 gg_id:366410 feces adult twins and mothers; TS3 clone TS3_a04e04 FJ3684
FJ676057.1 gg_id:522987 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6760
FJ368948.1 gg_id:358414 feces adult twins and mothers; TS4 clone TS4_a02d11 FJ3689
DQ904681.1 gg_id:167675 human fecal clone 001-d7 DQ904
FJ367435.1 gg_id:369311 feces adult twins and mothers; TS29 clone TS29_a03e05 FJ3674
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FJ683437.1 gg_id:522024 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6834
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FJ371863.1 gg_id:364576 feces adult twins and mothers; TS8 clone TS8_a03b01 FJ3718
DQ794141.1 gg_id:184017 human fecal clone RL176_aan58f01 DQ794
DQ797385.1 gg_id:177118 human fecal clone RL248_aai98f10 DQ797
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DQ905305.1 gg_id:173589 human fecal clone 013B-C3 DQ905
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AY977661.1 gg_id:115899 human cecum mucosal biopsy clone LD13 AY977
EU766645.1 gg_id:324915 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU766
EU768539.1 gg_id:312962 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C5 EU7685
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FJ679695.1 gg_id:520078 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6796
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FJ370175.1 gg_id:360481 feces adult twins and mothers; TS56 clone TS56_a01d01 FJ3701
FJ673279.1 gg_id:509946 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6732
FJ673248.1 gg_id:515026 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6732
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FJ368153.1 gg_id:360870 feces adult twins and mothers; TS30 clone TS30_a04h03 FJ3681
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FJ370921.1 gg_id:357718 feces adult twins and mothers; TS5 clone TS5_a02g11 FJ3709
FJ673101.1 gg_id:522788 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6731

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FJ368033.1 gg_id:365896 feces adult twins and mothers; TS30 clone TS30_a03a05 FJ3680
DQ801157.1 gg_id:183243 human fecal clone RL116_aae99c08 DQ801
FJ679875.1 gg_id:523155 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6798
FJ673177.1 gg_id:532034 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6731
EU768423.1 gg_id:312477 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C5 EU768
DQ326327.1 gg_id:149193 Metagenomic gut microbiome healthy human stool clone C315 DQ326
EU764558.1 gg_id:355240 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1 EU764
FJ370347.1 gg_id:358643 feces adult twins and mothers; TS56 clone TS56_a03g05 FJ3703
EU778247.1 gg_id:349382 feces clone RL387_aao92c08 EU778
FJ682228.1 gg_id:522028 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6822
FJ679783.1 gg_id:514644 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6797
FJ363269.1 gg_id:361887 feces adult twins and mothers; TS149 clone TS149_a01c06 FJ3632
DQ801692.1 gg_id:177072 human fecal clone RL201_aai45e11 DQ801
EF402548.1 gg_id:208161 human fecal clone SJTU_B_09_39 EF4025
DQ798083.1 gg_id:178796 human fecal clone RL302_aal95c11 DQ798
FJ680412.1 gg_id:520169 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6804
EU530340.1 gg_id:268093 mucosa adherent and invasive microbes profile adenoma colorectal cancer clone M4 EU530
EF404586.1 gg_id:212232 human fecal clone SJTU_C_13_14 EF4045
DQ796742.1 gg_id:181648 human fecal clone RL179_aao53h05 DQ796
FJ674232.1 gg_id:518469 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6742
FJ672979.1 gg_id:510804 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6729
AJ408966.1 gg_id:35563 human colonic clone HuCA11 AJ4089
FJ679091.1 gg_id:523363 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6790
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FJ674197.1 gg_id:519966 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6741
FJ682603.1 gg_id:517546 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6826
EU530466.1 gg_id:264386 mucosa adherent and invasive microbes profile adenoma colorectal cancer clone M7 EU530
FJ683111.1 gg_id:530863 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6831
EF404843.1 gg_id:214451 human fecal clone SJTU_G_09_17 EF4048
AY979427.1 gg_id:121148 human transverse colon mucosal biopsy clone M032 AY979
AY976159.1 gg_id:115926 human ascending colon mucosal biopsy clone LV59 AY976
EU762974.1 gg_id:334009 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU762
FJ672910.1 gg_id:525713 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6729
FJ682002.1 gg_id:530882 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6820
EU530352.1 gg_id:262491 mucosa adherent and invasive microbes profile adenoma colorectal cancer clone M4 EU530
FJ683338.1 gg_id:512733 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6833
FJ683940.1 gg_id:516959 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6839
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DQ797655.1 gg_id:189836 human fecal clone RL206_aaj14c08 DQ797

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AY977950.1 gg_id:118536 human cecum mucosal biopsy clone LG70 AY977
FJ673387.1 gg_id:524753 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6733
FJ371184.1 gg_id:369649 feces adult twins and mothers; TS6 clone TS6_a01h07 FJ3711
FJ370915.1 gg_id:366041 feces adult twins and mothers; TS5 clone TS5_a02g05 FJ3709
AY979470.1 gg_id:122222 human transverse colon mucosal biopsy clone M092 AY979
FJ679979.1 gg_id:515455 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6799
GQ047267.1 gg_id:403182 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1010g GQ047
FJ674186.1 gg_id:521986 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6741
DQ799695.1 gg_id:174015 human fecal clone RL182_aah31f02 DQ799
GQ106316.1 gg_id:380987 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw GQ106
FJ368141.1 gg_id:357932 feces adult twins and mothers; TS30 clone TS30_a04f07 FJ3681
EF071238.1 gg_id:183485 library survey and quantitative measurement major mucosa- IBD human colonic muc EF0712
GQ175442.1 gg_id:582425 Chicken intestinal microbiota modulations various feed supplementations DGGE anc GQ175
FJ676411.1 gg_id:527284 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6764
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FJ364308.1 gg_id:362640 feces adult twins and mothers; TS15 clone TS15_a01d09 FJ3643
DQ904672.1 gg_id:168550 human fecal clone 001-d10 DQ904
FJ367413.1 gg_id:368212 feces adult twins and mothers; TS29 clone TS29_a03c03 FJ3674
FJ682295.1 gg_id:529230 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6822
AY984418.1 gg_id:125596 human stool clone B328 AY984
FJ677882.1 gg_id:522565 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6778
EU768686.1 gg_id:325407 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C5 EU768
FJ672989.1 gg_id:530262 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6729
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DQ824866.1 gg_id:182546 human fecal clone RL185_aao70c04 DQ824
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FJ362604.1 gg_id:359991 feces adult twins and mothers; TS13 clone TS13_a01a04 FJ3626
DQ824923.1 gg_id:187440 human fecal clone RL185_aao71a08 DQ824
DQ798715.1 gg_id:188471 human fecal clone RL181_aao00e01 DQ798
DQ806296.1 gg_id:191926 human fecal clone RL186_aan90a08 DQ806
FJ682262.1 gg_id:519476 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6822
FJ679434.1 gg_id:520774 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6794
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DQ798741.1 gg_id:174949 human fecal clone RL181_aao00g06 DQ798

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EU776790.1 gg_id:354485 Mongoose lemur feces clone ML_aaj26g10 EU776
FJ371876.1 gg_id:364037 feces adult twins and mothers; TS8 clone TS8_a03c03 FJ3718
AY984825.1 gg_id:117416 human stool clone B788 AY984
FJ683631.1 gg_id:522895 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6836
DQ802096.1 gg_id:184026 human fecal clone RL241_aaj03a08 DQ802
AY978106.1 gg_id:116676 human cecum mucosal biopsy clone LI74 AY978
DQ905841.2 gg_id:168587 human fecal clone 29E-e9 DQ905
EU778267.1 gg_id:311473 feces clone RL387_aao91b03 EU778
DQ798294.1 gg_id:175197 human fecal clone RL181_aah40c08 DQ798
FJ680530.1 gg_id:523892 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6805
FJ371264.1 gg_id:362859 feces adult twins and mothers; TS6 clone TS6_a02h08 FJ3712
FJ364511.1 gg_id:363309 feces adult twins and mothers; TS15 clone TS15_a03g10 FJ3645
DQ823719.1 gg_id:177631 human fecal clone RL250_aaj78b05 DQ823
FJ363893.1 gg_id:365586 feces adult twins and mothers; TS14 clone TS14_a04f03 FJ3638
FJ363292.1 gg_id:358118 feces adult twins and mothers; TS149 clone TS149_a01e07 FJ3632
DQ797073.1 gg_id:199280 human fecal clone RL386_aao86f06 DQ797
DQ825260.1 gg_id:194237 human fecal clone RL185_aan87d08 DQ825
FJ368417.1 gg_id:363241 feces adult twins and mothers; TS3 clone TS3_a04b03 FJ3684
DQ798527.1 gg_id:189625 human fecal clone RL181_aan97g11 DQ798
DQ793443.1 gg_id:180165 human fecal clone RL199_aaj43g08 DQ793
FJ674179.1 gg_id:523438 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6741
DQ798705.1 gg_id:190561 human fecal clone RL181_aao00d02 DQ798
FJ363606.1 gg_id:370127 feces adult twins and mothers; TS14 clone TS14_a01c06 FJ3636
EU763100.1 gg_id:340083 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A> EU763
FJ673868.1 gg_id:516798 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6738
DQ797952.1 gg_id:187550 human fecal clone RL302_aal93g09 DQ797
AY976628.1 gg_id:115592 human cecum mucosal biopsy clone K185 AY976
DQ796725.1 gg_id:175411 human fecal clone RL179_aao53f10 DQ796
FJ682306.1 gg_id:521483 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6823
FJ683390.1 gg_id:525600 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6833
EF404495.1 gg_id:208261 human fecal clone SJTU_C_10_93 EF4044
AY979567.1 gg_id:120401 human transverse colon mucosal biopsy clone M232 AY979
FJ371786.1 gg_id:370259 feces adult twins and mothers; TS8 clone TS8_a02b10 FJ3717
FJ364386.1 gg_id:367288 feces adult twins and mothers; TS15 clone TS15_a02c09 FJ3643
AY984573.1 gg_id:117999 human stool clone B512 AY984
FJ365469.1 gg_id:362327 feces adult twins and mothers; TS20 clone TS20_a03c06 FJ3654
FJ371852.1 gg_id:362302 feces adult twins and mothers; TS8 clone TS8_a03a01 FJ3718
DQ801186.1 gg_id:189437 human fecal clone RL116_aaf00b11 DQ801
FJ677356.1 gg_id:512856 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6773
DQ800972.1 gg_id:183872 human fecal clone RL387_aao90b04 DQ800

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FJ674111.1 gg_id:531152 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6741
GQ493258.1 gg_id:554436 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
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FJ363807.1 gg_id:367928 feces adult twins and mothers; TS14 clone TS14_a03e10 FJ3638
FJ679348.1 gg_id:519744 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6793
FJ371375.1 gg_id:358117 feces adult twins and mothers; TS6 clone TS6_a04b12 FJ3713
FJ367066.1 gg_id:366315 feces adult twins and mothers; TS28 clone TS28_a03b05 FJ3670
FJ676310.1 gg_id:515950 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6763
FJ678060.1 gg_id:517235 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6780
FJ362986.1 gg_id:368011 feces adult twins and mothers; TS148 clone TS148_a01e10 FJ3629
FJ364439.1 gg_id:366516 feces adult twins and mothers; TS15 clone TS15_a03a02 FJ3644
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FJ674266.1 gg_id:512154 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6742
FJ364737.1 gg_id:364401 feces adult twins and mothers; TS19 clone TS19_a02d10 FJ3647
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DQ801272.1 gg_id:185246 human fecal clone RL388_aao93c07 DQ801
EU778265.1 gg_id:323557 feces clone RL388_aao94d09 EU778
DQ798404.1 gg_id:182641 human fecal clone RL181_aah42b01 DQ798
EU768521.1 gg_id:322716 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C5 EU7685
FJ681399.1 gg_id:530749 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6813
EU764987.1 gg_id:352648 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2 EU7649
FJ371734.1 gg_id:358134 feces adult twins and mothers; TS8 clone TS8_a01f03 FJ3717
EU765813.1 gg_id:307235 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B4 EU7658
FJ674074.1 gg_id:528122 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6740
EU778234.1 gg_id:349081 feces clone RL116_aaf02b06 EU778
FJ684453.1 gg_id:530787 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6844
EU767130.1 gg_id:354618 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU767
DQ797991.1 gg_id:178056 human fecal clone RL302_aal94c03 DQ797
FJ370413.1 gg_id:360290 feces adult twins and mothers; TS56 clone TS56_a04g08 FJ3704
FJ673187.1 gg_id:524511 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6731
FJ372110.1 gg_id:364108 feces adult twins and mothers; TS9 clone TS9_a01h03 FJ3721
FJ684625.1 gg_id:518196 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6846
EU768164.1 gg_id:353312 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C4 EU768
DQ905685.1 gg_id:165926 human fecal clone 014C-G2 DQ905
FJ368148.1 gg_id:368219 feces adult twins and mothers; TS30 clone TS30_a04g06 FJ3681
FJ368038.1 gg_id:359551 feces adult twins and mothers; TS30 clone TS30_a03b03 FJ3680

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FJ678955.1 gg_id:520398 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6789
FJ680925.1 gg_id:514232 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6809
FJ676032.1 gg_id:521684 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6760
FJ682075.1 gg_id:513892 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6820
FJ683291.1 gg_id:516284 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6832
FJ674196.1 gg_id:519723 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6741
FJ678852.1 gg_id:520763 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6788
FJ366549.1 gg_id:368072 feces adult twins and mothers; TS27 clone TS27_a01a10 FJ3665
FJ677213.1 gg_id:514787 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6772
DQ456476.1 gg_id:157645 pre-adolescent turkey cecum clone CFT214A6 DQ456
DQ800946.1 gg_id:186241 human fecal clone RL387_aao89g04 DQ800
DQ793487.1 gg_id:191141 human fecal clone RL199_aaj44d08 DQ793
FJ672951.1 gg_id:520500 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6729
FJ371153.1 gg_id:366167 feces adult twins and mothers; TS6 clone TS6_a01e10 FJ3711
EF400140.1 gg_id:214439 human fecal clone SJTU_E_09_36 EF4001
EU776883.1 gg_id:331861 Mongoose lemur feces clone ML_aaj27h08 EU776
DQ905706.1 gg_id:173135 human fecal clone 29A-a5 DQ905
FJ371246.1 gg_id:363885 feces adult twins and mothers; TS6 clone TS6_a02f10 FJ3712
DQ798093.1 gg_id:186928 human fecal clone RL302_aal95d09 DQ798
DQ801240.1 gg_id:174910 human fecal clone RL116_aaf02d04 DQ801
DQ805697.1 gg_id:193638 human fecal clone RL306aal89h10 DQ805
FJ363638.1 gg_id:358653 feces adult twins and mothers; TS14 clone TS14_a01f03 FJ3636
AY983802.1 gg_id:127508 human descending colon mucosal biopsy clone M857 AY983
FJ678737.1 gg_id:527250 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6787
DQ795930.1 gg_id:178865 human fecal clone RL202_aai49b02 DQ795
FJ370104.1 gg_id:370287 feces adult twins and mothers; TS55 clone TS55_a04d12 FJ3701
FJ676047.1 gg_id:528616 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6760
DQ798655.1 gg_id:179391 human fecal clone RL181_aan99f04 DQ798
DQ808591.1 gg_id:176396 human fecal clone RL239_aaj10e10 DQ808
FJ371097.1 gg_id:361306 feces adult twins and mothers; TS5 clone TS5_a04h06 FJ3710
DQ806591.1 gg_id:183000 human fecal clone RL186_aao46e01 DQ806
EF403860.1 gg_id:214234 human fecal clone SJTU_C_01_49 EF4038
DQ905186.1 gg_id:169306 human fecal clone 002C-h7 DQ905
FJ676092.1 gg_id:524421 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6760
EU767030.1 gg_id:315946 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU767
DQ806427.1 gg_id:175791 human fecal clone RL186_aan92c04 DQ806
DQ798416.1 gg_id:179829 human fecal clone RL181_aah42c09 DQ798
DQ798223.1 gg_id:176932 human fecal clone RL181_aah39a12 DQ798
FJ677305.1 gg_id:530886 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6773
DQ796705.1 gg_id:188452 human fecal clone RL179_aao53d09 DQ796

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DQ796847.1 gg_id:184231 human fecal clone RL179_aao55d05 DQ796
FJ370960.1 gg_id:366197 feces adult twins and mothers; TS5 clone TS5_a03c07 FJ3709
EU763792.1 gg_id:342779 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A5 EU763
FJ673785.1 gg_id:529284 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6737
FJ371147.1 gg_id:365835 feces adult twins and mothers; TS6 clone TS6_a01e04 FJ3711
GQ448258.1 gg_id:577127 Microbiome neonatal calves: shedding microorganisms fecal clone calf783_2wks_gr GQ448
FJ370249.1 gg_id:369759 feces adult twins and mothers; TS56 clone TS56_a02d04 FJ3702
FJ365152.1 gg_id:362683 feces adult twins and mothers; TS1 clone TS1_a03e03 FJ3651
DQ798369.1 gg_id:179321 human fecal clone RL181_aah41f06 DQ798
FJ371336.1 gg_id:367543 feces adult twins and mothers; TS6 clone TS6_a03g04 FJ3713
EF402817.1 gg_id:209333 human fecal clone SJTU_B_12_88 EF4028
EF403128.1 gg_id:207179 human fecal clone SJTU_A1_1_31 EF4031
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FJ371675.1 gg_id:359679 feces adult twins and mothers; TS8 clone TS8_a01a03 FJ3716
DQ805298.1 gg_id:191990 human fecal clone RL249_aaj84g02 DQ805
DQ825317.1 gg_id:188494 human fecal clone RL185_aan88d07 DQ825
FJ681707.1 gg_id:527647 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6817
AY983857.1 gg_id:121748 human descending colon mucosal biopsy clone M976 AY9838
DQ801459.1 gg_id:195653 human fecal clone RL388_aao95g10 DQ801
FJ369135.1 gg_id:368234 feces adult twins and mothers; TS4 clone TS4_a04f08 FJ3691
EU765784.1 gg_id:305773 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B4 EU765
EU773399.1 gg_id:338066 Black lemur feces clone BKLE_h03_1 EU773
FJ676620.1 gg_id:511300 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6766
EU778112.1 gg_id:305800 feces clone RL387_aao91d06 EU778
DQ806446.1 gg_id:187439 human fecal clone RL186_aan92e11 DQ806
FJ678558.1 gg_id:518265 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6785
DQ797469.1 gg_id:176953 human fecal clone RL248_aai99g02 DQ797
EU766774.1 gg_id:306661 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU766
EU778110.1 gg_id:325310 feces clone RL388_aao96c05 EU778
EF405102.1 gg_id:205664 human fecal clone SJTU_G_07_93 EF4051
DQ794050.1 gg_id:183259 human fecal clone RL176_aan57c08 DQ794
EU774236.1 gg_id:327585 Chimpanzee feces clone CHIMP1_aaj37c05 EU774
FJ363566.1 gg_id:364894 feces adult twins and mothers; TS149 clone TS149_a04g05 FJ3635
FJ368436.1 gg_id:369275 feces adult twins and mothers; TS3 clone TS3_a04c11 FJ3684
DQ797452.1 gg_id:190572 human fecal clone RL248_aai99e06 DQ797
FJ365840.1 gg_id:368102 feces adult twins and mothers; TS21 clone TS21_a03f09 FJ3658
FJ363037.1 gg_id:359542 feces adult twins and mothers; TS148 clone TS148_a02c01 FJ3630
DQ801524.1 gg_id:185679 human fecal clone RL388_aao96f03 DQ801
FJ367888.1 gg_id:357299 feces adult twins and mothers; TS2 clone TS2_a04g04 FJ3678
AY978232.1 gg_id:120586 human transverse colon mucosal biopsy clone F043 AY978

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FJ679163.1 gg_id:527463 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6791
EF403098.1 gg_id:216037 human fecal clone SJTU_B_10_61 EF403
EF404629.1 gg_id:206291 human fecal clone SJTU_C_13_72 EF404
FJ362929.1 gg_id:365179 feces adult twins and mothers; TS13 clone TS13_a04h05 FJ3629
EF403882.1 gg_id:210159 human fecal clone SJTU_C_01_81 EF4038
EU762976.1 gg_id:353328 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU762
DQ799125.1 gg_id:189425 human fecal clone RL205_aaj17h11 DQ799
EU765069.1 gg_id:318023 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2 EU765
FJ371388.1 gg_id:365191 feces adult twins and mothers; TS6 clone TS6_a04d02 FJ3713
FJ368195.1 gg_id:357057 feces adult twins and mothers; TS3 clone TS3_a01d02 FJ3681
EU766953.1 gg_id:342269 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU766
EU763850.1 gg_id:308850 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A5 EU763
EU764022.1 gg_id:333428 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A5 EU764
EU764359.1 gg_id:327190 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1 EU764
FJ675734.1 gg_id:529354 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6757
FJ681114.1 gg_id:528002 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6811
FJ363265.1 gg_id:367426 feces adult twins and mothers; TS149 clone TS149_a01c02 FJ3632
DQ325575.1 gg_id:148122 Metagenomic gut microbiome healthy human stool clone B071 DQ325
DQ802390.1 gg_id:174026 human fecal clone RL188_aah17b01 DQ802
DQ808569.1 gg_id:183333 human fecal clone RL239_aaj10c06 DQ808
FJ372331.1 gg_id:359063 feces adult twins and mothers; TS9 clone TS9_a04d03 FJ3723
FJ365338.1 gg_id:359646 feces adult twins and mothers; TS20 clone TS20_a01f11 FJ3653
FJ362983.1 gg_id:369741 feces adult twins and mothers; TS148 clone TS148_a01e07 FJ3629
FJ681527.1 gg_id:511454 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6815
FJ681525.1 gg_id:519470 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6815
FJ371371.1 gg_id:365514 feces adult twins and mothers; TS6 clone TS6_a04b08 FJ3713
EF404214.1 gg_id:208301 human fecal clone SJTU_C_06_52 EF4042
DQ797735.1 gg_id:176811 human fecal clone RL206_aaj15c06 DQ797
DQ802387.1 gg_id:193218 human fecal clone RL188_aah17a10 DQ802
DQ801698.1 gg_id:183272 human fecal clone RL201_aai45f07 DQ801
FJ683934.1 gg_id:520449 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6839
FJ367378.1 gg_id:357380 feces adult twins and mothers; TS29 clone TS29_a02g06 FJ3673
DQ795994.1 gg_id:185878 human fecal clone RL202_aai50a04 DQ795
DQ800176.1 gg_id:188379 human fecal clone RL303_aal69c01 DQ800
FJ365498.1 gg_id:361816 feces adult twins and mothers; TS20 clone TS20_a03e12 FJ3654
GQ898100.1 gg_id:549326 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do GQ898
DQ905073.1 gg_id:168039 human fecal clone 2-002-f8 DQ905
FJ674188.1 gg_id:525812 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6741
DQ808596.1 gg_id:194672 human fecal clone RL239_aaj10f03 DQ808
FJ682161.1 gg_id:522847 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6821

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DQ824062.1 gg_id:196818 human fecal clone RL204_aaj58h03 DQ824
FJ685187.1 gg_id:530922 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6851
FM873865.1 gg_id:370037 occupant source house mattress dust clone MB02A07 FM873
FJ678640.1 gg_id:520383 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6786
DQ802202.1 gg_id:189156 human fecal clone RL241_aaj04d07 DQ802
DQ798729.1 gg_id:188748 human fecal clone RL181_aao00f06 DQ798
FJ680125.1 gg_id:525032 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6801
DQ825062.1 gg_id:190667 human fecal clone RL185_aao72h05 DQ825
AY976163.1 gg_id:116614 human ascending colon mucosal biopsy clone LV63 AY976
EU763182.1 gg_id:304534 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU763
AY981860.1 gg_id:118738 human sigmoid colon mucosal biopsy clone NW64 AY981
FJ682340.1 gg_id:512027 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6823
FJ675866.1 gg_id:516407 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6758
FJ370371.1 gg_id:369756 feces adult twins and mothers; TS56 clone TS56_a04b01 FJ3703
FJ367318.1 gg_id:370209 feces adult twins and mothers; TS29 clone TS29_a02b02 FJ3673
FJ370292.1 gg_id:362950 feces adult twins and mothers; TS56 clone TS56_a03a03 FJ3702
FJ680864.1 gg_id:522506 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6808
DQ797569.1 gg_id:195296 human fecal clone RL206_aaj13b08 DQ797
EU762970.1 gg_id:344903 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU762
EU764795.1 gg_id:341292 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B EU764
DQ823827.1 gg_id:194156 human fecal clone RL250_aaj79f05 DQ823
DQ904651.1 gg_id:163289 human fecal clone 001-b12 DQ904
FJ674264.1 gg_id:522817 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6742
EU768309.1 gg_id:321223 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C EU768
FJ368096.1 gg_id:357577 feces adult twins and mothers; TS30 clone TS30_a03h12 FJ3680
FJ683802.1 gg_id:528836 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6838
FJ363799.1 gg_id:363481 feces adult twins and mothers; TS14 clone TS14_a03e01 FJ3637
GQ016078.1 gg_id:493589 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw GQ016
DQ824126.1 gg_id:176546 human fecal clone RL204_aaj59f10 DQ824
FJ682360.1 gg_id:524527 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6823
FJ364311.1 gg_id:360764 feces adult twins and mothers; TS15 clone TS15_a01d12 FJ3643
EU475256.1 gg_id:296250 bonobo feces clone BNO_aaa01d04 EU475
GQ079614.1 gg_id:462293 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1231h GQ079
FJ366185.1 gg_id:357470 feces adult twins and mothers; TS25 clone TS25_a03f10 FJ3661
FJ370813.1 gg_id:361408 feces adult twins and mothers; TS5 clone TS5_a01e11 FJ3708
DQ801695.1 gg_id:185663 human fecal clone RL201_aai45f02 DQ801
DQ798344.1 gg_id:190278 human fecal clone RL181_aah41c04 DQ798
FJ673805.1 gg_id:530252 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6738
DQ801134.1 gg_id:187888 human fecal clone RL387_aao92g05 DQ801

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FJ684079.1 gg_id:523830 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6840
FJ370286.1 gg_id:365598 feces adult twins and mothers; TS56 clone TS56_a02h06 FJ3702
FJ685011.1 gg_id:524400 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6850
DQ802801.1 gg_id:193378 human fecal clone RL188_aan96g03 DQ802
FJ676677.1 gg_id:510685 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6766
FJ682588.1 gg_id:524482 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6825
EU778627.1 gg_id:340204 Ring-tailed lemur feces clone RT_aai09d01 EU778
DQ904690.1 gg_id:168007 human fecal clone 001-e4 DQ904
DQ797233.1 gg_id:178267 human fecal clone RL386_aao88f12 DQ797
EU766846.1 gg_id:315226 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU766
FJ366972.1 gg_id:362118 feces adult twins and mothers; TS28 clone TS28_a02a03 FJ3669
FJ364419.1 gg_id:360543 feces adult twins and mothers; TS15 clone TS15_a02g02 FJ3644
EF402383.1 gg_id:212008 human fecal clone SJTU_B_07_15 EF4023
EF403845.1 gg_id:207336 human fecal clone SJTU_C_01_32 EF4038
DQ797376.1 gg_id:179644 human fecal clone RL248_aai98e11 DQ797
DQ904873.1 gg_id:169773 human fecal clone 001C-e12 DQ904
DQ823885.1 gg_id:180532 human fecal clone RL250_aaj80d09 DQ823
AF371723.1 gg_id:39948 swine intestine clone p-366-a3 AF371
FJ681951.1 gg_id:510322 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6819
FJ682732.1 gg_id:513225 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6827
FJ372292.1 gg_id:365149 feces adult twins and mothers; TS9 clone TS9_a03h10 FJ3722
DQ805429.1 gg_id:189660 human fecal clone RL203_aai62e03 DQ805
FJ679931.1 gg_id:527631 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6799
EU778303.1 gg_id:331363 feces clone RL388_aao93a11 EU778
GQ898754.1 gg_id:585524 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do GQ898
DQ798053.1 gg_id:197507 human fecal clone RL302_aal95a03 DQ798
DQ801515.1 gg_id:182931 human fecal clone RL388_aao96e06 DQ801
FJ682430.1 gg_id:530685 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6824
FJ680211.1 gg_id:526612 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6802
FJ679369.1 gg_id:519122 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6793
FJ370312.1 gg_id:367326 feces adult twins and mothers; TS56 clone TS56_a03c09 FJ3703
DQ809064.1 gg_id:195742 human fecal clone RL243_aai88h06 DQ809
FJ364975.1 gg_id:362407 feces adult twins and mothers; TS1 clone TS1_a01d06 FJ3649
DQ797365.1 gg_id:175570 human fecal clone RL248_aai98d09 DQ797
EU466841.1 gg_id:292490 African elephant feces clone AFEL2_aao30c02 EU466
FJ674077.1 gg_id:525715 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6740
GQ898171.1 gg_id:549196 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do GQ898
FJ678426.1 gg_id:522074 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6784
DQ799443.1 gg_id:195250 human fecal clone RL305aal86d01 DQ799

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FJ678870.1 gg_id:512472 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6788
EF400999.1 gg_id:203591 human fecal clone SJTU_D_04_49 EF4009
FJ680972.1 gg_id:519973 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6809
DQ806688.1 gg_id:183513 human fecal clone RL186_aao47e12 DQ806
EU766495.1 gg_id:305290 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU766
FJ362752.1 gg_id:367710 feces adult twins and mothers; TS13 clone TS13_a02g01 FJ3627
FJ372208.1 gg_id:359289 feces adult twins and mothers; TS9 clone TS9_a03a03 FJ3722
FJ367380.1 gg_id:365407 feces adult twins and mothers; TS29 clone TS29_a02g08 FJ3673
FJ363839.1 gg_id:360232 feces adult twins and mothers; TS14 clone TS14_a04a01 FJ3638
FJ678151.1 gg_id:528937 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6781
FJ680786.1 gg_id:526274 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6807
EU762845.1 gg_id:304517 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A> EU762
FJ677432.1 gg_id:528151 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6774
FJ368415.1 gg_id:358955 feces adult twins and mothers; TS3 clone TS3_a04b01 FJ3684
EF402952.1 gg_id:213907 human fecal clone SJTU_B_14_69 EF4029
FJ683751.1 gg_id:530843 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6837
DQ905111.1 gg_id:163491 human fecal clone 002C-b12 DQ905
FJ364490.1 gg_id:362754 feces adult twins and mothers; TS15 clone TS15_a03e11 FJ3644
FJ685392.1 gg_id:530094 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6853
FJ673343.1 gg_id:517507 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6733
DQ825000.1 gg_id:174877 human fecal clone RL185_aao72b01 DQ825
EU768621.1 gg_id:318450 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C5 EU768
FJ678887.1 gg_id:521067 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6788
FJ365105.1 gg_id:359049 feces adult twins and mothers; TS1 clone TS1_a02h06 FJ3651
FJ364590.1 gg_id:362559 feces adult twins and mothers; TS15 clone TS15_a04g06 FJ3645
FJ365386.1 gg_id:359852 feces adult twins and mothers; TS20 clone TS20_a02c08 FJ3653
FJ367541.1 gg_id:370253 feces adult twins and mothers; TS29 clone TS29_a04g06 FJ3675
FJ680223.1 gg_id:520109 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6802
EU763241.1 gg_id:307220 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A> EU763
FJ681568.1 gg_id:527811 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6815
FJ676504.1 gg_id:522876 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6765
FJ362885.1 gg_id:359008 feces adult twins and mothers; TS13 clone TS13_a04d04 FJ3628
FJ678804.1 gg_id:516818 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6788
FJ673487.1 gg_id:527547 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6734
DQ801384.1 gg_id:178047 human fecal clone RL388_aao94g07 DQ801
AY984170.1 gg_id:118701 human stool clone B054 AY984
AY979049.1 gg_id:126578 human transverse colon mucosal biopsy clone NJ45 AY979
FJ673097.1 gg_id:520459 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6730
FJ674043.1 gg_id:523328 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6740
FJ673534.1 gg_id:523016 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6735

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GQ898476.1 gg_id:585428 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ898
DQ326372.1 gg_id:149213 Metagenomic gut microbiome healthy human stool clone C386 DQ326
DQ796992.1 gg_id:195038 human fecal clone RL386_aao85e04 DQ796
DQ823803.1 gg_id:191333 human fecal clone RL250_aaj79c08 DQ823
FJ678240.1 gg_id:525494 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6782
FJ683918.1 gg_id:520517 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6839
FJ677025.1 gg_id:519119 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6770
DQ801244.1 gg_id:187010 human fecal clone RL116_aaf02f02 DQ801
GQ448921.1 gg_id:548379 Microbiome neonatal calves: shedding microorganisms fecal clone calf783_2wks_gr GQ448
FJ365385.1 gg_id:361941 feces adult twins and mothers; TS20 clone TS20_a02c07 FJ3653
FJ678517.1 gg_id:516135 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6785
GQ043044.1 gg_id:460138 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1012e GQ043
FJ682899.1 gg_id:525479 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6828
FJ362810.1 gg_id:363538 feces adult twins and mothers; TS13 clone TS13_a03e01 FJ3628
EU778238.1 gg_id:325784 feces clone RL388_aao96a06 EU778
AB185655.1 gg_id:107235 rumen clone F24-H11 AB185
DQ455829.1 gg_id:158222 pre-adolescent turkey cecum clone CFT19A8 DQ455
EU775925.1 gg_id:326785 Horse feces clone horsem_aai93f12 EU775
FJ362828.1 gg_id:366573 feces adult twins and mothers; TS13 clone TS13_a03f08 FJ3628
DQ815311.1 gg_id:167509 mouse cecum clone aab45c07 DQ815
EU504766.1 gg_id:259535 cecal contents Mus musculus strain C57BL/6J; myd2 clone myd2_aaa01g09 EU504
EU503968.1 gg_id:273637 cecal contents Mus musculus strain C57BL/6J; CRWD4 clone CRWD4_aaa03d07 EU503
EU474488.1 gg_id:301032 bighorn sheep feces clone BHSD_aaa02f09 EU474
EF401657.1 gg_id:205604 human fecal clone SJTU_D_14_93 EF4016
FJ367640.1 gg_id:368423 feces adult twins and mothers; TS2 clone TS2_a01h01 FJ3676
EF436308.2 gg_id:209712 library-based ruminal water buffalo (Bubalus bubalis) rumen fluid clone BRC22 EF4363
EU137434.1 gg_id:267999 Bartonella-positive fleas: and assembly patterns Oropsylla hirsuta (prairie dog flea) C EU1374
AY985959.1 gg_id:118285 human stool clone D258 AY985
DQ794276.1 gg_id:187564 human fecal clone RL176_aan60e05 DQ794
FJ823863.1 gg_id:526665 Controlling accumulation fermentation inhibitors biorefinery recycle water microbial FJ8238
GQ491174.1 gg_id:544996 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
DQ394655.1 gg_id:155341 on -Arctic peninsula Svalbard Norway determined genes and rumen isolates reindee DQ394
EU844238.1 gg_id:309451 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
EU776785.1 gg_id:313471 Mongoose lemur feces clone ML_aaj26e11 EU776
EF602811.1 gg_id:230941 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6028
AB234463.1 gg_id:149007 termite gut homogenate clone MgMjD-058 AB2344
DQ798394.1 gg_id:194661 human fecal clone RL181_aah41h12 DQ798
EU458004.1 gg_id:304013 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU458
AY916303.1 gg_id:114021 human sigmoid colon biopsy clone MM71 AY9163
EU763882.1 gg_id:331742 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A5 EU7638
FJ372305.1 gg_id:369053 feces adult twins and mothers; TS9 clone TS9_a04a11 FJ3723

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FJ366573.1 gg_id:363823 feces adult twins and mothers; TS27 clone TS27_a01c10 FJ3665
DQ456220.1 gg_id:158722 pre-adolescent turkey cecum clone CFT29G9 DQ456
DQ014822.1 gg_id:134301 mouse cecum clone M1_b06_3 DQ014
EU461564.1 gg_id:288270 black rhinoceros feces clone RH_aaj92e10 EU461
EU461544.1 gg_id:298072 black rhinoceros feces clone RH_aaj92b07 EU461
AB218336.1 gg_id:147024 Fecal microbial (dugong dugon) determined genes Dugong feces clone dgC-135 AB218
EU504992.1 gg_id:271491 cecal contents Mus musculus strain C57BL/6J; myd3 clone myd3_aaa01c11 EU504
GU302582.1 gg_id:585073 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU302
DQ801356.1 gg_id:195943 human fecal clone RL388_aao94d10 DQ801
FJ366352.1 gg_id:365719 feces adult twins and mothers; TS26 clone TS26_a01g07 FJ3663
DQ804825.1 gg_id:175497 human fecal clone RL385_aao81b11.Contig2 DQ804
EF604816.1 gg_id:229824 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6048
EU452624.1 gg_id:328445 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75 EU452
EU456254.1 gg_id:338796 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80 EU456
GQ896697.1 gg_id:532748 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do GQ896
FJ362655.1 gg_id:362777 feces adult twins and mothers; TS13 clone TS13_a01e10 FJ3626
GQ449217.1 gg_id:549950 Microbiome neonatal calves: shedding microorganisms fecal clone calf784_10wks_ GQ449
FJ363502.1 gg_id:363316 feces adult twins and mothers; TS149 clone TS149_a04a04 FJ3635
EF025275.1 gg_id:191239 Examination microbial ecology avian vivo bromodeoxyuridine intestine clone B5_N6 EF0252
DQ805440.1 gg_id:183410 human fecal clone RL203_aai62f07 DQ805
EU761793.1 gg_id:311033 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU761
EU843460.1 gg_id:321337 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
EU530368.1 gg_id:263665 mucosa adherent and invasive microbes profile adenoma colorectal cancer clone M EU530
EF400373.1 gg_id:206513 human fecal clone SJTU_E_12_37 EF4003
EF098593.1 gg_id:185752 mouse cecum clone SWPT16_aaa01h04 EF0985
FJ681249.1 gg_id:522699 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6812
DQ797153.1 gg_id:203545 human fecal clone RL386_aao87f05 DQ797
DQ824395.1 gg_id:195397 human fecal clone RL304_aal75e08 DQ824
GU304189.1 gg_id:548161 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU304
FJ365085.1 gg_id:366486 feces adult twins and mothers; TS1 clone TS1_a02f07 FJ3650
DQ799134.1 gg_id:191902 human fecal clone RL205_aaj18a10 DQ799
EU453686.1 gg_id:316428 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77 EU453
AB238598.1 gg_id:249174 Oscillibacter valericigenes str. Sjm18-20 (= NBRC 101213) AB238
FJ369766.1 gg_id:362078 feces adult twins and mothers; TS51 clone TS51_a04e10 FJ3697
DQ673487.1 gg_id:168795 rumen fluid clone GRC22 DQ673
DQ904783.1 gg_id:171303 human fecal clone 001B-e1 DQ904
EU462532.1 gg_id:297465 Sumatran orangutan feces clone orang1_aai56e09 EU462
EU509002.1 gg_id:274686 cecal contents Mus musculus strain C57BL/6J; MD7 clone MD7_aap41f02 EU509
EU505557.1 gg_id:276535 cecal contents Mus musculus strain C57BL/6J; myd5 clone myd5_aaa02f07 EU505
EF401625.1 gg_id:213633 human fecal clone SJTU_D_13_45 EF4016

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EU774621.1 gg_id:320768 Angola Colobus feces clone EAC_2_aaa02f02 EU7746
EU452440.1 gg_id:303454 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU4524
EU463672.1 gg_id:298918 domesticated horse feces clone horsej_aai90g11 EU4636
EU771312.1 gg_id:356187 Asiatic elephant feces clone AE1_aaa03d05 EU7713
EF096980.1 gg_id:192115 mouse cecum clone SWPT13_aaa03f07 EF0969
EU772150.1 gg_id:354379 Argali sheep feces clone AS1_aao40g10.Contig1 EU7721
DQ809326.1 gg_id:189943 human fecal clone RL184_aah19c02 DQ809
FJ366181.1 gg_id:361863 feces adult twins and mothers; TS25 clone TS25_a03f06 FJ3661
DQ793427.1 gg_id:192058 human fecal clone RL199_aaj43f01 DQ793
EU457751.1 gg_id:327701 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83M EU4577
EU455083.1 gg_id:322211 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75M EU4550
DQ808890.1 gg_id:195102 human fecal clone RL243_aai86f05 DQ808
EU475806.1 gg_id:296144 white-faced saki feces clone Saki_aaj61g02 EU4758
EF096534.1 gg_id:193435 mouse cecum clone obob2_aaa04e06 EF0965
EF602930.1 gg_id:235072 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6029
AY992715.1 gg_id:130454 mouse cecum clone C23_p23 AY9927
DQ905136.1 gg_id:165954 human fecal clone 002C-d1 DQ905
GQ897639.1 gg_id:536897 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ897
FJ365979.1 gg_id:360331 feces adult twins and mothers; TS25 clone TS25_a01d02 FJ3659
EU452820.1 gg_id:336127 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83M EU4528
EF096624.1 gg_id:198635 mouse cecum clone SWPT11_aaa02b09 EF0966
FJ681029.1 gg_id:520720 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6810
DQ815674.1 gg_id:164465 mouse cecum clone aab44f06 DQ815
DQ326565.1 gg_id:146558 Metagenomic gut microbiome healthy human stool clone C747 DQ326
EU775865.1 gg_id:336216 Horse feces clone horsem_aai95a08 EU7758
DQ808842.1 gg_id:181304 human fecal clone RL243_aai86a08 DQ808
DQ015246.1 gg_id:134096 mouse cecum clone M2_g12_3 DQ015
EU774932.1 gg_id:327337 Flying Fox feces clone FF_f03_1 EU7749
EF602809.1 gg_id:228426 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6028
DQ809986.1 gg_id:199055 human fecal clone RL184_aao66f12 DQ809
EU771406.1 gg_id:323903 Asiatic elephant feces clone AE2_aaa03h12 EU7714
DQ014634.1 gg_id:135369 mouse cecum clone M1_h06 DQ014
FJ879271.1 gg_id:427738 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8792
AY985603.1 gg_id:121620 human stool clone C593 AY9856
DQ796558.1 gg_id:190220 human fecal clone RL179aan74f10 DQ796
EU509249.1 gg_id:273592 cecal contents Mus musculus strain C57BL/6J; MD8 clone MD8_aap46f03 EU5092
EU461246.1 gg_id:295371 hamadryas baboon feces clone BAZ_aah91d08 EU4612
FJ362625.1 gg_id:365734 feces adult twins and mothers; TS13 clone TS13_a01c02 FJ3626
EU775024.1 gg_id:314582 Francois Langur feces clone FL_1aaa01h10 EU7750
DQ796802.1 gg_id:180980 human fecal clone RL179_aao54g01 DQ796

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EU764810.1 gg_id:330949 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2 EU7648
EU843610.1 gg_id:333248 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8436
DQ809094.1 gg_id:189555 human fecal clone RL308_aal81d05 DQ809
EU765801.1 gg_id:325064 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B4 EU7658
FJ363434.1 gg_id:361450 feces adult twins and mothers; TS149 clone TS149_a03c01 FJ3634
EU469102.1 gg_id:293060 Speke's gazelle feces clone SP3_e04 EU4691
FJ671876.1 gg_id:526225 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6718
EU463455.1 gg_id:287790 domesticated horse feces clone horsem_aai94c07 EU4634
EU775161.1 gg_id:320483 Francois Langur feces clone FL_1aaa04a09 EU7751
EU771243.1 gg_id:306711 Asiatic elephant feces clone AE3_aaa01e02 EU7712
EU469097.1 gg_id:299222 Speke's gazelle feces clone SP3_d08 EU4690
DQ795965.1 gg_id:193632 human fecal clone RL202_aai49e08 DQ795
AY684396.2 gg_id:110998 mucosal biopsies human intestine clone HuDI51 AY6843
EU765035.1 gg_id:306745 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2 EU7650
EU504706.1 gg_id:276511 cecal contents Mus musculus strain C57BL/6J; myd1 clone myd1_aaa04g08 EU5047
EF098196.1 gg_id:197863 mouse cecum clone SWPT14_aaa02h07 EF0981
EU466225.1 gg_id:298036 bighorn sheep feces clone BH1_aao28d06 EU4662
AY985428.1 gg_id:121349 human stool clone C372 AY9854
EU766503.1 gg_id:335417 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU7665
EU511173.1 gg_id:262677 cecal contents Mus musculus strain C57BL/6J; WD7 clone WD7_aal03h03 EU5111
EU765204.1 gg_id:356417 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B3 EU7652
DQ815864.1 gg_id:171239 mouse cecum clone aab23e01 DQ815
EU842347.1 gg_id:315851 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU8423
DQ815490.1 gg_id:164810 mouse cecum clone aab41e05 DQ815
EU472398.1 gg_id:299755 Angola colobus feces clone EAC_1aaa01c10 EU4723
EU508250.1 gg_id:276985 cecal contents Mus musculus strain C57BL/6J; MD26 clone MD26_aaa04e02 EU5082
EU506574.1 gg_id:260741 cecal contents Mus musculus strain C57BL/6J; MD19 clone MD19_aaa04e08 EU5065
AY983978.1 gg_id:117068 human descending colon mucosal biopsy clone MC71 AY9839
FJ681514.1 gg_id:529688 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6815
EU463554.1 gg_id:292439 domesticated horse feces clone horsem_aai96a07 EU4635
EU463726.1 gg_id:293353 domesticated horse feces clone horsej_aai91g05 EU4637
EU463427.1 gg_id:298457 domesticated horse feces clone horsem_aai93g03 EU4634
AB301912.1 gg_id:240231 Ruminococcus albus AB3019
FJ372107.1 gg_id:360830 feces adult twins and mothers; TS9 clone TS9_a01g12 FJ3721
FJ365585.1 gg_id:357253 feces adult twins and mothers; TS20 clone TS20_a04f02 FJ3655
FJ366914.1 gg_id:363146 feces adult twins and mothers; TS28 clone TS28_a01c11 FJ3669
FJ371844.1 gg_id:366240 feces adult twins and mothers; TS8 clone TS8_a02h01 FJ3718
FJ363657.1 gg_id:368173 feces adult twins and mothers; TS14 clone TS14_a01g10 FJ3636
FJ371275.1 gg_id:365709 feces adult twins and mothers; TS6 clone TS6_a03a09 FJ3712
GQ898568.1 gg_id:594381 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ898

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FJ368454.1 gg_id:362323 feces adult twins and mothers; TS3 clone TS3_a04e09 FJ3684
FJ366609.1 gg_id:361468 feces adult twins and mothers; TS27 clone TS27_a01f12 FJ3666
FJ363691.1 gg_id:358965 feces adult twins and mothers; TS14 clone TS14_a02b08 FJ3636
DQ905192.1 gg_id:173445 human fecal clone 013-a1 DQ905
EU768452.1 gg_id:320547 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C5 EU768
FJ365601.1 gg_id:363923 feces adult twins and mothers; TS20 clone TS20_a04g09 FJ3656
EU762103.1 gg_id:322081 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1 EU762
DQ807613.1 gg_id:182342 human fecal clone RL307_aam08h07 DQ807
FJ366911.1 gg_id:365471 feces adult twins and mothers; TS28 clone TS28_a01c08 FJ3669
DQ798028.1 gg_id:182455 human fecal clone RL302_aal94f12 DQ798
AY976187.1 gg_id:121324 human ascending colon mucosal biopsy clone LV95 AY976
EU761738.1 gg_id:352927 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1 EU761
AF104841.1 gg_id:16066 Ruminococcus flavefaciens str. AR72 AF1048
EU777840.1 gg_id:323801 European rabbit feces clone RA_c04_1 EU777
EU469685.1 gg_id:294797 flying fox feces clone FF_a06_1 EU469
EU468685.1 gg_id:291859 okapi feces clone OK2_e08_1 EU468
EF445196.1 gg_id:205179 rabbit cecum clone NED3F5 EF4451
EU779250.1 gg_id:324482 Trancaspian Urial feces clone TU1_aaa04c10 EU779
AF104846.1 gg_id:16065 Ruminococcus flavefaciens str. Y1 AF1048
FJ879092.1 gg_id:459944 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8790
EU468531.1 gg_id:290894 okapi feces clone OK1_b08_1 EU468
EU774461.1 gg_id:320332 mammals their gut microbes Eastern Black and White Colobus feces clone COL_aai14 EU774
FJ880174.1 gg_id:418064 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8801
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EU460043.1 gg_id:296857 mammals their gut microbes eastern black and white colobus feces clone COL_aai13 EU460
EF602945.1 gg_id:233404 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6029
FJ879630.1 gg_id:438358 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8796
EU465615.1 gg_id:288191 argali sheep feces clone AS1_aao39g11.Contig1 EU465
FJ880749.1 gg_id:460253 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8807
AF104837.1 gg_id:16040 Ruminococcus flavefaciens str. AR46 AF1048
FJ832845.1 gg_id:563574 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J3Q301_33A05 FJ8328
EU774973.1 gg_id:317714 Flying Fox feces clone FF_-aag84b01 EU774
FJ879772.1 gg_id:386333 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8797
AB034020.1 gg_id:45766 rumen clone 4C0d-7 AB034
FJ366125.1 gg_id:362036 feces adult twins and mothers; TS25 clone TS25_a03a05 FJ3661
EU469261.1 gg_id:298912 Speke's gazelle feces clone SP3_a07_1 EU469
FJ879853.1 gg_id:383102 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8798
FJ879578.1 gg_id:433149 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8795

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DQ394631.1 gg_id:153029 -Arctic peninsula Svalbard Norway determined genes and rumen isolates reindeer o DQ394
FJ880209.1 gg_id:407405 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8802
EU469949.1 gg_id:296346 trancaspain urial feces clone TU1_aaa01f10 EU469
EU779402.1 gg_id:343313 Grevy's Zebra feces clone GZ_aaa04c09 EU779
EU381701.1 gg_id:260559 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid EU381
EU475092.1 gg_id:301195 visayam warty pig feces clone VWP_aaa03c01 EU475
EU775809.1 gg_id:315666 Horse feces clone horsem_e12 EU775
FJ673061.1 gg_id:512575 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6730
EU774487.1 gg_id:356167 mammals their gut microbes Eastern Black and White Colobus feces clone COL_aai1 EU774
FJ682773.1 gg_id:522772 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6827
DQ882650.1 gg_id:172296 Ruminococcus sp. str. YE281 DQ882
EF401397.1 gg_id:207190 human fecal clone SJTU_D_09_78 EF4013
FJ673313.1 gg_id:514709 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6733
EU774954.1 gg_id:347335 Flying Fox feces clone FF_-aag84b12 EU774
FJ682475.1 gg_id:510095 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6824
AB034071.1 gg_id:29057 rumen clone 6C3d-10 AB034
FJ879569.1 gg_id:461354 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8795
DQ807559.1 gg_id:174923 human fecal clone RL307_aam08b12 DQ807
FJ881003.1 gg_id:385017 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8810
GU303205.1 gg_id:560753 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU303
FJ681243.1 gg_id:528589 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6812
FJ683277.1 gg_id:509351 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6832
FJ682760.1 gg_id:511748 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6827
AF132277.1 gg_id:72970 adult human fecal matter clone adhufec58 AF132
EU453081.1 gg_id:312665 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83 EU453
FJ880489.1 gg_id:415638 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8804
AJ515913.1 gg_id:102671 Ruminococcus sp. str. 18P13 AJ5159
FJ678989.1 gg_id:528232 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6789
GQ079248.1 gg_id:409845 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1230d GQ079
FJ366993.1 gg_id:358351 feces adult twins and mothers; TS28 clone TS28_a02b12 FJ3669
DQ905838.2 gg_id:163243 human fecal clone 29E-e5 DQ905
FJ363583.1 gg_id:365147 feces adult twins and mothers; TS14 clone TS14_a01a05 FJ3635
DQ800995.1 gg_id:191448 human fecal clone RL387_aao90f01 DQ800
EF088328.1 gg_id:199654 Clostridium islandicum str. AK1 EF0883
EU761602.1 gg_id:334170 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU761
FJ366126.1 gg_id:368142 feces adult twins and mothers; TS25 clone TS25_a03a06 FJ3661
EU453704.1 gg_id:309828 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83 EU453
EU773178.1 gg_id:349431 BigHorn sheep feces clone BHSD_aaa03h06 EU773
GQ042993.1 gg_id:431222 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1011h GQ042
FJ672106.1 gg_id:529789 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface FJ6721
EU470140.1 gg_id:291360 trancaspain urial feces clone TU2_aaa03c09 EU470

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AB494864.1 gg_id:535519 Fibrobacter succinogenes dominated consortium on hay stems sheep rumen clone N AB494
FJ881268.1 gg_id:381511 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8812
DQ807388.1 gg_id:195966 human fecal clone RL307_aam05h08 DQ807
EU762145.1 gg_id:350180 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1 EU762
FJ680003.1 gg_id:520618 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6800
AJ515914.1 gg_id:94504 Ruminococcus sp. str. 7L75 AJ5159
AY986181.1 gg_id:117716 human stool clone D538 AY986
GQ502527.1 gg_id:593965 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf4- GQ502
EF686574.1 gg_id:241489 Sequences Manifest Rumen Yunnan Yel Cattle (Bos Taurus) rumen fluid clone YNRC6 EF6865
FJ673393.1 gg_id:520904 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6733
GQ079249.1 gg_id:408551 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1230d GQ079
FJ367031.1 gg_id:364206 feces adult twins and mothers; TS28 clone TS28_a02f09 FJ3670
EF400797.1 gg_id:212533 human fecal clone SJTU_D_01_64 EF4007
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FJ683473.1 gg_id:516504 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6834
FJ683719.1 gg_id:529159 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6837
DQ793927.1 gg_id:196776 human fecal clone RL176_aah45d05 DQ793
FJ881336.1 gg_id:383369 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8813
EU381483.1 gg_id:259252 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid EU381
FJ682645.1 gg_id:528548 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6826
FJ683228.1 gg_id:527236 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6832
DQ801085.1 gg_id:183189 human fecal clone RL387_aao91h09 DQ801
FJ682883.1 gg_id:514296 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6828
DQ801034.1 gg_id:182668 human fecal clone RL387_aao91c01 DQ801
EU475067.1 gg_id:303213 visayam warty pig feces clone VWP_aaa03h09 EU475
FJ880441.1 gg_id:463901 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8804
EU201675.1 gg_id:240642 species intestinal microbiota between fiber- and liquid phase human fecal clone sd6 EU201
FJ880300.1 gg_id:460027 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8803
FJ683326.1 gg_id:530604 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6833
DQ014676.1 gg_id:130775 mouse cecum clone M1_d06_1 DQ014
EF401179.1 gg_id:216596 human fecal clone SJTU_D_06_75 EF4011
FJ682715.1 gg_id:520680 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6827
EU767484.1 gg_id:311384 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C EU767
FJ677927.1 gg_id:527685 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6779
DQ801328.1 gg_id:181220 human fecal clone RL388_aao94a10 DQ801
EU462655.1 gg_id:290967 Sumatran orangutan feces clone orang2_aai66g11 EU462
EU381835.1 gg_id:271639 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU381
EU777137.1 gg_id:347585 Okapi feces clone OK1_a08 EU777
FJ683874.1 gg_id:513947 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6838
FJ676801.1 gg_id:528312 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6768
AY858410.2 gg_id:112362 gastrointestinal tract Grant's gazelle clone GRANT74 AY858

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FJ366709.1 gg_id:369797 feces adult twins and mothers; TS27 clone TS27_a02h07 FJ3667
EU777134.1 gg_id:308293 Okapi feces clone OK1_f06 EU777
FJ673663.1 gg_id:521226 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6736
AB034039.1 gg_id:33321 rumen clone 5C0d-6 AB034
EU767319.1 gg_id:341274 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C2 EU767
EU748314.1 gg_id:311120 neotropical folivorous flying bird adult hoatzin crop clone hoa46_84D11 EU748
FJ683336.1 gg_id:517337 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6833
GQ175496.1 gg_id:548621 Chicken intestinal microbiota modulations various feed supplementations DGGE anc GQ175
DQ801337.1 gg_id:173810 human fecal clone RL388_aao94b09 DQ801
GQ079200.1 gg_id:440181 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1229f1 GQ079
DQ808310.1 gg_id:195868 human fecal clone RL180_aao75b04 DQ808
EU762806.1 gg_id:305114 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A> EU762
EU845601.1 gg_id:327387 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU845
FJ671379.1 gg_id:528679 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6713
DQ808451.1 gg_id:186429 human fecal clone RL180_aao76g01 DQ808
EU777639.1 gg_id:348060 Sumatran orangutan feces clone orang2_aai66f03 EU777
FJ683503.1 gg_id:532036 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6835
FJ683645.1 gg_id:530800 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6836
AB185796.1 gg_id:106698 rumen clone U29-F08 AB185
FJ367012.1 gg_id:367055 feces adult twins and mothers; TS28 clone TS28_a02d10 FJ3670
FJ673216.1 gg_id:515428 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6732
EF098027.1 gg_id:199742 mouse cecum clone SWPT12_aaa04c08 EF098
FJ880780.1 gg_id:385933 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8807
EF401603.1 gg_id:217078 human fecal clone SJTU_D_12_80 EF401
FJ673489.1 gg_id:525315 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6734
DQ808084.1 gg_id:193314 human fecal clone RL180_aan72b07 DQ808
GQ898105.1 gg_id:556976 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do : GQ898
AF018544.1 gg_id:16077 rumen fluid clone JW3 AF018
EU472362.1 gg_id:295892 Angola colobus feces clone EAC_1aaa02g07 EU472
EU842465.1 gg_id:341817 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
EU381723.1 gg_id:270733 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid ; EU381
GQ448900.1 gg_id:557051 Microbiome neonatal calves: shedding microorganisms fecal clone calf32_10wks_gr GQ448
DQ793356.1 gg_id:181961 human fecal clone RL199_aaj42f09 DQ793
DQ673540.1 gg_id:163800 rumen fluid clone GRC75 DQ673
FJ679803.1 gg_id:522426 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6798
DQ800439.1 gg_id:188212 human fecal clone RL183_aah24d07 DQ800
FJ682636.1 gg_id:514231 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6826
FJ879544.1 gg_id:445343 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8795
EU344189.1 gg_id:268936 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU344
FJ682735.1 gg_id:525180 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6827

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EU381595.1 gg_id:273843 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid EU381
FJ682919.1 gg_id:516302 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6829
FJ676403.1 gg_id:530207 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6764
EU466401.1 gg_id:293178 bighorn sheep feces clone BH2_aao23b06 EU466
EU381726.1 gg_id:268964 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid EU381
EF400818.1 gg_id:217014 human fecal clone SJTU_D_01_96 EF4008
EF515535.1 gg_id:223059 Electricigen Enrichment MFC full-scale anaerobic bioreactor sludge treating brewery EF5155
EU469287.1 gg_id:294007 Speke's gazelle feces clone SP3_d08_3 EU469
EU462675.1 gg_id:302094 Sumatran orangutan feces clone orang2_aai67b01 EU462
AJ515916.1 gg_id:94758 Ruminococcus sp. str. 25F6 AJ5159
FJ365090.1 gg_id:365676 feces adult twins and mothers; TS1 clone TS1_a02g01 FJ3650
EF436370.1 gg_id:205159 library-based ruminal water buffalo (Bubalus bubalis) rumen fluid clone BRC84 EF4363
FJ372101.1 gg_id:368749 feces adult twins and mothers; TS9 clone TS9_a01g06 FJ3721
FJ683482.1 gg_id:520858 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6834
FJ683285.1 gg_id:530742 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6832
EU472479.1 gg_id:297065 Angola colobus feces clone EAC_2_aaa02f09 EU472
GU304502.1 gg_id:562441 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU304
DQ795096.1 gg_id:175713 human fecal clone RL310_aam40b09 DQ795
FJ367666.1 gg_id:368428 feces adult twins and mothers; TS2 clone TS2_a02b06 FJ3676
EU467336.1 gg_id:297875 chimpanzee feces clone CHIMP1_c02 EU467
EF402085.1 gg_id:207480 human fecal clone SJTU_B_03_46 EF4020
FJ673679.1 gg_id:523326 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6736
FJ682787.1 gg_id:530594 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6827
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EU473649.1 gg_id:293409 banteng feces clone BG_aaa04a03.Contig1 EU473
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EU511872.1 gg_id:269378 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_aaf10b09 EU511
EU728796.1 gg_id:319681 Ruminococcus sp. str. DJF_VR87 EU728
FJ683078.1 gg_id:509155 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6830
FJ880361.1 gg_id:458950 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8803
EU764268.1 gg_id:304940 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU764
AB270050.1 gg_id:172453 Influence temperature and humidity on heifers rumen contents Holstein heifer (Bos AB270
EU762132.1 gg_id:349408 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU762
FJ680579.1 gg_id:514059 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6805
EU766698.1 gg_id:336413 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C EU766
EU777557.1 gg_id:304044 Sumatran orangutan feces clone orang1_aai55b05 EU777
FJ363111.1 gg_id:364931 feces adult twins and mothers; TS148 clone TS148_a03b10 FJ3631
DQ777945.1 gg_id:169698 rat feces clone R-1141(5) DQ777
GQ339149.1 gg_id:517495 Comprehensive Investigation on Iron Cycling Freshwater Seep ing Microscopy Cultiv GQ339

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FJ682062.1 gg_id:511125 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6820
FJ680636.1 gg_id:516987 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6806
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EU530308.1 gg_id:259951 mucosa adherent and invasive microbes profile adenoma colorectal cancer clone M4 EU5303
AJ515915.1 gg_id:94902 Ruminococcus sp. str. 25F8 AJ5159
EU469049.1 gg_id:298925 Speke's gazelle feces clone SP2_e03_1 EU469
DQ823690.1 gg_id:198813 human fecal clone RL250_aaj77f11 DQ823
EF686591.1 gg_id:242020 Sequences Manifest Rumen Yunnan Yel Cattle (Bos Taurus) rumen fluid clone YNRC8 EF6865
FJ363110.1 gg_id:367447 feces adult twins and mothers; TS148 clone TS148_a03b09 FJ3631
DQ394694.1 gg_id:156441 on -Arctic peninsula Svalbard Norway determined genes and rumen isolates reindee DQ394
EF402563.1 gg_id:208165 human fecal clone SJTU_B_09_56 EF4025
EF406472.1 gg_id:217186 mouse colon clone control_14days-C5 EF4064
EU472052.1 gg_id:294107 francois langur feces clone FL_1aaa01f10 EU472
AY916385.1 gg_id:114000 human stool clone D739 AY9163
EU767209.1 gg_id:331645 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C2 EU767
DQ394690.1 gg_id:155809 on -Arctic peninsula Svalbard Norway determined genes and rumen isolates reindee DQ394
FJ675754.1 gg_id:527270 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6757
DQ807190.1 gg_id:189116 human fecal clone RL244_aaj47d03 DQ807
FJ674069.1 gg_id:515630 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6740
EU469135.1 gg_id:302167 Speke's gazelle feces clone SP3_a09_1 EU469
FJ682410.1 gg_id:527856 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6824
EU774116.1 gg_id:318581 Chimpanzee feces clone CHIMP1_aaj39e09 EU774
EU475424.1 gg_id:295802 springbok feces clone SBSD_aaa04c06 EU475
EU843667.1 gg_id:322552 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
FJ685421.1 gg_id:527958 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6854
EU381538.1 gg_id:269531 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid EU381
AM404501.2 gg_id:563164 percent G+C fraction libraries number Actinobacteria human faecal clone AP08K.26 AM404
EU748111.1 gg_id:311383 neotropical folivorous flying bird adult hoatzin crop clone hoa2_42a10 EU748
GQ491920.1 gg_id:539328 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
FJ371896.1 gg_id:365465 feces adult twins and mothers; TS8 clone TS8_a03d11 FJ3718
GQ493718.1 gg_id:581908 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
FJ366766.1 gg_id:362381 feces adult twins and mothers; TS27 clone TS27_a03f03 FJ3667
DQ798110.1 gg_id:181710 human fecal clone RL302_aal95f05 DQ798
EF402950.1 gg_id:207652 human fecal clone SJTU_B_14_66 EF4029
EU460195.1 gg_id:300508 mammals their gut microbes eastern black and white colobus feces clone COL_aai16 EU460
EU460164.1 gg_id:290723 mammals their gut microbes eastern black and white colobus feces clone COL_aai15 EU460
EU774396.1 gg_id:323229 mammals their gut microbes Eastern Black and White Colobus feces clone COL_aai1 EU774
DQ673538.1 gg_id:172967 rumen fluid clone GRC73 DQ673

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GQ491705.1 gg_id:560898 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
FJ364282.1 gg_id:361072 feces adult twins and mothers; TS15 clone TS15_a01b03 FJ3642
GQ896914.1 gg_id:562943 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do GQ896
EU774563.1 gg_id:341482 Douc langur feces clone DL_2aaa04b11 EU774
DQ798279.1 gg_id:191890 human fecal clone RL181_aah40a10 DQ798
FJ366403.1 gg_id:356858 feces adult twins and mothers; TS26 clone TS26_a02f09 FJ3664
FJ363910.1 gg_id:369703 feces adult twins and mothers; TS14 clone TS14_a04g08 FJ3639
DQ794459.1 gg_id:186667 human fecal clone RL197_aah88b08 DQ794
AB185770.1 gg_id:104606 rumen clone U29-C11 AB185
FJ363821.1 gg_id:362970 feces adult twins and mothers; TS14 clone TS14_a03g05 FJ3638
FJ365359.1 gg_id:367180 feces adult twins and mothers; TS20 clone TS20_a02a02 FJ3653
FJ364504.1 gg_id:360766 feces adult twins and mothers; TS15 clone TS15_a03g02 FJ3645
FM873540.1 gg_id:367036 occupant source house mattress dust clone MA02D04 FM873
GQ043070.1 gg_id:381331 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1012h GQ043
FJ832323.1 gg_id:590062 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P1Q301_23G03 FJ8323
FJ365570.1 gg_id:357204 feces adult twins and mothers; TS20 clone TS20_a04d09 FJ3655
GQ493584.1 gg_id:541439 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
FJ372016.1 gg_id:357258 feces adult twins and mothers; TS8 clone TS8_a04g10 FJ3720
EU344162.1 gg_id:272649 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU344
EU460201.1 gg_id:299680 mammals their gut microbes eastern black and white colobus feces clone COL_aai16 EU460
DQ804617.1 gg_id:195090 human fecal clone RL187_aao70d11 DQ804
FJ365420.1 gg_id:368081 feces adult twins and mothers; TS20 clone TS20_a02f09 FJ3654
EU381440.1 gg_id:262572 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid EU381
FJ365555.1 gg_id:367799 feces adult twins and mothers; TS20 clone TS20_a04c05 FJ3655
FJ363045.1 gg_id:363989 feces adult twins and mothers; TS148 clone TS148_a02c09 FJ3630
AB034019.1 gg_id:33345 rumen clone 4C0d-6 AB034
AB034029.1 gg_id:19747 rumen clone 4C0d-16 AB034
DQ798127.1 gg_id:190960 human fecal clone RL302_aal95g12 DQ798
FJ366384.1 gg_id:366039 feces adult twins and mothers; TS26 clone TS26_a02d05 FJ3663
FJ367406.1 gg_id:364014 feces adult twins and mothers; TS29 clone TS29_a03b05 FJ3674
FJ833984.1 gg_id:512314 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P2Q202_78F10 FJ8339
EU381844.1 gg_id:262632 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU381
EU344365.1 gg_id:265090 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU344
EU530508.1 gg_id:270438 mucosa adherent and invasive microbes adenoma colorectal cancer profile non-ader EU530
FJ374224.1 gg_id:367864 Inter- and intraspecific humivorous scarab beetle larvae (Pachnoda spp.) larval hindg FJ3742
EU474848.1 gg_id:290278 takin feces clone TAK_aaa04h07 EU474
FJ881036.1 gg_id:380392 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8810
EF614895.1 gg_id:232257 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o EF6148
EU475330.1 gg_id:292243 rock hyrax feces clone RHSD_aaa03a07 EU475
EU777851.1 gg_id:345556 European rabbit feces clone RA_b02_1 EU777
DQ815323.1 gg_id:168054 mouse cecum clone aab45e04 DQ815

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GQ449203.1 gg_id:581463 Microbiome neonatal calves: shedding microorganisms fecal clone calf784_10wks_g GQ449
EU459351.1 gg_id:299233 cheetah feces clone CE3_aai05b03 EU459
EU009811.1 gg_id:253896 intestinal microbiota domestic and wild turkeys turkey cecum clone WTB_F48 EU009
AY791247.1 gg_id:109481 insect associated clone PBg1-130 AY791
DQ815450.1 gg_id:165952 mouse cecum clone aab48f03 DQ815
FJ365258.1 gg_id:369294 feces adult twins and mothers; TS1 clone TS1_a04g01 FJ3652
EU472325.1 gg_id:294908 Angola colobus feces clone EAC_1aaa01g09 EU472
FJ365014.1 gg_id:360002 feces adult twins and mothers; TS1 clone TS1_a01h01 FJ3650
EU507046.1 gg_id:270303 cecal contents Mus musculus strain C57BL/6J; MD21 clone MD21_aar10d04 EU507
FJ366853.1 gg_id:359339 feces adult twins and mothers; TS27 clone TS27_a04f04 FJ3668
X81125.1 gg_id:16072 Clostridium viride str. T2-7 (DSM 6836) X81125
EF614670.1 gg_id:234137 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o EF6146
EU470243.1 gg_id:295095 trancaspain urial feces clone TU2_aaa01f08 EU470
FJ680615.1 gg_id:519246 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6806
DQ809155.1 gg_id:198744 human fecal clone RL308_aal82e06 DQ809
DQ326189.1 gg_id:147297 Metagenomic gut microbiome healthy human stool clone C101 DQ326
EU509226.1 gg_id:275461 cecal contents Mus musculus strain C57BL/6J; MD8 clone MD8_aap46b06 EU509
FJ172853.1 gg_id:303627 Qinghai Yak Ruminal and Fungi China rumen clone RB-3F5 FJ1728
AB185764.1 gg_id:100135 rumen clone U29-C04 AB185
EU465598.1 gg_id:302257 argali sheep feces clone AS1_aao39a10.Contig1 EU465
DQ394300.1 gg_id:152583 Effect probiotics on gastrointestinal broilers intestine clone BY12 DQ394
EU844875.1 gg_id:342940 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
EU471673.1 gg_id:298819 Asiatic elephant feces clone AE1_aaa02c06 EU471
EU464154.1 gg_id:300628 reticulated giraffe feces clone gir_aah95a09 EU464
DQ057394.1 gg_id:130048 chicken ileum/cecum clone cc345 DQ057
EU511908.1 gg_id:260762 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_aak11a08 EU511
EU452998.1 gg_id:332814 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83 EU452
EU843264.1 gg_id:339035 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
DQ815824.1 gg_id:168145 mouse cecum clone aab22g08 DQ815
EF098064.1 gg_id:194182 mouse cecum clone SWPT14_aaa01a06 EF098
EU464416.1 gg_id:297278 hamadryas baboon feces clone AFBAB_aai04g02 EU464
FJ367833.1 gg_id:362395 feces adult twins and mothers; TS2 clone TS2_a04b03 FJ3678
AB234457.1 gg_id:149078 termite gut homogenate clone MgMjD-041 AB234
FJ681152.1 gg_id:530945 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6811
EU382058.1 gg_id:272613 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU382
EU506544.1 gg_id:270066 cecal contents Mus musculus strain C57BL/6J; MD19 clone MD19_aaa03g02 EU506
EU509962.1 gg_id:270866 cecal contents Mus musculus strain C57BL/6J; WD11 clone WD11_aak24d08 EU509
AJ488075.1 gg_id:66188 chlorobenzene-degrading consortium clone IA-24 AJ488
EU451755.1 gg_id:339667 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77 EU451
FJ365202.1 gg_id:365220 feces adult twins and mothers; TS1 clone TS1_a04a12 FJ3652

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EU776814.1 gg_id:339944 Mongoose lemur feces clone ML_aaj26e09 EU776
EU465532.1 gg_id:295223 argali sheep feces clone AS1_aao37a11.Contig1 EU465
EU458546.1 gg_id:301573 spotted hyena feces clone HY2_h08_2 EU458
FJ680266.1 gg_id:519941 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6802
AY992951.1 gg_id:130016 mouse cecum clone C22_k16 AY992
EU511675.1 gg_id:262671 cecal contents Mus musculus strain C57BL/6J; WD9 clone WD9_aak08g07 EU511
DQ815617.1 gg_id:167514 mouse cecum clone aab43f04 DQ815
EU844732.1 gg_id:340116 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
DQ805512.1 gg_id:181769 human fecal clone RL203_aai63f02 DQ805
EU468922.1 gg_id:289860 Speke's gazelle feces clone SP2_c09_1 EU468
FJ542840.1 gg_id:525763 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone A FJ5428
EU850604.1 gg_id:326444 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF436 EU850
EU774081.1 gg_id:352918 Chimpanzee feces clone CHIMP12_b04_1 EU774
NR_025025.1 gg_id:539939 Papillibacter cinnamivorans str. CIN1; DSM12816 NR_02
FJ374227.1 gg_id:369389 Inter- and intraspecific humivorous scarab beetle larvae (Pachnoda spp.) larval hindgu FJ3742
EF604698.1 gg_id:228902 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6046
FJ680261.1 gg_id:521792 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6802
EF096916.1 gg_id:175377 mouse cecum clone SWPT13_aaa02f07 EF0969
EU463678.1 gg_id:289426 domesticated horse feces clone horsej_aai90h08 EU463
EU506333.1 gg_id:270498 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aap63d10 EU506
DQ796729.1 gg_id:179422 human fecal clone RL179_aao53g02 DQ796
FJ684521.1 gg_id:532424 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6845
FJ880481.1 gg_id:373181 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8804
GQ047255.1 gg_id:375644 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1010e GQ047
EF403010.1 gg_id:204126 human fecal clone SJTU_B_15_54 EF403
EU465687.1 gg_id:302641 argali sheep feces clone AS2_aao33e07 EU465
AB198539.1 gg_id:135453 termite gut wall fraction clone RsW02-066 AB198
EU766175.1 gg_id:349740 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU766
FJ681934.1 gg_id:524439 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6819
EU470345.1 gg_id:292656 Grevy's zebra feces clone GZ_aaa01b08 EU470
AB192279.1 gg_id:143711 termite gut homogenate clone RPK-59 AB192
EU504413.1 gg_id:275288 cecal contents Mus musculus strain C57BL/6J; CRWD6 clone CRWD6_aaa03h04 EU504
EU470328.1 gg_id:297796 Grevy's zebra feces clone GZ_aaa04g03 EU470
DQ796579.1 gg_id:196210 human fecal clone RL179aan75b11 DQ796
DQ125557.1 gg_id:134357 uranium contaminated soil clone AKAU3538 DQ125
EU468690.1 gg_id:302712 okapi feces clone OK2_f06_1 EU468
EU871383.1 gg_id:351055 Genetic Bovine (Bos taurus) Rumen Thailand clone CF225 EU871
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EU505544.1 gg_id:258903 cecal contents Mus musculus strain C57BL/6J; myd5 clone myd5_aaa02d10 EU505

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EU765286.1 gg_id:344815 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B3 EU765
EU775069.1 gg_id:327573 Francois Langur feces clone FL_1aaa03e06 EU775
EF605057.1 gg_id:233530 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF605
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EU472220.1 gg_id:288423 francois langur feces clone FL_2aaa01e02 EU472
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EU777228.1 gg_id:305121 Okapi feces clone OK1_d05 EU777
EU507866.1 gg_id:273781 cecal contents Mus musculus strain C57BL/6J; MD24 clone MD24_aaa02d03 EU507
EU779203.1 gg_id:319642 Trancaspian Urial feces clone TU2_aaa03h10 EU779
EU504299.1 gg_id:268671 cecal contents Mus musculus strain C57BL/6J; CRWD6 clone CRWD6_aaa01h12 EU504
EU512008.1 gg_id:273519 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_aak12f05 EU512
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AF001761.1 gg_id:16027 rumen clone RF29 AF001
EU885041.1 gg_id:347991 microbial hindgut chamber Pomacanthus sexstriatus GI tract clone A2H7 EU885
FJ365158.1 gg_id:357678 feces adult twins and mothers; TS1 clone TS1_a03e11 FJ3651
EU779132.1 gg_id:356550 Trancaspian Urial feces clone TU2_aaa04c08 EU779
EU473497.1 gg_id:293727 Somali wild ass feces clone WA_aaa01h08 EU473
AY992778.1 gg_id:133495 mouse cecum clone C22_a17 AY992
EF401851.1 gg_id:216263 human fecal clone SJTU_D_05_87 EF4018
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EF445154.1 gg_id:210292 rabbit cecum clone NED2F7 EF4451
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EU779391.1 gg_id:345353 Somali Wild Ass feces clone WA_aaa01c12 EU779
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EU508202.1 gg_id:274847 cecal contents Mus musculus strain C57BL/6J; MD26 clone MD26_aaa03b05 EU508
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EU773165.1 gg_id:352908 BigHorn sheep feces clone BHSD_aaa01b04 EU773
GQ175508.1 gg_id:589507 Chicken intestinal microbiota modulations various feed supplementations DGGE and GQ175

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FJ880941.1 gg_id:410327 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8809
EU469833.1 gg_id:293546 western lowland gorilla feces clone GOR_aag72a09 EU469
EU772173.1 gg_id:312152 Argali sheep feces clone AS1_aao37d04.Contig1 EU772
AB185773.1 gg_id:105047 rumen clone U29-D02 AB185
EU850524.1 gg_id:331952 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF310 EU850
EU470209.1 gg_id:298302 trancaspain urial feces clone TU2_aaa02h10 EU470
EU472107.1 gg_id:290859 francois langur feces clone FL_1aaa01e09 EU472
EU463636.1 gg_id:292001 domesticated horse feces clone horsej_aai90b08 EU463
EU773172.1 gg_id:320029 BigHorn sheep feces clone BH2_aao23c10 EU773
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DQ014986.1 gg_id:131359 mouse cecum clone M1_1b09_1 DQ014
FJ881217.1 gg_id:371870 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8812
EU009770.1 gg_id:247551 intestinal microbiota domestic and wild turkeys turkey cecum clone DTB_AF39 EU009
FJ680773.1 gg_id:515004 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6807
EU454896.1 gg_id:327567 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83 EU454
EU772027.1 gg_id:354741 Argali sheep feces clone AS1_aao37a07.Contig1 EU772
EF071402.1 gg_id:187846 library survey and quantitative measurement major mucosa- IBD human colonic muc EF0714
EU844698.1 gg_id:306375 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
EU773275.1 gg_id:319693 BigHorn sheep feces clone BH1_aao25d09 EU773
AY858503.2 gg_id:110968 gastrointestinal tract eland clone ELAND_41 AY858
FJ680312.1 gg_id:532384 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6803
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FJ879227.1 gg_id:445626 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8792
EU506351.1 gg_id:271290 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aap64a01 EU506
EU776815.1 gg_id:333249 Mongoose lemur feces clone ML_aae88a09 EU776
EU779144.1 gg_id:321963 Trancaspian Urial feces clone TU2_aaa03b05 EU779
EU506252.1 gg_id:276388 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aap61d11 EU506
FJ680395.1 gg_id:515362 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6803
EU474545.1 gg_id:297237 bighorn sheep feces clone BHSD_aaa04e05 EU474
DQ809638.1 gg_id:195252 human fecal clone RL184_aan81h11 DQ809
FJ880264.1 gg_id:431899 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8802
FJ880708.1 gg_id:372146 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8807
GQ897911.1 gg_id:589989 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ897
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EU776496.1 gg_id:330252 Red Kangaroo feces clone KO1_aai41c09 EU776
DQ815620.1 gg_id:166466 mouse cecum clone aab43f08 DQ815
CU927388.1 gg_id:557458 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU927
EF401251.1 gg_id:207166 human fecal clone SJTU_D_07_85 EF4012

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DQ801156.1 gg_id:198841 human fecal clone RL116_aae99c04 DQ801
EU504194.1 gg_id:274083 cecal contents Mus musculus strain C57BL/6J; CRWD5 clone CRWD5_aaa03g11 EU504
EU777204.1 gg_id:347980 Okapi feces clone OK3_d02_3 EU777
FJ880790.1 gg_id:463116 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8807
FJ673102.1 gg_id:517347 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6731
EU468528.1 gg_id:293630 okapi feces clone OK1_a08_1 EU468
EU507527.1 gg_id:277388 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_2aaa04e12 EU507
EF098062.1 gg_id:190396 mouse cecum clone SWPT14_aaa01a03 EF098
FJ371773.1 gg_id:365161 feces adult twins and mothers; TS8 clone TS8_a02a09 FJ3717
AY854298.1 gg_id:110901 herbivore gastrointestinal tract clone Thompsons100 AY854
EF097074.1 gg_id:196191 mouse cecum clone SWPT18_aaa01a07 EF097
EU464390.1 gg_id:303345 hamadryas baboon feces clone AFBAB_aai04b12 EU464
CU926151.1 gg_id:562681 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU926
EU468950.1 gg_id:294437 Speke's gazelle feces clone SP2_g12 EU468
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EF096746.1 gg_id:193198 mouse cecum clone SWPT11_aaa04a09 EF0967
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EU771790.1 gg_id:333206 African elephant feces clone AFEL3_aao14d01 EU771
EU464228.1 gg_id:292382 reticulated giraffe feces clone gir_aah96f04 EU464
EU458586.1 gg_id:292513 European rabbit feces clone RA_d11 EU458
EU794151.1 gg_id:307643 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_H9 EU794
EU471983.1 gg_id:293667 francois langur feces clone FL_1aaa01h03 EU471
DQ808904.1 gg_id:175511 human fecal clone RL243_aai86g11 DQ808
FJ366541.1 gg_id:363783 feces adult twins and mothers; TS27 clone TS27_a01a02 FJ3665
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EU456560.1 gg_id:321019 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU456
EU452476.1 gg_id:313021 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83N EU452
EU506190.1 gg_id:273910 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aaa03a05 EU506
EU469336.1 gg_id:287585 springbok feces clone SBK_f11 EU469
EU766271.1 gg_id:340006 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU766
EU475523.1 gg_id:289882 springbok feces clone SBSD_aaa01f06 EU475
EU509854.1 gg_id:264775 cecal contents Mus musculus strain C57BL/6J; WD11 clone WD11_aak22e06 EU509
EU776270.1 gg_id:344111 Red Kangaroo feces clone KO2_aai18g10 EU776

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EF099665.1 gg_id:196556 mouse cecum clone SWPT4_aaa02f04 EF0996
EU622645.1 gg_id:281242 -feed administered sub-therapeutic chlorotetracycline alters structure and but not a EU622
EF097943.1 gg_id:194809 mouse cecum clone SWPT12_aaa02e11 EF0979
EU504880.1 gg_id:266512 cecal contents Mus musculus strain C57BL/6J; myd2 clone myd2_aaa03f12 EU5048
EU465571.1 gg_id:292962 argali sheep feces clone AS1_aao38b02.Contig1 EU465
FJ879507.1 gg_id:400748 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8795
EU506869.1 gg_id:266845 cecal contents Mus musculus strain C57BL/6J; MD21 clone MD21_aar07e08 EU5068
EU472333.1 gg_id:297020 Angola colobus feces clone EAC_1aaa02f01 EU4723
FJ681547.1 gg_id:527760 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6815
EF096100.1 gg_id:192849 mouse cecum clone lean2_aaa04b06 EF0961
AM405156.2 gg_id:564320 percent G+C fraction libraries number Actinobacteria human faecal clone AP11K.15 AM405
EU506930.1 gg_id:264668 cecal contents Mus musculus strain C57BL/6J; MD21 clone MD21_aar08e06 EU5069
EU773138.1 gg_id:329808 BigHorn sheep feces clone BH1_aao27h11 EU7731
EU470403.1 gg_id:290531 Grevy's zebra feces clone GZ_aaa01c07 EU4704
EF098922.1 gg_id:199445 mouse cecum clone SWPT1_aaa03c09 EF0989
AF371795.1 gg_id:48325 swine intestine clone p-2027-s959-5 AF3717
FJ880774.1 gg_id:377756 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8807
DQ825126.1 gg_id:186321 human fecal clone RL185_aan85f09 DQ825
GU302815.1 gg_id:593396 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU302
DQ815699.1 gg_id:162151 mouse cecum clone aab21b05 DQ815
EU779200.1 gg_id:348872 Trancaspian Urial feces clone TU2_aaa03a08 EU7792
EU463773.1 gg_id:299331 domesticated horse feces clone horsej_aai92f01 EU4637
EF434333.1 gg_id:205309 gastrointestinal tract microbiota microarray reference pool created pooling products EF4343
EU506958.1 gg_id:269532 cecal contents Mus musculus strain C57BL/6J; MD21 clone MD21_aar08h10 EU5069
EU843115.1 gg_id:353088 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8431
FJ833519.1 gg_id:557177 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J1Q301_40H05 FJ8335
DQ014588.1 gg_id:131678 mouse cecum clone M1_d04 DQ014
AF129864.1 gg_id:16031 microbial anaerobic digestor determined clone BC09 AF1298
DQ326172.1 gg_id:146132 Metagenomic gut microbiome healthy human stool clone C071 DQ326
EU511693.1 gg_id:263255 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_aaf07a12 EU5116
AY244908.1 gg_id:85153 cow rumen clone BF30 AY2449
EU532006.1 gg_id:268937 Predominant role host genetics controlling gut microbiota FMF remission stool clone EU5320
FJ371294.1 gg_id:357511 feces adult twins and mothers; TS6 clone TS6_a03c05 FJ3712
FJ674035.1 gg_id:529236 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6740
AB264082.1 gg_id:194322 Fecal microbial (dugong dugon) determined genes Dugong feces clone dgD-185 AB2640
EU773210.1 gg_id:306212 BigHorn sheep feces clone BH1_aao27f06 EU7732
EU772832.1 gg_id:308307 Bush dog feces clone bdog1_aai77b11 EU7728
EU458006.1 gg_id:327808 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83 EU4580
EU451213.1 gg_id:327675 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80 EU4512
EF454073.2 gg_id:224826 termite hindgut clone 290cost002-P3L-1599 EF4540

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EU468277.1 gg_id:294117 domesticated horse feces clone horsej_c02 EU468
EU509543.1 gg_id:272048 cecal contents Mus musculus strain C57BL/6J; MD9 clone MD9_aap60e08 EU509
EU622710.1 gg_id:278359 -feed administered sub-therapeutic chlorotetracycline alters structure and but not a EU622
EF602807.1 gg_id:230994 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6028
EU468306.1 gg_id:289975 domesticated horse feces clone horsem_e06_1 EU468
GQ451226.1 gg_id:592773 Fecal Yunnan snub-nosed monkey feces clone J132 GQ451
EU458596.1 gg_id:292888 European rabbit feces clone RA_a12_1 EU458
EU510699.1 gg_id:277228 cecal contents Mus musculus strain C57BL/6J; WD5 clone WD5_aak39e11 EU510
EU344213.1 gg_id:258933 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU344
EU344226.1 gg_id:268753 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU344
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EU381463.1 gg_id:261686 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid EU381
EU474449.1 gg_id:299201 bighorn sheep feces clone BHSD_aaa02c08 EU474
DQ815474.1 gg_id:164242 mouse cecum clone aab41c04 DQ815
FJ880592.1 gg_id:433422 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8805
EU469205.1 gg_id:301405 Speke's gazelle feces clone SP3_a12_1 EU469
DQ673520.1 gg_id:172035 rumen fluid clone GRC55 DQ673
EF099878.1 gg_id:194478 mouse cecum clone SWPT5_aaa01f08 EF0998
EU509449.1 gg_id:273706 cecal contents Mus musculus strain C57BL/6J; MD9 clone MD9_aap58e09 EU509
EF097158.1 gg_id:173971 mouse cecum clone SWPT18_aaa02c05 EF0971
GU174120.1 gg_id:543168 Microbial Bactrian camel estimated rumen clone XJC50 GU174
EU509440.1 gg_id:270062 cecal contents Mus musculus strain C57BL/6J; MD9 clone MD9_aap58d07 EU509
FJ880832.1 gg_id:455786 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8808
EF099659.1 gg_id:184823 mouse cecum clone SWPT4_aaa02e08 EF0996
EF025238.1 gg_id:182479 Examination microbial ecology avian vivo bromodeoxyuridine intestine clone B5_B31 EF0252
EU779173.1 gg_id:305394 Trancaspian Urial feces clone TU2_aaa04c09 EU779
AY916365.1 gg_id:113336 human stool clone D330 AY9163
FJ681328.1 gg_id:511240 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6813
EU470398.1 gg_id:300619 Grevy's zebra feces clone GZ_aaa03g04 EU470
AF129861.1 gg_id:16034 anaerobic digestor clone BA18 AF1298
EU457607.1 gg_id:349783 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H78 EU457
EU472116.1 gg_id:295144 francois langur feces clone FL_1aaa01h04 EU472
EU469146.1 gg_id:299718 Speke's gazelle feces clone SP3_c02_1 EU469
EU506974.1 gg_id:275040 cecal contents Mus musculus strain C57BL/6J; MD21 clone MD21_aar09c01 EU506
AB189696.1 gg_id:113007 termite gut homogenate clone Tc-64 AB189
EU844447.1 gg_id:310518 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
AF371933.1 gg_id:41628 swine intestine clone p-5013-2Wa5 AF371
EF099118.1 gg_id:179933 mouse cecum clone SWPT2_aaa02e09 EF0991
AB486052.1 gg_id:579562 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC AB486

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EU509869.1 gg_id:264539 cecal contents Mus musculus strain C57BL/6J; WD11 clone WD11_aak22h01 EU5098
EU509336.1 gg_id:259091 cecal contents Mus musculus strain C57BL/6J; MD8 clone MD8_aap48c05 EU5093
EU471605.1 gg_id:301418 Asiatic elephant feces clone AE1_aaa03h12 EU4716
DQ532267.1 gg_id:170620 Geographical Variation Microbial Burden and Spacecraft Assembly Johnson Space Ce DQ532
EU465548.1 gg_id:298616 argali sheep feces clone AS1_aao37d10.Contig1 EU4655
DQ014996.1 gg_id:133446 mouse cecum clone M1_1d03_1 DQ014
EF603680.1 gg_id:234600 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6036
EU461342.1 gg_id:291171 red kangaroo feces clone KO2_aai18a02 EU4613
EU358720.1 gg_id:326879 structure archaeal denaturing gel electrophoresis and sequencing mesophilic biogas EU3587
EU463535.1 gg_id:298695 domesticated horse feces clone horsem_aai95f08 EU4635
EU458633.1 gg_id:291920 European rabbit feces clone RA_c10_1 EU4586
EU509225.1 gg_id:262672 cecal contents Mus musculus strain C57BL/6J; MD8 clone MD8_aap46b05 EU5092
FJ684123.1 gg_id:521615 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6841
AB185802.1 gg_id:102301 rumen clone U29-G04 AB1858
FJ680288.1 gg_id:525143 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6802
EU776832.1 gg_id:336032 Mongoose lemur feces clone ML_aae88b01 EU7768
EU779365.1 gg_id:329869 Somali Wild Ass feces clone WA_aaa03g09 EU7793
AB486861.1 gg_id:578216 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCORC AB4868
DQ794759.1 gg_id:186541 human fecal clone RL240_aaj32a06 DQ794
AB185813.1 gg_id:107450 rumen clone U29-H08 AB1858
EU506784.1 gg_id:271281 cecal contents Mus musculus strain C57BL/6J; MD20 clone MD20_aap56c02 EU5067
FJ880114.1 gg_id:433722 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8801
EU844375.1 gg_id:340263 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8443
FJ880118.1 gg_id:418903 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8801
FJ365102.1 gg_id:364621 feces adult twins and mothers; TS1 clone TS1_a02h02 FJ3651
EF402847.1 gg_id:215231 human fecal clone SJTU_B_13_26 EF4028
EU773239.1 gg_id:312805 BigHorn sheep feces clone BH1_aao26d11 EU7732
DQ809188.1 gg_id:186037 human fecal clone RL308_aal83a11 DQ809
EU511248.1 gg_id:258340 cecal contents Mus musculus strain C57BL/6J; WD8 clone WD8_aak17a12 EU5112
EF602935.1 gg_id:234474 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6029
DQ905668.1 gg_id:165979 human fecal clone 014C-E4 DQ905
FJ881201.1 gg_id:379762 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8812
EU451818.1 gg_id:313324 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU4518
FJ679087.1 gg_id:512339 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6790
AB192035.1 gg_id:143918 termite gut homogenate clone M2PB4-66 AB1920
EU453946.1 gg_id:328060 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83N EU4539
EU462528.1 gg_id:300388 Sumatran orangutan feces clone orang1_aai56d11 EU4625
FJ978658.1 gg_id:434584 feces clone CL_F_333 FJ9786
FJ681272.1 gg_id:525681 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6812
GQ502526.1 gg_id:571808 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf4- GQ502

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EU463410.1 gg_id:296065 domesticated horse feces clone horsem_aai93d03 EU463
EU775729.1 gg_id:326022 Horse feces clone horsem_aai93b08 EU775
GQ491853.1 gg_id:577408 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
AF376229.1 gg_id:46657 ckncm325-B3-50 clone AF376
AY992419.1 gg_id:133769 mouse cecum clone C23_c21 AY992
EF097039.1 gg_id:197925 mouse cecum clone SWPT13_aaa04e08 EF097
AF371792.1 gg_id:25957 swine intestine clone p-2479-18B5 AF371
EU773132.1 gg_id:340732 BigHorn sheep feces clone BH1_aao27g09 EU773
EU506308.1 gg_id:261877 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aap63a07 EU506
EF098273.1 gg_id:195904 mouse cecum clone SWPT14_aaa04a05 EF098
EU885034.1 gg_id:339994 microbial hindgut chamber Pomacanthus sexstriatus GI tract clone A2C1 EU885
EU462489.1 gg_id:289958 Sumatran orangutan feces clone orang1_aai55f11 EU462
FJ880091.1 gg_id:407216 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ880
AB307642.1 gg_id:272210 clay wall used Japanese traditional buildings clone R70 AB307
DQ799877.1 gg_id:193310 human fecal clone RL247_aaj21c06 DQ799
EU507770.1 gg_id:268725 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_aaa04e05 EU507
DQ057415.1 gg_id:131039 chicken ileum/cecum clone oc30 DQ057
EU453106.1 gg_id:304019 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83 EU453
AB192010.1 gg_id:144056 termite gut homogenate clone M2PT2-13 AB192
GQ448400.1 gg_id:571165 Microbiome neonatal calves: shedding microorganisms fecal clone calf783_6wks_gr GQ448
FJ368251.1 gg_id:358150 feces adult twins and mothers; TS3 clone TS3_a02a08 FJ368
AM176887.1 gg_id:161109 Recovery mangrove sediment clone SZB63 AM176
EU885033.1 gg_id:315891 microbial hindgut chamber Pomacanthus sexstriatus GI tract clone A2B3 EU885
EU775785.1 gg_id:348949 Horse feces clone horsem_aai93g06 EU775
GQ451286.1 gg_id:594119 Fecal Yunnan snub-nosed monkey feces clone J287 GQ451
EU507013.1 gg_id:273022 cecal contents Mus musculus strain C57BL/6J; MD21 clone MD21_aar09g09 EU507
EU779486.1 gg_id:338681 Grevy's Zebra feces clone GZ_aaa04a02 EU779
GQ448458.1 gg_id:565308 Microbiome neonatal calves: shedding microorganisms fecal clone calf783_10wks_g GQ448
EU508142.1 gg_id:271619 cecal contents Mus musculus strain C57BL/6J; MD26 clone MD26_aaa01d04 EU508
GU304152.1 gg_id:580305 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU304
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DQ805454.1 gg_id:178841 human fecal clone RL203_aai62h05 DQ805
DQ793317.1 gg_id:193865 human fecal clone RL199_aaj42b08 DQ793
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EF098326.1 gg_id:195497 mouse cecum clone SWPT14_aaa04g10 EF098
EU509792.1 gg_id:266715 cecal contents Mus musculus strain C57BL/6J; WD11 clone WD11_aak21b03 EU509
EU842787.1 gg_id:308413 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
EU871413.1 gg_id:321628 Genetic Bovine (Bos taurus) Rumen Thailand clone CF386 EU871
FJ880997.1 gg_id:373909 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8809
EF434371.1 gg_id:209327 human infant gastrointestinal tract microbiota stool mother babies 13 and 14 7 mont EF4343

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FJ881346.1 gg_id:454021 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8813
EU461799.1 gg_id:287883 white-faced saki feces clone Saki_aaj61c06 EU461
EU457236.1 gg_id:326950 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75M EU457
FJ366005.1 gg_id:369544 feces adult twins and mothers; TS25 clone TS25_a01f04 FJ3660
GQ502525.1 gg_id:578230 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf4- GQ502
EU771554.1 gg_id:350467 Hamadryas Baboon feces clone AFBAB_aai02d07 EU771
EU506866.1 gg_id:276749 cecal contents Mus musculus strain C57BL/6J; MD21 clone MD21_aar07e05 EU5068
EF603969.1 gg_id:231028 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6039
EU777238.1 gg_id:317218 Okapi feces clone OK3_b10 EU777
EU771370.1 gg_id:345938 Asiatic elephant feces clone AE2_aaa01h05 EU7713
EU509664.1 gg_id:276522 cecal contents Mus musculus strain C57BL/6J; WD10 clone WD10_aak46g10 EU509
EU842226.1 gg_id:335384 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU8422
DQ327001.1 gg_id:148379 Metagenomic gut microbiome healthy human stool clone E502 DQ327
EU794177.1 gg_id:313908 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_A02 EU7941
EU466381.1 gg_id:302069 bighorn sheep feces clone BH2_aao22g11 EU4663
EU464525.1 gg_id:301028 African elephant feces clone AFEL_aai30e12 EU4645
FJ393118.1 gg_id:358001 Fusing Biology Engineering Improve Power Output Microbial Fuel Cells microbial fuel FJ3931
EF604700.1 gg_id:234202 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6047
EU764407.1 gg_id:322133 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1 EU7644
EU469147.1 gg_id:292438 Speke's gazelle feces clone SP3_c03_1 EU4691
EU509134.1 gg_id:276902 cecal contents Mus musculus strain C57BL/6J; MD7 clone MD7_aap44e04 EU5091
FJ880490.1 gg_id:436835 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8804
FJ681177.1 gg_id:516395 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6811
DQ815618.1 gg_id:170926 mouse cecum clone aab43f05 DQ815
AB234447.1 gg_id:148791 termite gut homogenate clone MgMjD-018 AB2344
AY212772.1 gg_id:101572 equine manure clone wet70 AY2127
EU843894.1 gg_id:331387 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8438
EF445187.1 gg_id:216140 rabbit cecum clone NED3D6 EF4451
AY976153.1 gg_id:117430 human ascending colon mucosal biopsy clone LV48 AY9761
FJ365228.1 gg_id:367866 feces adult twins and mothers; TS1 clone TS1_a04d04 FJ3652
EU777385.1 gg_id:348651 Sumatran orangutan feces clone orang1_aai53h04 EU7773
AY916184.1 gg_id:113111 human ascending colon biopsy clone LV67 AY9161
EU458679.1 gg_id:295715 European rabbit feces clone RA_h01_3 EU4586
EU842293.1 gg_id:309123 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU8422
EU467441.1 gg_id:295906 Sumatran orangutan feces clone orang1_c01 EU4674
EU470041.1 gg_id:294340 trancaspain urial feces clone TU1_aaa02a08 EU4700
FJ879644.1 gg_id:422337 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8796
DQ326566.1 gg_id:148532 Metagenomic gut microbiome healthy human stool clone C748 DQ326
EU506557.1 gg_id:265758 cecal contents Mus musculus strain C57BL/6J; MD19 clone MD19_aaa04b04 EU5065
EU842386.1 gg_id:321135 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU8423
FJ678622.1 gg_id:528111 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6786

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AY975617.1 gg_id:115444 human ascending colon mucosal biopsy clone NB69 AY9756
GU304498.1 gg_id:543553 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU304
EF399731.1 gg_id:209830 human fecal clone SJTU_E_02_68 EF3997
EU505664.1 gg_id:276996 cecal contents Mus musculus strain C57BL/6J; myd5 clone myd5_aaa04d06 EU5056
DQ801199.1 gg_id:178252 human fecal clone RL116_aaf00g02 DQ801
FJ880144.1 gg_id:424613 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8801
EU777857.1 gg_id:355155 European rabbit feces clone RA_b07 EU7778
FJ880076.1 gg_id:422278 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8800
EF097727.1 gg_id:190646 mouse cecum clone SWPT20_aaa02g10 EF0977
EU473597.1 gg_id:288349 Somali wild ass feces clone WA_aaa02g11 EU4735
EU774656.1 gg_id:351422 Angola Colobus feces clone EAC_2_aaa04h09 EU7746
FJ879462.1 gg_id:382733 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8794
EU458617.1 gg_id:293735 European rabbit feces clone RA_f11 EU4586
EU506600.1 gg_id:270508 cecal contents Mus musculus strain C57BL/6J; MD20 clone MD20_aap53b03 EU5066
DQ793945.1 gg_id:186640 human fecal clone RL176_aah45f04 DQ793
EF097537.1 gg_id:198821 mouse cecum clone SWPT19_aaa04a09 EF0975
EU778171.1 gg_id:353173 feces clone RL388_aao93e04 EU7781
AB198472.1 gg_id:135737 termite gut wall fraction clone RsW01-038 AB1984
DQ815459.1 gg_id:171864 mouse cecum clone aab48g10 DQ815
EU506211.1 gg_id:260799 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aaa03h12 EU5062
EU509851.1 gg_id:275622 cecal contents Mus musculus strain C57BL/6J; WD11 clone WD11_aak22e03 EU5098
FJ366802.1 gg_id:369416 feces adult twins and mothers; TS27 clone TS27_a04a08 FJ3668
EU773296.1 gg_id:338000 BigHorn sheep feces clone BHSD_aaa03c07 EU7732
EU463669.1 gg_id:287931 domesticated horse feces clone horsej_aai90g05 EU4636
EU773231.1 gg_id:314186 BigHorn sheep feces clone BH1_aao25h07 EU7732
EU475075.1 gg_id:287835 visayam warty pig feces clone VWP_aaa03h03 EU4750
FJ367779.1 gg_id:363229 feces adult twins and mothers; TS2 clone TS2_a03e05 FJ3677
EU471638.1 gg_id:300851 Asiatic elephant feces clone AE1_aaa02g01 EU4716
GQ079310.1 gg_id:386396 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1231c GQ079
EU507314.1 gg_id:258637 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_2aaa01e06 EU5073
EU474530.1 gg_id:291888 bighorn sheep feces clone BHSD_aaa02b07 EU4745
EU506880.1 gg_id:274508 cecal contents Mus musculus strain C57BL/6J; MD21 clone MD21_aar07g01 EU5068
EU777156.1 gg_id:326925 Okapi feces clone OK2_f08_3 EU7771
AB034042.1 gg_id:17907 rumen clone 5C0d-9 AB0340
AF371791.1 gg_id:16559 swine intestine clone p-1617-c5 AF3717
EF096046.1 gg_id:178180 mouse cecum clone lean2_aaa02g07 EF0960
EU457632.1 gg_id:334251 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83 EU4576
EU009861.1 gg_id:240271 intestinal microbiota domestic and wild turkeys turkey cecum clone WTB_Z48 EU0098
FJ365000.1 gg_id:358904 feces adult twins and mothers; TS1 clone TS1_a01f08 FJ3650

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EU468603.1 gg_id:290441 okapi feces clone OK1_h02_2 EU468
EU474862.1 gg_id:299736 takin feces clone TAK_aaa03a09 EU474
EU774668.1 gg_id:351100 Angola Colobus feces clone EAC_2_aaa03g09 EU774
EF603972.1 gg_id:232943 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6039
EU506398.1 gg_id:270870 cecal contents Mus musculus strain C57BL/6J; MD19 clone MD19_aaa01b10 EU506
FJ879124.1 gg_id:378376 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8791
EU465599.1 gg_id:295748 argali sheep feces clone AS1_aao39a12.Contig1 EU465
FJ681681.1 gg_id:531339 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6816
EU777625.1 gg_id:329861 Sumatran orangutan feces clone orang1_aai56c01 EU777
FJ677944.1 gg_id:520833 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6779
EU622764.1 gg_id:278667 -feed administered sub-therapeutic chlorotetracycline alters structure and but not a EU622
EF404912.1 gg_id:208751 human fecal clone SJTU_G_08_79 EF4049
EU458619.1 gg_id:291348 European rabbit feces clone RA_g05_1 EU458
EU775085.1 gg_id:353620 Francois Langur feces clone FL_1aaa01f09 EU775
EU774718.1 gg_id:324219 Angola Colobus feces clone EAC_2_aaa04f11 EU774
EU777117.1 gg_id:338991 Okapi feces clone OK1_b05_2 EU777
DQ800867.1 gg_id:178242 human fecal clone RL183_aao04e06 DQ800
FJ366788.1 gg_id:362813 feces adult twins and mothers; TS27 clone TS27_a03h03 FJ3667
EU777072.1 gg_id:336005 Okapi feces clone OK3_g10_1 EU777
EU779162.1 gg_id:315683 Trancaspian Urial feces clone TU2_aaa01f06 EU779
FJ880155.1 gg_id:400545 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8801
EF614841.1 gg_id:234630 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o EF6148
EU459641.1 gg_id:293767 ring-tailed lemur feces clone RT_aai09g11 EU459
FJ879015.1 gg_id:427159 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8790
EU463652.1 gg_id:296591 domesticated horse feces clone horsej_aai90d12 EU463
EU763460.1 gg_id:327692 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU763
DQ777916.1 gg_id:171499 rat feces clone R-1268 DQ777
FJ833370.1 gg_id:578399 Microbial Ecology Crop Folivorous Hoatzin crop contents clone A3Q301_90B12 FJ8333
EU458608.1 gg_id:295662 European rabbit feces clone RA_d09 EU458
EU344276.1 gg_id:277185 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU344
EU470451.1 gg_id:302165 Grevy's zebra feces clone GZ_aaa02d10 EU470
EU468576.1 gg_id:302061 okapi feces clone OK1_c08_3 EU468
EU509562.1 gg_id:275576 cecal contents Mus musculus strain C57BL/6J; MD9 clone MD9_aap60h04 EU509
EU466209.1 gg_id:300969 bighorn sheep feces clone BH1_aao28a09 EU466
FJ880004.1 gg_id:412229 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8800
EU457289.1 gg_id:342402 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H80 EU457
GQ448399.1 gg_id:511180 Microbiome neonatal calves: shedding microorganisms fecal clone calf783_6wks_gr GQ448
EU622765.1 gg_id:278758 -feed administered sub-therapeutic chlorotetracycline alters structure and but not a EU622
EU531935.1 gg_id:265234 Predominant role host genetics controlling gut microbiota FMF remission stool clone EU531
EU465629.1 gg_id:288944 argali sheep feces clone AS1_aao40b11.Contig1 EU465

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EU843150.1 gg_id:310031 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8431
DQ815858.1 gg_id:166226 mouse cecum clone aab23c10 DQ815
EU844883.1 gg_id:317405 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8448
EU772004.1 gg_id:323702 Argali sheep feces clone AS2_aao36g03 EU7720
DQ243771.1 gg_id:143396 Archaeal and Geochemically Hot Springs Yellowstone National Park USA Obsidian Pc DQ243
EU469210.1 gg_id:292548 Speke's gazelle feces clone SP3_b05_2 EU4692
EU458577.1 gg_id:297073 European rabbit feces clone RA_b02 EU4585
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FJ880460.1 gg_id:466851 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8804
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DQ795724.1 gg_id:183479 human fecal clone RL245_aai81c09 DQ795
EU511442.1 gg_id:269418 cecal contents Mus musculus strain C57BL/6J; WD8 clone WD8_aak20d04 EU5114
EF096031.1 gg_id:183985 mouse cecum clone lean2_aaa02d05 EF0960
EU771896.1 gg_id:317870 Southern three-banded armadillo feces clone arma_a03 EU7718
GQ867355.1 gg_id:591284 and prevalence blaTEM genes Arctic seals colon content clone WSp112 GQ867
EF096279.1 gg_id:185967 mouse cecum clone obob1_aaa04a07 EF0962
EU471906.1 gg_id:300186 Asiatic elephant feces clone AE3_aaa02c07 EU4719
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EU747962.1 gg_id:303763 neotropical folivorous flying bird adult hoatzin crop clone hoa11_26B04 EU7479
EU504516.1 gg_id:260720 cecal contents Mus musculus strain C57BL/6J; myd1 clone myd1_aaa01f12 EU5045
EU511746.1 gg_id:265963 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_aaf08d08 EU5117
FJ833392.1 gg_id:580128 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J1Q101_40H05 FJ8333
FJ679065.1 gg_id:520809 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6790
AF371805.1 gg_id:51722 swine intestine clone p-1877-s962-3 AF3718
EU774701.1 gg_id:347085 Angola Colobus feces clone EAC_2_aaa02e10 EU7747
DQ394593.1 gg_id:155059 -Arctic peninsula Svalbard Norway determined genes and rumen isolates reindeer o DQ394
EF400162.1 gg_id:216310 human fecal clone SJTU_E_09_66 EF4001
DQ015070.1 gg_id:132441 mouse cecum clone M2_f11 DQ015
AY991978.1 gg_id:132424 mouse cecum clone C20_n22 AY9919
EU776363.1 gg_id:335362 Red Kangaroo feces clone KO1_aai43b06 EU7763
EF605058.1 gg_id:231459 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6050
EU505144.1 gg_id:273462 cecal contents Mus musculus strain C57BL/6J; myd3 clone myd3_aaa03e05 EU5051
FJ881001.1 gg_id:468255 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8810
FJ680493.1 gg_id:531808 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6804
EU473598.1 gg_id:290698 Somali wild ass feces clone WA_aaa02h04 EU4735
EF454508.2 gg_id:224436 termite hindgut clone 290cost002-P3L-2244 EF4545
GU174135.1 gg_id:539506 Microbial Bactrian camel estimated rumen clone XJC128 GU174
EU747942.1 gg_id:328823 neotropical folivorous flying bird adult hoatzin crop clone hoa13_91C12 EU7479

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EU465621.1 gg_id:301410 argali sheep feces clone AS1_aao40a08.Contig1 EU465
EU622694.1 gg_id:278901 -feed administered sub-therapeutic chlorotetracycline alters structure and but not a EU622
EU506877.1 gg_id:276273 cecal contents Mus musculus strain C57BL/6J; MD21 clone MD21_aar07f08 EU5068
AB270051.1 gg_id:166168 Influence temperature and humidity on heifers rumen contents Holstein heifer (Bos AB270
FJ879323.1 gg_id:408513 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8793
EF096450.1 gg_id:189527 mouse cecum clone obob2_aaa03a07 EF0964
EU779309.1 gg_id:309070 Visayam Warty Pig feces clone VWP_aaa02g07 EU7793
EU775150.1 gg_id:314421 Francois Langur feces clone FL_1aaa02a01 EU7751
EF603178.1 gg_id:228975 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6031
EU772202.1 gg_id:329529 Argali sheep feces clone AS1_aao39g01.Contig1 EU7722
EF644508.1 gg_id:253716 Structure and performance microbial involved reductive dechlorination 1122-tetrach EF6445
DQ805484.1 gg_id:181448 human fecal clone RL203_aai63c05 DQ805
GU120121.1 gg_id:538805 Real time ruminal microbial sheep fed hay or corn:hay mix adherent fraction rumen GU120
EU460085.1 gg_id:296424 mammals their gut microbes eastern black and white colobus feces clone COL_aai14 EU460
EU454100.1 gg_id:309302 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83M EU4541
FJ881171.1 gg_id:413391 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8811
EU453959.1 gg_id:341713 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H79S EU4539
EU843243.1 gg_id:336486 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8432
FJ369537.1 gg_id:358078 feces adult twins and mothers; TS51 clone TS51_a01g04 FJ3695
DQ815409.1 gg_id:170399 mouse cecum clone aab47f08 DQ815
EU507544.1 gg_id:270027 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_2aaa04g11 EU5075
EU451074.1 gg_id:355178 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H80M EU4510
EU470093.1 gg_id:292704 trancaspain urial feces clone TU1_aaa03h12 EU4700
DQ014710.1 gg_id:135420 mouse cecum clone M1_g07_1 DQ014
EU777884.1 gg_id:341092 European rabbit feces clone RA_g01 EU7778
FJ368283.1 gg_id:366143 feces adult twins and mothers; TS3 clone TS3_a02d09 FJ3682
GQ011731.1 gg_id:497935 Topographical and Temporal Human Skin Microbiome skin nare clone nbw744d05c1 GQ011
EU358724.1 gg_id:334839 structure archaeal denaturing gel electrophoresis and sequencing mesophilic biogas EU3587
EU773998.1 gg_id:331659 Cheetah feces clone CE3_aai07f02 EU7739
DQ801008.1 gg_id:194735 human fecal clone RL387_aao90g09 DQ801
EU842331.1 gg_id:332860 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU8423
EF098919.1 gg_id:177578 mouse cecum clone SWPT1_aaa03c05 EF0989
EU775419.1 gg_id:351927 Western lowland gorilla feces clone GOR_aag73e08 EU7754
FJ880305.1 gg_id:398138 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8803
FJ680934.1 gg_id:508925 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6809
EU506923.1 gg_id:273345 cecal contents Mus musculus strain C57BL/6J; MD21 clone MD21_aar08d09 EU5069
AB192011.1 gg_id:144692 termite gut homogenate clone M1NP1-81 AB1920
EU503919.1 gg_id:273549 cecal contents Mus musculus strain C57BL/6J; CRWD4 clone CRWD4_aaa02f03 EU5039
FJ881052.1 gg_id:397444 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8810
EU771330.1 gg_id:336513 Asiatic elephant feces clone AE2_aaa02f07 EU7713
EU468977.1 gg_id:292793 Speke's gazelle feces clone SP2_c06 EU4689

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EF097622.1 gg_id:180235 mouse cecum clone SWPT20_aaa01d09 EF0976
DQ806289.1 gg_id:180565 human fecal clone RL186_aan89h10 DQ806
GQ491367.1 gg_id:549281 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
EU458674.1 gg_id:288936 European rabbit feces clone RA_f11_2 EU458
DQ455867.1 gg_id:158230 pre-adolescent turkey cecum clone CFT19E6 DQ455
EU850450.1 gg_id:333245 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF12 EU850
AF001758.1 gg_id:16019 rumen clone RF26 AF001
FJ683056.1 gg_id:523244 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6830
FJ681401.1 gg_id:531867 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6814
EF406825.1 gg_id:205987 mouse colon clone infected_28days-D10 EF4068
EU511801.1 gg_id:260417 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_09d04.Contig2 EU5118
DQ799972.1 gg_id:190124 human fecal clone RL247_aaj22e08 DQ799
EU776838.1 gg_id:310416 Mongoose lemur feces clone ML_aae89e01 EU7768
DQ795909.1 gg_id:183187 human fecal clone RL245_aai84f06 DQ795
DQ327133.1 gg_id:145883 Metagenomic gut microbiome healthy human stool clone E652 DQ327
EU773365.1 gg_id:332481 BigHorn sheep feces clone BH1_aao26a07 EU7733
EU774411.1 gg_id:326991 mammals their gut microbes Eastern Black and White Colobus feces clone COL_aai1 EU7744
EU888005.1 gg_id:315439 Microbial structure hydrolytic stage two-stage anaerobic digestion grass silage leach EU8880
EU465646.1 gg_id:293696 argali sheep feces clone AS1_aao40f11.Contig1 EU4656
EF406869.1 gg_id:206744 mouse colon clone infected_28days-G8 EF4068
FJ172851.1 gg_id:336231 Qinghai Yak Ruminal and Fungi China rumen clone RB-3E10 FJ1728
EU459663.1 gg_id:297045 ring-tailed lemur feces clone RT_aai10d08 EU4596
FJ880548.1 gg_id:439880 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8805
EU344680.1 gg_id:264114 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU3446
AB234482.1 gg_id:146578 termite gut homogenate clone MgMjR-021 AB2344
DQ796871.1 gg_id:197125 human fecal clone RL179_aao55g01 DQ796
EU468696.1 gg_id:290392 okapi feces clone OK2_g05_1 EU4686
EU467108.1 gg_id:288100 mongoose lemur feces clone ML_aae88d09 EU4671
FJ367531.1 gg_id:365767 feces adult twins and mothers; TS29 clone TS29_a04f07 FJ3675
DQ326345.1 gg_id:145888 Metagenomic gut microbiome healthy human stool clone C336 DQ326
FJ367522.1 gg_id:357913 feces adult twins and mothers; TS29 clone TS29_a04e09 FJ3675
EF402491.1 gg_id:212641 human fecal clone SJTU_B_08_60 EF4024
EU462180.1 gg_id:291266 black-handed spider monkey feces clone SPIM_aaj36f07 EU4621
DQ904856.1 gg_id:173724 human fecal clone 001C-c7 DQ904
FJ365644.1 gg_id:365410 feces adult twins and mothers; TS21 clone TS21_a01c11 FJ3656
FJ367519.1 gg_id:364229 feces adult twins and mothers; TS29 clone TS29_a04e06 FJ3675
DQ825169.1 gg_id:178670 human fecal clone RL185_aan86c02 DQ825
DQ794729.1 gg_id:186912 human fecal clone RL240_aaj31f06 DQ794
FJ362635.1 gg_id:361266 feces adult twins and mothers; TS13 clone TS13_a01c12 FJ3626
FJ367119.1 gg_id:368394 feces adult twins and mothers; TS28 clone TS28_a03g02 FJ3671

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DQ800988.1 gg_id:199182 human fecal clone RL387_aao90d10 DQ800
FJ367903.1 gg_id:358152 feces adult twins and mothers; TS2 clone TS2_a04h08 FJ3679
DQ805771.1 gg_id:182051 human fecal clone RL306aal90g11 DQ805
DQ801641.1 gg_id:186456 human fecal clone RL117_aae93c11 DQ801
FJ365197.1 gg_id:361811 feces adult twins and mothers; TS1 clone TS1_a04a07 FJ3651
EU771688.1 gg_id:349437 African elephant feces clone AFYEL_aaj67g07 EU771
AF376218.1 gg_id:73575 ckncm314-B7-17 clone AF3762
FJ683715.1 gg_id:524587 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6837
FJ366945.1 gg_id:359422 feces adult twins and mothers; TS28 clone TS28_a01f06 FJ3669
DQ797744.1 gg_id:174636 human fecal clone RL206_aaj15d05 DQ797
EU767217.1 gg_id:325765 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C2 EU767
DQ801018.1 gg_id:187632 human fecal clone RL387_aao91a03 DQ801
EU765302.1 gg_id:319980 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B3 EU765
EU778932.1 gg_id:336217 Black-handed Spider Monkey feces clone SPIM_g09 EU778
EU773495.1 gg_id:311824 Bonobo feces clone BNO_aaa01e06 EU773
EF434341.1 gg_id:214444 human infant gastrointestinal tract microbiota stool mother baby 3 day delivery clon EF4343
DQ794628.1 gg_id:196233 human fecal clone RL240_aaj30d10 DQ794
EU766126.1 gg_id:344856 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU766
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DQ798600.1 gg_id:199246 human fecal clone RL181_aan98g09 DQ798
DQ797494.1 gg_id:182059 human fecal clone RL248_aaj00a11 DQ797
EU768767.1 gg_id:330678 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C5 EU768
DQ905339.1 gg_id:170592 human fecal clone 013B-F1 DQ905
DQ456222.1 gg_id:157966 pre-adolescent turkey cecum clone CFT29G11 DQ456
DQ793929.1 gg_id:198885 human fecal clone RL176_aah45d07 DQ793
FJ363399.1 gg_id:368137 feces adult twins and mothers; TS149 clone TS149_a02g05 FJ3633
DQ810085.1 gg_id:194784 human fecal clone RL184_aao67h08 DQ810
DQ905150.1 gg_id:170385 human fecal clone 002C-e3 DQ905
DQ808308.1 gg_id:199463 human fecal clone RL180_aao75b02 DQ808
FJ367475.1 gg_id:364674 feces adult twins and mothers; TS29 clone TS29_a04a04 FJ3674
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DQ798340.1 gg_id:194552 human fecal clone RL181_aah41b08 DQ798
AF376220.1 gg_id:72147 ckncm316-B4-5 clone AF3762
DQ325549.1 gg_id:150385 Metagenomic gut microbiome healthy human stool clone B006 DQ325
DQ905891.1 gg_id:162492 human fecal clone 29c-c1 DQ905
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EF403280.1 gg_id:212619 human fecal clone SJTU_A1_3_61 EF4032

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AF371716.1 gg_id:46691 swine intestine clone p-2814-24E5 AF3717
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EU767122.1 gg_id:342124 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU767
FJ363687.1 gg_id:359284 feces adult twins and mothers; TS14 clone TS14_a02b04 FJ3636
FJ363795.1 gg_id:367084 feces adult twins and mothers; TS14 clone TS14_a03d09 FJ3637
DQ455909.1 gg_id:158360 pre-adolescent turkey cecum clone CFT111A10 DQ455
EU728786.1 gg_id:334557 Subdoligranulum sp. str. DJF_VR33k2 EU728
GQ175440.1 gg_id:594206 Chicken intestinal microbiota modulations various feed supplementations DGGE anc GQ175
AB264065.1 gg_id:187741 Fecal microbial (dugong dugon) determined genes Dugong feces clone dgD-25 AB264
DQ793941.1 gg_id:193786 human fecal clone RL176_aah45e09 DQ793
DQ798183.1 gg_id:186702 human fecal clone RL302_aal96e09 DQ798
EU461689.1 gg_id:301750 mongoose lemur feces clone ML_aaj27b12 EU461
EU768362.1 gg_id:335270 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C5 EU768
EU766446.1 gg_id:339125 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU766
EU768798.1 gg_id:319831 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C5 EU768
DQ794902.1 gg_id:181213 human fecal clone RL310_aam37g03 DQ794
DQ797996.1 gg_id:178744 human fecal clone RL302_aal94c11 DQ797
FJ682973.1 gg_id:514399 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6829
DQ810168.1 gg_id:184292 human fecal clone RL184_aao68g11 DQ810
DQ905437.1 gg_id:168776 human fecal clone 013C-F11 DQ905
FJ372141.1 gg_id:367989 feces adult twins and mothers; TS9 clone TS9_a02b11 FJ3721
FJ365745.1 gg_id:367703 feces adult twins and mothers; TS21 clone TS21_a02e04 FJ3657
DQ807932.1 gg_id:176619 human fecal clone RL180_aan69d03 DQ807
DQ809649.1 gg_id:178390 human fecal clone RL184_aan82b04 DQ809
DQ795975.1 gg_id:188631 human fecal clone RL202_aai49f12 DQ795
FJ363732.1 gg_id:361579 feces adult twins and mothers; TS14 clone TS14_a02f05 FJ3637
FJ368274.1 gg_id:360904 feces adult twins and mothers; TS3 clone TS3_a02c10 FJ3682
DQ799468.1 gg_id:193053 human fecal clone RL305aal86f07 DQ799

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EF445171.1 gg_id:205155 rabbit cecum clone NED1B8 EF4451
DQ801703.1 gg_id:185329 human fecal clone RL201_aai45g05 DQ801
DQ823743.1 gg_id:188160 human fecal clone RL250_aaj78d11 DQ823
FJ367539.1 gg_id:368178 feces adult twins and mothers; TS29 clone TS29_a04g04 FJ3675
DQ793937.1 gg_id:197542 human fecal clone RL176_aah45e04 DQ793
DQ905796.2 gg_id:163561 human fecal clone 29E-a8 DQ905
FJ367386.1 gg_id:357496 feces adult twins and mothers; TS29 clone TS29_a02h03 FJ3673
DQ809792.1 gg_id:178470 human fecal clone RL184_aan84c07 DQ809
DQ801603.1 gg_id:195608 human fecal clone RL117_aae92d11 DQ801
EU764665.1 gg_id:322947 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1 EU764
FJ369707.1 gg_id:369903 feces adult twins and mothers; TS51 clone TS51_a03h01 FJ3697
DQ808067.1 gg_id:174837 human fecal clone RL180_aan71g05 DQ808
DQ456024.1 gg_id:157417 pre-adolescent turkey cecum clone CFT112D5 DQ456
DQ794206.1 gg_id:194933 human fecal clone RL176_aan59d12 DQ794
FJ371854.1 gg_id:368906 feces adult twins and mothers; TS8 clone TS8_a03a03 FJ3718
DQ801585.1 gg_id:190660 human fecal clone RL117_aae92a08 DQ801
FJ367477.1 gg_id:366886 feces adult twins and mothers; TS29 clone TS29_a04a06 FJ3674
GQ491881.1 gg_id:586525 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
EU765568.1 gg_id:306962 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B3 EU765
FJ366821.1 gg_id:362432 feces adult twins and mothers; TS27 clone TS27_a04c06 FJ3668
FJ683678.1 gg_id:509821 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6836
DQ797710.1 gg_id:176442 human fecal clone RL206_aaj14h09 DQ797
FJ365885.1 gg_id:369922 feces adult twins and mothers; TS21 clone TS21_a04b11 FJ3658
DQ825076.1 gg_id:196616 human fecal clone RL185_aan85a12 DQ825
GQ898028.1 gg_id:572956 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ898
FJ365932.1 gg_id:364083 feces adult twins and mothers; TS21 clone TS21_a04g10 FJ3659
FJ677101.1 gg_id:529556 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6771
DQ456177.1 gg_id:158252 pre-adolescent turkey cecum clone CFT29C8 DQ456
FJ366691.1 gg_id:361827 feces adult twins and mothers; TS27 clone TS27_a02f11 FJ3666
FJ372109.1 gg_id:358744 feces adult twins and mothers; TS9 clone TS9_a01h02 FJ3721
EU766189.1 gg_id:354737 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU766
DQ904685.1 gg_id:167251 human fecal clone 001-e11 DQ904
EU764575.1 gg_id:348449 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1 EU764
FJ366231.1 gg_id:367348 feces adult twins and mothers; TS25 clone TS25_a04c05 FJ3662
DQ905880.2 gg_id:164867 human fecal clone 29c-a4 DQ905
DQ905769.2 gg_id:167863 human fecal clone 29A-f12 DQ905
FJ365793.1 gg_id:361283 feces adult twins and mothers; TS21 clone TS21_a03b03 FJ3657
DQ905791.2 gg_id:165346 human fecal clone 29E-a3 DQ905

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DQ794362.1 gg_id:193007 human fecal clone RL197_aah86d10 DQ794
FJ366400.1 gg_id:363257 feces adult twins and mothers; TS26 clone TS26_a02f05 FJ3664
DQ794224.1 gg_id:197701 human fecal clone RL176_aan59g02 DQ794
FJ372259.1 gg_id:361667 feces adult twins and mothers; TS9 clone TS9_a03e08 FJ3722
FJ368378.1 gg_id:366286 feces adult twins and mothers; TS3 clone TS3_a03f07 FJ3683
FJ372007.1 gg_id:367712 feces adult twins and mothers; TS8 clone TS8_a04f10 FJ3720
FJ367415.1 gg_id:360771 feces adult twins and mothers; TS29 clone TS29_a03c05 FJ3674
EU459904.1 gg_id:293874 Prevost's squirrel feces clone SQ_aah81a02 EU4599
FJ375910.1 gg_id:323534 and prevalence blaTEM genes polar bear feces clone PBM_a2 FJ3759
DQ801353.1 gg_id:181976 human fecal clone RL388_aao94d07 DQ801
DQ798168.1 gg_id:198554 human fecal clone RL302_aal96d01 DQ798
DQ794297.1 gg_id:185762 human fecal clone RL176_aan60g10 DQ794
GQ175410.1 gg_id:565952 Chicken intestinal microbiota modulations various feed supplementations DGGE anc GQ175
EF400910.1 gg_id:212549 human fecal clone SJTU_D_03_29 EF4009
FJ363972.1 gg_id:361798 feces adult twins and mothers; TS150 clone TS150_a01e06 FJ3639
EU767998.1 gg_id:347967 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C4 EU7679
DQ796772.1 gg_id:199502 human fecal clone RL179_aao54c08 DQ796
DQ808683.1 gg_id:199269 human fecal clone RL239_aaj11g11 DQ808
FJ363956.1 gg_id:361122 feces adult twins and mothers; TS150 clone TS150_a01c12 FJ3639
EU509787.1 gg_id:271488 cecal contents Mus musculus strain C57BL/6J; WD11 clone WD11_aak21a08 EU5097
FJ683794.1 gg_id:531444 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6837
DQ795560.1 gg_id:195561 human fecal clone RL178_aan66c03 DQ795
EU766373.1 gg_id:332702 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU7663
EF404114.1 gg_id:211295 human fecal clone SJTU_C_04_87 EF4041
AY169430.1 gg_id:81198 Faecalibacterium prausnitzii AY1694
DQ057482.2 gg_id:134174 str. ic1395 DQ057
DQ905832.2 gg_id:170094 human fecal clone 29E-d11 DQ905
FJ676304.1 gg_id:523814 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6763
EU009761.1 gg_id:237211 intestinal microbiota domestic and wild turkeys turkey cecum clone DTB_AB8 EU0097
FJ362743.1 gg_id:366267 feces adult twins and mothers; TS13 clone TS13_a02f03 FJ3627
DQ810028.1 gg_id:193622 human fecal clone RL184_aao67c03 DQ810
DQ798283.1 gg_id:183674 human fecal clone RL181_aah40b05 DQ798
FJ367251.1 gg_id:362328 feces adult twins and mothers; TS29 clone TS29_a01c11 FJ3672
DQ808060.1 gg_id:191541 human fecal clone RL180_aan71f03 DQ808
GQ896642.1 gg_id:568845 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do s GQ896
DQ806793.1 gg_id:178419 human fecal clone RL186_aao48g07 DQ806
GQ897259.1 gg_id:584951 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ897
AY916158.1 gg_id:113956 human transverse colon biopsy clone M479 AY9161
EU778922.1 gg_id:306633 Black-handed Spider Monkey feces clone SPIM_aaj36g11 EU7789

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FJ367399.1 gg_id:357525 feces adult twins and mothers; TS29 clone TS29_a03a09 FJ3673
DQ905064.1 gg_id:170262 human fecal clone 2-002-f10 DQ905
EU461598.1 gg_id:295083 mongoose lemur feces clone ML_aaj25c08 EU461
EF071254.1 gg_id:178512 library survey and quantitative measurement major mucosa- IBD human colonic muc EF0712
GQ897730.1 gg_id:593300 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ897
DQ825124.1 gg_id:196499 human fecal clone RL185_aan85f07 DQ825
GQ175380.1 gg_id:511009 Chicken intestinal microbiota modulations various feed supplementations DGGE anc GQ175
DQ455878.1 gg_id:157455 pre-adolescent turkey cecum clone CFT19F7 DQ455
EU763901.1 gg_id:345683 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A5 EU763
EU462171.1 gg_id:297013 black-handed spider monkey feces clone SPIM_aaj36d03 EU462
DQ801092.1 gg_id:176861 human fecal clone RL387_aao92a10 DQ801
EU778057.1 gg_id:307224 Rock hyrax feces clone RHSD_aaa03e07_1 EU778
DQ809793.1 gg_id:190067 human fecal clone RL184_aan84c10 DQ809
DQ793432.1 gg_id:174458 human fecal clone RL199_aaj43f06 DQ793
EU766782.1 gg_id:336071 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU766
FJ833044.1 gg_id:546069 Microbial Ecology Crop Folivorous Hoatzin crop contents clone A1Q201_14F02 FJ8330
DQ794181.1 gg_id:194219 human fecal clone RL176_aan59b08 DQ794
DQ797283.1 gg_id:178578 human fecal clone RL248_aai97c11 DQ797
DQ806652.1 gg_id:195391 human fecal clone RL186_aao47b11 DQ806
FJ904264.1 gg_id:552251 Further evidence absence horsehair worms (Nematomorpha: Gordiidae) Gordius robı FJ9042
DQ327429.1 gg_id:145346 Metagenomic gut microbiome healthy human stool clone E988 DQ327
EF603324.1 gg_id:229642 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6033
EU506238.1 gg_id:276137 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aap61c04 EU506
EU509367.1 gg_id:259581 cecal contents Mus musculus strain C57BL/6J; MD8 clone MD8_aap48f12 EU509
EF603651.1 gg_id:230125 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6036
DQ805523.1 gg_id:177311 human fecal clone RL203_aai63g02 DQ805
EU778221.1 gg_id:306021 feces clone RL387_aao90e02 EU778
EU462031.1 gg_id:290645 black-handed spider monkey feces clone SPIM_aaj33f07 EU462
AM278254.2 gg_id:234724 fecal microbiota irritable bowel syndrome patients significantly that healthy subject AM278
EF604546.1 gg_id:228893 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6045
EF445283.1 gg_id:216004 dairy cow rumen clone NED4G8 EF4452
AY858434.2 gg_id:111671 gastrointestinal tract Grant's gazelle clone GRANT15 AY8584
EU469998.1 gg_id:296456 trancaspain urial feces clone TU1_aaa03e06 EU469
EU381467.1 gg_id:275170 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid ı EU381
EU468548.1 gg_id:291584 okapi feces clone OK1_e02_1 EU468
EU459548.1 gg_id:293827 capybara feces clone CAP_aah99f08 EU459
EU885025.1 gg_id:304728 microbial hindgut chamber Pomacanthus sexstriatus GI tract clone A3D10 EU885
AY985261.1 gg_id:119310 human stool clone C142 AY985
EU778974.1 gg_id:353817 Prevost's squirrel feces clone SQ_aah81b08 EU778
AB089046.1 gg_id:78294 termite gut homogenate clone Rs-C61 bacterium AB089

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EU777853.1 gg_id:342571 European rabbit feces clone RA_g09 EU777
DQ808989.1 gg_id:189844 human fecal clone RL243_aai87h07 DQ808
EU466083.1 gg_id:303148 bighorn sheep feces clone BH1_aao25e08 EU466
DQ804796.1 gg_id:183299 human fecal clone RL187_aao72g10 DQ804
EU470212.1 gg_id:291405 trancaspain urial feces clone TU2_aaa01d03 EU470
AM697026.1 gg_id:223318 sequencing libraries indoor dust clone BF0001B052 AM697
AY916375.1 gg_id:113620 human stool clone D577 AY916
GQ079311.1 gg_id:435792 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1231c GQ079
EU844792.1 gg_id:355063 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
EU468771.1 gg_id:295107 okapi feces clone OK3_d08 EU468
EU507525.1 gg_id:265635 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_2aaa04e09 EU507
DQ794266.1 gg_id:196637 human fecal clone RL176_aan60d03 DQ794
EU462535.1 gg_id:298204 Sumatran orangutan feces clone orang1_aai56e12 EU462
DQ798661.1 gg_id:192677 human fecal clone RL181_aan99f11 DQ798
AB288904.1 gg_id:201203 termite gut homogenate clone BOf5-23 AB288
EU774126.1 gg_id:352182 Chimpanzee feces clone CHIMP1_aaj39f05 EU774
DQ905206.1 gg_id:165257 human fecal clone 013-b3 DQ905
DQ799538.1 gg_id:194197 human fecal clone RL305aal87d11 DQ799
DQ793626.1 gg_id:180995 human fecal clone RL246_aai74f03 DQ793
GQ493785.1 gg_id:591839 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
EU622690.1 gg_id:279659 -feed administered sub-therapeutic chlorotetracycline alters structure and but not a EU622
AB088959.1 gg_id:77706 termite gut homogenate clone Rs-B44 AB088
EU842424.1 gg_id:349962 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
DQ168656.1 gg_id:158569 sediment-free PCB-dechlorinating enrichment culture clone JN18_V41_S DQ168
AY991981.1 gg_id:135396 mouse cecum clone C20_o04 AY991
EU468795.1 gg_id:299019 okapi feces clone OK3_c07_1 EU468
FJ677881.1 gg_id:530146 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6778
EU451989.1 gg_id:320505 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU451
EU463774.1 gg_id:300041 domesticated horse feces clone horsej_aai92f03 EU463
EU842712.1 gg_id:346029 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
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DQ824345.1 gg_id:187264 human fecal clone RL304_aal74g08 DQ824
DQ015569.1 gg_id:130945 mouse cecum clone M3_f07_1 DQ015
FJ364993.1 gg_id:360916 feces adult twins and mothers; TS1 clone TS1_a01f01 FJ3649
AY980462.1 gg_id:123025 human rectum mucosal biopsy clone X044 AY980
EU504886.1 gg_id:275779 cecal contents Mus musculus strain C57BL/6J; myd2 clone myd2_aaa03g09 EU504
EU468744.1 gg_id:292147 okapi feces clone OK3_e09 EU468
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EF434358.1 gg_id:207991 human infant gastrointestinal tract microbiota stool mother babies 13 and 14 7 mont EF4343

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AM697405.1 gg_id:221429 sequencing libraries indoor dust clone BF0001D020 AM697
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AB089039.1 gg_id:77833 termite gut homogenate clone Rs-K92 bacterium AB089
FJ371922.1 gg_id:366885 feces adult twins and mothers; TS8 clone TS8_a03g03 FJ3719
DQ797006.1 gg_id:187006 human fecal clone RL386_aao85f09 DQ797
EU622658.1 gg_id:278098 -feed administered sub-therapeutic chlorotetracycline alters structure and but not a EU622
EU766883.1 gg_id:347024 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU766
DQ803678.1 gg_id:198988 human fecal clone RL200_aai57a11 DQ803
EU887971.1 gg_id:323501 Microbial structure hydrolytic stage two-stage anaerobic digestion grass silage leach EU887
EU506802.1 gg_id:260776 cecal contents Mus musculus strain C57BL/6J; MD20 clone MD20_aap56f01 EU506
EF603362.1 gg_id:232918 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6033
EU452114.1 gg_id:332037 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83 EU452
DQ815954.1 gg_id:167276 mouse cecum clone aab24g06 DQ815
EF603499.1 gg_id:232260 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6034
FJ679323.1 gg_id:517248 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6793
EU471941.1 gg_id:296850 Asiatic elephant feces clone AE3_aaa04e06 EU471
DQ793811.1 gg_id:178684 human fecal clone RL176_aah43f06 DQ793
EU469735.1 gg_id:291917 flying fox feces clone FF_h04_1 EU469
DQ795793.1 gg_id:194778 human fecal clone RL245_aai82e04 DQ795
GQ897459.1 gg_id:540055 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do GQ897
FJ368429.1 gg_id:366722 feces adult twins and mothers; TS3 clone TS3_a04c03 FJ3684
EU509946.1 gg_id:262944 cecal contents Mus musculus strain C57BL/6J; WD11 clone WD11_aak24b08 EU509
DQ905341.1 gg_id:173282 human fecal clone 013B-F5 DQ905
FJ879345.1 gg_id:394512 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8793
EU452674.1 gg_id:332282 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU452
AY916207.1 gg_id:112958 human cecum biopsy clone LF02 AY916
EU455446.1 gg_id:355041 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H74 EU455
AJ488078.1 gg_id:66186 chlorobenzene-degrading consortium clone IB-18 AJ488
FJ879403.1 gg_id:392407 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8794
EU451140.1 gg_id:329458 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU451
AY570589.1 gg_id:108465 -temperature biodegraded Canadian oil reservoir clone PL-38B12 AY570
AY487928.1 gg_id:100412 Acetanaerobacterium elongatum str. Z7 AY487
EF402779.1 gg_id:207624 human fecal clone SJTU_B_12_36 EF4027
EU845152.1 gg_id:347819 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU845
EU775744.1 gg_id:339121 Horse feces clone horsem_aai94d08 EU775
FJ269107.1 gg_id:338187 dissimilatory ferric iron reducers arsenic contaminated Hunan south China paddy soil FJ2691
FJ367099.1 gg_id:358674 feces adult twins and mothers; TS28 clone TS28_a03e06 FJ3670
EF604611.1 gg_id:231168 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6046
GQ502524.1 gg_id:590995 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf4- GQ502

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EU506329.1 gg_id:260859 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aap63d05 EU506
EU506188.1 gg_id:268806 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aaa02g02 EU506
DQ805002.1 gg_id:187524 human fecal clone RL385_aao83h09 DQ805
DQ796382.1 gg_id:189994 human fecal clone RL179_aah26e06 DQ796
EU463788.1 gg_id:291111 domesticated horse feces clone horsej_aai92h01 EU463
DQ904661.1 gg_id:168845 human fecal clone 001-c11 DQ904
AY622268.1 gg_id:100124 subsurface soil clone S-F26 AY622
EU452362.1 gg_id:312979 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75 EU452
DQ905623.1 gg_id:170271 human fecal clone 014B-H9 DQ905
DQ807121.1 gg_id:179301 human fecal clone RL244_aaj46e08 DQ807
EU469245.1 gg_id:289125 Speke's gazelle feces clone SP3_g02_1 EU469
FJ825458.1 gg_id:550485 Microbial during start-up mesophilic biogas plant clone 135_BE5_6 FJ8254
AB270141.1 gg_id:172165 Influence temperature and humidity on heifers rumen contents Holstein heifer (Bos AB270
AY984523.1 gg_id:123415 human stool clone B450 AY984
EU506576.1 gg_id:272283 cecal contents Mus musculus strain C57BL/6J; MD19 clone MD19_aaa04f01 EU506
EU765144.1 gg_id:314884 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B EU765
GQ867487.1 gg_id:579293 and prevalence blaTEM genes Arctic seals colon content clone CSG58 GQ867
EU531982.1 gg_id:276231 Predominant role host genetics controlling gut microbiota FMF remission stool clone EU531
DQ800460.1 gg_id:174827 human fecal clone RL183_aah24h03 DQ800
EU472119.1 gg_id:296626 francois langur feces clone FL_1aaa02g05 EU472
EU456056.1 gg_id:315580 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80 EU456
EF071169.1 gg_id:195415 library survey and quantitative measurement major mucosa- IBD human colonic muc EF0711
EU462752.1 gg_id:302382 Sumatran orangutan feces clone orang2_aai68e04 EU462
AB234479.1 gg_id:148075 termite gut homogenate clone MgMjR-012 AB234
GU303965.1 gg_id:538145 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU303
DQ015351.1 gg_id:131324 mouse cecum clone M3_a07 DQ015
EU461068.1 gg_id:289969 red kangaroo feces clone KO1_aai43e06 EU461
GQ448715.1 gg_id:532859 Microbiome neonatal calves: shedding microorganisms fecal clone calf784_10wks_ GQ448
DQ817325.1 gg_id:173276 mouse cecum clone aaa73d09 DQ817
AJ576369.1 gg_id:103744 hindgut homogenate Pachnoda ephippiata larva clone PeH56 AJ5763
EU771106.1 gg_id:333205 Asiatic elephant feces clone AE3_aaa02b02 EU771
EU506196.1 gg_id:261365 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aaa03c05 EU506
GQ047291.1 gg_id:423254 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1011a GQ047
EF603339.1 gg_id:234992 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6033
DQ800226.1 gg_id:181527 human fecal clone RL303_aal69h06 DQ800
EU506587.1 gg_id:263968 cecal contents Mus musculus strain C57BL/6J; MD19 clone MD19_aaa04g10 EU506
EU794136.1 gg_id:307564 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_AE37 EU794
FJ368767.1 gg_id:362041 feces adult twins and mothers; TS49 clone TS49_a04c07 FJ3687
EU455609.1 gg_id:345861 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H80 EU455
EU454483.1 gg_id:310557 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77 EU454

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EU467284.1 gg_id:291196 hamadryas baboon feces clone BAZ_a12 EU467
EU453205.1 gg_id:350575 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU453
FJ368179.1 gg_id:365529 feces adult twins and mothers; TS3 clone TS3_a01b08 FJ3681
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EU472376.1 gg_id:297774 Angola colobus feces clone EAC_1aaa04b03 EU4723
EU766492.1 gg_id:328236 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU7664
EU772256.1 gg_id:333948 Argali sheep feces clone AS2_aao34b08 EU772
FJ368800.1 gg_id:362922 feces adult twins and mothers; TS49 clone TS49_a04g02 FJ3688
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EF603352.1 gg_id:232042 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6033
DQ809978.1 gg_id:189758 human fecal clone RL184_aao66f03 DQ809
EU871402.1 gg_id:305146 Genetic Bovine (Bos taurus) Rumen Thailand clone CF342 EU8714
GQ175456.1 gg_id:535444 Chicken intestinal microbiota modulations various feed supplementations DGGE and GQ175
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EU506686.1 gg_id:258926 cecal contents Mus musculus strain C57BL/6J; MD20 clone MD20_aap54e03 EU5066
EU505553.1 gg_id:272277 cecal contents Mus musculus strain C57BL/6J; myd5 clone myd5_aaa02e12 EU5055
GQ451212.1 gg_id:575559 Fecal Yunnan snub-nosed monkey feces clone J66 GQ451
DQ015035.1 gg_id:131182 mouse cecum clone M2_c06 DQ015
GQ491889.1 gg_id:560663 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
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EU507209.1 gg_id:271754 cecal contents Mus musculus strain C57BL/6J; MD22 clone MD22_aaa03e10 EU5072
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EU509855.1 gg_id:258260 cecal contents Mus musculus strain C57BL/6J; WD11 clone WD11_aak22e08 EU5098
EU773500.1 gg_id:325524 Bonobo feces clone BNO_aaa04e04 EU7735
EU778735.1 gg_id:322931 Springbok feces clone SBSD_aaa04b06_1 EU7787
EU767072.1 gg_id:307566 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU7670
EU259422.1 gg_id:253559 Rumen yak (Bos grunniens) sequences rumen fluid clone YRC46 EU2594
FJ672969.1 gg_id:530829 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6729
EU358715.1 gg_id:351451 structure archaeal denaturing gel electrophoresis and sequencing mesophilic biogas EU3587
EU468521.1 gg_id:287988 okapi feces clone OK1_h03_1 EU4685
DQ796435.1 gg_id:198029 human fecal clone RL179_aah28d02 DQ796
EU764739.1 gg_id:347893 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2 EU7647
EU474451.1 gg_id:291314 bighorn sheep feces clone BHSD_aaa02b12 EU4744
FJ364955.1 gg_id:360031 feces adult twins and mothers; TS1 clone TS1_a01b10 FJ3649
EU461035.1 gg_id:291117 red kangaroo feces clone KO1_aai42g02 EU4610

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EF603271.1 gg_id:229291 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6032
GQ502529.1 gg_id:589530 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf4- GQ502
EU768072.1 gg_id:314565 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C4 EU768
EU850470.1 gg_id:304165 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF49 EU850
EU510224.1 gg_id:270297 cecal contents Mus musculus strain C57BL/6J; WD3 clone WD3_aak03b09 EU510
EF603286.1 gg_id:234373 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6032
EU763025.1 gg_id:304725 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU763
AY976193.1 gg_id:125597 human ascending colon mucosal biopsy clone LW10 AY976
DQ327508.1 gg_id:145878 Metagenomic gut microbiome healthy human stool clone EA83 DQ327
DQ325649.1 gg_id:146048 Metagenomic gut microbiome healthy human stool clone B215 DQ325
EF603298.1 gg_id:232031 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6032
FJ365192.1 gg_id:368412 feces adult twins and mothers; TS1 clone TS1_a04a02 FJ3651
EF099963.1 gg_id:195689 mouse cecum clone SWPT5_aaa02h03 EF0999
DQ800544.1 gg_id:195667 human fecal clone RL183_aah29d10 DQ800
EU455299.1 gg_id:333969 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N EU455
EU506732.1 gg_id:276761 cecal contents Mus musculus strain C57BL/6J; MD20 clone MD20_aap55c08 EU506
GQ896776.1 gg_id:590125 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do GQ896
EU768021.1 gg_id:328363 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C4 EU768
AF371766.1 gg_id:107272 swine intestine clone p-4546-4Wb3 AF371
EU774361.1 gg_id:353322 Chimpanzee feces clone CHIMP1_aaj37f02 EU774
DQ793759.1 gg_id:177903 human fecal clone RL246_aai76h04 DQ793
EF559116.1 gg_id:220174 mesophilic anaerobic digester clone C35_D7_H_B_C05 EF5591
DQ116011.1 gg_id:130793 bovine teat canal clone D-74 DQ116
FJ366095.1 gg_id:367681 feces adult twins and mothers; TS25 clone TS25_a02f06 FJ3660
EU772286.1 gg_id:340066 Argali sheep feces clone AS2_aao36e12 EU772
GQ448532.1 gg_id:510233 Microbiome neonatal calves: shedding microorganisms fecal clone calf784_6wks_gr GQ448
EU158190.1 gg_id:235474 Clostridium sp. str. SW512 EU158
AM277638.2 gg_id:233253 fecal microbiota irritable bowel syndrome patients significantly that healthy subject AM277
EF603366.1 gg_id:229110 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6033
EU778786.1 gg_id:349884 Springbok feces clone SBSD_aaa02e08_1 EU778
DQ800873.1 gg_id:185826 human fecal clone RL183_aao04f02 DQ800
FJ363634.1 gg_id:363716 feces adult twins and mothers; TS14 clone TS14_a01e11 FJ3636
DQ794088.1 gg_id:187393 human fecal clone RL176_aan57h02 DQ794
EF603784.1 gg_id:244484 Salmonella enterica serovar typhimurium exploits inflammation compete intestinal n EF6037
EU454869.1 gg_id:311725 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU4548
FJ366738.1 gg_id:361920 feces adult twins and mothers; TS27 clone TS27_a03c09 FJ3667
FJ440066.1 gg_id:546958 Megamonas hypermegale colonization correlates Campylobacter jejuni exclusion pou FJ4400
FJ680947.1 gg_id:531238 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6809
FJ366104.1 gg_id:361201 feces adult twins and mothers; TS25 clone TS25_a02g04 FJ3661
EU779323.1 gg_id:342446 Visayam Warty Pig feces clone VWP_aaa02g01 EU779
EU511636.1 gg_id:271303 cecal contents Mus musculus strain C57BL/6J; WD9 clone WD9_aak08a08 EU511

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EU509971.1 gg_id:273737 cecal contents Mus musculus strain C57BL/6J; WD11 clone WD11_aak24f03 EU509
GQ491419.1 gg_id:558068 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
GQ491157.1 gg_id:581278 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
EU842952.1 gg_id:303785 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU842
EU748046.1 gg_id:355404 neotropical folivorous flying bird adult hoatzin crop clone hoa2_43g04 EU748
EU465638.1 gg_id:301382 argali sheep feces clone AS1_aao40e01.Contig1 EU465
EU844075.1 gg_id:328379 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
FJ374214.1 gg_id:369525 Inter- and intraspecific humivorous scarab beetle larvae (Pachnoda spp.) larval hindgu FJ3742
FN436123.1 gg_id:539296 Molekularbiologische Charakterisierung der bakteriellen Populationsdynamik eines t FN436
FJ363880.1 gg_id:361066 feces adult twins and mothers; TS14 clone TS14_a04d11 FJ3638
EU506986.1 gg_id:274921 cecal contents Mus musculus strain C57BL/6J; MD21 clone MD21_aar09d08 EU506
EF603494.1 gg_id:234342 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6034
FJ881322.1 gg_id:459119 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8813
EU006198.1 gg_id:256016 Salmonella enterica serovar typhimurium exploits inflammation compete intestinal r EU006
AJ608244.1 gg_id:149660 human biopsies ulcerative colitis biopsy clone UC7-69 AJ6082
DQ802767.1 gg_id:199696 human fecal clone RL188_aan96c12 DQ802
EU764801.1 gg_id:331168 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2 EU7648
GQ451266.1 gg_id:565404 Fecal Yunnan snub-nosed monkey feces clone J245 GQ451
FJ368624.1 gg_id:361341 feces adult twins and mothers; TS49 clone TS49_a02e05 FJ3686
EU474535.1 gg_id:289015 bighorn sheep feces clone BHSD_aaa04h11 EU474
DQ456247.1 gg_id:158456 pre-adolescent turkey cecum clone CFT211A12 DQ456
EF686627.1 gg_id:257352 Sequences Manifest Rumen Yunnan Yel Cattle (Bos Taurus) rumen fluid clone YNRC1 EF6866
EF445160.1 gg_id:215193 rabbit cecum clone NED3A12 EF4451
FJ365131.1 gg_id:370011 feces adult twins and mothers; TS1 clone TS1_a03c05 FJ3651
EF603330.1 gg_id:230238 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6033
EU453550.1 gg_id:341015 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77 EU453
EU507924.1 gg_id:268722 cecal contents Mus musculus strain C57BL/6J; MD24 clone MD24_aaa03e09 EU507
DQ904669.1 gg_id:164541 human fecal clone 001-c7 DQ904
AB288879.1 gg_id:200879 termite gut homogenate clone BOf1-09 AB288
EU507998.1 gg_id:276229 cecal contents Mus musculus strain C57BL/6J; MD25 clone MD25_aaa01e10 EU507
AY916333.1 gg_id:114325 human stool clone C342 AY916
GQ451236.1 gg_id:578147 Fecal Yunnan snub-nosed monkey feces clone J158 GQ451
FJ371419.1 gg_id:358780 feces adult twins and mothers; TS6 clone TS6_a04g03 FJ3714
EU508713.1 gg_id:269238 cecal contents Mus musculus strain C57BL/6J; MD4 clone MD4_aap49g09 EU508
DQ796608.1 gg_id:192022 human fecal clone RL179aan75g07 DQ796
DQ325941.1 gg_id:147410 Metagenomic gut microbiome healthy human stool clone B814 DQ325
FJ363232.1 gg_id:362622 feces adult twins and mothers; TS148 clone TS148_a04g08 FJ3632
DQ793709.1 gg_id:176372 human fecal clone RL246_aai76a06 DQ793
EU772408.1 gg_id:315393 Hamadryas Baboon feces clone BAZ_aah91d12 EU772
DQ815688.1 gg_id:173264 mouse cecum clone aab21a03 DQ815
EF603333.1 gg_id:228320 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6033

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EU453520.1 gg_id:343276 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83 EU453
EU170433.1 gg_id:240700 Clostridium sp. str. W72 EU170
FJ365004.1 gg_id:366702 feces adult twins and mothers; TS1 clone TS1_a01g01 FJ3650
DQ793719.1 gg_id:185168 human fecal clone RL246_aai76b08 DQ793
EU463106.1 gg_id:294065 naked mole-rat feces clone molerat_aai70a01 EU463
AB307643.1 gg_id:268556 clay wall used Japanese traditional buildings clone B42 AB307
DQ800879.1 gg_id:198184 human fecal clone RL183_aao04f08 DQ800
EU457334.1 gg_id:331013 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80 EU457
EF400652.1 gg_id:210777 human fecal clone SJTU_E_16_56 EF4006
DQ015580.1 gg_id:131378 mouse cecum clone M3_g06_2 DQ015
DQ394651.1 gg_id:155932 on -Arctic peninsula Svalbard Norway determined genes and rumen isolates reindee DQ394
DQ808780.1 gg_id:190703 human fecal clone RL243_aai85b07 DQ808
FJ366863.1 gg_id:357503 feces adult twins and mothers; TS27 clone TS27_a04g03 FJ3668
EU843786.1 gg_id:343476 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
EU509268.1 gg_id:263766 cecal contents Mus musculus strain C57BL/6J; MD8 clone MD8_aap46h08 EU509
AM693109.2 gg_id:525997 Microbial level alterations overall gastrointestinal microbiota diarrhoea-predominar AM693
EF404038.1 gg_id:213124 human fecal clone SJTU_C_03_83 EF404
EF603287.1 gg_id:231021 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6032
GQ449055.1 gg_id:561879 Microbiome neonatal calves: shedding microorganisms fecal clone calf783_10wks_ GQ449
EF409954.1 gg_id:211472 Isolation equol-producing fecal clone QE4 EF4099
EU470456.1 gg_id:297964 Grevy's zebra feces clone GZ_aaa02h03 EU470
AY916351.1 gg_id:113822 human stool clone D036 AY9163
FJ364575.1 gg_id:361644 feces adult twins and mothers; TS15 clone TS15_a04e11 FJ3645
AF376224.1 gg_id:50072 ckncm320-B3-25 clone AF3762
EU775897.1 gg_id:330061 Horse feces clone horsem_aai93d07 EU7758
DQ800561.1 gg_id:178571 human fecal clone RL183_aah29g05 DQ800
DQ905474.1 gg_id:170185 human fecal clone 014-b10 DQ905
DQ803929.1 gg_id:189820 human fecal clone RL200_aai60a09 DQ803
EU764469.1 gg_id:311864 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B EU7644
EU469193.1 gg_id:291668 Speke's gazelle feces clone SP3_h03_1 EU469
EU468601.1 gg_id:302588 okapi feces clone OK1_g10_1 EU468
FJ673780.1 gg_id:527976 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6737
GQ175446.1 gg_id:566899 Chicken intestinal microbiota modulations various feed supplementations DGGE an GQ175
AY854329.1 gg_id:110824 herbivore gastrointestinal tract clone Thompsons41 AY8543
EU461148.1 gg_id:294246 hamadryas baboon feces clone BAZ_aah89b06 EU461
EU508360.1 gg_id:271519 cecal contents Mus musculus strain C57BL/6J; MD27 clone MD27_aaa03g03 EU508
DQ237939.1 gg_id:143881 influence fumarate disodium on ruminal metabolism goats goat rumen clone M2 DQ237
FJ368475.1 gg_id:362854 feces adult twins and mothers; TS3 clone TS3_a04g11 FJ3684
EU761698.1 gg_id:338035 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU761

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DQ673514.1 gg_id:161997 rumen fluid clone GRC49 DQ673
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AY980635.1 gg_id:122955 human rectum mucosal biopsy clone LL09 AY9806
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EU468515.1 gg_id:292708 okapi feces clone OK1_f10 EU4685
EF603304.1 gg_id:230751 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6033
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EU794105.1 gg_id:345871 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_W46 EU7941
DQ014883.1 gg_id:130110 mouse cecum clone M1_h02_3 DQ014
GU174108.1 gg_id:592004 Microbial Bactrian camel estimated rumen clone XJC79 GU174
EU842993.1 gg_id:308786 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8429
AB234478.1 gg_id:146871 termite gut homogenate clone MgMjW-23 AB2344
FJ366107.1 gg_id:364527 feces adult twins and mothers; TS25 clone TS25_a02g07 FJ3661
DQ815960.1 gg_id:169219 mouse cecum clone aab24h04 DQ815
EU504849.1 gg_id:270413 cecal contents Mus musculus strain C57BL/6J; myd2 clone myd2_aaa03c03 EU5048
EU511174.1 gg_id:270030 cecal contents Mus musculus strain C57BL/6J; WD7 clone WD7_aal03h04 EU5111
DQ793285.1 gg_id:189122 human fecal clone RL199_aaj41g04 DQ793
EU887972.1 gg_id:323591 Microbial structure hydrolytic stage two-stage anaerobic digestion grass silage leach EU8879
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FJ371344.1 gg_id:370052 feces adult twins and mothers; TS6 clone TS6_a03h02 FJ3713
EU006164.1 gg_id:236225 Salmonella enterica serovar typhimurium exploits inflammation compete intestinal r EU0061
DQ798670.1 gg_id:199475 human fecal clone RL181_aan99g11 DQ798
EF603268.1 gg_id:232658 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6032
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DQ795049.1 gg_id:178859 human fecal clone RL310_aam39e10 DQ795
FJ367663.1 gg_id:369320 feces adult twins and mothers; TS2 clone TS2_a02b03 FJ3676
EU453675.1 gg_id:313431 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N EU4536
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GQ897679.1 gg_id:559659 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ897
EU774417.1 gg_id:309482 mammals their gut microbes Eastern Black and White Colobus feces clone COL_aai14 EU7744
EU463401.1 gg_id:299759 domesticated horse feces clone horsem_aai93c02 EU4634

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EF445157.1 gg_id:216557 rabbit cecum clone NED1A10 EF4451
GU304029.1 gg_id:590712 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU304
DQ673580.1 gg_id:171848 rumen fluid clone GRC115 DQ673
EU465584.1 gg_id:296437 argali sheep feces clone AS1_aao38f10.Contig1 EU465
FJ880813.1 gg_id:437273 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8808
EU461017.1 gg_id:302744 red kangaroo feces clone KO1_aai42d09 EU461
EU470386.1 gg_id:293477 Grevy's zebra feces clone GZ_aaa02e11 EU470
EU382005.1 gg_id:272899 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU382
GU303495.1 gg_id:582952 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU303
EU470037.1 gg_id:303164 trancaspain urial feces clone TU1_aaa03b09 EU470
DQ801064.1 gg_id:193895 human fecal clone RL387_aao91f04 DQ801
EU250958.1 gg_id:363509 degraded cellulose lindane NSC-7 NFC-7 grown 50 degrees Celsius compost compose EU250
DQ793756.1 gg_id:188225 human fecal clone RL246_aai76g11 DQ793
AB185540.1 gg_id:104439 rumen clone F23-D09 AB185
EU464078.1 gg_id:303244 reticulated giraffe feces clone gir_aah93b06 EU464
EU469077.1 gg_id:296415 Speke's gazelle feces clone SP3_a12 EU469
EU462596.1 gg_id:295615 Sumatran orangutan feces clone orang2_aai65h01 EU462
EU506620.1 gg_id:258946 cecal contents Mus musculus strain C57BL/6J; MD20 clone MD20_aap53e02 EU506
EF096988.1 gg_id:198512 mouse cecum clone SWPT13_aaa03g08 EF0969
EU842961.1 gg_id:315150 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU842
EU466444.1 gg_id:287377 bighorn sheep feces clone BH2_aao23g10 EU466
FJ681223.1 gg_id:528725 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6812
EU842439.1 gg_id:340770 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
EU794257.1 gg_id:344025 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_J17 EU794
AB198524.1 gg_id:135518 termite gut wall fraction clone RsW02-034 AB198
EF454875.2 gg_id:221978 termite hindgut clone 290cost002-P3L-568 EF4548
EU465567.1 gg_id:299012 argali sheep feces clone AS1_aao37h07.Contig1 EU465
AY858483.2 gg_id:109604 gastrointestinal tract eland clone ELAND_3 AY8584
EU794310.1 gg_id:307291 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_P3 EU7943
AB185579.1 gg_id:103145 rumen clone F24-A06 AB185
EU794264.1 gg_id:354632 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_L34 EU794
AF050582.1 gg_id:16073 contaminated aquifer clone WCHB1-54 AF050
EU794192.1 gg_id:323910 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_E02 EU794
AM183003.1 gg_id:251289 and its spatial composts compost clone SMA17 AM183
EU844610.1 gg_id:311446 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
AB009176.1 gg_id:16063 rumen clone RFN17 bacterium AB009
EU775199.1 gg_id:329360 Reticulated giraffe feces clone gir_aah94d12 EU775
DQ801076.1 gg_id:176718 human fecal clone RL387_aao91g09 DQ801
EU794129.1 gg_id:356245 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_AE6 EU794

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EU471995.1 gg_id:298553 francois langur feces clone FL_1aaa03c03 EU471
AB233996.1 gg_id:156549 anaerobic reactor clone B-3 AB233
GQ451308.1 gg_id:592857 Fecal Yunnan snub-nosed monkey feces clone J325 GQ451
EU453210.1 gg_id:349798 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77 EU453
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AB198484.1 gg_id:135720 termite gut wall fraction clone RsW01-056 AB198
EU466282.1 gg_id:289200 bighorn sheep feces clone BH2_aao21c11 EU466
GU454868.1 gg_id:518493 Understanding short-chain fatty acids accumulation enhanced alkaline digestion: kir GU454
EU461091.1 gg_id:301917 red kangaroo feces clone KO1_aai44a02 EU461
EU468985.1 gg_id:301716 Speke's gazelle feces clone SP2_d07_1 EU468
GU174133.1 gg_id:551562 Microbial Bactrian camel estimated rumen clone XJC124 GU174
EU844169.1 gg_id:326767 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
EU461512.1 gg_id:303394 black rhinoceros feces clone RH_aaj91c12 EU461
EU462243.1 gg_id:299441 chimpanzee feces clone CHIMP1_aaj38c11 EU462
AB185776.1 gg_id:105514 rumen clone U29-D05 AB185
EU762139.1 gg_id:307647 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU762
EU468725.1 gg_id:290201 okapi feces clone OK2_g04_1 EU468
EU794278.1 gg_id:325883 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_H46 EU794
EU509875.1 gg_id:270519 cecal contents Mus musculus strain C57BL/6J; WD11 clone WD11_aak22h11 EU509
DQ797051.1 gg_id:199149 human fecal clone RL386_aao86c11 DQ797
EU850568.1 gg_id:303584 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF379 EU850
EU381809.1 gg_id:273552 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU381
FJ681730.1 gg_id:522625 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6817
FJ681667.1 gg_id:517931 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6816
EU773299.1 gg_id:329112 BigHorn sheep feces clone BHSD_aaa04e12 EU773
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EU469314.1 gg_id:293987 Speke's gazelle feces clone SP3_h03_3 EU469
FJ681337.1 gg_id:518060 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6813
DQ456148.1 gg_id:157036 pre-adolescent turkey cecum clone CFT29A2 DQ456
EU776470.1 gg_id:340210 Red Kangaroo feces clone KO2_aai17e12 EU776

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GQ449144.1 gg_id:511242 Microbiome neonatal calves: shedding microorganisms fecal clone calf784_6wks_gr GQ449
EU773276.1 gg_id:349695 BigHorn sheep feces clone BH2_aao22h09 EU773
EU771349.1 gg_id:321127 Asiatic elephant feces clone AE2_aaa02h02 EU771
EU776451.1 gg_id:354054 Red Kangaroo feces clone KO2_aai17g04 EU776
EU844199.1 gg_id:304015 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
EU472419.1 gg_id:293879 Angola colobus feces clone EAC_1aaa03d10 EU472
DQ801138.1 gg_id:181671 human fecal clone RL387_aao92g09 DQ801
EU776342.1 gg_id:320831 Red Kangaroo feces clone KO1_aai42g11 EU776
EF686635.1 gg_id:237134 Sequences Manifest Rumen Yunnan Yel Cattle (Bos Taurus) rumen fluid clone YNRC1 EF6866
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EU464112.1 gg_id:296798 reticulated giraffe feces clone gir_aah93h11 EU464
AF050581.1 gg_id:16062 contaminated aquifer clone WCHB1-49 AF050
EU470437.1 gg_id:289438 Grevy's zebra feces clone GZ_aaa03g08 EU470
EU843153.1 gg_id:353179 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
EU463648.1 gg_id:288212 domesticated horse feces clone horsej_aai90d05 EU463
EU773265.1 gg_id:333820 BigHorn sheep feces clone BHSD_aaa03a03 EU773
EU470173.1 gg_id:292016 trancaspain urial feces clone TU2_aaa03h02 EU470
EU794179.1 gg_id:331046 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_A15 EU794
EU470148.1 gg_id:300089 trancaspain urial feces clone TU2_aaa02b09 EU470
EU470366.1 gg_id:287724 Grevy's zebra feces clone GZ_aaa01d12 EU470
GQ502523.1 gg_id:583328 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf4- GQ502
DQ805504.1 gg_id:187508 human fecal clone RL203_aai63e04 DQ805
EU458486.1 gg_id:291270 spotted hyena feces clone HY2_h02 EU458
EU772024.1 gg_id:335757 Argali sheep feces clone AS2_aao36e09 EU772
GQ451202.1 gg_id:578310 Fecal Yunnan snub-nosed monkey feces clone J52 GQ451
GQ448531.1 gg_id:594107 Microbiome neonatal calves: shedding microorganisms fecal clone calf784_6wks_gr GQ448
EU779127.1 gg_id:328671 Trancaspian Urial feces clone TU2_aaa02e08 EU779
DQ801040.1 gg_id:196502 human fecal clone RL387_aao91c07 DQ801
AB192042.1 gg_id:142583 termite gut homogenate clone M1NP1-42 AB192
AB198499.1 gg_id:135452 termite gut wall fraction clone RsW01-073 AB198
EF686609.1 gg_id:239644 Sequences Manifest Rumen Yunnan Yel Cattle (Bos Taurus) rumen fluid clone YNRC9 EF6866
EU468734.1 gg_id:297952 okapi feces clone OK3_b09 EU468
FJ366638.1 gg_id:362693 feces adult twins and mothers; TS27 clone TS27_a02a10 FJ3666
GQ448437.1 gg_id:547348 Microbiome neonatal calves: shedding microorganisms fecal clone calf783_10wks_g GQ448
FJ684375.1 gg_id:528722 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6843
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EU779349.1 gg_id:344615 Somali Wild Ass feces clone WA_aaa04g06 EU779
FJ680570.1 gg_id:522248 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6805
EU844036.1 gg_id:344137 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844

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EU509795.1 gg_id:264941 cecal contents Mus musculus strain C57BL/6J; WD11 clone WD11_aak21b06 EU509
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EU499919.1 gg_id:279555 Sulfobacillus thermosulfidooxidans str. N19-50-01 EU499
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AY079150.1 gg_id:60544 Sulfobacillus sibiricus str. N1 AY079
EU419151.1 gg_id:270741 Microbial and ecology selected andesitic hydrothermal acidic hydrothermally modifi EU419
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AB454087.1 gg_id:323069 Thermaerobacter sp. str. Ni80 AB4540
EU214629.1 gg_id:331773 Thermaerobacter subterraneus ir-12 EU2146
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AB011495.1 gg_id:13721 Thermaerobacter marianensis AB0114
AB254790.1 gg_id:160816 Biogenic Fe-oxyhydroxides nodules (takashikozo) encrusted iron-oxide reducing sedi AB2547
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AF465653.1 gg_id:25424 G+C Gram-positive clone YNPRH70A AF4656
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AF391988.1 gg_id:27433 thermal soil clone YNPFFP9 AF3919
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AP006840.1 gg_id:129187 Symbiobacterium thermophilum IAM 14863 str. IAM14863 AP006
AB361629.1 gg_id:243859 Symbiobacterium sp. str. KY38 AB361
AB455238.1 gg_id:322976 Symbiobacterium sp. str. KY46 AB455
AB455239.1 gg_id:344098 Symbiobacterium sp. str. KA13 AB455
DQ112187.1 gg_id:132753 Syntrophomonas sporosyntrophas str. Y4-1 DQ112
FJ799130.1 gg_id:559105 Microbial Responsible Intermediates Degradation Anaerobic Digestion System Deterr FJ7991
AF050586.1 gg_id:13690 contaminated aquifer clone WCHB1-82 AF050
AF482445.1 gg_id:77471 granular sludge clone R5p27 AF482
DQ984666.1 gg_id:257916 Anaerobic degradation unsaturated or saturated long chain fatty acids (LCFA) preser DQ984
AY290767.1 gg_id:87293 Syntrophomonas curvata str. GB8-1 AY290
AB252683.1 gg_id:172658 and activities propionate-oxidizing that affected propionate concentration anaerobic AB252
AB186861.1 gg_id:103994 polychlorinated dioxin dechlorinating microcosm clone TSBW01 AB186
AB248633.1 gg_id:146259 mesophilic anaerobic butyrate-degrading reactor clone BHB04 AB248
EF559161.1 gg_id:217350 mesophilic anaerobic digester clone G35_D8_L_B_A02 EF5591
AM947547.1 gg_id:259682 Minor changes detected microbial structure and after three week thermophilic dige AM947
CR933176.1 gg_id:110152 Evry municipal wastewater treatment plant clone 008H01_B_SD_P15 CR933
AB248623.1 gg_id:149149 mesophilic anaerobic butyrate-degrading reactor clone BLB01 AB248
FJ799160.1 gg_id:511304 Microbial Responsible Intermediates Degradation Anaerobic Digestion System Deterr FJ7991
AB234271.1 gg_id:150183 Biotransformation Polychlorinated Dioxins Microbial Dynamics Sediment Microcosm AB234
X99980.1 gg_id:13689 Thermosyntropha lipolytica str. JW265 X99980
DQ339710.1 gg_id:208155 assessment complex microbial degrading long chain fatty acids (LCFA) methanogeni DQ339
DQ080135.1 gg_id:137138 reductive dechlorination 2345-tetrachlorobiphenyl three s: evidence involvement D DQ080
AB192059.1 gg_id:141089 termite gut homogenate clone M1PL1-18 AB192
AB248632.1 gg_id:145683 mesophilic anaerobic butyrate-degrading reactor clone BHB03 AB248
AB234008.1 gg_id:154827 anaerobic reactor clone B-15 AB234
NR_028910.1 gg_id:552212 Pelospora glutarica str. WoGl3; DSM 6652 NR_02
EF515712.1 gg_id:222308 Electricigen Enrichment MFC full-scale anaerobic bioreactor sludge treating brewery EF5157
FJ799131.1 gg_id:510041 Microbial Responsible Intermediates Degradation Anaerobic Digestion System Deterr FJ7991
AB274497.1 gg_id:203894 packed-bed reactor clone CFB-8 AB274
AB021305.1 gg_id:13691 Syntrophothermus lipocalidus str. TGB-C1 AB021
AB539943.1 gg_id:567072 Evidence syntrophic acetate oxidation coupled hydrogenotrophic methanogenesis -t AB539
X76743.1 gg_id:13762 Clostridium thermoamylolyticum str. DSM2335 X76743
AY350594.2 gg_id:221143 Thermoanaerobacterium aciditolerans str. 761-119 AY350
EU999016.1 gg_id:322435 Predominance Methanolobus and Methanoculleus spp. Archaeal Saline Gas Field Fo EU999
FJ268955.1 gg_id:356922 Thermoanaerobacterium saccharolyticum str. B6A FJ2689
EU563363.1 gg_id:272616 Thermoanaerobacterium saccharolyticum str. D22 EU563
FM999998.1 gg_id:532726 Thermoanaerobacterium sp. PO-2009 FM999
L09172.1 gg_id:13755 Thermoanaerobacterium xylanolyticum str. LXIIT L09172
AY140670.1 gg_id:59208 Thermoanaerobacterium bryantii str. mel9 AY140
AY331143.1 gg_id:106330 Mahella australiensis str. 50-1-BON AY331
AF247003.1 gg_id:27592 Thermoanaerobacterium thermosaccharolyticum str. D120-70 AF247

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s__Desulfosporomusa polytropa	50530
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EF507903.1 gg_id:239939 Caldanaerobium fijiensis str. JW/YJL-F3 EF5079
EF060090.1 gg_id:199473 Acidaminococcus fermentans str. ADV 6092.03 EF0600
EF060091.1 gg_id:176163 Acidaminococcus fermentans str. ADV 1338.05 EF0600
EU728758.1 gg_id:337187 Acidaminococcus sp. str. DJF_RP55 EU7287
EF028685.1 gg_id:199297 Acidaminococcus intestinalis str. LBN 321 EF0286
EU773566.1 gg_id:307454 Goeldi's Marmoset feces clone CAL_b10_1 EU7735
NR_028812.1 gg_id:539819 Anaeroglobus geminatus str. AIP313.00; CIP 106856; CCUG 4477 NR_028
AY372050.1 gg_id:94360 Anaerospora hongkongensis str. HKU15 AY3720
AY728067.1 gg_id:104334 decayed velvetleaf seed clone S1-6-CL2 AY7280
DQ816346.1 gg_id:172987 mouse cecum clone aaa80f06 DQ816
EU981222.1 gg_id:340874 sulfate reducing living bench scale aquifer packed bed clone A7_FB EU9812
AB288880.1 gg_id:201846 termite gut homogenate clone BOf1-11 AB2888
EF454547.2 gg_id:224315 termite hindgut clone 290cost002-P3L-2304 EF4545
FJ542917.1 gg_id:510013 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone A FJ5429
AM158322.1 gg_id:156235 Sporomusa rhizae str. RS AM158
AJ279799.1 gg_id:21147 Sporomusa malonica str. DSM 5090 Type AJ2797
AJ279801.1 gg_id:25868 Sporomusa sphaeroides str. DSM 2875 Type AJ2798
NR_025415.1 gg_id:541895 Sporomusa acidovorans str. DSM 3132 NR_025
GQ047238.1 gg_id:466398 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1010d GQ047
FJ372052.1 gg_id:364054 feces adult twins and mothers; TS9 clone TS9_a01c02 FJ3720
DQ794346.1 gg_id:187487 human fecal clone RL197_aah86a07 DQ794
EU762181.1 gg_id:340520 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A› EU7621
DQ803760.1 gg_id:180927 human fecal clone RL200_aai58a11 DQ803
NZ_ACIM02000001.1 gg_id:470239 Dialister invisus str. DSM 15470 NZ_AC
FJ370202.1 gg_id:369002 feces adult twins and mothers; TS56 clone TS56_a01g01 FJ3702
FJ363905.1 gg_id:358364 feces adult twins and mothers; TS14 clone TS14_a04g03 FJ3639
AF473837.2 gg_id:136415 Dialister micraerophilus str. ADV 04.01 AF4738
U13040.1 gg_id:13826 Dialister pneumosintes str. SC3D U13040
FM872697.1 gg_id:365104 occupant source house floor dust clone FA02F02 FM872
EU461194.1 gg_id:290748 hamadryas baboon feces clone BAZ_aah90c07 EU4611
DQ071524.1 gg_id:229365 microbial cecum captive and free-living capercaillies (Tetrao urogallus) clone TuCc32 DQ071
FJ364585.1 gg_id:363398 feces adult twins and mothers; TS15 clone TS15_a04g01 FJ3645
FJ833261.1 gg_id:512439 Microbial Ecology Crop Folivorous Hoatzin crop contents clone A3Q302_40H05 FJ8332
FJ832358.1 gg_id:593767 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P1Q301_87G11 FJ8323
DQ326331.1 gg_id:145728 Metagenomic gut microbiome healthy human stool clone C320 DQ326
EU464320.1 gg_id:293799 hamadryas baboon feces clone AFBAB_aai02f07 EU4643
FJ834270.1 gg_id:564560 Microbial Ecology Crop Folivorous Hoatzin crop contents clone A2Q401_63G08 FJ8342
AY850119.1 gg_id:109904 Dialister sp. str. ADV 1053.03 AY8501
EU773545.1 gg_id:349811 Goeldi's Marmoset feces clone CAL_e11 EU7735
EU764686.1 gg_id:325573 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1 EU7646
DQ353930.1 gg_id:145968 Fecal Wild Gorilla (Gorilla beringei) wild gorilla feces clone Z83 DQ353

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EU464269.1 gg_id:287863 hamadryas baboon feces clone AFBAB_aai01d11 EU4642
DQ325965.1 gg_id:148937 Metagenomic gut microbiome healthy human stool clone B855 DQ325
AY958942.1 gg_id:128228 Microbes on human vaginal epithelium clone rRNA169 AY9589
DQ809210.1 gg_id:196169 human fecal clone RL308_aal83d11 DQ809
GQ014629.1 gg_id:495037 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw762b GQ014
GQ156497.1 gg_id:590051 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
DQ353912.1 gg_id:146557 Fecal Wild Gorilla (Gorilla beringei) wild gorilla feces clone Z25 DQ353
FJ833651.1 gg_id:563580 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J1Q402_64H08 FJ8336
DQ325967.1 gg_id:146807 Metagenomic gut microbiome healthy human stool clone B859 DQ325
GQ082178.1 gg_id:382947 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw GQ082
DQ325932.1 gg_id:150078 Metagenomic gut microbiome healthy human stool clone B792 DQ325
NR_028862.1 gg_id:585826 Allisonella histaminiformans str. MR2; DSM 15230 NR_028
EU009856.1 gg_id:255834 intestinal microbiota domestic and wild turkeys turkey cecum clone WTB_X48 EU0098
FJ832445.1 gg_id:582014 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P3Q101_25A04 FJ8324
EU475193.1 gg_id:295381 bonobo feces clone BNO_aaa01c01 EU4751
AY959160.1 gg_id:130495 Microbes on human vaginal epithelium clone rRNA387 AY9591
FJ832730.1 gg_id:562702 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J3Q101_38F05 FJ8327
EU775402.1 gg_id:342839 Western lowland gorilla feces clone GOR_aag73e12 EU7754
DQ071435.1 gg_id:228821 microbial cecum captive and free-living capercaillies (Tetrao urogallus) clone TuCw4 DQ071
FJ489245.1 gg_id:513909 Megamonas hypermegale str. ABXD_AE27 FJ4892
DQ071446.1 gg_id:228113 microbial cecum captive and free-living capercaillies (Tetrao urogallus) clone TuCw1 DQ071
NR_025514.1 gg_id:552592 Megamonas hypermegale str. DSM 1672 NR_025
EU465518.1 gg_id:287786 lion feces clone LI3_aah78g03 EU4655
EU939429.1 gg_id:343257 Fecal wild pygmy loris feces clone WF16S_275 EU9394
U95029.1 gg_id:53032 Megasphaera elsdenii str. S3 U95029
AY038996.1 gg_id:24370 Megasphaera elsdenii str. YJ-4 AY0389
DQ905695.1 gg_id:170226 human fecal clone 014C-G12 DQ905
DQ904992.1 gg_id:170296 human fecal clone 002-g5 DQ904
DQ278866.1 gg_id:151623 Megasphaera sp. TrE9262 DQ278
DQ904832.1 gg_id:168912 human fecal clone 001C-a6 DQ904
DQ904811.1 gg_id:173152 human fecal clone 001B-g7 DQ904
ABWK02000005.1 gg_id:579171 Mitsuokella multacida str. DSM 20544 ABWK0
NZ_ABWK02000010.1 gg_id:470692 Mitsuokella multacida str. DSM 20544 NZ_AB
AY985193.1 gg_id:119553 human stool clone C039 AY9851
DQ325931.1 gg_id:148483 Metagenomic gut microbiome healthy human stool clone B785 DQ325
AY982411.1 gg_id:117325 human sigmoid colon mucosal biopsy clone MK92 AY9824
AY977807.1 gg_id:123930 human cecum mucosal biopsy clone LE93 AY9778
NR_028840.1 gg_id:590732 Mitsuokella jalaludinii str. M9; DSM 13811 NR_028
DQ223731.1 gg_id:140868 Pectinatus haikarae str. VTT E-88329; DSM 16980 DQ223

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EF404155.1 gg_id:206419 human fecal clone SJTU_C_05_48 EF4041
GQ493381.1 gg_id:587536 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
FJ368136.1 gg_id:357831 feces adult twins and mothers; TS30 clone TS30_a04f02 FJ3681
DQ805306.1 gg_id:183098 human fecal clone RL249_aaj84h07 DQ805
GQ492054.1 gg_id:594375 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
FJ362702.1 gg_id:367004 feces adult twins and mothers; TS13 clone TS13_a02b03 FJ3627
EU009791.1 gg_id:255530 intestinal microbiota domestic and wild turkeys turkey cecum clone WTB_A48 EU009
EF400225.1 gg_id:212456 human fecal clone SJTU_E_10_50 EF4002
X72867.1 gg_id:13860 Phascolarctobacterium faecium X72867
GQ492591.1 gg_id:575113 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
EU009762.1 gg_id:239970 intestinal microbiota domestic and wild turkeys turkey cecum clone DTB_AC19 EU009
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AY878646.1 gg_id:112413 Selenomonas noxia str. AIP 45-92 AY8786
AY947498.2 gg_id:114498 subgingival plaque clone OH4A AY9474
AY878645.1 gg_id:111934 Selenomonas noxia str. AIP 518-78 AY8786
AF161581.1 gg_id:13799 Selenomonas ruminantium str. K2 AF1615
EU381812.1 gg_id:276744 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU3818
AY685145.1 gg_id:99746 Selenomonas ruminantium L6 AY6851
EU327399.1 gg_id:237808 Selenomonas ruminantium str. LongL1 EU3273
AB198429.1 gg_id:257094 Selenomonas ruminantium str. S36 AB1984
DQ673518.1 gg_id:165042 rumen fluid clone GRC53 DQ673
EF112197.1 gg_id:178224 Selenomonas ruminantium str. 65 EF1121
AB003379.1 gg_id:13812 Selenomonas ruminantium str.JCM6582 AB0033
AF001774.1 gg_id:13813 rumen clone RFP7 AF0017
ACKP02000033.1 gg_id:589013 Selenomonas sputigena str. ATCC 35185 ACKP0
AF373023.1 gg_id:17310 Selenomonas sputigena str. ATCC35185 AF3730
EF195237.1 gg_id:180877 Selenomonas sp. str. MCB2 EF1952
AY685142.1 gg_id:99281 Selenomonas ruminantium M40 AY6851
AY207052.1 gg_id:83279 human mouth clone P2PA_80 AY2070
AF287790.1 gg_id:23591 human subgingival plaque clone DM071 AF2877
NR_028796.1 gg_id:550364 Selenomonas noxia str. ATCC 43541 NR_02
EU669564.1 gg_id:292356 Profiles Root Caries Elderly Patients supragingival plaque tooth root surface clone O EU6695
AY349403.1 gg_id:93019 human oral cavity clone FT050 AY3494
DQ673510.1 gg_id:168649 rumen fluid clone GRC45 DQ673
AM419977.1 gg_id:252996 Noma subgingival plaque clone 101H05(oral) AM419
AF538861.1 gg_id:59529 Selenomonas sp. oral clone P4PA_36 P2 AF5388
AY878647.1 gg_id:112215 Selenomonas sp. str. AIP 308-97 AY8786
FM873718.1 gg_id:368850 occupant source house mattress dust clone MA03E01 FM873

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AY349409.1 gg_id:92349 human oral cavity clone JI021 AY3494
AM420026.1 gg_id:254272 Noma subgingival plaque clone 201F02(oral) AM420
GU302661.1 gg_id:586155 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU302
EU850496.1 gg_id:329400 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF265 EU8504
AY278627.1 gg_id:86707 Selenomonas genomosp. C1 AY2786
AM420028.1 gg_id:252936 Noma subgingival plaque clone 201F04(oral) AM420
AY341820.1 gg_id:92263 Selenomonas genomosp. P5 AY3418
AM419959.1 gg_id:241050 Noma subgingival plaque clone 101C02(oral) AM419
GQ006802.1 gg_id:502861 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu87h08c GQ006
GQ006643.1 gg_id:503020 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu86a02c GQ006
AM420074.1 gg_id:238385 Noma subgingival plaque clone 301F12(oral) AM420
EU669566.1 gg_id:295019 Profiles Root Caries Elderly Patients supragingival plaque tooth root surface clone O(EU6695
AM420113.1 gg_id:240321 Noma subgingival plaque clone 303G10(oral) AM420
DQ394645.1 gg_id:155308 -Arctic peninsula Svalbard Norway determined genes and rumen isolates reindeer o DQ394
DQ145536.1 gg_id:141405 Geosinus fermentans str. R7 DQ145
NZ_AAWL01000001.1 gg_id:192281 Thermosinus carboxydivorans str. Nor1 NZ_AA
AJ009486.1 gg_id:13842 TCB-transforming consortium clone SJA-112 AJ0094
DQ125719.1 gg_id:134207 uranium contaminated soil clone AKAU3815 DQ125
AF275913.1 gg_id:72075 anaerobic digestor clone AA01 AF2759
AB195907.1 gg_id:109195 Anaerobic sludge clone N39 AB1959
AB486682.1 gg_id:559077 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCOR(AB4866
EU864464.1 gg_id:310615 structures under selection pressure levels antibiotics Xiao River receiving treated ox EU8644
AB240309.1 gg_id:141751 microbial structure Phragmites rhizosphere biofilm reed bed reactor laboratory clon AB2403
AB487569.1 gg_id:571451 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNSR0 AB4875
FJ673072.1 gg_id:516219 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6730
AB486151.1 gg_id:586628 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC AB4861
FJ683262.1 gg_id:512213 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6832
EU843176.1 gg_id:304446 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8431
AJ006980.1 gg_id:13862 Succinispira mobilis str. 19gly1 AJ0069
EU344280.1 gg_id:273405 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU3442
FJ683898.1 gg_id:521321 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6838
AF407698.1 gg_id:60600 Great Artesian Basin clone G07 AF4076
FJ880994.1 gg_id:405629 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8809
NR_025298.1 gg_id:575973 Anaeroarcus burkinensis str. DSM 6283 NR_025
FJ676048.1 gg_id:530548 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6760
GQ038559.1 gg_id:383518 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu4 GQ038
AY244964.1 gg_id:84451 cow rumen clone BS10 AY2449
FJ799146.1 gg_id:583522 Microbial Responsible Intermediates Degradation Anaerobic Digestion System Deterr FJ7991
FJ672960.1 gg_id:519106 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6729
DQ801441.1 gg_id:198328 human fecal clone RL388_aao95e11 DQ801

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EU775040.1 gg_id:351818 Francois Langur feces clone FL_2aaa04b12 EU775
AB487852.1 gg_id:548067 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNSR AB487
FJ681608.1 gg_id:517653 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6816
FJ386549.1 gg_id:364845 vaccination sludge backf pumping house Xilang municipal wastewater treatment plar FJ3865
FJ834254.1 gg_id:575321 Microbial Ecology Crop Folivorous Hoatzin crop contents clone A2Q401_14F02 FJ8342
EU773455.1 gg_id:328240 Black lemur feces clone BKLE_g09_1 EU773
DQ833299.1 gg_id:170560 Anaerobic Reductive Dechlorination Vinyl Chloride ly Enriched Bachman Aquifer Sed DQ833
FJ684672.1 gg_id:532119 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6846
FJ678209.1 gg_id:528615 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6782
AY684401.2 gg_id:110815 mucosal biopsies human intestine clone HuAC20 AY684
AB486629.1 gg_id:577345 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCOR AB486
EU531895.1 gg_id:263067 Predominant role host genetics controlling gut microbiota FMF remission stool clone EU531
AF071415.1 gg_id:13851 Anaeromusa acidaminophila str. DSM 3853 AF071
EU469036.1 gg_id:303124 Speke's gazelle feces clone SP2_c09_3 EU469
DQ824735.1 gg_id:179447 human fecal clone RL185_aaj72d08 DQ824
FJ683901.1 gg_id:521470 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6839
GU304004.1 gg_id:549795 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU304
FJ673979.1 gg_id:516340 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6739
DQ833301.1 gg_id:164274 Anaerobic Reductive Dechlorination Vinyl Chloride ly Enriched Bachman Aquifer Sed DQ833
FJ682035.1 gg_id:525023 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6820
EU307091.1 gg_id:251142 Changes microbial metabolic and along hydrogeochemically variable profile unsatura EU307
AB034135.1 gg_id:48795 rumen clone 4C28d-2 AB034
DQ904885.1 gg_id:163607 human fecal clone 001C-f2 DQ904
GQ005015.1 gg_id:504647 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu65h1 GQ005
FJ676618.1 gg_id:532032 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6766
FJ678334.1 gg_id:527813 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6783
AB486685.1 gg_id:572648 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCOR AB486
FJ678463.1 gg_id:527603 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6784
EU845665.1 gg_id:336552 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU845
FJ682745.1 gg_id:527983 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6827
FJ684630.1 gg_id:514989 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6846
EU774198.1 gg_id:346793 Chimpanzee feces clone CHIMP1_aaj39c11 EU774
EU307090.1 gg_id:243204 Changes microbial metabolic and along hydrogeochemically variable profile unsatura EU307
EU775009.1 gg_id:316336 Francois Langur feces clone FL_2aaa02b05 EU775
EU747937.1 gg_id:337267 neotropical folivorous flying bird adult hoatzin crop clone hoa13_77E10 EU747
DQ310746.1 gg_id:199797 Recurring seasonal dynamics microbial stream habitats riverine sediment clone WC DQ310
AY995255.1 gg_id:123766 human vagina clone FX8B2-5 AY995
AY667269.1 gg_id:103280 TCE-dechlorinating groundwater clone TANB127 AY667
FJ674118.1 gg_id:518615 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6741

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GQ179679.1 gg_id:455949 Heterogeneity vaginal microbial within individuals vagina clone VE44F01 GQ179
FJ678138.1 gg_id:521053 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6781
FJ678575.1 gg_id:531578 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6785
FJ682764.1 gg_id:518322 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6827
AY672080.2 gg_id:149234 Microbial on patients stomatitis and healthy biofilm denture wearers clone DWE10 AY672
DQ217599.1 gg_id:139963 Zymophilus raffinosivorans str. VTT E-90406; DSM 20765; ATCC 496 DQ217
FJ673355.1 gg_id:525608 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6733
FJ679306.1 gg_id:520520 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6793
FJ372095.1 gg_id:363046 feces adult twins and mothers; TS9 clone TS9_a01f12 FJ3720
AB034141.1 gg_id:28188 rumen clone 3C28d-10 AB034
AY985859.1 gg_id:117810 human stool clone D133 AY985
DQ113674.1 gg_id:132784 dog colon clone C2-26 DQ113
AB185750.1 gg_id:103463 rumen clone U29-B01 AB185
GU303125.1 gg_id:570205 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU303
EU842705.1 gg_id:318812 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
FJ674045.1 gg_id:521328 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6740
AB034079.1 gg_id:51519 rumen clone 3C3d-10 AB034
FJ680777.1 gg_id:510572 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6807
EU747918.1 gg_id:346208 neotropical folivorous flying bird adult hoatzin crop clone hoa12_26B04 EU747
FJ673180.1 gg_id:514372 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6731
AB486409.1 gg_id:546268 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC AB486
AF371705.1 gg_id:45688 swine intestine clone p-286-a3 AF371
AB486202.1 gg_id:575498 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC AB486
FJ684083.1 gg_id:520119 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6840
AJ009494.1 gg_id:13843 anaerobic TCB-transforming consortium clone SJA-143 AJ0094
GQ060518.1 gg_id:462753 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw02g03 GQ060
GQ451274.1 gg_id:514095 Fecal Yunnan snub-nosed monkey feces clone J269 GQ451
AF357557.1 gg_id:72198 mpn-isolate group 9 AF357
AF371701.1 gg_id:34987 swine intestine clone p-2365-55G5 AF371
AB198438.1 gg_id:237356 Selenomonas ruminantium str. S206 AB198
AF473834.1 gg_id:38606 Megasphaera micronuciformis str. AIP 412.00; CIP 107280 AF473
EU382011.1 gg_id:268506 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU382
EU794209.1 gg_id:334383 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_O30 EU794
EU475011.1 gg_id:296159 red river hog feces clone RRH_aaa03c07 EU475
FJ674071.1 gg_id:521929 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6740
FJ372342.1 gg_id:368157 feces adult twins and mothers; TS9 clone TS9_a04e03 FJ3723
EF063619.1 gg_id:193173 Microbial ecology autotrophic denitrifying anaerobic methanogenic UASB reactor clo EF0636
DQ223729.1 gg_id:140753 Megasphaera sueciensis str. VTT E-97791 DQ223
EU779137.1 gg_id:354926 Trancaspian Urial feces clone TU1_aaa03b10 EU779
FN563256.1 gg_id:554464 Impact changing HRT OLR on prokaryotes involved biomethanizitaion and fuzzy logic FN563
EU747978.1 gg_id:349584 neotropical folivorous flying bird adult hoatzin crop clone hoa13_48H06 EU747

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AB486952.1 gg_id:541359 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCOR(AB486
AY959093.1 gg_id:131417 Microbes on human vaginal epithelium clone rRNA320 AY959(
FJ675815.1 gg_id:531229 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6758
FJ678660.1 gg_id:519991 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6786
FJ673588.1 gg_id:526829 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6735
FJ673153.1 gg_id:529494 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6731
AB198425.1 gg_id:246110 Selenomonas ruminantium str. S2 AB198
EU850607.1 gg_id:334117 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF440 EU850
AB034134.1 gg_id:42912 rumen clone 4C28d-6 AB034
AB218316.1 gg_id:148501 Fecal microbial (dugong dugon) determined genes Dugong feces clone dgB-66 AB218
AY958931.1 gg_id:153751 Microbes on human vaginal epithelium clone rRNA158 AY958
GQ004077.1 gg_id:505586 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu68d0 GQ004
AB486076.1 gg_id:569899 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC AB486
AB487430.1 gg_id:540748 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNIR0 AB487
FJ682840.1 gg_id:520575 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6828
FJ393127.1 gg_id:362899 Fusing Biology Engineering Improve Power Output Microbial Fuel Cells microbial fuel FJ3931
U81750.2 gg_id:13861 fluidized bed anaerobic digestor fed vinasses (waste wine distillery) clone vadinHB04 U8175
FJ833201.1 gg_id:594131 Microbial Ecology Crop Folivorous Hoatzin crop contents clone A3Q102_39G05 FJ8332
FJ673713.1 gg_id:524216 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6737
GQ006579.1 gg_id:503085 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu85b11c GQ006
FJ386554.1 gg_id:369923 vaccination sludge backf pumping house Xilang municipal wastewater treatment plar FJ3865
FJ673625.1 gg_id:530256 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6736
EF399619.1 gg_id:206942 human fecal clone SJTU_E_01_29 EF3996
EU009839.1 gg_id:254812 intestinal microbiota domestic and wild turkeys turkey cecum clone WTB_Q48 EU009
EU234118.1 gg_id:252011 receiving river and un techniques anaerobic process WWTP treating penicillin G prod EU234
AB198432.1 gg_id:242601 Selenomonas ruminantium str. S109 AB198
DQ295866.1 gg_id:191985 Pelosinus fermentans str. UFO1 DQ295
FJ172883.1 gg_id:352391 Qinghai Yak Ruminal and Fungi China rumen clone RB-2F2 FJ1728
FJ680477.1 gg_id:523055 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6804
FJ682404.1 gg_id:513552 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6824
AB486876.1 gg_id:578241 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCOR(AB486
EU259482.1 gg_id:241086 Rumen yak (Bos grunniens) sequences rumen fluid clone YRC106 EU259
AY981016.1 gg_id:116502 human rectum mucosal biopsy clone V190 AY981(
FJ680012.1 gg_id:515217 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6800
FJ677302.1 gg_id:528220 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6773
DQ795993.1 gg_id:188086 human fecal clone RL202_aai50a03 DQ795
GU214167.1 gg_id:593991 and biota slimes Canadian paper mills slime mill taken wet section around papermal GU214
DQ777892.2 gg_id:166356 rat feces clone R-1170 DQ777
AB034191.1 gg_id:38984 Anaerovibrio lipolyticus str. ATCC 33276 AB034
EU748414.1 gg_id:328699 neotropical folivorous flying bird adult hoatzin crop clone hoa5_08h08 EU748

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AY244972.1 gg_id:83021 cow rumen clone BS18 AY2449
FJ683141.1 gg_id:528857 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6831
NR_029357.1 gg_id:547456 Propionispira arboris str. 12B4; DSM 2179 NR_02
GQ004964.1 gg_id:504698 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu65d0 GQ004
EU344158.1 gg_id:260291 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU3441
FJ825568.1 gg_id:559706 Microbial during start-up mesophilic biogas plant clone 21_BS5_39 FJ8255
AB198435.1 gg_id:236008 Selenomonas ruminantium str. S150 AB1984
AB486785.1 gg_id:541916 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCOR(AB4867
EU461059.1 gg_id:288601 red kangaroo feces clone KO1_aai43d02 EU461(
DQ168841.1 gg_id:154690 Fermentative biohydrogen production heated anaerobic sludge clone J25 DQ168
EU468247.1 gg_id:290103 domesticated horse feces clone horsej_h07 EU4682
EU463594.1 gg_id:302001 domesticated horse feces clone horsej_aai89d11 EU4635
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AY514996.1 gg_id:99976 Veillonella rodentium str. ATCC 17743 AY5149
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GQ086352.1 gg_id:443529 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ086
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EF434331.1 gg_id:210713 gastrointestinal tract microbiota microarray reference pool created pooling products EF4343
GQ091818.1 gg_id:411006 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ091
EF515580.1 gg_id:218801 Electricigen Enrichment MFC full-scale anaerobic bioreactor sludge treating brewery EF5155
GQ338722.1 gg_id:573384 and function human intestinal microbiota ileostomy effluent healthy patient clone A GQ338
EU460862.1 gg_id:301827 short-beaked echidna feces clone ECH_aai39e05 EU4608
GQ101329.1 gg_id:453095 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw493g GQ101
GQ006752.1 gg_id:502912 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu87c06c GQ006
GQ022064.1 gg_id:487605 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu3 GQ022
FJ374768.1 gg_id:585419 Veillonella sp. str. S101 FJ3747
GQ109121.1 gg_id:448078 Topographical and Temporal Human Skin Microbiome skin palm clone nbw608f12c1 GQ109
GQ031217.1 gg_id:422979 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor GQ031
GQ055579.1 gg_id:381881 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1117e1 GQ055
GQ011614.1 gg_id:498054 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw794c08 GQ011
GQ113791.1 gg_id:414090 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw(GQ113
GQ030037.1 gg_id:437122 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw866c0 GQ030
AY995768.1 gg_id:119118 Veillonella atypica str. ATCC 17744 AY9957
GQ030108.1 gg_id:459734 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw867c0(GQ030

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GQ030048.1 gg_id:430534 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw866d0 GQ030
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GQ005607.1 gg_id:504056 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl GQ005
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GQ086284.1 gg_id:422736 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ086

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o__Desulfitobacterales	f__Desulfitobacteraceae
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o__Desulfitobacterales	f__Desulfitobacteraceae
o__Halanaerobiales	f__Halanaerobiaceae
o__Halanaerobiales	f__Halanaerobiaceae
o__Halanaerobiales	f__Halanaerobiaceae
o__Halanaerobiales	f__Halanaerobiaceae

g__Veillonella
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g__Veillonella
g__Veillonella
g__Veillonella
g__Desulfitobacter
g__Desulfitobacter
g__Desulfitobacter
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__Halanaerobium
g__Halothermothrix
g__unclassified
g__unclassified