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AY177799.1 gg_id:78421 Antarctic sediment clone SB2_13
EU542440.1 gg_id:270723 Effects chemical structure concentration on pathways microbial during dechlorinatio
DQ394960.1 gg_id:155401 harbor sediment clone VHS-B3-73
EU542523.1 gg_id:267799 Effects chemical structure concentration on pathways microbial during dechlorinatio
EF125387.1 gg_id:193460 soil naked tidal flat sediment near mangrove clone MSB-1B10
NR_025746.1 gg_id:544425 Desulfofaba fastidiosa str. P2; ATCC BAA-815; DSM 15249
EU048629.1 gg_id:249788 Microbial surface marine sediment Xisha Trough South China Sea clone MD2902-B24
AM039960.1 gg_id:132592 marine sediment clone 50FS
AJ535249.1 gg_id:77873 marine sediment above hydrate ridge clone Hyd89-61 proteobacterium
CU927052.1 gg_id:569189 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
AF022936.1 gg_id:10867 Desulfocella halophila str. GSL-But2
CU927196.1 gg_id:554689 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
DQ831552.1 gg_id:162529 Activity and sulphate-reducing contrasting sediments River Colne estuary UK marine
NR_028780.1 gg_id:551572 Desulforegula conservatrix str. Mb1Pa; DSM 13527
FN429809.1 gg_id:556083 Biogeochemistry -activity cold seep Larsen B area western Weddell Sea Antarctica m
DQ431904.1 gg_id:204801 microorganisms catalyzing nitrogen removal and organic matter metabolism perme
DQ831554.1 gg_id:171484 Activity and sulphate-reducing contrasting sediments River Colne estuary UK marine
AM490744.1 gg_id:568791 Linking and functional nutrient spiraling mats (USA) microbial mat sulfidic cave sprir
EU488036.1 gg_id:560020 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and
AM745204.1 gg_id:287932 Impact oil er hydrocarbons on microbial and activity Gulf Mexico cold seep marine s
AY851292.1 gg_id:150305 Algidimarina butyricum str. AK-B
DQ811797.1 gg_id:167399 mangrove soil clone MSB-3C3
GU080089.1 gg_id:578329 Combined and proteomic approaches identify involved anaerobic 2-methylnaphthal
DQ397436.1 gg_id:159112 Guerrero Negro hypersaline microbial mat clone 062DZ56
AF418174.1 gg_id:71864 Desulfovibrio baarsii str. DSM 2075
GQ356991.1 gg_id:580063 Metal Dependent Marine Methane Oxidation methane seep sediment clone FeSO4_
AM490746.1 gg_id:591624 Linking and functional nutrient spiraling mats (USA) microbial mat sulfidic cave sprir
AM176857.1 gg_id:160904 Recovery mangrove sediment clone SZB57
GQ357013.1 gg_id:510495 Metal Dependent Marine Methane Oxidation methane seep sediment clone FeLive(
AM040123.1 gg_id:147720 sandy sediments clone Sylt 27
EU617854.1 gg_id:316203 Seasonal variation microbial Yel Sea sediment clone C13S-20
EU048693.1 gg_id:250681 and archaeal surface marine sediment Slope South China Sea clone MD2896-B42
DQ431902.1 gg_id:207781 microorganisms catalyzing nitrogen removal and organic matter metabolism perme
FJ484778.1 gg_id:542328 microbial autonomous rover world's deepest phreatic sinkhole wall biomat El Zacator
DQ811819.1 gg_id:169367 mangrove soil clone MSB-4H12
DQ811816.1 gg_id:166688 mangrove soil clone MSB-4G6
DQ404782.1 gg_id:155938 contaminated sediment clone 661234
AF002671.1 gg_id:10776 Desulfobacca acetoxidans
FJ902442.1 gg_id:548667 phreatic limestone sinkholes northeastern Mexico water column surface cenote Cara
FJ810575.1 gg_id:373867 Subsurface ecosystem resilience: Long-term attenuation subsurface contaminants su

AB530220.1	537927	2661.2	2947.3	3763.0	3523.9	2478.7	2677.0
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DQ394960.1	155401	3468.3	4156.5	2423.0	1961.1	4747.0	4797.8
EU542523.1	267799	5792.6	6881.1	7775.2	3667.6	8016.1	6536.1
EF125387.1	193460	1299.3	3176.8	4904.4	2480.0	3415.5	6218.5
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AM039960.1	132592	159.7	538.2	114.6	89.5	795.8	82.2
AJ535249.1	77873	1558.5	2493.1	2321.2	1593.0	1190.5	2574.1
CU927052.1	569189	4167.8	3876.1	4422.6	4474.3	4860.6	4720.6
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CU927196.1	554689	192.0	339.2	450.3	116.1	148.4	139.6
DQ831552.1	162529	100.3	96.8	196.0	165.6	58.9	59.5
NR_028780.1	551572	40.5	72.0	89.5	62.7	70.7	32.6
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AF523963.1 gg_id:101995 forested wetland clone FW106
FJ902422.1 gg_id:586511 phreatic limestone sinkholes northeastern Mexico water column surface cenote Cara
FJ484032.1 gg_id:537190 microbial autonomous rover world's deepest phreatic sinkhole wall biomat El Zacator
FJ484530.1 gg_id:554210 microbial autonomous rover world's deepest phreatic sinkhole wall biomat El Zacator
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AY340836.1 gg_id:91627 sulfate-reducing fluidized-bed reactor clone SR_FBR_L13
AB262720.1 gg_id:239069 microorganisms shal subsurface Sarobetsu mire peat soil clone HSM050P-B-9
FJ516878.1 gg_id:558853 semiarid 'Tablas de Daimiel National Park' wetland (Central Spain) unravelled upper s
DQ676381.1 gg_id:221935 Archaeal sediment and plankton freshwater pond suboxic freshwater-pond clone M
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FJ437843.1 gg_id:511708 Benthic okenone production Fayetteville New York Green Lake 25 m water depth clor
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AF282178.1 gg_id:31004 marine sediment clone Btol
AJ316021.1 gg_id:42269 Desulfomonile sp. clone 624
AM086646.1 gg_id:140135 Desulfomonile tiedjei str. DSM 6799
DQ133909.1 gg_id:164530 Dominant microbial biofilms frasassi cave system Italy limestone-corroding stream b
CT574193.1 gg_id:151947 Evry municipal wastewater treatment plant clone 060B12_B_SD_P93
CU917968.1 gg_id:562603 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
CT573954.1 gg_id:153501 Evry municipal wastewater treatment plant clone 009F10_B_SD_P15
CT573960.1 gg_id:155759 Evry municipal wastewater treatment plant clone 009F03_B_SD_P15
FJ462108.1 gg_id:581591 Microbial ecology industrial digestor mesophilic anaerobic reactor fed effluent chemi
EU407209.1 gg_id:275861 household biogas digester clone GW-26
CT574120.1 gg_id:155635 Evry municipal wastewater treatment plant clone 061D05_B_SD_P93
AJ133795.1 gg_id:10858 Syntrophus sp
EU104840.1 gg_id:265855 sulfate-reducing and methanogen sulfate-fed reactors libraries anaerobic biofilm rea
CT574027.1 gg_id:151989 Evry municipal wastewater treatment plant clone 008C04_B_SD_P15
CT574029.1 gg_id:156244 Evry municipal wastewater treatment plant clone 008C02_B_SD_P15
AB252682.1 gg_id:168756 and activities propionate-oxidizing that affected propionate concentration anaerobic
CR933148.1 gg_id:110803 Evry municipal wastewater treatment plant clone 012B10_B_SD_P15
CU919519.1 gg_id:547047 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
DQ676391.1 gg_id:227149 Archaeal and plankton freshwater pond suboxic freshwater-pond sediment clone M
CT574164.1 gg_id:152984 Evry municipal wastewater treatment plant clone 060F04_B_SD_P93
DQ501304.1 gg_id:187961 Seasonal dynamics free-living and particle- four lakes northeastern Germany freshw
GU202945.1 gg_id:592840 Effect pH on anode microbes MFC microbial fuel cell inoculated activated sludge wa
CT573944.1 gg_id:154331 Evry municipal wastewater treatment plant clone 009H01_B_SD_P15
EU407210.1 gg_id:276971 household biogas digester clone GW-27
EU522631.1 gg_id:262404 hydrocarbon-degrading methanogenic microbial consortia settling basin Northern Al
AY661413.1 gg_id:107448 anaerobic hybrid reactor clone TTA_H37
AB234260.1 gg_id:145632 Biotransformation Polychlorinated Dioxins Microbial Dynamics Sediment Microcosm

AB426203.1	268764	1485.7	2788.5	6885.8	927.5	479.5	2569.0
AF523963.1	101995	12.2	39.8	646.8	54.8	37.0	22.0
FJ902422.1	586511	2459.8	2390.3	6057.5	1716.5	2660.2	1965.1
FJ484032.1	537190	4448.8	5733.9	7381.6	6184.9	8001.9	8523.8
FJ484530.1	554210	10926.1	10055.8	10571.6	8229.8	9536.7	8357.8
DQ404621.1	152758	3072.7	4866.7	3037.6	3813.5	5022.2	5692.8
AB426195.1	268751	3773.7	4572.4	9767.4	3821.1	1799.0	4587.8
AY340836.1	91627	49.6	82.3	174.2	61.9	87.2	43.2
AB262720.1	239069	277.2	863.0	3697.7	276.5	257.9	719.5
FJ516878.1	558853	3808.6	3884.7	8593.9	5852.9	3366.5	3315.7
DQ676381.1	221935	7091.6	6528.4	2537.9	3095.6	2478.6	1896.2
AM490653.1	580869	178.3	436.0	977.0	168.2	297.9	711.0
FJ437843.1	511708	297.7	842.9	739.2	111.8	112.8	123.2
AF282177.1	30060	10813.0	9151.3	3788.6	5876.5	8745.2	9355.8
AF282178.1	31004	352.7	277.8	311.4	425.0	104.0	174.5
AJ316021.1	42269	8082.7	10357.2	14901.9	8407.7	9942.4	11045.3
AM086646.1	140135	260.3	447.6	659.8	187.0	215.2	406.7
DQ133909.1	164530	277.1	591.6	1461.5	426.3	172.0	533.6
CT574193.1	151947	623.6	544.2	1137.7	412.1	540.0	475.8
CU917968.1	562603	4344.4	3787.2	1790.8	5808.8	7939.6	6589.7
CT573954.1	153501	6375.6	6550.4	2409.8	5512.2	7250.1	8397.9
CT573960.1	155759	1914.9	2373.8	4466.5	1808.1	1202.0	2148.8
FJ462108.1	581591	2227.7	2702.7	2921.3	1239.5	1579.0	1267.4
EU407209.1	275861	6183.9	9376.4	11481.4	5846.0	8870.8	8882.1
CT574120.1	155635	7176.5	6814.5	3693.0	7184.2	5858.7	6653.5
AJ133795.1	10858	46.4	49.8	39.7	56.7	69.9	33.9
EU104840.1	265855	4612.4	4882.8	4254.4	3379.1	4388.0	4144.1
CT574027.1	151989	316.4	349.7	965.5	227.8	71.6	91.4
CT574029.1	156244	3254.5	4253.1	2191.5	3313.7	6526.8	7290.6
AB252682.1	168756	27.5	46.5	47.1	57.3	63.1	23.3
CR933148.1	110803	30.0	29.9	50.8	50.7	64.0	28.8
CU919519.1	547047	2046.7	1406.6	1765.5	2307.3	1805.0	1694.4
DQ676391.1	227149	761.6	1210.5	969.6	811.4	1200.1	857.0
CT574164.1	152984	5282.5	5374.6	5001.8	6959.3	4799.0	5973.4
DQ501304.1	187961	7559.4	10844.3	8527.8	8535.3	15068.5	10368.5
GU202945.1	592840	432.8	1085.0	2162.3	352.5	48.9	49.1
CT573944.1	154331	12288.5	12882.1	14635.3	10042.0	14315.6	14383.0
EU407210.1	276971	6771.5	8018.2	10572.8	6443.3	8194.5	7452.4
EU522631.1	262404	538.8	871.0	3048.1	559.1	54.8	13.1
AY661413.1	107448	5628.6	7448.9	5503.8	6199.6	10091.0	7541.3
AB234260.1	145632	2685.7	4033.9	5366.9	1347.5	2500.8	2701.9

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FJ461976.1 gg_id:586848 Microbial ecology industrial digestor mesophilic anaerobic reactor fed effluent chemi
CU925368.1 gg_id:547613 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
EU399668.1 gg_id:271079 and localization microbial consortium full-scale granular activated carbon anaerobic
AB186854.1 gg_id:99369 polychlorinated dioxin dechlorinating microcosm clone TSBZ03
AF229793.1 gg_id:37165 terephthalate-degrading consortium clone TA20
AJ306771.1 gg_id:66928 DCP-dechlorinating consortium clone SHA-42
AB288891.1 gg_id:203169 termite gut homogenate clone BOf2-22
FJ462058.1 gg_id:593849 Microbial ecology industrial digestor mesophilic anaerobic reactor fed effluent chemi
EU522634.1 gg_id:269542 hydrocarbon-degrading methanogenic microbial consortia settling basin Northern Al
DQ521796.1 gg_id:159708 Anaerobic Methane Oxidizing ANME-1b Archaea Hypersaline Sediments Gulf Mexic
AB179694.1 gg_id:102521 groundwater 0.2 m-captured fraction clone KNA6-EB24
DQ521792.1 gg_id:160618 Anaerobic Methane Oxidizing ANME-1b Archaea Hypersaline Sediments Gulf Mexic
FJ902117.1 gg_id:579169 phreatic limestone sinkholes northeastern Mexico orange biomat 8m deep cenote Ca
AJ535254.1 gg_id:77896 marine sediment above hydrate ridge clone Hyd89-52 proteobacterium
FJ462062.1 gg_id:587689 Microbial ecology industrial digestor mesophilic anaerobic reactor fed effluent chemi
AM746089.1 gg_id:299409 Impact oil er hydrocarbons on microbial and activity Gulf Mexico cold seep marine s
DQ811814.1 gg_id:173034 mangrove soil clone MSB-4G3
CU922340.1 gg_id:534010 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
FN429788.1 gg_id:546409 Biogeochemistry -activity cold seep Larsen B area western Weddell Sea Antarctica m
AB252432.1 gg_id:153221 Microbial extremely CO2 rich deep-sea sediment Marine sediments Yonaguni Knoll I
EU644230.1 gg_id:283767 and Samoylov Island Lena active layer -centred polygon near surface horizon; Rim_T
DQ067032.1 gg_id:133542 Lake Washington sediment clone pLW-41
DQ404844.1 gg_id:150930 contaminated sediment clone 655974
FJ902148.1 gg_id:592355 phreatic limestone sinkholes northeastern Mexico orange biomat 8m deep cenote Ca
DQ415841.1 gg_id:158424 Dominant microbial limestone-corroding biofilms frasassi system Italy Frasassi sulfid
AF420337.1 gg_id:67800 hydrothermal sediment clone AF420337
GU180161.1 gg_id:538685 Impact coplanar PCBs on microbial activity anaerobic estuarine sediments sediment
EU101287.1 gg_id:237813 Sulfide/oxygen supply ratio predicts outcome competition among sulfur-oxidizing wa
EU542439.1 gg_id:274550 Effects chemical structure concentration on pathways microbial during dechlorinatio
FN429791.1 gg_id:586738 Biogeochemistry -activity cold seep Larsen B area western Weddell Sea Antarctica m
AY053494.1 gg_id:34985 gas hydrate clone AT425_EubF5
FJ437824.1 gg_id:509369 Benthic okenone production Fayetteville New York Green Lake chemocline 20.5 m wa
DQ988259.1 gg_id:185953 Microbial lab-scale A1-A2-O fixed biofilm system coking wastewater treatment with
FJ462006.1 gg_id:569259 Microbial ecology industrial digestor mesophilic anaerobic reactor fed effluent chemi
AF354149.1 gg_id:71121 marine methane seep clone 1513
AM712339.1 gg_id:252529 detection and ly microbial Brothers Seamount Kermadec Arc New Zealand biofilm h
EU522632.1 gg_id:269237 hydrocarbon-degrading methanogenic microbial consortia settling basin Northern Al
AB177179.1 gg_id:128221 seafloor methane hydrate clone ODP1230B23.08
CR933196.1 gg_id:110185 Evry municipal wastewater treatment plant clone 008B10_B_SD_P15
AY542210.1 gg_id:114116 Gulf Mexico seafloor sediments clone GoM HDB-32
AB426198.1 gg_id:259940 -situ identification study benzene-degrading s under methanogenic condition anaerc

FJ461976.1	586848	9109.2	12026.2	8631.4	8686.4	12053.1	8862.1
CU925368.1	547613	4659.7	4847.5	5714.1	2596.2	1103.9	1744.5
EU399668.1	271079	1760.2	3550.4	4936.7	762.2	1759.9	1517.3
AB186854.1	99369	4443.7	5021.0	10482.5	3139.3	4609.2	3762.3
AF229793.1	37165	4642.6	5563.5	5441.6	4597.4	2931.7	4325.6
AJ306771.1	66928	582.9	1140.3	3897.4	683.2	1440.9	1815.2
AB288891.1	203169	927.7	1778.0	3460.4	675.2	2024.3	1562.7
FJ462058.1	593849	22850.7	22125.0	20678.7	20648.9	19479.6	17710.6
EU522634.1	269542	1044.1	2181.3	3298.6	688.1	1620.1	789.3
DQ521796.1	159708	680.4	725.2	658.6	204.5	171.6	131.9
AB179694.1	102521	111.0	275.9	685.5	274.3	117.6	114.4
DQ521792.1	160618	769.3	880.1	1409.5	587.6	848.3	167.7
FJ902117.1	579169	866.4	2121.6	3600.3	629.1	2728.9	1996.0
AJ535254.1	77896	2903.7	4605.9	2786.5	2060.2	2677.1	3000.2
FJ462062.1	587689	825.1	1296.1	1796.1	490.3	120.8	322.9
AM746089.1	299409	1826.1	4261.6	3935.4	1718.1	1494.9	1619.2
DQ811814.1	173034	32.8	52.2	46.3	42.1	57.6	30.7
CU922340.1	534010	1224.7	3552.5	6158.0	2474.3	1825.6	1832.7
FN429788.1	546409	6250.0	6565.8	7423.2	7096.9	4237.9	4969.7
AB252432.1	153221	58.2	142.9	267.0	118.1	105.0	173.1
EU644230.1	283767	7169.3	8528.8	10684.9	6716.2	9851.0	8177.8
DQ067032.1	133542	1329.9	2266.0	7120.8	1263.6	746.8	1793.4
DQ404844.1	150930	547.8	1546.5	2443.8	311.2	79.8	154.4
FJ902148.1	592355	7622.8	7247.0	6337.4	6051.0	11097.4	9507.5
DQ415841.1	158424	44.0	155.4	117.5	57.1	57.4	24.0
AF420337.1	67800	2152.1	2560.5	3478.4	1559.9	2432.9	2515.9
GU180161.1	538685	7285.9	8063.7	8213.0	6739.8	5652.4	9952.5
EU101287.1	237813	5788.9	5892.8	3610.7	4663.4	6690.0	6296.7
EU542439.1	274550	5226.1	6754.7	3701.3	3681.2	6306.9	3316.8
FN429791.1	586738	2346.5	2529.8	4572.2	1405.4	759.1	1275.1
AY053494.1	34985	1737.6	2007.6	2986.9	1414.9	1281.7	1148.8
FJ437824.1	509369	2245.8	3614.7	7088.9	2825.2	3143.9	3242.6
DQ988259.1	185953	11720.1	13336.7	9651.8	8287.9	8241.6	6167.1
FJ462006.1	569259	2863.3	3267.2	3509.0	3749.9	5185.2	4513.1
AF354149.1	71121	1161.3	1805.0	4742.7	2623.7	1539.3	2333.4
AM712339.1	252529	2425.5	3427.1	4445.7	2336.9	2895.4	2728.7
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AB177179.1	128221	30.2	60.8	153.0	86.7	60.6	67.5
CR933196.1	110185	208.2	684.6	806.9	456.9	1307.1	316.9
AY542210.1	114116	2327.1	2897.6	2712.4	1036.0	2972.9	3479.4
AB426198.1	259940	347.3	1021.2	728.4	277.6	956.7	1877.5

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EU592411.1 gg_id:535455 Seasonal changes Salton Sea hypersaline sediment clone SSS15N
EU644111.1 gg_id:280179 and Samoylov Island Lena active layer -centred polygon near permafrost table; Rim_
AY211657.1 gg_id:95801 Gulf Mexico seafloor sediment clone GoM GC185 503E
AY211680.1 gg_id:96542 Gulf Mexico seafloor sediment clone GoM GC234 621E
AF482437.1 gg_id:77432 granular sludge clone R2b29
FJ902092.1 gg_id:566804 phreatic limestone sinkholes northeastern Mexico orange biomat 8m deep cenote Ca
DQ521786.1 gg_id:160206 Anaerobic Methane Oxidizing ANME-1b Archaea Hypersaline Sediments Gulf Mexic
FJ462010.1 gg_id:593726 Microbial ecology industrial digestor mesophilic anaerobic reactor fed effluent chemi
AJ583188.1 gg_id:94853 radioactive site ground water clone S15B-MN12
EU644229.1 gg_id:282165 and Samoylov Island Lena active layer -centred polygon near surface horizon; Rim_T
AB525446.1 gg_id:570354 Segregated ANME-1 and -2 cold-seep marine sediments deep-sea methane seep sed
DQ787721.1 gg_id:162776 holocene lake sediment clone SLB628
FJ902107.1 gg_id:580738 phreatic limestone sinkholes northeastern Mexico orange biomat 8m deep cenote Ca
AM745217.1 gg_id:294031 Impact oil er hydrocarbons on microbial and activity Gulf Mexico cold seep marine s
AF385080.1 gg_id:28552 Desulfacinum subterraneum str. 101
AF170418.1 gg_id:73225 Desulfacinum sp. str. M40/2 CIV-2.3
DQ006288.1 gg_id:123413 Desulfatimicrobium mahresensis str. SA1
FN356276.1 gg_id:558010 Prokaryotic structure sulfate reducer activity -temperature reservoirs and without ni
FN356315.1 gg_id:570270 Prokaryotic structure sulfate reducer activity -temperature reservoirs and without ni
NR_027598.1 gg_id:544627 Syntrophobacter fumaroxidans MPOB str. MPOB; DSM 10017
AAJF01000012.1 gg_id:134597 Syntrophobacter fumaroxidans str. MPOB
GQ261306.1 gg_id:543826 Study on Sediment sediment Dongping Lake clone 1S2-18
AB232801.1 gg_id:138526 Microbial mesophilic chemostat cultivation propionate-degrading methanogenic con
FJ535519.1 gg_id:538615 Microbial digestion swine wastewater anaerobic UASB reactor clone SWADLP2-18
GU208398.1 gg_id:581775 Study on Sediment Dongping Lake sediment clone Fh1-17
GQ402720.1 gg_id:583853 Accessing microbial biodiversity and metabolic potential tropical -based approach p
CU920959.1 gg_id:535086 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
CU924062.1 gg_id:573309 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
CU921674.1 gg_id:543856 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
FJ484661.1 gg_id:571785 microbial autonomous rover world's deepest phreatic sinkhole wall biomat El Zacator
X70905.1 gg_id:10750 Syntrophobacter wolinii str. defined co Desulfovibrio sp. DSM 2805
EF515568.1 gg_id:222770 Electricigen Enrichment MFC full-scale anaerobic bioreactor sludge treating brewery
AB232820.1 gg_id:139158 Microbial mesophilic chemostat cultivation propionate-degrading methanogenic con
DQ415751.1 gg_id:157212 Dominant microbial limestone-corroding biofilms frasassi system Italy Frasassi sulfid
CU921434.1 gg_id:549201 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
FN646446.1 gg_id:589878 candidate division OP3 cells limonene Limonene degrading methanogenic s clone Li
X94911.1 gg_id:10755 Syntrophobacter sp
GQ402673.1 gg_id:585966 Accessing microbial biodiversity and metabolic potential tropical -based approach p
EF688226.1 gg_id:329449 Detection microbial sludge anaerobic wastewater treatment system clone 5E3_cons
DQ404834.1 gg_id:155072 contaminated sediment clone 655963
U25627.1 gg_id:10762 Thermodesulforhabdus norvegica str. A8444

EU592411.1	535455	6917.9	9587.3	14878.7	5568.8	8012.2	8096.9
EU644111.1	280179	1056.9	1471.0	2206.1	1493.8	1470.2	1555.3
AY211657.1	95801	5007.3	5607.4	7136.6	5449.9	6439.3	5646.5
AY211680.1	96542	1813.9	3531.2	4680.4	2298.1	1517.4	2884.2
AF482437.1	77432	20900.4	20030.7	12456.3	17559.3	16296.3	13356.3
FJ902092.1	566804	1046.6	1584.1	4296.4	789.1	73.7	31.4
DQ521786.1	160206	6855.4	7841.6	4999.3	7666.6	5828.5	7306.7
FJ462010.1	593726	14779.9	14766.9	7886.6	9525.5	16493.0	10585.1
AJ583188.1	94853	282.4	597.9	695.5	194.9	331.4	413.8
EU644229.1	282165	11409.2	12832.6	5682.2	7546.9	6879.2	5176.3
AB525446.1	570354	2465.7	2973.1	2391.6	2355.8	3690.6	2392.9
DQ787721.1	162776	551.2	1520.5	4063.8	679.2	170.1	596.0
FJ902107.1	580738	3764.3	6023.8	6951.6	4679.9	7362.3	6696.6
AM745217.1	294031	3380.9	9803.1	7563.7	6961.2	3042.2	9738.9
AF385080.1	28552	621.7	647.7	376.9	327.4	169.1	155.8
AF170418.1	73225	4546.9	5016.3	5716.8	3401.2	3767.2	4032.4
DQ006288.1	123413	36.2	234.9	511.5	123.5	161.7	27.2
FN356276.1	558010	1967.0	2751.1	3662.1	1609.7	2182.1	2228.3
FN356315.1	570270	12411.0	13744.5	10294.8	11627.7	15575.7	17786.9
NR_027598.1	544627	114.7	454.8	480.3	183.7	171.9	74.7
AAJF01000012.1	134597	914.9	1437.4	1144.5	1196.7	882.1	1063.3
GQ261306.1	543826	285.8	961.3	1316.7	129.7	148.5	212.3
AB232801.1	138526	831.2	867.4	2064.5	406.6	223.7	273.5
FJ535519.1	538615	195.4	667.0	1597.3	144.5	91.2	155.5
GU208398.1	581775	5607.3	5941.1	7134.0	3274.2	5463.9	4333.3
GQ402720.1	583853	179.2	548.5	1517.8	162.8	117.1	138.8
CU920959.1	535086	4177.9	4521.3	5156.7	4023.8	12963.7	10142.5
CU924062.1	573309	87.3	172.2	333.4	155.3	344.4	488.3
CU921674.1	543856	9825.6	13476.4	7598.2	10559.6	11836.5	11655.1
FJ484661.1	571785	1668.7	1674.2	5280.1	2300.2	785.8	1861.4
X70905.1	10750	32.7	54.4	324.4	39.6	69.1	28.4
EF515568.1	222770	3206.3	2797.7	1535.0	3855.9	3502.1	4348.0
AB232820.1	139158	86.3	274.4	473.6	94.0	221.4	1035.0
DQ415751.1	157212	7825.6	7413.0	5947.4	4393.1	4639.1	3908.6
CU921434.1	549201	2302.9	1913.1	2073.9	1975.3	1410.7	2024.6
FN646446.1	589878	508.2	1610.3	4657.8	889.1	974.5	1106.6
X94911.1	10755	129.3	348.6	909.9	327.5	371.7	149.3
GQ402673.1	585966	2958.9	3707.6	3905.8	2098.1	3356.1	3299.4
EF688226.1	329449	7177.4	6798.1	10688.7	5907.7	6142.5	5058.7
DQ404834.1	155072	5416.1	3282.3	5488.8	5830.7	1948.8	2967.6
U25627.1	10762	47.3	106.4	211.0	79.3	96.1	85.6

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EF018960.1 gg_id:213030 aspen rhizosphere clone Amb_16S_1474
EU134394.1 gg_id:237260 tallgrass prarie soil clone FFCH612
GQ389113.1 gg_id:535437 quality deterioration drinking system during serious red water outbreak clone S67
FJ205268.1 gg_id:558961 Prokaryotic deep-sea region East Lau Spreading Centre active hydrothermal field sedi
EU373905.1 gg_id:267944 southern Cretan margin (eastern Mediterranean Sea) canyon and slope sediment clc
GU208360.1 gg_id:560302 Study on Sediment Dongping Lake sediment clone Td4-7
EF019335.1 gg_id:206015 aspen rhizosphere clone Elev_16S_545
FJ478988.1 gg_id:560191 species richness estimates obtained nearly and simulated pyrosequencing-generated
EU335317.1 gg_id:248449 Changes microbial metabolic and along hydrogeochemically variable profile unsatura
AM936205.1 gg_id:559827 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
GQ472446.1 gg_id:568881 Microbial Dongping Lake lake sediment clone 5T1-3
AF523967.1 gg_id:63257 forested wetland clone FW136
AY963427.1 gg_id:152097 structures and correlated ecological factors soils two evergreen broad-leaved forests
FJ478874.1 gg_id:593126 species richness estimates obtained nearly and simulated pyrosequencing-generated
FJ479469.1 gg_id:572414 species richness estimates obtained nearly and simulated pyrosequencing-generated
AB426233.1 gg_id:275505 -situ identification study benzene-degrading s under methanogenic condition anaerc
GU208380.1 gg_id:565064 Study on Sediment Dongping Lake sediment clone Td2-11
AB128874.1 gg_id:103274 deep marine sediments Nankai Trough Japan; ODP Leg 190 clone 1174-1091-4
EU134559.1 gg_id:243792 tallgrass prarie soil clone FFCH3288
AY921794.1 gg_id:113824 farm soil clone AKYG681
FJ478660.1 gg_id:573531 species richness estimates obtained nearly and simulated pyrosequencing-generated
GQ259289.1 gg_id:564500 Microbial activities coastal marine sediments and water column Svalbard deep sedir
AF523886.1 gg_id:55388 forested wetland clone RCP2-54
FJ479115.1 gg_id:540681 species richness estimates obtained nearly and simulated pyrosequencing-generated
FJ479389.1 gg_id:559874 species richness estimates obtained nearly and simulated pyrosequencing-generated
AM072417.1 gg_id:138410 Untersuchung Verschiebung der bakteriellen Populationen mit U(VI) inokulierten Bc
FJ479315.1 gg_id:575779 species richness estimates obtained nearly and simulated pyrosequencing-generated
GQ302546.1 gg_id:581532 prokaryotic sediment Shawan methods cold spring clone sw-xj100
GU056068.1 gg_id:552030 Biologic Techniques Applied Microbial Prospecting China: Ban 876 Gas Oil Field Bein
FJ479231.1 gg_id:593037 species richness estimates obtained nearly and simulated pyrosequencing-generated
AJ296569.1 gg_id:38614 uranium mining mill tailing clone GR-WP33-30
CU921195.1 gg_id:543214 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
GU118124.1 gg_id:547351 Threatened Corals Provide Microbial Habitats clone Apal_A09
EF600558.1 gg_id:302892 soil clone E5-2
EU202780.1 gg_id:326405 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo
FJ479565.1 gg_id:510105 species richness estimates obtained nearly and simulated pyrosequencing-generated
AJ581602.1 gg_id:93483 soil near uranium mill tailings clone KCM-B-53
EF032748.1 gg_id:191331 cyanobacterial mat in lava cave clone HAVOmat120
AM997325.1 gg_id:555867 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A
FJ478489.1 gg_id:572174 species richness estimates obtained nearly and simulated pyrosequencing-generated
GQ500719.1 gg_id:581516 Surveys Biofilms and Sediments Mammoth Cave Karst Aquifers Charon's Cascade sa

EF018960.1	213030	5309.2	4917.7	7677.2	8175.4	6168.5	7592.8
EU134394.1	237260	101.5	207.1	1761.3	179.4	152.1	495.9
GQ389113.1	535437	628.2	1385.0	3271.8	1742.5	528.6	903.3
FJ205268.1	558961	355.9	990.2	1340.8	1218.4	442.3	610.3
EU373905.1	267944	47.3	166.1	1349.6	90.0	177.5	347.6
GU208360.1	560302	4071.7	5016.5	6476.4	6002.1	3784.8	4559.8
EF019335.1	206015	2111.6	2888.6	4346.5	1830.4	1945.6	2481.9
FJ478988.1	560191	69.5	196.1	362.6	144.0	74.6	57.2
EU335317.1	248449	15.1	20.8	73.6	46.8	60.6	19.1
AM936205.1	559827	11067.1	12591.3	7500.4	8814.4	11762.2	12317.7
GQ472446.1	568881	2840.2	4461.2	3236.0	2438.3	1455.9	3191.6
AF523967.1	63257	3962.3	3349.3	2662.4	4755.8	2249.5	2266.1
AY963427.1	152097	33.5	77.4	159.5	100.9	63.5	53.1
FJ478874.1	593126	459.3	1242.6	3988.6	374.2	377.4	1477.3
FJ479469.1	572414	7355.8	8415.9	6605.8	7710.1	4346.5	5695.7
AB426233.1	275505	4313.7	5019.5	7698.4	2558.7	4538.7	6091.4
GU208380.1	565064	9012.0	10240.8	10550.0	9369.5	7899.5	8861.3
AB128874.1	103274	47.7	68.3	41.9	53.7	74.7	37.1
EU134559.1	243792	6887.3	8056.4	9053.7	4109.9	4043.4	4995.4
AY921794.1	113824	899.9	1270.1	2525.0	2432.2	1487.7	1771.8
FJ478660.1	573531	5435.6	5908.5	7346.2	3214.4	3474.4	5575.3
GQ259289.1	564500	11344.2	13022.4	9263.7	7648.4	11094.7	9368.7
AF523886.1	55388	27.9	92.3	67.3	63.4	64.6	37.4
FJ479115.1	540681	6340.1	11152.0	21841.6	6477.5	13082.3	15591.2
FJ479389.1	559874	3504.5	4129.8	5963.5	4107.0	3965.9	4443.8
AM072417.1	138410	2865.2	2686.2	4319.8	1187.5	1880.2	2351.5
FJ479315.1	575779	7002.1	7318.3	2562.3	6962.6	9794.9	9292.6
GQ302546.1	581532	5686.4	5657.5	5945.2	9393.3	8317.5	8918.4
GU056068.1	552030	295.8	658.2	2311.1	668.6	642.5	970.9
FJ479231.1	593037	781.3	1640.8	3427.6	834.4	584.9	963.8
AJ296569.1	38614	4226.1	5641.5	2225.6	4366.9	4637.7	3682.0
CU921195.1	543214	4499.7	6300.3	4428.1	1894.2	2188.3	2310.5
GU118124.1	547351	72.1	99.1	357.1	51.8	73.1	72.9
EF600558.1	302892	14933.6	16914.2	14440.3	8422.4	14422.4	13595.1
EU202780.1	326405	2239.4	1567.8	3279.4	1561.9	1819.0	2762.4
FJ479565.1	510105	9176.6	10415.7	6456.2	11175.2	12853.6	10646.3
AJ581602.1	93483	5280.1	6122.5	4436.6	6409.1	6878.2	7081.1
EF032748.1	191331	5437.7	7056.3	7663.7	5608.2	9824.6	11363.4
AM997325.1	555867	2235.8	2428.8	5066.8	1315.4	1469.7	1959.4
FJ478489.1	572174	4445.4	6444.9	7738.2	4527.5	4434.7	5108.8
GQ500719.1	581516	3194.5	4536.3	3479.4	3335.5	1430.6	2925.8

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FJ478475.1 gg_id:585889 species richness estimates obtained nearly and simulated pyrosequencing-generated
DQ811806.1 gg_id:165767 mangrove soil clone MSB-4C10
GQ262847.1 gg_id:549915 Structure Simulated Level Waste Site simulated level waste site clone F1_28X2
EF018612.1 gg_id:215602 aspen rhizosphere clone Amb_16S_891
EF032749.1 gg_id:192369 cyanobacterial mat in lava cave clone HAVOmat133
EF590024.2 gg_id:228859 changes structure sediments Songhua River contaminated nitrobenzene -DGGE cloni
EU617849.1 gg_id:331603 Seasonal variation microbial Yel Sea sediment clone D13S-11
GU061491.1 gg_id:560172 and function microbial mesoscale eddy perturbations South China Sea clone CE1-DC
FJ478639.1 gg_id:593827 species richness estimates obtained nearly and simulated pyrosequencing-generated
GU230392.1 gg_id:586588 Multilevel approach along Rio de la Plata-South Atlantic Ocean coastal sediment clo
EF032751.1 gg_id:195011 cyanobacterial mat in lava cave clone HAVOmat82
AB240314.1 gg_id:144627 microbial structure Phragmites rhizosphere biofilm reed bed reactor laboratory clone
AJ519632.1 gg_id:77057 uranium mill tailings soil sample clone Sh765B-AG-71 proteobacterium
AY289452.1 gg_id:89599 soil clone ABS-13
FJ152850.1 gg_id:315633 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX5A_
AM997396.1 gg_id:572529 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A
AM936195.1 gg_id:548041 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
EU050854.1 gg_id:254522 libraries sediment Kings Bay Svalbard Arctic clone ss1_B_02_28
AJ518789.1 gg_id:75247 uranium mining waste pile near Johanngeorgenstadt soil clone JG37-AG-2
EF018554.1 gg_id:205913 aspen rhizosphere clone Amb_16S_816
EU386119.1 gg_id:276230 Biogeographical and microbes sediments on subseafloor sediment South China Sea c
EU134520.1 gg_id:240393 tallgrass prarie soil clone FFCH8074
FJ755756.1 gg_id:578972 vertical archaeal water and Lake Taihu sediment clone LT-SB-B12
EU134328.1 gg_id:249749 tallgrass prarie soil clone FFCH11550
EU202763.1 gg_id:324982 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo
AB234261.1 gg_id:147174 Biotransformation Polychlorinated Dioxins Microbial Dynamics Sediment Microcosm
AB252957.1 gg_id:168547 Identification Shibayama lagoon Ishikawa Japan iron-oxidation biofilm clone 023
EU881148.1 gg_id:323943 Karst region primary forest soil clone KPF200711-152
EF471464.1 gg_id:262091 Fast Screening and Estuarine Operon Libraries whole surface water Chesapeake Bay
EF019530.1 gg_id:214844 aspen rhizosphere clone Elev_16S_1033
GQ246353.1 gg_id:509231 Temporal and spatial China North Yel Sea sediments clone Cm1-16
FJ479302.1 gg_id:535350 species richness estimates obtained nearly and simulated pyrosequencing-generated
AB252435.1 gg_id:152635 Microbial extremely CO2 rich deep-sea sediment Marine sediments Yonaguni Knoll I
EF076107.1 gg_id:244235 Sponge- microorganisms: ecology and biotechnological potential Bahamas: Little San
FJ478944.1 gg_id:512156 species richness estimates obtained nearly and simulated pyrosequencing-generated
AY963383.1 gg_id:152964 structures and correlated ecological factors soils two evergreen broad-leaved forests
AF234748.1 gg_id:48147 sludge clone H16
EF516526.1 gg_id:226074 grassland soil clone FCPP428
AM935117.1 gg_id:565668 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
AM889194.1 gg_id:593414 structure superficial sediments Bizerte (Tunisia) southern Mediterranean coastal an
EF125461.1 gg_id:182959 mangrove soil clone MSB-2H1

FJ478475.1	585889	10331.4	12079.7	11959.3	10752.4	8227.9	10240.0
DQ811806.1	165767	471.7	777.9	1294.7	886.4	1457.1	1116.8
GQ262847.1	549915	625.2	1578.6	3318.7	460.8	559.2	840.7
EF018612.1	215602	2207.3	2126.6	1661.4	5728.9	895.7	1510.9
EF032749.1	192369	249.3	686.9	2076.1	252.6	325.9	680.8
EF590024.2	228859	1362.8	1963.3	3855.1	1909.5	1340.5	3891.6
EU617849.1	331603	12713.3	11904.1	11103.3	9743.6	16780.6	13775.7
GU061491.1	560172	167.6	1285.0	1559.8	180.2	645.2	1447.4
FJ478639.1	593827	6958.4	7969.7	7494.9	7386.2	8517.3	6708.9
GU230392.1	586588	128.1	507.9	1862.4	221.4	158.3	270.3
EF032751.1	195011	826.8	831.1	790.2	1288.9	2489.5	2537.6
AB240314.1	144627	6670.0	7151.3	5778.5	4411.7	4682.7	6004.0
AJ519632.1	77057	18.6	49.8	148.7	59.8	91.2	170.4
AY289452.1	89599	38.4	135.5	487.2	62.9	184.6	168.6
FJ152850.1	315633	2692.1	3452.1	4174.5	2846.5	2306.9	3294.4
AM997396.1	572529	5425.6	7545.9	12907.6	4744.4	5674.0	7487.8
AM936195.1	548041	4831.9	5000.5	5686.8	3550.4	4581.6	5965.2
EU050854.1	254522	2717.6	2321.9	4991.9	4691.9	2619.8	3599.7
AJ518789.1	75247	1107.1	1442.4	3785.4	659.3	834.6	1505.9
EF018554.1	205913	2100.7	2515.6	4567.5	1942.8	2421.9	2638.8
EU386119.1	276230	2627.2	2987.2	4122.7	3369.1	8034.3	4252.4
EU134520.1	240393	11118.7	11796.7	11443.1	9472.8	15504.1	13929.1
FJ755756.1	578972	5808.0	6822.9	7342.4	7127.7	8191.6	7267.2
EU134328.1	249749	6088.6	7276.4	6000.9	6681.0	7951.6	7677.7
EU202763.1	324982	6399.5	5864.0	5259.3	9017.7	9762.7	9716.1
AB234261.1	147174	102.7	134.7	231.7	78.4	722.1	407.8
AB252957.1	168547	203.9	799.6	2849.4	281.2	213.0	611.3
EU881148.1	323943	706.3	2045.0	3462.0	949.6	763.3	1375.1
EF471464.1	262091	1442.0	2260.4	3927.5	2994.2	6148.4	4751.1
EF019530.1	214844	127.2	387.5	849.7	165.9	119.1	93.7
GQ246353.1	509231	733.4	1859.7	3235.6	1645.1	908.9	1455.8
FJ479302.1	535350	6738.4	5944.9	5523.1	6236.7	6219.6	7722.4
AB252435.1	152635	17581.4	15797.2	12830.8	13368.1	16686.8	14215.3
EF076107.1	244235	7713.6	8621.2	10607.9	8260.8	15288.0	11800.5
FJ478944.1	512156	267.3	623.3	2402.5	220.7	274.2	350.2
AY963383.1	152964	45.3	88.6	162.6	66.5	65.2	37.3
AF234748.1	48147	414.8	234.8	455.5	121.4	568.0	347.0
EF516526.1	226074	477.8	1780.9	5577.6	1287.8	2182.9	3742.6
AM935117.1	565668	3334.3	3312.1	3210.2	5066.1	2305.0	4088.3
AM889194.1	593414	3549.6	3502.0	3960.6	3904.3	3748.3	6310.6
EF125461.1	182959	36.3	96.1	174.0	49.0	69.2	33.9

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DQ906885.1 gg_id:241976 Oman subsurface soil clone 11B-13
AJ347034.1 gg_id:104678 sponge clone TK13
AF026987.1 gg_id:10763 hot spring clone OPB33
EU700154.1 gg_id:294756 Study on Shantou Bay Marine Sediments Microorganisms sediment clone STU12
EF442978.1 gg_id:257733 Desulforhabdus sp. str. DDT
EU542438.1 gg_id:262663 Effects chemical structure concentration on pathways microbial during dechlorinatio
DQ984662.1 gg_id:242560 Anaerobic degradation unsaturated or saturated long chain fatty acids (LCFA) prese
GQ487978.1 gg_id:542670 Microbial metal soil polluted heavy metals clone G19-236
X83274.1 gg_id:10759 Desulforhabdus amnigena str. ASRB1
AJ237605.1 gg_id:10754 Syntrophobacter sp str. TsuA1
AM176868.1 gg_id:160457 Recovery mangrove sediment clone SZB17
GU180163.1 gg_id:578505 Impact coplanar PCBs on microbial activity anaerobic estuarine sediments sediment
DQ303457.1 gg_id:151758 Desulfoglaeba alkanexedens str. ALDC
DQ676446.1 gg_id:219894 Archaeal and plankton freshwater pond suboxic freshwater-pond sediment clone M
FN646458.1 gg_id:591519 candidate division OP3 cells limonene Limonene degrading methanogenic s clone Li
GU208388.1 gg_id:587929 Study on Sediment Dongping Lake sediment clone Td2-21
AJ306776.1 gg_id:66924 DCP-dechlorinating consortium clone SHA-117
AM176858.1 gg_id:161119 Recovery mangrove sediment clone SZB9
GQ402743.1 gg_id:543482 Accessing microbial biodiversity and metabolic potential tropical -based approach p
CU919420.1 gg_id:538867 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
AY297973.1 gg_id:89577 thermophilic anaerobic terephthalate-degrading sludge clone TTA_B25
CT573926.1 gg_id:153737 Evry municipal wastewater treatment plant clone 012B11_B_SD_P15
AB091329.1 gg_id:60011 UASB granular sludge clone UI
AF229787.1 gg_id:29387 terephthalate-degrading consortium clone TA14
CT573826.1 gg_id:152222 Evry municipal wastewater treatment plant clone 013H09_B_SD_P15
EU542505.1 gg_id:275595 Effects chemical structure concentration on pathways microbial during dechlorinatio
EU399669.1 gg_id:262088 and localization microbial consortium full-scale granular activated carbon anaerobic
EU399678.1 gg_id:275018 and localization microbial consortium full-scale granular activated carbon anaerobic
AJ009465.1 gg_id:10718 TCB-transforming consortium clone SJA-51
EF198029.1 gg_id:180225 Microbial structures and thermophilic methanogenic consortia anaerobic mesophilic
AF523969.1 gg_id:63254 forested wetland clone FW121
EU399661.1 gg_id:263368 and localization microbial consortium full-scale granular activated carbon anaerobic
EU399675.1 gg_id:265878 and localization microbial consortium full-scale granular activated carbon anaerobic
GQ844327.1 gg_id:569150 Microbial full-scale produced water treatment plant biofilm anoxic tank clone BB-B2
CT573958.1 gg_id:151218 Evry municipal wastewater treatment plant clone 009F06_B_SD_P15
CT574144.1 gg_id:156077 Evry municipal wastewater treatment plant clone 060H12_B_SD_P93
CT574201.1 gg_id:151230 Evry municipal wastewater treatment plant clone 060B01_B_SD_P93
GU208245.1 gg_id:541892 Study on Sediment Dongping Lake sediment clone 6B1-7
CT574119.1 gg_id:152546 Evry municipal wastewater treatment plant clone 061D06_B_SD_P93
AY862530.1 gg_id:109749 rice slurry clone TPD-48

FJ873368.1	544213	5181.7	6945.2	11349.7	4805.3	7959.7	7959.4
DQ906885.1	241976	3751.4	4028.3	4427.1	2623.3	2950.4	3729.4
AJ347034.1	104678	1518.6	2773.7	5143.2	2620.8	1385.6	3381.8
AF026987.1	10763	183.6	368.7	656.4	299.3	374.9	274.5
EU700154.1	294756	1899.8	3504.7	6507.1	1745.8	1905.8	1831.9
EF442978.1	257733	106.6	375.9	865.5	383.8	312.8	184.5
EU542438.1	262663	799.3	1070.4	3558.4	1160.2	537.7	328.7
DQ984662.1	242560	557.8	940.4	1769.6	277.5	471.7	980.9
GQ487978.1	542670	9625.2	10649.2	10522.1	7876.8	16252.1	12401.6
X83274.1	10759	805.8	1604.1	2038.6	1337.8	2978.2	1578.0
AJ237605.1	10754	30.7	74.3	125.5	50.8	52.1	47.0
AM176868.1	160457	25.5	34.8	17.6	51.0	46.7	22.1
GU180163.1	578505	1463.8	1389.7	5832.8	1515.4	2497.3	1540.4
DQ303457.1	151758	75.6	79.7	82.6	68.8	88.9	44.6
DQ676446.1	219894	71.7	326.9	626.0	83.5	145.9	296.0
FN646458.1	591519	5372.2	7010.4	12636.5	6482.4	10231.4	10395.9
GU208388.1	587929	3399.3	4233.7	5641.5	6136.5	2554.9	2455.2
AJ306776.1	66924	44.8	103.6	53.3	61.5	58.6	58.5
AM176858.1	161119	50.8	92.8	107.3	67.4	89.2	26.4
GQ402743.1	543482	1178.0	1783.1	5025.9	2257.6	2591.9	3211.3
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CT573926.1	153737	12945.7	13413.9	14103.3	11581.9	15066.6	15415.1
AB091329.1	60011	3616.8	3425.5	5541.6	3259.6	2737.9	3571.0
AF229787.1	29387	2724.2	1946.5	466.9	2058.5	2584.6	2115.5
CT573826.1	152222	434.2	653.4	984.1	440.5	1543.8	710.5
EU542505.1	275595	3368.9	3874.9	3116.5	5172.6	6521.2	4509.8
EU399669.1	262088	4955.3	4966.9	6937.6	4333.2	5559.1	6505.1
EU399678.1	275018	11462.9	11238.2	8793.0	8428.9	9408.7	8873.8
AJ009465.1	10718	30.6	58.5	99.2	61.7	77.8	55.6
EF198029.1	180225	6085.0	5026.3	5473.9	7375.1	6373.7	9064.9
AF523969.1	63254	1205.8	1388.8	2097.5	1028.2	1547.6	796.7
EU399661.1	263368	26.2	58.1	187.8	52.4	35.3	22.7
EU399675.1	265878	10586.2	9192.5	7359.2	10328.5	9581.5	9179.8
GQ844327.1	569150	5057.6	6374.0	8577.1	6884.2	3063.5	4535.2
CT573958.1	151218	1358.2	1540.5	983.6	2359.1	2994.7	3172.3
CT574144.1	156077	9060.6	10020.9	7449.7	5979.7	8008.9	7684.5
CT574201.1	151230	93.8	159.0	423.2	96.5	510.7	160.7
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CT574119.1	152546	1479.7	926.2	806.5	1900.0	397.1	804.3
AY862530.1	109749	2950.2	2531.5	1720.2	2768.0	1634.5	2515.3

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DQ513073.1 gg_id:160937 Microbial life fluids ridge flank crustal fluid clone FS266-12B-03
DQ396250.1 gg_id:151404 deep-sea octacoral clone ctg_NISA104
GQ348270.1 gg_id:546068 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
GQ348264.1 gg_id:590521 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
GQ349049.1 gg_id:566231 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
GQ348844.1 gg_id:541085 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
GQ348190.1 gg_id:583411 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
GQ351086.1 gg_id:590469 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
GQ337095.1 gg_id:560221 Hydrography shapes biogeography deep Arctic Ocean water depth 1000m clone BB(
GQ350665.1 gg_id:593832 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
GQ347064.1 gg_id:589130 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
GQ348641.1 gg_id:571912 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
FJ545636.1 gg_id:559552 Diveristy Seawater and Sediment Northern North Yel Sea seawater clone W2-63
GQ337087.1 gg_id:572986 Hydrography shapes biogeography deep Arctic Ocean water depth 1191m clone NB:
DQ300620.1 gg_id:145501 microbial ocean's interior amplicon single fosmid library pool 130m depth HOT static
GU083677.1 gg_id:581115 Microorganism Xiarinur soda lake sediment clone x72
FJ152921.1 gg_id:317973 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX4CI
AY048892.1 gg_id:23990 rhizosphere clone Q3-6C17
DQ501327.1 gg_id:198258 Seasonal dynamics free-living and particle- four lakes northeastern Germany freshw
EU050847.1 gg_id:237789 libraries sediment Kings Bay Svalbard Arctic clone ss1_B_03_45
EU487900.1 gg_id:574097 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and
EU491765.1 gg_id:261919 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39
EF573310.1 gg_id:233830 Coco's Island site 23 marine clone S23_1409
FJ155019.1 gg_id:330963 seasonal fluctuation coastal Bohai Bay sequencing and RFLP ocean water clone BX
GQ348578.1 gg_id:576386 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
AF371949.1 gg_id:23625 swine intestine clone p-4193-6Wa5
FJ484808.1 gg_id:509157 microbial autonomous rover world's deepest phreatic sinkhole wall biomat El Zacator
EU220836.1 gg_id:274794 Spirobacillus cienkowskii
GQ337121.1 gg_id:577297 Hydrography shapes biogeography deep Arctic Ocean water depth 395m clone CB0:
CU466767.1 gg_id:336493 Evry wastewater treatment plant anoxic basin clone
GU061838.1 gg_id:578641 and function microbial mesoscale eddy perturbations South China Sea clone CEP-DC
U70713.1 gg_id:4709 Cape Hatteras picoplankton clone OM27
FJ203134.1 gg_id:355193 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c
EF574353.1 gg_id:234197 site S25 near Coco's Island marine clone S25_697
EU101270.1 gg_id:257793 Sulfide/oxygen supply ratio predicts outcome competition among sulfur-oxidizing wa
DQ330714.1 gg_id:159120 Guerrero Negro hypersaline microbial mat clone 01D1q147
EU491257.1 gg_id:269593 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak
DQ395799.1 gg_id:155720 deep-sea octacoral clone ctg_CGOF235
EU925894.1 gg_id:346201 sediments sediment station DBS1 northern Bering Sea clone 115G73
GQ263929.1 gg_id:513958 Structure Simulated Level Waste Site simulated level waste site clone WC2_181

GQ347002.1	534292	12371.1	10525.2	12210.9	8735.6	11186.5	10923.6
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DQ396250.1	151404	4937.0	3293.5	6166.8	7092.1	12385.0	6850.1
GQ348270.1	546068	7109.3	6688.7	8778.4	6096.5	5604.2	7363.3
GQ348264.1	590521	13013.7	9536.5	12933.3	12159.1	10133.4	11542.0
GQ349049.1	566231	13811.4	10090.6	12636.5	12255.3	8230.6	9177.7
GQ348844.1	541085	5588.8	5820.6	5833.8	5482.4	5886.2	5591.1
GQ348190.1	583411	9306.0	8049.0	10820.7	9704.6	8927.0	11277.0
GQ351086.1	590469	6471.0	4649.0	5852.8	6114.8	3852.3	4526.8
GQ337095.1	560221	4999.1	5476.4	9400.2	7738.5	7211.0	8757.1
GQ350665.1	593832	119.5	78.9	135.9	797.0	171.7	95.7
GQ347064.1	589130	17304.7	14565.3	7755.7	14119.1	15159.9	13551.7
GQ348641.1	571912	7029.7	8784.5	4308.3	6963.7	3899.9	4594.0
FJ545636.1	559552	7314.2	3104.3	3541.9	5784.0	2031.4	5475.3
GQ337087.1	572986	5207.0	3437.9	1691.1	7089.9	5291.8	5260.6
DQ300620.1	145501	210.1	335.2	445.8	458.7	107.1	131.4
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FJ152921.1	317973	2817.9	3064.9	5064.1	2942.4	7747.3	4387.7
AY048892.1	23990	111.9	351.2	577.4	352.4	213.5	223.7
DQ501327.1	198258	1765.3	1996.0	1462.6	477.6	1585.5	1248.1
EU050847.1	237789	6518.9	7320.7	9870.8	6378.1	4378.9	6960.6
EU487900.1	574097	6392.8	6831.1	3796.4	2640.1	4545.6	3768.0
EU491765.1	261919	10298.5	10010.7	7024.3	10054.3	8069.9	8714.1
EF573310.1	233830	39.3	35.3	37.4	61.3	74.4	30.5
FJ155019.1	330963	418.7	857.3	1484.4	362.6	2541.2	612.3
GQ348578.1	576386	2564.4	2684.6	1250.2	2374.0	3158.7	2683.5
AF371949.1	23625	417.1	1432.8	2380.4	1154.7	791.1	922.1
FJ484808.1	509157	282.0	910.5	1147.5	317.7	161.1	104.3
EU220836.1	274794	6009.9	6374.4	4826.4	2901.6	2124.7	2614.8
GQ337121.1	577297	45.4	73.4	62.9	82.7	142.4	70.7
CU466767.1	336493	1487.6	2884.7	6766.1	2314.7	3649.3	4563.7
GU061838.1	578641	925.5	2078.3	1216.8	1360.0	1894.4	2080.9
U70713.1	4709	40.4	70.3	151.2	128.6	1289.2	426.8
FJ203134.1	355193	3628.9	4954.1	3921.1	4065.4	5034.8	5293.1
EF574353.1	234197	871.2	400.4	1231.7	338.9	612.0	907.9
EU101270.1	257793	9038.7	8471.5	7138.9	10790.6	7276.7	6642.9
DQ330714.1	159120	4582.8	5298.5	3745.0	2769.2	3763.9	4258.5
EU491257.1	269593	8880.8	8823.4	11987.6	9003.8	9310.1	9697.7
DQ395799.1	155720	3809.7	4237.7	4256.9	3192.7	7936.7	6078.1
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GQ263929.1	513958	776.7	1458.1	4582.0	887.5	883.6	1409.2

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FJ902004.1 gg_id:573340 phreatic limestone sinkholes northeastern Mexico biomat sediment cenote La Palita
FJ484648.1 gg_id:572347 microbial autonomous rover world's deepest phreatic sinkhole wall biomat El Zacator
GQ472419.1 gg_id:547121 Microbial Dongping Lake lake sediment clone 4F2-23
AB238778.1 gg_id:147775 shal subsurface Sarobetsu Mire peat soil clone HSM-SS-015
AM086107.1 gg_id:149503 Abundance and archaea mesotrophic Lake Kinneret lake profundal sediment clone
AJ519663.1 gg_id:76094 uranium mill tailings soil sample clone GuBH2-AD/TzT-67 proteobacterium
FJ716435.1 gg_id:509967 Uncultivated archaea sulfate-reducing biofilm Frasassi cave system anoxic lake water
EF590018.2 gg_id:231749 changes structure sediments Songhua River contaminated nitrobenzene -DGGE cloni
FJ484742.1 gg_id:534747 microbial autonomous rover world's deepest phreatic sinkhole wall biomat El Zacator
AB300111.1 gg_id:219858 Wide ancient microbial DNAs Quaternary sediments holocene mud sediment clone K
EU589306.1 gg_id:265934 China Ningxia rice paddy field soil clone 2_E4
FJ902299.1 gg_id:575054 phreatic limestone sinkholes northeastern Mexico biomat rock outcrop cenote La Pal
FJ484802.1 gg_id:537592 microbial autonomous rover world's deepest phreatic sinkhole wall biomat El Zacator
AB300078.1 gg_id:223240 Wide ancient microbial DNAs Quaternary sediments holocene mud sediment clone A
EF999397.1 gg_id:255615 Vertical and Methanotrophs Estuarine Sediments Pearl River Estuary sediments 50cn
DQ811808.1 gg_id:165809 mangrove soil clone MSB-4C2
DQ083114.1 gg_id:137474 Functional and responses microbial century-old field soil clone S34
EU528195.1 gg_id:285313 Seasonal Dynamics Mudflat Mouth Major Kentucky Lake Reservoir Tributary sedime
AM934934.1 gg_id:549065 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
DQ067029.1 gg_id:129752 Lake Washington sediment clone pLW-45
FJ538146.1 gg_id:566857 metagenomics study rice treated milk vetch and no-tillage paddy field soil clone MBN
EU335163.1 gg_id:239473 Changes microbial metabolic and along hydrogeochemically variable profile saturate
CU922370.1 gg_id:552630 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
GU180168.1 gg_id:590108 Impact coplanar PCBs on microbial activity anaerobic estuarine sediments sediment
CU918113.1 gg_id:567976 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
CU921396.1 gg_id:561911 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
EU407211.1 gg_id:266671 household biogas digester clone GW-28
CU921615.1 gg_id:549289 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
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EF574365.1 gg_id:228280 site S25 near Coco's Island marine clone S25_709
EF575257.1 gg_id:228296 site S25 near Coco's Island marine clone S25_1601
FJ155026.1 gg_id:330159 seasonal fluctuation coastal Bohai Bay sequencing and RFLP ocean water clone W
EF573912.1 gg_id:228667 site S25 near Coco's Island marine clone S25_256
EU592442.1 gg_id:537106 Seasonal changes Salton Sea hypersaline sediment clone SSS66N
EU592440.1 gg_id:589629 Seasonal changes Salton Sea hypersaline sediment clone SSS64N
EU488121.1 gg_id:560324 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and
EU488297.1 gg_id:556385 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and
DQ463694.2 gg_id:165464 distinct Lake Tanganyika anoxic hypolimnion clone TK-SH10
DQ394901.1 gg_id:156343 harbor sediment clone VHS-B1-26
GQ261790.1 gg_id:544072 shifts taxa and response localized organic loading deep sea sediment whale falls clo

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FJ902004.1	573340	4330.0	5077.9	3935.0	3933.9	2942.6	2215.9
FJ484648.1	572347	4193.7	5815.3	8413.1	3649.5	3331.4	3588.0
GQ472419.1	547121	2662.5	5984.5	8945.7	3604.9	9303.0	7838.5
AB238778.1	147775	2529.6	3682.0	5400.0	3577.1	2919.3	4269.2
AM086107.1	149503	13675.3	14418.3	7348.9	11082.5	13636.6	10711.6
AJ519663.1	76094	93.2	125.4	254.3	67.0	69.5	49.3
FJ716435.1	509967	690.5	1388.3	1222.6	222.0	1175.3	409.0
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FJ484742.1	534747	2693.6	4886.2	5424.9	1828.8	3660.2	3915.6
AB300111.1	219858	62.7	185.0	170.3	76.0	147.3	78.6
EU589306.1	265934	1553.6	2638.6	6026.0	1724.2	3038.9	4664.6
FJ902299.1	575054	2154.3	3516.2	5640.3	1327.4	3480.3	2624.8
FJ484802.1	537592	7310.9	6377.7	4022.3	7507.4	7303.3	7121.2
AB300078.1	223240	537.0	1539.6	2579.4	629.4	373.1	232.7
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DQ811808.1	165809	177.2	353.0	1510.5	174.5	162.5	195.3
DQ083114.1	137474	1085.3	2135.6	3260.1	1128.1	3302.6	3889.0
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AM934934.1	549065	9887.8	11117.1	7319.5	10709.6	11260.1	11678.0
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EU335163.1	239473	4241.2	6392.0	10182.4	5448.1	9081.8	9293.3
CU922370.1	552630	1595.6	2724.6	3452.7	2363.2	6026.1	5601.4
GU180168.1	590108	3927.2	3933.9	5571.1	4213.1	4254.1	4997.9
CU918113.1	567976	2734.8	3388.7	4740.8	3143.6	2906.7	3191.8
CU921396.1	561911	1178.8	2476.0	5729.6	1258.9	2964.3	3305.4
EU407211.1	266671	7000.8	7053.4	7164.7	5453.7	5873.4	5174.8
CU921615.1	549289	5468.0	5745.4	3960.5	5831.7	8495.2	7626.5
EF575193.1	234927	304.5	959.7	852.2	250.3	387.9	1098.7
EF574365.1	228280	2205.6	3543.2	2302.6	2446.9	1988.7	3279.4
EF575257.1	228296	1840.3	2499.1	1915.0	1359.7	2901.8	3538.6
FJ155026.1	330159	9759.3	10818.3	11103.5	11775.0	11957.0	12054.1
EF573912.1	228667	1140.8	1727.8	1657.4	1643.6	2469.6	2582.9
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DQ394901.1	156343	46.5	59.9	40.5	58.5	63.7	37.1
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DQ811792.1 gg_id:167519 mangrove soil clone MSB-3A9
EF520534.1 gg_id:232980 structure lakes: what controls ? acid-impacted lake clone ADK-BTe02-06
EU861868.1 gg_id:343349 effects chronic fertilization on alpine tundra microbial implications carbon and nitrog
EU803844.1 gg_id:337066 It's all ranking aquatic Lake Gatun clone 5C231481
DQ451526.1 gg_id:156878 forest soil clone FAC87
DQ811827.1 gg_id:170103 mangrove soil clone MSB-5C4
EF208655.1 gg_id:202296 Vertical and horizontal structure microbial sandy carbonate sediment clone CI35cm.2
EF125419.1 gg_id:199002 soil naked tidal flat sediment near mangrove clone MSB-1F8
EU491252.1 gg_id:276800 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak
DQ925889.1 gg_id:255773 Microbes and Thermal Gradients Temperature Hydrothermal Chimneys hydrotherm
EU050850.1 gg_id:238559 libraries sediment Kings Bay Svalbard Arctic clone ss1_B_09_96
FJ535320.1 gg_id:536335 within iron-containing flocculent mats submarine volcanoes along Kermadec Arc sedi
AM712338.1 gg_id:255844 detection and ly microbial Brothers Seamount Kermadec Arc New Zealand biofilm h
AF420341.2 gg_id:67796 hydrothermal sediment clone AF420341
AJ441235.1 gg_id:57453 hydrothermal vent polychaete mucous clone P. palm A 205
AF420340.1 gg_id:67797 hydrothermal sediment clone AF420340
FJ712464.1 gg_id:517432 and Archaea Gas Hydrate Sediments (East Sea) Kazan Mud Volcano Anaximander Mo
DQ017948.1 gg_id:136786 upland stream clone S-Btb7_40
EU134544.1 gg_id:253026 tallgrass prarie soil clone FFCH2390
FJ592579.1 gg_id:509119 Fumarole-supported islands biodiversity within hyperarid -elevation landscape on Pu
EF573992.1 gg_id:230171 site S25 near Coco's Island marine clone S25_336
EF574948.1 gg_id:230813 site S25 near Coco's Island marine clone S25_1292
GQ347789.1 gg_id:541766 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
EU048624.1 gg_id:236563 Microbial surface marine sediment Xisha Trough South China Sea clone MD2902-B18
EU386045.1 gg_id:274122 Biogeographical and microbes sediments on subseafloor sediment South China Sea c
EU373913.1 gg_id:275503 southern Cretan margin (eastern Mediterranean Sea) canyon and slope sediment clc
FJ745210.1 gg_id:570846 Transporter genes expressed coastal response dissolved organic carbon surface wate
GQ346753.1 gg_id:568507 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
EU134378.1 gg_id:256515 tallgrass prarie soil clone FFCH5621
AB486345.1 gg_id:559850 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC
DQ267495.1 gg_id:149878 Metagenomic group plankton 500m depth mesopelagic Antarctic waters clone
EF574148.1 gg_id:230908 site S25 near Coco's Island marine clone S25_492
DQ154849.1 gg_id:139171 Diel Migration Restructures Hypersaline Microbial Mat hypersaline microbial mat cl
FJ485412.1 gg_id:558030 microbial autonomous rover world's deepest phreatic sinkhole wall biomat El Zacator
AJ241001.1 gg_id:10681 Norway:(Svalbard)Hornsund clone Sva0485
AM882628.1 gg_id:350620 Structure along hydrocarbon contamination coastal sediment oil polluted water pet
EF632708.1 gg_id:256201 Unique microbial contrasting aquatic altitude Andean Altiplano (northern Chile) wate
DQ103652.1 gg_id:131834 hypersaline endoevaporitic microbial mat clone E6aH12
AM040101.1 gg_id:149432 sandy sediments clone Sylt 5

DQ394969.1	151807	7452.7	7701.2	6279.6	7248.6	6263.3	8888.8
AB100007.1	79461	37.7	62.4	76.0	56.7	46.6	43.2
DQ811792.1	167519	127.3	516.8	1676.7	176.3	125.8	277.4
EF520534.1	232980	67.1	111.2	132.9	118.1	121.0	65.5
EU861868.1	343349	469.5	1382.4	2886.9	347.7	664.9	737.5
EU803844.1	337066	501.8	1096.7	2433.1	725.9	843.3	1294.5
DQ451526.1	156878	4172.4	5581.4	4989.4	4482.6	2672.4	3344.2
DQ811827.1	170103	9496.9	7320.3	5538.7	7500.3	10650.0	9177.7
EF208655.1	202296	1078.7	992.9	1149.8	654.8	404.1	715.1
EF125419.1	199002	1496.4	2441.0	5557.1	2594.0	2579.3	2279.2
EU491252.1	276800	1945.0	2407.5	6434.2	3882.7	2142.7	3537.7
DQ925889.1	255773	2717.8	2929.6	2924.1	2779.2	3242.5	2333.0
EU050850.1	238559	4733.9	5776.4	4377.7	5678.4	7050.9	6027.4
FJ535320.1	536335	1979.1	2434.8	3940.9	1856.7	3481.5	2650.5
AM712338.1	255844	2367.0	3872.3	6716.1	4551.1	3910.8	4244.0
AF420341.2	67796	709.5	1762.4	1381.5	484.2	658.1	666.3
AJ441235.1	57453	3379.7	3878.0	2702.2	2908.8	885.5	1618.2
AF420340.1	67797	115.3	273.0	335.0	98.3	387.7	39.0
FJ712464.1	517432	2509.2	2198.4	3590.5	3179.3	2122.0	1635.0
DQ017948.1	136786	135.8	334.1	429.2	157.5	375.4	206.7
EU134544.1	253026	3339.4	4747.1	7619.0	5810.2	4607.0	4871.5
FJ592579.1	509119	7088.3	7074.4	6486.6	7344.5	9514.2	7957.5
EF573992.1	230171	3822.3	3242.9	946.6	751.6	699.0	1018.7
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GQ347789.1	541766	1417.9	2462.4	1827.5	1859.1	2631.1	2766.9
EU048624.1	236563	12439.8	14561.3	19093.8	10773.5	15233.8	12255.2
EU386045.1	274122	83.2	127.8	130.8	192.0	258.9	146.0
EU373913.1	275503	11846.0	11921.5	8248.5	9510.1	10093.0	9080.0
FJ745210.1	570846	6179.6	7477.0	5619.4	6774.7	10454.8	8452.9
GQ346753.1	568507	13850.9	12990.3	8583.6	11454.4	15337.2	13427.9
EU134378.1	256515	9317.1	9690.0	11549.2	10812.6	15640.5	11751.0
AB486345.1	559850	5050.9	6210.9	12994.1	8141.1	9945.7	10528.1
DQ267495.1	149878	51.7	101.8	284.3	86.4	68.7	30.7
EF574148.1	230908	53.2	121.1	258.0	147.6	77.2	54.0
DQ154849.1	139171	40.9	145.1	46.6	57.2	41.9	27.2
FJ485412.1	558030	5599.1	7780.4	14735.0	7064.6	12184.6	12427.2
AJ241001.1	10681	3932.7	5658.9	10232.4	3622.5	6170.4	8362.5
AM882628.1	350620	8702.1	9241.8	8551.5	6558.4	6815.6	7714.4
EF632708.1	256201	7877.0	5789.9	6664.6	3636.8	3188.1	4563.7
DQ103652.1	131834	1544.4	1272.7	1331.0	1448.5	1698.5	1352.4
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FJ717005.1 gg_id:553766 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United Kingc
AF382143.1 gg_id:79548 bacterioplankton clone ZA3735c
GQ337096.1 gg_id:548348 Hydrography shapes biogeography deep Arctic Ocean water depth 1000m clone BB(
FM242399.1 gg_id:328281 sequences sediment clone 86 T12d-oil
EU735646.1 gg_id:322881 archaeal structures and pristine soils China oil contaminated soil Jidong Oilfield clone
EU734937.1 gg_id:327296 assemblages sediment station DBSE Northern Bering Sea clone 028C19
AY375082.1 gg_id:98535 deep sea sediment clone B109
AJ240985.1 gg_id:10661 Norway:(Svalbard)Hornsund clone Sva0853
AM882631.1 gg_id:306845 Structure along hydrocarbon contamination coastal sediment oil polluted water pet
DQ464344.1 gg_id:157072 Arcobacter skirrowii str. 449/80
AY314755.1 gg_id:105549 Arcobacter cryaerophilus CCUG 17802
EU106662.1 gg_id:260782 Arcobacter nitrofigilis str. F2176
FJ203148.1 gg_id:334326 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c
AB262383.1 gg_id:161324 Microbial Ishigaki-jima Island Japan sea water Ishigaki Port clone IG-1-21
AB262379.1 gg_id:160905 Microbial Ishigaki-jima Island Japan sea water Ishigaki Port clone IG-1-16
AY922188.1 gg_id:113246 whalefall clone 131599
GQ348908.1 gg_id:558608 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
FJ497477.1 gg_id:589078 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun
AF513455.1 gg_id:60384 Arcobacter sp. str. LA31B
DQ071284.1 gg_id:139697 dominate filamentous sulfur mat 13 degree north field East Pacific Rise deep-sea hy
AF314538.1 gg_id:36386 Arcobacter butzleri oN_107_00
AB013832.1 gg_id:11163 NB1-k clone NB1-k
EU052247.1 gg_id:248438 degradation kinetics and current efficiency cells supplied anode microbial fuel cell fe
FJ202344.1 gg_id:314840 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k
EF648116.1 gg_id:251292 dynamics during produced water treatment aerobic activated sludge clone XJ22
AY225610.1 gg_id:96366 pumice fragments exposed to Mid-Atlantic Ridge vent clone AT-pp13
GU061286.1 gg_id:546186 Evaluation culturing methods cultivate previously Yel Sea intertidal beach seawater
AJ607391.1 gg_id:102614 Arcobacter cibarius str. LMG 21996
EF515495.1 gg_id:222170 Electricigen Enrichment MFC full-scale anaerobic bioreactor sludge treating brewery
AY922205.1 gg_id:113754 whalefall clone 131644
FJ202783.1 gg_id:349369 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k
FJ403064.1 gg_id:357886 Disease- changes healthy and diseased colonies Caribbean coral Montastrea faveolat
EF123613.1 gg_id:239833 Microbial disease microbial mats on Siderastrea siderea three regions wider Caribbea
AJ271654.1 gg_id:51975 Arcobacter sp. D1a1
AM084124.1 gg_id:140216 Arcobacter sp. str. R-28214
AY570641.1 gg_id:108516 biodegraded Canadian oil reservoir clone PL-8D4
FN429802.1 gg_id:534177 Biogeochemistry -activity cold seep Larsen B area western Weddell Sea Antarctica m
FJ202326.1 gg_id:315205 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k
DQ917897.1 gg_id:227146 Microbial profiles bleached and wild-type Muricea elongata Arcobacter clone ME15
AY035822.1 gg_id:70950 enriched coastal seawater overlying anoxic marine sediment sulfidicus
EU050947.1 gg_id:255076 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_02_37

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AF382143.1	79548	5036.2	4182.0	6263.3	5394.6	7530.6	6567.8
GQ337096.1	548348	4249.4	4959.2	7332.7	5637.2	5886.2	8143.4
FM242399.1	328281	8589.9	7666.8	5176.0	6226.6	6894.2	4886.6
EU735646.1	322881	1224.2	1975.5	3636.8	2767.2	1793.3	2128.9
EU734937.1	327296	1710.7	3888.6	4388.1	2525.8	2509.1	3154.6
AY375082.1	98535	4491.8	8252.8	11269.2	4727.3	9959.1	10326.7
AJ240985.1	10661	5097.8	4673.8	2469.1	3694.6	3173.4	5083.3
AM882631.1	306845	10121.8	12376.5	11075.3	10289.7	8825.8	4622.0
DQ464344.1	157072	1727.8	332.9	2172.7	1362.9	100.0	167.8
AY314755.1	105549	3471.0	766.8	6741.5	2234.7	1027.7	494.5
EU106662.1	260782	3276.0	2358.0	7805.4	4722.6	3958.6	3315.5
FJ203148.1	334326	9171.4	7588.5	6397.9	7246.8	3844.3	3238.8
AB262383.1	161324	3704.3	3476.6	1150.9	5386.2	10097.0	7085.0
AB262379.1	160905	11460.1	8193.5	6370.3	10240.8	9818.0	8469.0
AY922188.1	113246	25.9	17.3	52.2	73.6	59.0	18.5
GQ348908.1	558608	16895.6	14407.8	14241.6	12559.6	12945.6	12557.4
FJ497477.1	589078	3241.3	3428.0	2580.4	4132.7	857.5	619.3
AF513455.1	60384	3320.5	2178.3	2647.6	1258.6	566.2	1162.8
DQ071284.1	139697	2858.1	2168.2	440.5	3534.8	4776.1	3505.9
AF314538.1	36386	5846.2	1364.5	11288.3	4235.2	1302.7	1685.9
AB013832.1	11163	1521.4	531.5	3960.0	2413.2	138.7	373.9
EU052247.1	248438	4437.6	2108.7	3255.4	2697.1	990.7	419.7
FJ202344.1	314840	8934.8	7481.6	11253.7	8653.8	6844.6	5726.3
EF648116.1	251292	3620.0	3287.6	4818.2	3624.7	2351.4	4629.0
AY225610.1	96366	2091.7	1394.9	2253.6	1092.9	650.7	1387.5
GU061286.1	546186	4677.8	4151.0	8767.7	9495.2	4777.2	4550.3
AJ607391.1	102614	8649.4	4423.1	13252.1	6226.0	3497.2	2904.4
EF515495.1	222170	6384.0	3672.9	6387.8	9346.3	2244.4	4744.6
AY922205.1	113754	424.8	43.6	2417.0	578.2	71.4	30.2
FJ202783.1	349369	3112.8	480.7	2327.7	1710.8	187.5	348.7
FJ403064.1	357886	6325.4	3175.0	10933.1	5323.6	1717.6	1975.7
EF123613.1	239833	6384.1	7494.3	10216.1	6148.5	8004.6	6962.6
AJ271654.1	51975	2008.8	1191.0	2547.2	1599.9	1222.8	2137.2
AM084124.1	140216	7151.4	986.2	15798.6	6133.2	285.9	797.8
AY570641.1	108516	67.4	28.8	77.6	115.8	89.8	115.2
FN429802.1	534177	2134.1	1134.0	2218.9	1103.2	171.4	346.3
FJ202326.1	315205	6802.9	6558.4	9445.2	7467.8	8578.7	8074.9
DQ917897.1	227146	10291.7	10390.8	11909.1	8212.3	10856.4	9646.5
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s__Campylobacter subantarcticus	54222

DQ357825.1 gg_id:150082 Marine Hatchery: Balance Between Pathogenic and Potentially Probiotic Strains adu
DQ676433.1 gg_id:224791 Archaeal sediment and plankton freshwater pond suboxic freshwater-pond clone M
AB030594.1 gg_id:50542 groundwater clone 1021
EU265967.1 gg_id:567689 transition and zone within near-shore anoxic basin: Nitinat Lake depth 50 m clone Ni
FJ660508.1 gg_id:561979 Correlation functional stability and dynamics full-scale wastewater treatment plant a
EF688595.1 gg_id:284348 Biogeochemistry iron- and sulfur-precipitating microbial mats (Nile Mediterranean) s
GU061298.1 gg_id:560130 Evaluation culturing methods cultivate previously Yel Sea intertidal beach seawater
FJ717168.1 gg_id:571505 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United King
AY621116.1 gg_id:106004 Arcobacter butzleri str. ATCC 49616
EF031092.1 gg_id:186810 Prokaryotic Tirez La Macha Spain endorheic hypersaline atalasohaline lake clone SalB
AY697901.1 gg_id:105639 Antarctica clone F3C43
AB234539.1 gg_id:149689 termite gut homogenate clone MgMjD-024
FJ203095.1 gg_id:346863 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c
AB262386.1 gg_id:159735 Microbial Ishigaki-jima Island Japan sea water Ishigaki Port clone IG-1-27
EU236320.1 gg_id:292623 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg1bF7
AB015259.1 gg_id:11183 deepest cold-seep area Japan Trench clone JTB360 proteobacterium
AJ810558.1 gg_id:105006 superficial sediments clone
DQ464340.1 gg_id:158050 Arcobacter butzleri str. 520H-2004
GQ340204.1 gg_id:583784 Prokaryotic Marathonas Reservoir Greece water column clone VE07-08-BAC
AB013833.1 gg_id:11181 NB1-l clone NB1-l
GQ349268.1 gg_id:581309 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
EU781617.1 gg_id:322902 Bacteroides ureolyticus 4
GQ167663.1 gg_id:581365 Campylobacter concisus str. ATCC 51561
EU869312.1 gg_id:334581 Campylobacter cuniculorum str. 119/07
NC_009715.1 gg_id:242986 Campylobacter curvus str. 525.92
AY621301.1 gg_id:103129 Campylobacter fetus str. 23D
AF219233.1 gg_id:69901 Campylobacter fetus MGH 97-2126
DQ174168.1 gg_id:151146 Campylobacter gracilis str. ATCC 33236
DQ174161.1 gg_id:155173 Campylobacter helveticus str. NCTC 12470
DQ174163.1 gg_id:154260 Campylobacter helveticus str. NCTC 12472
U03022.1 gg_id:11247 Campylobacter helveticus
CP000776.1 gg_id:257761 Campylobacter hominis str. ATCC BAA-381
AF043422.1 gg_id:11239 Campylobacter cf. lanienae str. UB 992
AF550661.1 gg_id:57347 Campylobacter mucosalis str. ATCC 49353
FJ983015.1 gg_id:430191 Aspects Oral Microbiome root canal clone
NZ_ACFU01000050.1 gg_id:469893 Campylobacter rectus str. RM3267
NZ_ACVQ01000030.1 gg_id:470642 Campylobacter showae str. RM3277
EU781616.1 gg_id:326311 Campylobacter showae 3
X67775.1 gg_id:11227 Campylobacter sputorum str. biovar sputorum;LMG 7795
AB181364.1 gg_id:100818 Campylobacter lari str. A3
AB181358.1 gg_id:105325 Campylobacter lari str. NCTC12893

DQ357825.1	150082	4167.5	1929.6	7538.3	4094.9	1639.7	1766.4
DQ676433.1	224791	5326.8	4677.5	8720.5	6011.3	10041.7	6657.0
AB030594.1	50542	7889.2	6453.4	9322.5	9813.8	5171.8	5874.3
EU265967.1	567689	6580.5	5724.7	9826.8	6810.6	4832.5	5208.7
FJ660508.1	561979	5982.4	2719.8	8973.6	5368.4	1214.0	1931.1
EF688595.1	284348	2633.0	2558.1	4745.1	2125.7	5802.1	2041.7
GU061298.1	560130	11632.9	10374.6	6762.6	12525.0	13447.4	13689.3
FJ717168.1	571505	124.0	88.0	581.2	218.7	219.5	56.5
AY621116.1	106004	6659.4	1372.9	12703.5	4715.9	1304.6	1685.9
EF031092.1	186810	7767.6	9234.8	5253.6	9331.4	9756.4	7015.6
AY697901.1	105639	685.2	130.1	2509.8	687.6	198.4	152.6
AB234539.1	149689	793.7	93.0	1515.0	519.2	83.6	39.1
FJ203095.1	346863	9616.1	7420.7	9980.1	6588.2	6356.7	6226.1
AB262386.1	159735	10801.9	7304.2	6693.7	9397.0	9286.9	8251.9
EU236320.1	292623	1406.9	1502.1	1887.1	1952.3	765.0	1547.9
AB015259.1	11183	618.9	133.0	356.6	139.5	224.6	182.8
AJ810558.1	105006	2178.9	2572.2	1013.5	2957.5	3130.8	4485.7
DQ464340.1	158050	14627.0	11077.8	15779.1	10601.9	11828.2	12809.6
GQ340204.1	583784	14459.7	11148.8	11971.9	10048.1	9361.6	7517.5
AB013833.1	11181	8849.0	9478.7	9115.8	10002.0	15069.3	14924.9
GQ349268.1	581309	7455.3	5906.5	8221.4	5712.4	3730.1	4615.8
EU781617.1	322902	4497.8	4274.7	2726.8	3546.9	2216.1	2701.3
GQ167663.1	581365	517.2	81.4	1964.2	409.4	140.6	166.9
EU869312.1	334581	72.2	119.3	456.6	178.5	136.5	217.1
NC_009715.1	242986	329.9	322.7	424.2	167.2	162.6	226.2
AY621301.1	103129	3489.1	4533.0	9810.2	3866.3	3873.2	3805.8
AF219233.1	69901	1213.4	1996.8	8094.2	1784.7	3949.7	1936.4
DQ174168.1	151146	26.5	47.3	81.8	107.9	67.6	53.8
DQ174161.1	155173	1033.8	1496.7	2324.9	2252.5	1299.9	1226.1
DQ174163.1	154260	743.4	1239.8	2990.7	1898.7	1416.8	1021.1
U03022.1	11247	5082.2	4714.7	7050.4	6399.6	6838.4	5187.7
CP000776.1	257761	34.1	20.4	59.0	70.7	65.0	32.7
AF043422.1	11239	1303.4	1275.4	1870.7	2229.7	486.3	920.2
AF550661.1	57347	1328.7	1229.7	2316.2	1109.6	843.0	637.1
FJ983015.1	430191	5432.0	6112.4	2573.2	5811.7	8973.6	6920.0
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EU781616.1	326311	1162.2	2279.9	2762.9	1124.9	1345.4	1666.7
X67775.1	11227	81.5	72.1	108.8	86.0	65.5	33.0
AB181364.1	100818	3462.3	4894.2	3862.2	6221.4	7123.7	4743.9
AB181358.1	105325	10430.9	9439.8	8363.4	10923.8	7614.3	6323.1

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AB181357.1 gg_id:105165 Campylobacter lari str. NCTC12892
AB181359.1 gg_id:105482 Campylobacter lari str. NCTC12894
AF550640.1 gg_id:57368 Campylobacter upsaliensis str. LMG 8851
AF550632.1 gg_id:102123 Campylobacter lari str. LMG 11251
GQ167658.1 gg_id:586732 Campylobacter upsaliensis str. RM3195
DQ174156.1 gg_id:154704 Campylobacter showae str. CCUG 11641
EU289113.1 gg_id:238608 microbiome cloacal openings urogenital and anal tracts tammar wallaby Macropus e
FJ832837.1 gg_id:542539 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J3Q301_10B02
AF219235.1 gg_id:70687 Campylobacter hyointestinalis MGH 97-2652
AB301962.1 gg_id:219863 Campylobacter subsp. hyointestinalis str. 2831-1
AF550641.1 gg_id:57366 Campylobacter upsaliensis str. LMG 8853
EU289065.1 gg_id:253584 microbiome cloacal openings urogenital and anal tracts tammar wallaby Macropus e
AY554142.1 gg_id:113002 Campylobacter sp. str. BTP1
AY554144.1 gg_id:113756 Campylobacter sp. str. WB1
GQ167676.1 gg_id:542181 Campylobacter coli str. ATCC 33559
AF372091.1 gg_id:66989 Campylobacter jejuni str. NCTC 11351
EU559332.1 gg_id:549039 Campylobacter sp. str. MIT 97-5311
AJ276874.1 gg_id:69947 Campylobacter faecalis str. 1433 stool sample isolate
AB301961.1 gg_id:219965 Campylobacter subsp. hyointestinalis str. 2728-1
AF550628.1 gg_id:55836 Campylobacter jejuni str. H99/240
AF550647.1 gg_id:57361 Campylobacter helveticus str. CCUG 30563
DQ174159.1 gg_id:154512 Campylobacter upsaliensis str. NZ5564-94
AM933372.1 gg_id:541426 Campylobacter subantarcticus str. LMG 24374
GQ451185.1 gg_id:533613 Fecal Yunnan snub-nosed monkey feces clone J16
AF097688.1 gg_id:11237 Campylobacter hyointestinalis subsp. lawsonii str. CHY8 subsp.
AB066098.1 gg_id:54599 Campylobacter lari str. CF89-12 Japanese strain
AJ620504.1 gg_id:108770 Campylobacter insulaenigrae str. NCTC 12927
DQ174164.1 gg_id:152100 Campylobacter helveticus str. E504-90
EU623474.1 gg_id:278725 Campylobacter sp. str. 24/06
AF550620.1 gg_id:57384 Campylobacter coli str. LMG 9220
DQ174146.1 gg_id:151930 Campylobacter lari str. NZ145-95
FJ609419.1 gg_id:573432 Campylobacter jejuni str. PRCC-3
EF621895.1 gg_id:243035 Campylobacter canadensis str. L268
AF550655.1 gg_id:57353 Campylobacter showae str. LMG 12636
EU470464.1 gg_id:302158 Grevy's zebra feces clone GZ_aaa03d07
AY288304.1 gg_id:86812 Campylobacter lanienae str. L52
EF621896.1 gg_id:240175 Campylobacter canadensis str. L267
NR_028692.1 gg_id:561090 Sulfurospirillum barnesii str. SES-3; ATCC 700032
EF462744.1 gg_id:295702 meta-genome level extreme microbial symbiosis dorsal surface deep sea hydrotherm
AB355036.1 gg_id:244687 Monitoring and archaeal two heavy polluted areas lake Egypt based on surface wate

AB181356.1	105014	675.7	891.4	1248.8	1683.4	608.6	51.0
AB181357.1	105165	680.2	824.0	1259.5	1712.4	630.7	142.9
AB181359.1	105482	2916.3	3115.8	2340.7	4041.5	2620.6	1925.4
AF550640.1	57368	687.2	964.1	5262.5	3052.4	1522.4	631.6
AF550632.1	102123	2163.2	3033.3	4205.0	3034.8	2335.2	3173.8
GQ167658.1	586732	1661.4	981.1	11249.2	2428.0	304.9	2439.3
DQ174156.1	154704	1325.2	3193.6	2028.9	1030.5	724.3	1439.3
EU289113.1	238608	2772.1	2830.3	5180.7	3665.1	3645.3	5246.9
FJ832837.1	542539	4853.3	4737.9	5479.1	4492.4	8860.8	4458.4
AF219235.1	70687	2248.7	1442.9	12861.2	2140.6	2800.7	2593.6
AB301962.1	219863	2930.4	1058.0	1242.2	2281.2	716.2	1811.9
AF550641.1	57366	2356.6	5351.5	8911.7	2953.3	3074.1	2486.2
EU289065.1	253584	1615.8	2649.3	1931.0	803.1	1279.8	1024.4
AY554142.1	113002	1817.7	3177.0	3894.3	1609.5	1284.0	1441.6
AY554144.1	113756	198.5	182.9	723.9	623.3	76.7	137.6
GQ167676.1	542181	616.9	655.9	785.0	1530.0	187.0	434.6
AF372091.1	66989	586.8	862.1	1186.6	857.6	610.9	53.6
EU559332.1	549039	5768.9	6164.7	13394.1	7582.6	6100.1	7202.7
AJ276874.1	69947	41.7	23.7	33.6	65.0	64.4	27.9
AB301961.1	219965	46.8	42.0	253.8	123.4	101.2	150.9
AF550628.1	55836	1868.0	3762.0	3680.3	2590.1	1392.5	472.3
AF550647.1	57361	4261.8	4870.0	7351.5	5791.8	6209.2	5333.7
DQ174159.1	154512	394.1	937.5	2924.4	888.5	1043.4	729.0
AM933372.1	541426	1595.1	2798.4	2612.1	2154.8	1266.9	1166.5
GQ451185.1	533613	2026.5	2191.5	4548.6	3971.3	10130.5	3691.1
AF097688.1	11237	946.1	1663.8	2003.9	724.9	1280.8	1006.5
AB066098.1	54599	1905.3	2360.9	2324.6	3456.8	1982.6	1440.4
AJ620504.1	108770	3398.4	4182.9	5166.8	4265.4	2471.1	2683.1
DQ174164.1	152100	200.7	689.5	1798.8	547.7	737.5	454.1
EU623474.1	278725	2317.9	2995.9	3481.8	3960.2	3359.9	3473.8
AF550620.1	57384	617.7	794.7	819.9	1159.4	223.3	450.3
DQ174146.1	151930	4181.4	5469.0	7073.7	5493.6	3350.2	4515.5
FJ609419.1	573432	7181.9	8106.6	6811.5	9002.3	7238.7	7121.3
EF621895.1	243035	6664.3	8311.4	6577.3	8048.4	10645.4	8958.6
AF550655.1	57353	1239.4	2375.8	5496.0	2047.0	1724.3	718.3
EU470464.1	302158	1596.5	649.0	5870.7	1183.4	528.5	1900.3
AY288304.1	86812	5440.6	4558.3	8865.7	3173.3	4396.8	5770.3
EF621896.1	240175	5978.3	7669.7	12929.3	7147.1	15001.7	7649.8
NR_028692.1	561090	10845.3	8915.5	5858.2	6994.7	6435.0	8471.5
EF462744.1	295702	2714.3	3383.2	5531.0	3533.4	5312.6	5695.5
AB355036.1	244687	1110.4	697.2	5143.3	1225.8	308.4	512.4

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s__Helicobacter apodemus	54130

FJ792436.1 gg_id:546339 Unexpectedly archaeal species shift between rare and dominant over thousand year
FJ791877.1 gg_id:573109 Unexpectedly archaeal species shift between rare and dominant over thousand year
FJ792027.1 gg_id:534646 Unexpectedly archaeal species shift between rare and dominant over thousand year
U85964.1 gg_id:11189 Sulfurospirillum arsenophilum str. MIT-13
AB286550.1 gg_id:206504 Reducing production and domination comamonadaceae reducing oxygen supply was
AY548994.2 gg_id:103740 marine bone clone boneC3F4
FJ792107.1 gg_id:534811 Unexpectedly archaeal species shift between rare and dominant over thousand year
FJ792301.1 gg_id:562673 Unexpectedly archaeal species shift between rare and dominant over thousand year
AY548973.1 gg_id:102465 marine bone clone boneC15D1
DQ295747.1 gg_id:160847 Epsilonproteobacteria terrestrial caves and springs microbial mat sulfidic Warm spri
DQ925871.1 gg_id:249367 Microbes and Thermal Gradients Temperature Hydrothermal Chimneys hydrotherm
DQ228579.1 gg_id:141569 and physiological significance attached microorganisms rock-hosted deep-sea carbo
AF357199.1 gg_id:22148 Sulfurospirillum sp. str. 18.1
FJ792478.1 gg_id:534881 Unexpectedly archaeal species shift between rare and dominant over thousand year
AY672509.1 gg_id:99157 hydrothermal vent 9 degrees North East Rise Pacific Ocean clone CH1_28_BAC_16SrR
AY327877.2 gg_id:88092 surface vent snail foot clone SF_C11-F3
FJ640810.1 gg_id:512603 GeoChip-based metabolic microbial hydrothermal vent chimney 4143-1 Mothra field
AY280408.1 gg_id:100828 exterior deep-sea hydrothermal vent sulfide chimney Juan de Fuca Ridge Pacific Oce
AB234540.1 gg_id:146284 termite gut homogenate clone MgMjR-060
AY280434.1 gg_id:106449 exterior deep-sea hydrothermal vent sulfide chimney Juan de Fuca Ridge Pacific Oce
AB192073.1 gg_id:143275 termite gut homogenate clone M2PT2-04
FN356324.1 gg_id:580201 Prokaryotic structure sulfate reducer activity -temperature reservoirs and without ni
FJ485111.1 gg_id:541385 microbial autonomous rover world's deepest phreatic sinkhole water column El Zacat
AY266270.1 gg_id:103575 oil production water clone CT1
DQ925875.1 gg_id:244236 Microbes and Thermal Gradients Temperature Hydrothermal Chimneys hydrotherm
FJ156092.1 gg_id:461508 Arcobacter mytili str. T234
AJ969453.1 gg_id:159487 Microbial black smoker s Mid Atlantic Ridge ecological implications rock fragments ch
AB231076.1 gg_id:147107 termite gut wall clone NkW01-035
AJ441214.1 gg_id:106099 hydrothermal vent polychaete mucous clone P. palm C/A 39
AJ576349.1 gg_id:102626 hindgut homogenate Pachnoda ephippiata larva clone PeH32
AY192528.1 gg_id:111196 Flexispira rappini str. 205-2
AY192526.1 gg_id:109700 Flexispira rappini str. 204-1
AY126479.1 gg_id:131724 Flexispira rappini str. 205-1
AF396078.1 gg_id:20816 Helicobacter cinaedi 30327
AF396081.1 gg_id:49270 Helicobacter cinaedi 31111
AB275325.1 gg_id:196588 Helicobacter cinaedi str. PAGU0621 (= 56)
AF302108.1 gg_id:69782 Helicobacter sp. str. HC15880
AF118017.1 gg_id:11022 Flexispira rappini str. H1353
AF497810.1 gg_id:56169 Helicobacter cinaedi str. 94105
AF497807.1 gg_id:60772 Flexispira rappini str. FR106
AF072471.1 gg_id:10989 Helicobacter mesocricetorum str. MU97-1514

FJ792436.1	546339	6999.4	5445.7	9250.6	6308.9	5011.9	4480.2
FJ791877.1	573109	3463.6	3645.7	3778.4	4012.6	4557.4	3780.1
FJ792027.1	534646	1825.7	1102.5	2471.5	860.6	859.3	374.7
U85964.1	11189	43.1	60.4	2202.7	89.6	70.2	26.1
AB286550.1	206504	55.7	126.9	551.6	184.5	387.1	141.1
AY548994.2	103740	2879.1	3300.2	4467.6	3909.2	1514.2	2506.0
FJ792107.1	534811	4828.9	2623.3	2258.5	4634.0	3070.1	3610.7
FJ792301.1	562673	8838.9	7885.6	7008.8	10098.1	13953.8	11308.1
AY548973.1	102465	5722.7	3662.4	2526.7	8577.7	2308.2	4334.1
DQ295747.1	160847	740.5	659.5	1327.3	2069.7	357.8	1142.9
DQ925871.1	249367	155.3	322.1	629.5	182.7	594.5	562.7
DQ228579.1	141569	506.0	109.7	462.7	444.6	405.5	734.4
AF357199.1	22148	1178.3	48.0	1776.9	735.6	58.0	31.4
FJ792478.1	534881	8001.0	6089.7	4536.9	6507.5	7601.7	6998.6
AY672509.1	99157	333.0	475.7	902.8	193.2	172.4	110.9
AY327877.2	88092	27.5	21.6	133.2	82.5	54.7	14.6
FJ640810.1	512603	27.5	26.3	67.5	172.1	57.3	39.2
AY280408.1	100828	23.1	24.9	34.0	35.5	67.5	18.2
AB234540.1	146284	3984.8	3646.3	1787.7	849.2	162.1	219.7
AY280434.1	106449	31.3	26.9	64.4	161.9	62.7	25.1
AB192073.1	143275	126.0	98.2	87.6	127.6	239.6	64.4
FN356324.1	580201	3930.5	2717.3	939.4	4798.5	5451.9	3767.2
FJ485111.1	541385	74.8	161.4	385.0	115.3	105.5	112.3
AY266270.1	103575	4095.3	2967.3	5554.9	4962.1	2824.9	3830.6
DQ925875.1	244236	9284.1	9207.4	11480.1	10679.6	7954.8	10137.4
FJ156092.1	461508	3663.8	1800.9	11341.9	4245.8	4083.7	2561.8
AJ969453.1	159487	2295.5	2067.3	577.7	1751.0	2748.9	1809.3
AB231076.1	147107	28.2	40.0	53.1	67.1	53.4	18.3
AJ441214.1	106099	109.5	144.8	166.1	110.0	235.1	111.8
AJ576349.1	102626	2872.6	2708.9	4835.7	3918.9	3058.8	2268.0
AY192528.1	111196	4596.3	5000.5	3448.9	4181.5	6927.2	3737.4
AY192526.1	109700	3952.5	4901.4	3007.8	5666.0	6726.9	4770.9
AY126479.1	131724	3291.8	4459.7	3400.9	5519.6	8589.2	5400.5
AF396078.1	20816	2743.2	3329.9	4106.4	4599.1	4320.6	3430.5
AF396081.1	49270	11867.0	9357.9	8104.3	12262.8	14400.3	11911.2
AB275325.1	196588	3406.9	3464.8	2550.3	3971.4	2595.8	1784.8
AF302108.1	69782	7180.8	7145.2	4445.7	6687.7	4351.9	4654.6
AF118017.1	11022	2372.3	3072.8	2965.4	5152.8	4010.3	3206.8
AF497810.1	56169	2809.3	2479.6	2420.1	5193.7	4480.5	3517.0
AF497807.1	60772	1612.3	1327.5	1999.1	3403.9	3720.8	2337.0
AF072471.1	10989	1757.4	3657.6	3577.5	3815.1	7076.4	5534.0

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AY009130.1 gg_id:37836 Helicobacter apodemus str. YMRC 00419
AY323502.1 gg_id:105862 Helicobacter canadensis ISL 793/92
DQ438113.1 gg_id:154548 Helicobacter canadensis str. L172
AY631946.1 gg_id:106403 Helicobacter canis str. MIT 51402
L13464.1 gg_id:11062 Helicobacter canis
DQ307736.1 gg_id:154375 Helicobacter equorum str. EqF2
AF506785.1 gg_id:72292 Helicobacter heilmannii str. WD1
AY686607.1 gg_id:111336 Helicobacter felis str. Lee DS2
M57398.2 gg_id:10994 Helicobacter felis str. CS1; ATCC 49179
AF103882.1 gg_id:11030 Helicobacter felis str. 1136-7
AY561831.1 gg_id:106123 Helicobacter ganmani str. ES-5
AY631951.1 gg_id:101810 Helicobacter ganmani str. MIT 99-5102
U07573.2 gg_id:11042 Helicobacter hepaticus str. Hh-1
AY554124.1 gg_id:114186 Helicobacter kirbridei str. BTP1F
AF333339.1 gg_id:27055 Helicobacter sp. str. MIT 99-5504
AF010140.1 gg_id:11040 Helicobacter muridarum str. UNSW 1.7st
M35048.2 gg_id:11057 Helicobacter mustelae str. ATCC 43772
AY554133.1 gg_id:113226 Helicobacter peregrinus str. RTP4S
DQ062214.1 gg_id:132728 Helicobacter sp. AGN-1
X67854.1 gg_id:11080 Helicobacter pylori str. ATCC 49396T
Z25741.1 gg_id:11013 Helicobacter pylori str. NCTC 11637
DQ062215.1 gg_id:132837 Helicobacter sp. GA-3
AY593989.1 gg_id:101118 Helicobacter pylori str. LPB 424-01
AF057163.1 gg_id:10974 Helicobacter sp
AF535198.1 gg_id:57708 Helicobacter pylori str. Lit81
M88137.2 gg_id:10945 Helicobacter trogontum str. ATCC 43966
AY034820.1 gg_id:47556 Helicobacter rappini str. H 95 S
AF225548.1 gg_id:28994 Helicobacter trogontum str. ATCC 49310
U96296.1 gg_id:10983 Helicobacter rodentium str. MIT 95-1707
AF506791.1 gg_id:64310 Helicobacter heilmannii str. P5
AF506790.1 gg_id:71558 Helicobacter heilmannii str. P4
AF506787.1 gg_id:73122 Helicobacter heilmannii str. P1
AY554121.1 gg_id:114199 Helicobacter vulpecula str. BTP7C
FJ667779.1 gg_id:548699 Helicobacter sp. 'pancake tortoise' str. FL-2007
AF292378.1 gg_id:72792 Helicobacter cetorum str. MIT 99-5656
AY554137.1 gg_id:113171 Helicobacter sp. str. BTP3S
M88152.2 gg_id:11054 Helicobacter sp. '91-266-11 Fox' str. 91-266-11 Fox
X81028.1 gg_id:10960 Helicobacter sp. str. Mainz
L36141.1 gg_id:10982 Helicobacter pullorum str. NCTC 12824
AF058768.1 gg_id:11034 Helicobacter heilmannii 1
AF506794.1 gg_id:64304 Helicobacter heilmannii str. TD1

AY009130.1	37836	8638.2	8626.1	5431.0	6312.4	6578.3	6004.6
AY323502.1	105862	193.8	214.4	915.0	165.7	254.1	227.1
DQ438113.1	154548	201.1	256.6	1628.3	343.0	264.7	316.7
AY631946.1	106403	1551.8	1658.3	3823.1	3590.2	3008.1	1879.2
L13464.1	11062	4645.3	5990.4	6726.2	4860.1	6402.4	4806.7
DQ307736.1	154375	57.1	166.3	3573.2	207.1	166.6	239.4
AF506785.1	72292	2604.1	3001.9	1508.2	2917.2	1778.5	1777.9
AY686607.1	111336	4236.7	4543.5	2294.4	4200.5	3640.4	3653.9
M57398.2	10994	2583.0	3050.4	1715.7	2666.6	1861.0	1484.6
AF103882.1	11030	12381.7	10921.6	6070.9	11650.9	15580.4	13233.0
AY561831.1	106123	137.8	147.1	289.8	158.0	73.6	46.4
AY631951.1	101810	43.1	64.4	76.5	81.9	128.0	46.8
U07573.2	11042	2231.9	2665.1	8512.2	1924.1	3642.5	3511.3
AY554124.1	114186	188.2	436.9	1250.5	284.9	116.4	117.5
AF333339.1	27055	1125.8	800.9	835.2	242.8	565.8	469.0
AF010140.1	11040	847.6	459.2	1003.2	2305.5	194.0	252.9
M35048.2	11057	4067.2	4535.7	2872.1	5263.1	3328.6	2603.9
AY554133.1	113226	992.0	1407.5	3689.2	731.6	664.2	1376.1
DQ062214.1	132728	501.3	1138.5	1194.3	397.9	1564.4	1645.9
X67854.1	11080	9684.8	9149.1	3572.8	7114.1	7802.2	7357.3
Z25741.1	11013	166.7	222.2	600.9	336.2	118.0	480.7
DQ062215.1	132837	1145.9	976.4	7373.6	1320.5	1071.0	1526.7
AY593989.1	101118	4326.0	4444.5	3555.7	3381.7	4821.9	5919.9
AF057163.1	10974	1783.8	1906.9	3702.6	865.2	1284.2	2196.7
AF535198.1	57708	6855.8	5535.4	3931.6	6514.9	6891.1	6872.2
M88137.2	10945	1696.6	1791.1	3720.1	3998.6	4091.7	2347.2
AY034820.1	47556	2392.3	882.1	1886.8	2024.1	1032.8	1250.2
AF225548.1	28994	1628.6	2746.2	1803.6	3800.4	4004.8	3378.6
U96296.1	10983	174.8	173.4	923.7	206.0	291.0	218.4
AF506791.1	64310	84.2	106.9	181.8	385.0	80.8	55.0
AF506790.1	71558	223.7	199.4	449.5	1397.7	211.2	68.4
AF506787.1	73122	763.6	1063.9	400.1	1371.8	124.5	87.8
AY554121.1	114199	1474.1	1311.1	2057.3	751.8	912.6	754.0
FJ667779.1	548699	3919.9	3289.3	4492.1	2492.2	1505.8	1365.9
AF292378.1	72792	3423.6	5022.4	4202.3	5397.8	5392.4	5364.8
AY554137.1	113171	195.9	51.6	170.7	209.4	71.5	26.3
M88152.2	11054	895.6	777.4	4589.1	975.6	407.5	520.7
X81028.1	10960	2877.0	3395.7	5118.4	5062.8	5698.1	4879.1
L36141.1	10982	910.3	1039.0	1561.9	1180.2	2486.0	2152.7
AF058768.1	11034	2616.5	2858.9	1756.6	3089.1	1852.8	1583.1
AF506794.1	64304	1735.9	2605.5	4005.7	3168.8	3844.1	4002.8

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AY634601.1 gg_id:109137 stomach clone
AF334681.1 gg_id:17771 Helicobacter cf. pullorum str. W.Tee-Cro
AF333341.1 gg_id:36371 Helicobacter marmotae str. MIT 98-6070
AY143177.1 gg_id:76377 Helicobacter cetorum str. MIT 01-6202
U96300.1 gg_id:11047 Helicobacter trogontum str. ATCC 43968
AF237612.1 gg_id:26677 Helicobacter sp. str. Wee Tee
AY034817.1 gg_id:49918 Helicobacter rappini str. 1 SU
Y18028.1 gg_id:10969 Helicobacter heilmannii str. AF53
AB006148.1 gg_id:11016 Helicobacter suncus str. Kaz-2
AJ249858.1 gg_id:41542 Helicobacter sp. blood isolate 964
AF127027.1 gg_id:10980 Candidatus Helicobacter bovis
AF506778.1 gg_id:64319 Helicobacter heilmannii str. C4E
AF103880.1 gg_id:11028 Helicobacter felis str. 390-9
M88151.2 gg_id:10993 Helicobacter sp. CLO-3 str. CCUG 14564
DQ415545.1 gg_id:153639 Helicobacter anseris str. MIT 04-9362
AY203900.1 gg_id:82216 Helicobacter sp. MIT 02-5519C
AY634603.1 gg_id:109139 stomach clone
DQ415546.1 gg_id:153064 Helicobacter brantae str. MIT 04-9366
AY686609.1 gg_id:110529 Helicobacter trogontum str. MIT 95-5368
AF246986.1 gg_id:16388 Helicobacter winghamensis str. NLEP 98-202
AF103883.1 gg_id:11031 Helicobacter bizzozeronii str. 865-2
AF142062.1 gg_id:11063 Helicobacter sp. 'feline isolate'
AF302105.1 gg_id:50310 Helicobacter pametensis str. ATCC51478
AF333340.1 gg_id:49735 Helicobacter sp. str. MIT 99-5507
AF506780.1 gg_id:72724 Helicobacter heilmannii str. CM1
AY634577.1 gg_id:109104 stomach clone
AY554139.1 gg_id:114285 Helicobacter sp. str. LNB2F
AF506782.1 gg_id:64314 Helicobacter heilmannii str. MM1
AY554140.1 gg_id:113412 Helicobacter sp. str. WB1F
U46129.1 gg_id:11050 Helicobacter cholecystus str. Hkb-1
DQ438119.1 gg_id:152253 Helicobacter canadensis str. L222
AF297868.1 gg_id:48289 Helicobacter aurati str. MIT 97-5075c
AF302107.1 gg_id:47191 Helicobacter bizzozeronii str. ATCC700031
AY742308.1 gg_id:102634 Helicobacter sp. str. MIT 02-6899
DQ004689.2 gg_id:133982 Helicobacter cynogastricus str. JKM4
AF103881.1 gg_id:11029 Helicobacter felis str. 144-10
AB080644.1 gg_id:49390 Sulfuricurvum kujiense str. YK-3
DQ295616.1 gg_id:161607 Epsilonproteobacteria terrestrial caves and springs microbial mat sulfidic spring Pah
EU542457.1 gg_id:267730 Effects chemical structure concentration on pathways microbial during dechlorinatio
FJ793154.1 gg_id:522980 Archaea and Hot Spring Thailand Tao Dam hot spring clone TDB04
AB080645.1 gg_id:41311 Sulfuricurvum kujiense str. YK-4

AY634601.1	109137	2485.9	2845.9	2151.4	3064.6	895.5	1145.1
AF334681.1	17771	219.4	345.4	3077.2	197.7	360.1	238.7
AF333341.1	36371	727.3	650.7	3613.4	1340.9	660.0	502.3
AY143177.1	76377	3820.2	5137.1	3307.8	4558.7	7387.5	6902.3
U96300.1	11047	506.0	464.4	2246.5	547.6	106.2	108.7
AF237612.1	26677	890.0	683.1	2527.3	1265.1	454.8	485.0
AY034817.1	49918	1547.2	953.5	3352.8	2041.2	937.0	1094.6
Y18028.1	10969	5465.5	5761.3	4492.0	4489.4	3844.4	2923.2
AB006148.1	11016	647.5	169.5	2296.1	2477.3	724.3	628.4
AJ249858.1	41542	5796.0	5987.2	5277.9	4508.8	7234.6	6042.3
AF127027.1	10980	126.0	508.3	1670.0	916.1	191.1	275.1
AF506778.1	64319	6126.6	5981.6	2875.8	6131.2	4683.1	4322.1
AF103880.1	11028	6049.7	7053.5	4252.0	6152.2	6229.3	6137.6
M88151.2	10993	1163.5	1782.2	4769.9	3100.5	2215.4	1888.9
DQ415545.1	153639	636.5	360.5	2090.3	2673.1	1208.2	1187.9
AY203900.1	82216	1490.6	1105.4	1830.0	2284.9	704.2	925.3
AY634603.1	109139	9800.0	7744.7	4380.2	5978.8	2146.2	2463.7
DQ415546.1	153064	175.1	321.1	1780.3	528.7	111.7	180.2
AY686609.1	110529	245.3	150.8	2671.8	1970.9	119.0	51.5
AF246986.1	16388	309.2	667.8	3068.4	981.7	206.7	215.9
AF103883.1	11031	9206.8	7452.8	7890.4	9060.0	7133.4	7341.1
AF142062.1	11063	11163.9	10106.3	5524.0	8839.7	13233.5	11625.2
AF302105.1	50310	33.3	39.1	99.1	540.9	48.5	47.8
AF333340.1	49735	2610.4	3016.6	2523.6	5559.6	3263.8	1693.9
AF506780.1	72724	1338.3	2245.4	669.7	3599.4	588.6	693.4
AY634577.1	109104	3192.9	3227.6	2715.8	2859.9	2770.4	2177.5
AY554139.1	114285	357.8	440.5	1127.5	282.4	421.5	470.2
AF506782.1	64314	238.5	294.1	649.1	1010.2	822.8	1444.3
AY554140.1	113412	1219.8	1858.7	2098.4	1940.9	961.1	1737.9
U46129.1	11050	1572.2	1931.1	2945.9	2322.4	2329.2	2512.9
DQ438119.1	152253	630.6	152.4	3404.2	403.7	455.7	264.5
AF297868.1	48289	683.8	353.2	1974.1	503.0	407.7	172.8
AF302107.1	47191	4069.7	4064.3	4010.5	7200.5	7488.5	6090.3
AY742308.1	102634	2081.4	1494.0	5102.4	3066.9	1607.0	1515.6
DQ004689.2	133982	1535.0	1778.0	1094.8	1887.1	1451.2	1194.4
AF103881.1	11029	9656.8	8293.4	7669.5	7788.4	6992.6	6787.8
AB080644.1	49390	226.9	315.8	5278.4	1265.4	163.5	267.5
DQ295616.1	161607	2894.4	3137.5	5715.8	2995.6	2396.5	2403.3
EU542457.1	267730	4094.9	4026.2	4444.1	3951.6	4320.6	5386.9
FJ793154.1	522980	2696.2	2539.0	7924.6	3097.9	717.1	1201.6
AB080645.1	41311	1838.5	1314.9	8330.5	1762.2	1004.2	2023.9

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FJ484902.1 gg_id:563044 microbial autonomous rover world's deepest phreatic sinkhole water column El Zacat
FJ484970.1 gg_id:513207 microbial autonomous rover world's deepest phreatic sinkhole water column El Zacat
GQ261311.1 gg_id:538468 Study on Sediment sediment Dongping Lake clone 1S3-8
DQ295705.1 gg_id:161331 Epsilonproteobacteria terrestrial caves and springs microbial mat sulfidic stream Mil
AY510188.1 gg_id:109996 microbial mat cave sulfidic spring clone LKC3_57B.17
DQ295661.1 gg_id:161483 Epsilonproteobacteria terrestrial caves and springs microbial mat sulfidic spring resu
DQ295560.1 gg_id:160845 Epsilonproteobacteria terrestrial caves and springs microbial mat sulfidic cave strea
EU884105.1 gg_id:326035 Recently Evolved Symbiosis Between Chemoautotrophic and Cave-Dwelling Amphip
AF407391.1 gg_id:30295 MCB-contaminated groundwater-treating reactor clone RA9C8
AY191481.1 gg_id:93946 microbial mat sulfidic cave spring clone LKC1.114_6
AY191468.1 gg_id:93668 microbial mat sulfidic cave spring clone LKC1.21_5
AY510191.1 gg_id:109873 microbial mat cave sulfidic spring clone LKC3_19.39
DQ295690.1 gg_id:160741 Epsilonproteobacteria terrestrial caves and springs floating microbial mat sulfidic gr
DQ295702.1 gg_id:160766 Epsilonproteobacteria terrestrial caves and springs microbial mat sulfidic stream Mil
GQ406165.1 gg_id:512611 Benthic submerged sinkhole ecosystems sediment clone BK-20-18
EU101041.1 gg_id:238274 Sulfide/oxygen supply ratio predicts outcome competition among sulfur-oxidizing wa
AB030601.1 gg_id:21738 groundwater clone 1043
AB030605.1 gg_id:22082 groundwater clone 1028
EU884110.1 gg_id:329225 Recently Evolved Symbiosis Between Chemoautotrophic and Cave-Dwelling Amphip
AY191482.1 gg_id:93762 microbial mat sulfidic cave spring clone LKC1.114_7
GQ390203.1 gg_id:557628 oxic-anoxic interface meromictic crater lake Lac Pavin clone Eub62D4
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DQ787703.1 gg_id:171036 holocene lake sediment clone SLB59
EF467565.1 gg_id:203699 situ microelectrode voltammetry sulfur-oxidizing biofilms Frasassi sulfidic cave strear
AY191466.1 gg_id:103936 microbial mat sulfidic cave spring clone LKC1.21_1
AB240521.1 gg_id:143003 microbial structure rhizosphere biofilm Sapporo root-base (80 160 mm) Phragmites S
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AY510167.1 gg_id:110035 microbial mat cave sulfidic spring clone LKC3_22.72
DQ295745.1 gg_id:159690 Epsilonproteobacteria terrestrial caves and springs microbial mat sulfidic Warm spri
AY510168.1 gg_id:110808 microbial mat cave sulfidic spring clone LKC3_57B.54
DQ295557.1 gg_id:160445 Epsilonproteobacteria terrestrial caves and springs microbial mat sulfidic cave strea
DQ787698.1 gg_id:162117 holocene lake sediment clone SLB422
AY532544.1 gg_id:99687 uranium-contaminated aquifer clone 1013-1-CG22
AY510194.1 gg_id:111128 microbial mat cave sulfidic spring clone LKC3_57B.49
AF367495.1 gg_id:43869 deep-sea hydrothermal vent clone VC1.2-cl50
AF367492.1 gg_id:70730 deep-sea hydrothermal vent clone VC1.2-cl32
GQ433935.1 gg_id:541504 Subseafloor ocean crust microbial observatories: (F-through Osmo Colonization Syst

AB030603.1	48041	2465.0	2289.3	7583.1	3057.8	2534.9	2179.2
FJ484985.1	512690	4540.5	4273.0	4976.3	4081.3	3777.8	3543.3
FJ484902.1	563044	6377.9	6967.0	5943.8	5744.4	7152.6	7115.3
FJ484970.1	513207	2107.1	2007.3	6995.0	2775.2	1548.6	1413.4
GQ261311.1	538468	311.7	436.6	3234.5	295.8	578.2	424.4
DQ295705.1	161331	718.5	556.9	6043.2	1439.7	238.2	252.1
AY510188.1	109996	985.2	684.9	5392.5	2054.1	120.6	357.8
DQ295661.1	161483	466.0	402.9	4259.1	1210.0	350.1	387.0
DQ295560.1	160845	2677.8	4606.0	5449.9	3420.5	8100.3	6428.4
EU884105.1	326035	771.7	253.6	15240.9	1620.5	407.1	1653.1
AF407391.1	30295	141.7	160.9	12579.1	991.4	110.5	201.4
AY191481.1	93946	1040.7	1420.1	10923.2	2418.8	327.4	954.6
AY191468.1	93668	1212.3	2113.3	5907.0	2421.3	5773.2	7288.7
AY510191.1	109873	2921.0	4111.8	10864.9	3753.4	5309.0	3757.2
DQ295690.1	160741	4483.7	4281.4	17438.7	6792.1	6081.8	8726.5
DQ295702.1	160766	73.9	70.2	5809.5	772.1	76.4	30.4
GQ406165.1	512611	2885.7	5096.1	7717.8	3852.6	7858.5	6818.5
EU101041.1	238274	8975.4	9255.6	12214.0	7113.7	5436.6	5230.5
AB030601.1	21738	2192.3	1771.0	12331.0	2875.4	880.7	1818.3
AB030605.1	22082	5002.7	5535.6	11443.7	3972.9	2607.0	3276.7
EU884110.1	329225	1689.7	3162.1	6134.7	897.6	2700.6	4953.7
AY191482.1	93762	12858.6	14592.2	10264.2	11410.3	15013.4	15283.8
GQ390203.1	557628	493.0	552.1	6204.1	1201.2	193.6	871.3
AY510172.1	109530	12051.3	11269.5	14309.4	11223.0	9916.7	10440.0
DQ787703.1	171036	8752.9	8145.6	4594.8	11038.8	12904.9	13006.1
EF467565.1	203699	164.5	412.6	4569.7	523.6	594.4	327.1
AY191466.1	103936	2277.0	2602.5	5857.5	2160.6	3898.6	5124.6
AB240521.1	143003	4728.8	5470.1	11043.8	5240.8	2447.7	2525.3
GQ472372.1	553344	35.8	26.3	1840.2	276.2	41.0	16.1
DQ787688.1	172663	919.5	1067.8	4515.2	2027.8	631.9	1480.5
DQ295722.1	159773	9271.1	10534.4	8771.3	9417.9	8113.3	8490.3
AY510167.1	110035	2312.5	2691.1	8686.4	2564.6	2375.6	2497.6
DQ295745.1	159690	409.3	405.1	7054.7	592.4	187.0	189.0
AY510168.1	110808	6126.8	5641.6	8386.2	6106.8	4008.6	5988.5
DQ295557.1	160445	2416.2	2817.4	13285.7	3357.8	2308.6	2726.4
DQ787698.1	162117	4263.1	4235.3	5317.6	4666.9	5251.6	6030.9
AY532544.1	99687	5729.5	7245.5	10901.1	5686.7	4852.9	8040.7
AY510194.1	111128	5058.2	6245.0	9109.5	7005.1	12565.4	14756.8
AF367495.1	43869	538.3	341.7	1400.0	385.7	773.3	1141.8
AF367492.1	70730	4004.7	4259.5	3351.2	4999.3	6731.6	4177.3
GQ433935.1	541504	2711.4	1941.7	4786.2	2841.7	4631.9	2528.2

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U15101.1 gg_id:11096 hydrothermal vent clone PVB_OTU_2
NC_007575.1 gg_id:144857 Thiomicrospira denitrificans str. ATCC 33889
FJ437888.1 gg_id:547212 Benthic okenone production Fayetteville New York Green Lake 25 m water depth clor
AF121884.1 gg_id:11109 phenol-degrading consortium clone Phenol-1
DQ295573.1 gg_id:160062 Epsilonproteobacteria terrestrial caves and springs microbial mat sulfidic cave spring
FJ615170.1 gg_id:593488 Microbial dynamics seasonally fjord: British Columbia Saanich Inlet depth 10m anoxic
EU491812.1 gg_id:268142 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39
DQ234141.2 gg_id:142794 determined library mangrove clone DS057
FJ497618.1 gg_id:563303 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun
FJ717090.1 gg_id:551059 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United Kingc
DQ676325.1 gg_id:224044 Archaeal and plankton freshwater pond suboxic freshwater-pond sediment clone M
AY211683.1 gg_id:96203 Gulf Mexico seafloor sediment clone GoM GC234 633E
AY225615.1 gg_id:97077 iron-rich substrate exposed to Mid-Atlantic Ridge vent clone AT-cs10
FN397808.1 gg_id:424252 geomicrobiological investigation sediments Gulf Cadiz GeoB 9072-1 anoxic sub-surfa
AJ441199.1 gg_id:57482 hydrothermal vent polychaete mucous clone P. palm C/A 78
AF355050.1 gg_id:48010 marine clone Arctic96B-13
GQ356982.1 gg_id:592000 Metal Dependent Marine Methane Oxidation methane seep sediment clone FeSO4_
AY225612.1 gg_id:97721 organic-rich substrate exposed to Mid-Atlantic Ridge vent clone AT-co23
DQ676368.1 gg_id:222158 Archaeal sediment and plankton freshwater pond suboxic freshwater-pond clone M
FJ497273.1 gg_id:590030 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun
EF218993.1 gg_id:215778 and Eukaryotic Hydrothermal Site East Rise Ridge Flank Abyssal Hill hydrothermal site
DQ228650.1 gg_id:141130 Microbial colonizing mineral surfaces within sulfide-microbial incubator clone CH2b1
EF219001.1 gg_id:209624 and Eukaryotic Hydrothermal Site East Rise Ridge Flank Abyssal Hill hydrothermal site
U15106.1 gg_id:11103 hydrothermal vent clone PVB_OTU_6
AY280406.1 gg_id:100516 exterior deep-sea hydrothermal vent sulfide chimney Juan de Fuca Ridge Pacific Oce
GQ848465.1 gg_id:578863 Microbial sediments vents along East Lau Spreading Centre deep sea hydrothermal
FJ535290.1 gg_id:546926 within iron-containing flocculent mats submarine volcanoes along Kermadec Arc iron
FJ717130.1 gg_id:551352 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United Kingc
FJ717171.1 gg_id:533593 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United Kingc
EF379628.1 gg_id:205139 sea water Victoria Harbor (Hong Kong) area clone VH-PA7-38
EU652649.1 gg_id:279233 Seasonal variation microbial Yel Sea sediment clone B8S-4
DQ836759.1 gg_id:169835 attached biomass denitrifying bioreactor clone DB-83
AY218555.1 gg_id:82461 penguin droppings sediments clone KD1-140
EU652651.1 gg_id:278362 Seasonal variation microbial Yel Sea sediment clone A8S-94
FM242221.1 gg_id:343001 sequences sediment clone 259 T0h-oil
EU652650.1 gg_id:277911 Seasonal variation microbial Yel Sea sediment clone C8S-4
FJ717108.1 gg_id:569301 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United Kingc
FJ535347.1 gg_id:510699 within iron-containing flocculent mats submarine volcanoes along Kermadec Arc sedi
AB530237.1 gg_id:584301 Monitoring Suez and Tokyo bays based on analyses marine sediment clone Tokyo..B
AB188787.1 gg_id:113750 cold seep sediment clone SB5-24
AB193899.1 gg_id:108823 deep-sea vent clone Mb-NB05

U15101.1	11096	206.6	480.0	4264.7	797.0	192.3	141.2
NC_007575.1	144857	150.3	193.6	1906.2	285.3	126.1	87.0
FJ437888.1	547212	71.1	89.0	962.0	719.5	90.8	73.6
AF121884.1	11109	117.7	92.7	729.0	85.9	212.6	70.5
DQ295573.1	160062	5848.3	5620.5	14336.5	9348.5	6011.4	7491.1
FJ615170.1	593488	499.6	526.5	2956.8	1413.9	1858.2	1400.2
EU491812.1	268142	1818.1	2351.7	7813.4	3405.4	6366.8	5862.5
DQ234141.2	142794	51.2	55.0	1567.1	173.4	76.5	34.1
FJ497618.1	563303	457.7	80.7	288.0	339.7	184.3	154.4
FJ717090.1	551059	2278.1	3479.6	6282.9	1757.6	4229.4	3204.5
DQ676325.1	224044	1225.6	632.9	818.2	327.1	405.9	261.1
AY211683.1	96203	43.9	92.6	808.8	102.7	73.8	74.3
AY225615.1	97077	504.3	379.3	1445.5	329.0	152.1	187.5
FN397808.1	424252	1472.0	1347.0	3276.5	2531.0	392.2	1090.8
AJ441199.1	57482	122.4	164.9	235.6	101.5	122.6	93.0
AF355050.1	48010	263.4	95.3	511.0	168.6	45.8	56.7
GQ356982.1	592000	7219.0	5621.9	10255.6	5231.3	4936.5	4892.6
AY225612.1	97721	68.1	55.5	150.7	92.9	101.2	38.1
DQ676368.1	222158	1671.7	963.6	1661.0	2026.5	1300.5	832.7
FJ497273.1	590030	864.5	855.1	4537.0	1731.5	614.2	1219.2
EF218993.1	215778	157.1	209.0	1318.4	344.6	219.7	141.1
DQ228650.1	141130	295.2	348.2	4870.9	334.2	717.9	440.1
EF219001.1	209624	22.9	70.7	67.4	69.2	77.6	34.4
U15106.1	11103	25.2	46.1	72.6	57.5	68.5	40.1
AY280406.1	100516	219.4	170.9	3573.7	580.5	410.3	360.8
GQ848465.1	578863	57.8	65.8	2984.6	256.7	79.2	39.7
FJ535290.1	546926	1180.5	1448.6	1971.9	687.8	387.4	462.1
FJ717130.1	551352	278.9	556.7	5084.8	397.1	629.7	482.8
FJ717171.1	533593	5107.3	6021.3	9652.8	3995.7	7268.9	5167.5
EF379628.1	205139	7839.1	6287.8	3351.9	9216.2	8390.8	8989.4
EU652649.1	279233	1839.5	1547.3	1106.3	595.2	388.6	656.7
DQ836759.1	169835	1026.4	1410.7	5797.0	1875.9	2697.1	2244.9
AY218555.1	82461	7263.9	7147.8	6501.1	4200.3	4059.7	3248.2
EU652651.1	278362	3254.1	2765.7	1844.2	3719.0	1082.5	2641.6
FM242221.1	343001	689.5	1162.8	1956.4	1105.9	2214.9	3397.9
EU652650.1	277911	11960.6	10460.2	8799.6	8532.8	9684.3	8101.3
FJ717108.1	569301	2151.9	3300.5	7945.1	1344.9	3641.6	3533.3
FJ535347.1	510699	3151.5	4283.7	4593.8	3389.2	10026.1	6348.4
AB530237.1	584301	4723.4	5123.6	5030.1	3430.2	2726.3	3134.7
AB188787.1	113750	509.1	2846.5	821.0	349.1	236.3	1726.4
AB193899.1	108823	127.3	144.7	800.2	231.3	137.4	131.4

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s__Sulfurovum sp. NBC37-1	54823
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AF367490.1 gg_id:73836 deep-sea hydrothermal vent clone VC1.2-cl26
GQ261804.1 gg_id:560545 shifts taxa and response localized organic loading deep sea sediment whale falls clo
AY922199.1 gg_id:112883 whalefall clone 131631
DQ228651.1 gg_id:142365 Microbial colonizing mineral surfaces within sulfide-microbial incubator clone CH2b1
FJ717087.1 gg_id:562754 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United King
AY216438.1 gg_id:82215 temperate estuarine mud clone KM51
EU491805.1 gg_id:273299 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39
AY225613.1 gg_id:98692 pumice fragments exposed to Mid-Atlantic Ridge vent clone AT-pp6
AB189375.1 gg_id:113264 cold seep sediment clone JT75-307
FJ497428.1 gg_id:572725 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun
AY672505.1 gg_id:107511 hydrothermal vent 9 degrees North East Rise Pacific Ocean clone CH1_22_BAC_16Sr
AB015257.1 gg_id:11113 deepest cold-seep area Japan Trench clone JTB146 proteobacterium
AJ441200.1 gg_id:57484 hydrothermal vent polychaete mucous clone P. palm C 92
EF999352.1 gg_id:237892 Vertical and Methanotrophs Estuarine Sediments Pearl River Estuary sediments 6cm
AM982624.1 gg_id:278960 microbial and slurry pig saw dust spent bedding clone PISD-AJC10
FJ535284.1 gg_id:512607 within iron-containing flocculent mats submarine volcanoes along Kermadec Arc iron
EF218991.1 gg_id:206907 and Eukaryotic Hydrothermal Site East Rise Ridge Flank Abyssal Hill hydrothermal site
AY532570.1 gg_id:105327 uranium-contaminated aquifer clone 1013-28-CG21
FJ497261.1 gg_id:566005 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun
AB235234.1 gg_id:141016 symbiont
FJ437839.1 gg_id:513719 Benthic okenone production Fayetteville New York Green Lake 25 m water depth clo
AB176111.1 gg_id:175999 Microbial Hydrothermal System Suiyo Seamount on Izu-Ogasawara Arc vent area wa
FM203379.1 gg_id:370488 Biogeography filamentous and epsilonproteobacterial ectosymbionts vent shrimp e
AJ515714.1 gg_id:94683 deep-sea shrimp gut clone 4
FM203398.1 gg_id:371282 Biogeography filamentous and epsilonproteobacterial ectosymbionts vent shrimp e
AP009179.1 gg_id:249880 Sulfurovum sp. str. NBC37-1
EF462799.1 gg_id:293907 meta-genome level extreme microbial symbiosis dorsal surface deep sea hydrothern
AJ515716.1 gg_id:94327 deep-sea shrimp gut clone 15
EU555122.1 gg_id:259007 Microbial Sulfide Hydrothermal Vent Field Juan de Fuca Ridge Dudley hydrothermal
AY672497.1 gg_id:102782 hydrothermal vent 9 degrees North East Rise Pacific Ocean clone CH1_1_BAC_16SrR
FJ792125.1 gg_id:510296 Unexpectedly archaeal species shift between rare and dominant over thousand year
FJ535278.1 gg_id:554288 within iron-containing flocculent mats submarine volcanoes along Kermadec Arc iron
AY531596.1 gg_id:100070 Indian Ocean hydrothermal vent clone SF_C23-C4_shell
DQ228647.1 gg_id:144474 Microbial colonizing mineral surfaces within sulfide-microbial incubator clone CH2b1
AY542560.1 gg_id:113844 Gulf Mexico seafloor sediment clone GoM GB425 02B-28
GQ249521.1 gg_id:580475 Microbial anaerobic sediments Bay Cadiz (Spain) marine sediment: 6-8 cm layer clo
GQ357025.1 gg_id:533206 Metal Dependent Marine Methane Oxidation methane seep sediment clone FeOrig
AF449231.1 gg_id:61878 Riftia pachyptila's tube clone R103-B15
AB476184.1 gg_id:536849 Compositional and functional transition epibiotic microbial hydrothermal vent galat
AY531576.1 gg_id:107839 Indian Ocean hydrothermal vent clone SF_C23-G3
FJ535277.1 gg_id:540587 within iron-containing flocculent mats submarine volcanoes along Kermadec Arc iron

AF367490.1	73836	1305.6	1204.0	2135.3	920.4	2704.5	1893.1
GQ261804.1	560545	1978.9	1679.7	6757.0	3670.8	3174.6	3031.8
AY922199.1	112883	14581.0	11436.3	15406.9	11280.5	13757.2	14089.0
DQ228651.1	142365	41.2	43.9	73.0	57.2	64.6	27.2
FJ717087.1	562754	4377.0	3846.1	4363.5	3638.6	1834.9	2556.3
AY216438.1	82215	41.4	53.5	54.0	50.2	99.1	47.1
EU491805.1	273299	8272.3	7493.9	2506.0	7109.1	2568.2	3243.3
AY225613.1	98692	199.3	239.5	330.3	499.0	166.5	250.2
AB189375.1	113264	37.1	61.7	255.1	124.6	190.2	126.3
FJ497428.1	572725	639.6	670.2	1238.1	575.0	810.2	834.3
AY672505.1	107511	758.0	530.7	5501.5	1355.2	680.8	602.5
AB015257.1	11113	29.7	25.3	22.9	45.3	52.8	25.1
AJ441200.1	57484	56.0	63.6	66.1	142.3	87.0	32.9
EF999352.1	237892	4473.9	2582.3	7110.8	4497.6	4214.9	3194.2
AM982624.1	278960	7472.6	7291.9	3506.1	4103.5	5789.7	4557.7
FJ535284.1	512607	8162.8	7297.2	4870.4	6239.1	5728.7	6727.3
EF218991.1	206907	604.1	526.5	3550.1	673.9	690.1	948.2
AY532570.1	105327	1487.3	1464.3	3061.6	1678.7	2022.9	783.1
FJ497261.1	566005	3302.7	1826.1	8473.2	2999.4	1289.2	2025.8
AB235234.1	141016	44.8	44.3	59.2	60.4	72.1	51.1
FJ437839.1	513719	7893.8	8250.7	16452.8	8089.8	10457.6	9317.5
AB176111.1	175999	22.6	30.7	1076.3	159.5	52.3	15.1
FM203379.1	370488	5422.1	4891.8	6639.6	2758.8	2980.1	2596.8
AJ515714.1	94683	666.2	1485.1	2968.5	489.4	250.9	469.0
FM203398.1	371282	2591.9	2736.0	966.9	701.6	928.2	667.2
AP009179.1	249880	365.2	948.8	1852.8	361.3	988.3	517.7
EF462799.1	293907	8459.5	11566.5	6570.3	5632.7	7031.4	12129.7
AJ515716.1	94327	416.2	50.8	1105.1	217.1	53.0	20.6
EU555122.1	259007	14487.3	12289.7	6587.7	12770.4	16563.8	13724.8
AY672497.1	102782	33.6	39.6	59.2	63.6	99.2	20.5
FJ792125.1	510296	1341.1	3079.9	7020.2	1948.1	646.4	1117.1
FJ535278.1	554288	1030.1	990.3	3387.4	423.0	165.3	151.5
AY531596.1	100070	6108.0	4684.0	7663.4	8929.7	5341.7	4407.3
DQ228647.1	144474	378.4	613.1	686.9	153.4	429.0	245.8
AY542560.1	113844	141.3	88.3	381.4	117.3	247.8	75.2
GQ249521.1	580475	4433.9	4581.9	1163.1	6068.2	6357.6	5572.0
GQ357025.1	533206	35.8	36.2	87.1	64.0	189.0	41.7
AF449231.1	61878	120.6	235.8	1111.4	120.0	1379.3	536.6
AB476184.1	536849	1695.3	1896.0	924.6	1534.2	823.0	914.3
AY531576.1	107839	3050.8	2625.9	1234.2	2044.3	2726.2	2212.6
FJ535277.1	540587	10600.8	10636.6	6438.5	7936.9	11218.6	9239.6

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AY225616.1 gg_id:96100 organic-rich substrate exposed to Mid-Atlantic Ridge vent clone AT-co11
AB440165.1 gg_id:552622 Farming and harvesting filamentous vent- galatheid crab (Decapoda; Anomura) vent
EU487998.1 gg_id:570269 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and
FJ497296.1 gg_id:541606 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun
GU369887.1 gg_id:519900 and mats vents Arc white filamentous microbial mat photic shal hydrothermal vent
FJ535276.1 gg_id:511548 within iron-containing flocculent mats submarine volcanoes along Kermadec Arc iron
AY549001.2 gg_id:101316 marine bone clone sacC13A3
FJ535285.1 gg_id:554836 within iron-containing flocculent mats submarine volcanoes along Kermadec Arc iron
AY225623.1 gg_id:98432 iron-rich substrate exposed to Mid-Atlantic Ridge vent clone AT-cs15
AY531587.1 gg_id:104132 Indian Ocean hydrothermal vent clone SF_C23-D11_shell
AY672538.1 gg_id:105257 hydrothermal vent 9 degrees North East Rise Pacific Ocean clone CH9_1_BAC_16SrR
AB440171.1 gg_id:569838 Farming and harvesting filamentous vent- galatheid crab (Decapoda; Anomura) vent
AY531601.1 gg_id:104446 Indian Ocean hydrothermal vent clone SF_C23-C7_shell
FJ535304.1 gg_id:554479 within iron-containing flocculent mats submarine volcanoes along Kermadec Arc iron
EU652643.1 gg_id:278085 Seasonal variation microbial Yel Sea sediment clone B8S-12
EU555129.1 gg_id:268986 Microbial Sulfide Hydrothermal Vent Field Juan de Fuca Ridge Dudley hydrothermal
DQ071277.1 gg_id:139667 dominate filamentous sulfur mat 13 degree north field East Pacific Rise deep-sea hy
EF462802.1 gg_id:289264 meta-genome level extreme microbial symbiosis dorsal surface deep sea hydrotherm
AJ441206.1 gg_id:57471 hydrothermal vent polychaete mucous clone P. palm C/A 113
EF462624.1 gg_id:296130 meta-genome level extreme microbial symbiosis dorsal surface deep sea hydrotherm
AB530172.1 gg_id:559058 Monitoring Suez and Tokyo bays based on analyses marine sediment clone Suez..Ba
FM165251.1 gg_id:558481 seep chitineous tube vestimentiferan tubeworm Lamellibrachia sp. cold seeps clone
AF420359.1 gg_id:67782 hydrothermal sediment clone AF420359
AB205405.1 gg_id:115002 Alviniconcha aff. hessleri gill endosymbiont
EF462766.1 gg_id:300444 meta-genome level extreme microbial symbiosis dorsal surface deep sea hydrotherm
AY531572.1 gg_id:107247 Indian Ocean hydrothermal vent clone SF_C23-G9
FJ712419.1 gg_id:526671 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) K
AF029044.1 gg_id:11139 Benzene mineralizing consortium complete clone SB-17
EF462668.1 gg_id:299697 meta-genome level extreme microbial symbiosis dorsal surface deep sea hydrotherm
AY531593.1 gg_id:99597 Indian Ocean hydrothermal vent clone SF_C23-E5_shell
AY225618.1 gg_id:98223 organic-rich substrate exposed to Mid-Atlantic Ridge vent clone AT-co12
AY672511.1 gg_id:103076 hydrothermal vent 9 degrees North East Rise Pacific Ocean clone CH1_3f_BAC_16SrF
DQ270643.1 gg_id:142040 hydrothermal carbonate chimney clone LC1133B-58
EU107475.1 gg_id:349595 Identification Ectosymbiont on Hair Inhabiting Hydrothermal Vents hair Shinkaia cro
AY225625.1 gg_id:98807 iron-rich substrate exposed to Mid-Atlantic Ridge vent clone AT-cs7
FM165253.1 gg_id:558667 seep chitineous tube vestimentiferan tubeworm Lamellibrachia sp. cold seeps clone
AB099998.1 gg_id:79591 inactive deep-sea hydrothermal vent chimneys clone IndB1-30
DQ394973.1 gg_id:153118 harbor sediment clone VHS-B3-94
EF462777.1 gg_id:288783 meta-genome level extreme microbial symbiosis dorsal surface deep sea hydrotherm
AY531595.1 gg_id:99906 Indian Ocean hydrothermal vent clone SF_C23-E10_shell
EU265786.1 gg_id:258528 epibiotic assemblage recently described Yeti Kiwa hirsuta (Kiwidae) surface crab hyc

AY225616.1	96100	1891.8	1983.6	1110.6	1811.4	2308.6	1657.5
AB440165.1	552622	3159.1	2472.9	4704.3	3959.5	4472.4	3275.7
EU487998.1	570269	10102.7	10790.2	12878.4	7660.0	9870.4	7612.1
FJ497296.1	541606	1158.9	1324.3	570.6	698.8	729.2	376.6
GU369887.1	519900	996.3	1059.7	4990.2	917.1	2552.2	1315.4
FJ535276.1	511548	205.1	64.5	918.7	201.1	1389.9	226.1
AY549001.2	101316	1049.2	89.1	1095.1	234.5	72.6	61.1
FJ535285.1	554836	2089.2	2005.6	7990.2	2148.7	4466.4	2350.8
AY225623.1	98432	143.7	239.4	209.2	128.7	504.3	213.6
AY531587.1	104132	3269.8	4206.2	2964.4	3102.8	3722.8	2951.2
AY672538.1	105257	121.8	185.6	134.5	625.9	461.6	254.7
AB440171.1	569838	152.2	367.9	404.3	182.7	94.8	121.5
AY531601.1	104446	1827.3	2486.9	1388.3	1370.4	2848.0	1985.7
FJ535304.1	554479	4956.8	4563.3	1942.2	3625.0	5058.9	4754.4
EU652643.1	278085	10116.1	10061.5	7385.8	8032.3	10193.0	10564.5
EU555129.1	268986	146.5	340.5	896.5	116.0	113.2	90.4
DQ071277.1	139667	3058.6	1914.3	2323.2	3217.4	2694.2	2578.7
EF462802.1	289264	13294.3	13208.4	10465.2	12016.3	17840.7	13195.0
AJ441206.1	57471	4999.2	4752.9	4178.4	5076.1	5773.2	4662.7
EF462624.1	296130	3495.2	3797.5	2977.7	3023.1	5227.3	5978.6
AB530172.1	559058	4108.2	4491.0	6371.1	4794.8	8603.9	5473.6
FM165251.1	558481	8001.4	7821.7	3606.7	5265.8	8811.8	6319.3
AF420359.1	67782	2333.6	3240.5	2268.6	1387.4	4147.2	3106.8
AB205405.1	115002	6095.4	5828.2	3995.8	4161.3	6914.9	6291.4
EF462766.1	300444	330.9	640.1	413.4	721.8	998.1	965.1
AY531572.1	107247	124.7	108.2	530.9	130.0	101.7	64.5
FJ712419.1	526671	1523.0	1536.0	3281.9	2326.8	3764.9	2510.7
AF029044.1	11139	134.4	135.6	282.0	89.4	65.6	50.4
EF462668.1	299697	8893.3	10095.7	7303.6	11057.2	11282.9	12307.5
AY531593.1	99597	40.0	47.5	60.3	55.8	87.4	27.1
AY225618.1	98223	753.5	1137.9	1613.6	1512.5	386.1	1080.6
AY672511.1	103076	6357.4	6328.1	5384.0	5646.9	4687.3	4143.6
DQ270643.1	142040	973.4	1336.4	1381.8	284.5	1133.9	601.7
EU107475.1	349595	1215.3	919.7	2374.7	309.9	303.5	386.8
AY225625.1	98807	101.3	98.8	2538.9	224.2	89.6	167.0
FM165253.1	558667	50.5	153.6	418.4	88.2	237.5	80.0
AB099998.1	79591	1498.0	1401.9	1337.6	555.9	1260.2	817.1
DQ394973.1	153118	7900.3	7167.7	7903.7	6008.2	5617.3	5311.2
EF462777.1	288783	8645.7	7797.6	3579.6	8411.5	7600.3	10131.3
AY531595.1	99906	217.9	1105.8	2521.4	632.6	782.4	1643.1
EU265786.1	258528	1007.4	2654.6	3520.1	709.3	236.7	1133.6

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FM179904.1 gg_id:317544 Biogeochemical processes microbial Gullfaks and Tommeliten methane seeps (Nortl
AY280405.1 gg_id:100364 exterior deep-sea hydrothermal vent sulfide chimney Juan de Fuca Ridge Pacific Oce
AJ575963.1 gg_id:95437 deep sea hydrothermal vent clone T3-Hot3-706
AY531597.1 gg_id:100222 Indian Ocean hydrothermal vent clone SF_C23-B7_shell
AM176867.1 gg_id:161081 Recovery mangrove sediment clone SZB13
EU265795.1 gg_id:262084 epibiotic assemblage recently described Yeti Kiwa hirsuta (Kiwidae) surface crab hyc
EU662602.1 gg_id:577333 Productivity- Chemolithoautotrophically Based Sulfidic Karst Systems floating microb
AB476188.1 gg_id:536599 Compositional and functional transition epibiotic microbial hydrothermal vent galath
AY197378.1 gg_id:83351 Guaymas Basin hydrothermal vent sediments clone B01R006
FJ535271.1 gg_id:544300 within iron-containing flocculent mats submarine volcanoes along Kermadec Arc iron
EF462600.1 gg_id:303123 meta-genome level extreme microbial symbiosis dorsal surface deep sea hydrotherm
EU265785.1 gg_id:277410 epibiotic assemblage recently described Yeti Kiwa hirsuta (Kiwidae) surface crab hyc
DQ394894.1 gg_id:151332 harbor sediment clone VHS-B1-11
AY531575.1 gg_id:107689 Indian Ocean hydrothermal vent clone SF_C23-G4
AY531585.1 gg_id:103824 Indian Ocean hydrothermal vent clone SF_C23-C11_shell
AY225614.1 gg_id:96015 iron-rich substrate exposed to Mid-Atlantic Ridge vent clone AT-cs3
AB232530.1 gg_id:151369 Prokaryotic gills deep-sea hydrothermal vent shrimp gill Alvinocaris longirostris clone
DQ270645.1 gg_id:143843 hydrothermal carbonate chimney clone LC1133B-68
AY531600.1 gg_id:104287 Indian Ocean hydrothermal vent clone SF_C23-C8_shell
AY531591.1 gg_id:99285 Indian Ocean hydrothermal vent clone SF_C23-B1_shell
AY327882.1 gg_id:90455 surface vent snail foot clone SF_C4-D5
AY225624.1 gg_id:97289 pumice fragments exposed to Mid-Atlantic Ridge vent clone AT-pp27
AF420351.1 gg_id:67787 hydrothermal sediment clone AF420351
EU617859.1 gg_id:345356 Seasonal variation microbial Yel Sea sediment clone D13S-42
FJ799124.1 gg_id:510696 Microbial Responsible Intermediates Degradation Anaerobic Digestion System Deterr
AY225622.1 gg_id:97434 iron-rich substrate exposed to Mid-Atlantic Ridge vent clone AT-cs8
EF462801.1 gg_id:299935 meta-genome level extreme microbial symbiosis dorsal surface deep sea hydrotherm
DQ270655.1 gg_id:141448 hydrothermal carbonate chimney clone LC1404B-6
FJ535259.1 gg_id:542712 within iron-containing flocculent mats submarine volcanoes along Kermadec Arc iron
GQ167319.1 gg_id:562624 Microbial Life -13C Brine Ice-Sealed Antarctic ice-entrained brine 16.5 m Lake Vida c
FJ535292.1 gg_id:551198 within iron-containing flocculent mats submarine volcanoes along Kermadec Arc iron
AF449253.1 gg_id:61855 Riftia pachyptila's tube clone R76-B151
AY672522.1 gg_id:99252 hydrothermal vent 9 degrees North East Rise Pacific Ocean clone CH3_9_BAC_16SrRN
DQ071276.1 gg_id:140018 dominate filamentous sulfur mat 13 degree north field East Pacific Rise deep-sea hy
EF462733.1 gg_id:291526 meta-genome level extreme microbial symbiosis dorsal surface deep sea hydrotherm
AY704398.1 gg_id:112176 oceanic crust clone FS275-77B-03
AB440161.1 gg_id:549495 Farming and harvesting filamentous vent- galatheid crab (Decapoda; Anomura) vent
EF462696.1 gg_id:289073 meta-genome level extreme microbial symbiosis dorsal surface deep sea hydrotherm
AY531570.1 gg_id:106942 Indian Ocean hydrothermal vent clone SF_C23-H11
AB239758.1 gg_id:149235 filamentous epibiont Vulcanolepas osheai
FJ535270.1 gg_id:533833 within iron-containing flocculent mats submarine volcanoes along Kermadec Arc iron

FM179904.1	317544	2963.6	2388.5	3989.2	3639.0	3279.0	3187.3
AY280405.1	100364	297.8	672.3	1705.1	480.3	157.9	201.6
AJ575963.1	95437	3373.8	5474.5	9963.0	1918.6	829.6	2595.7
AY531597.1	100222	75.6	134.8	131.6	129.5	134.8	96.4
AM176867.1	161081	4295.0	4045.4	12669.9	6003.0	5366.5	6090.1
EU265795.1	262084	2047.0	3255.9	290.0	1022.3	1545.7	1063.9
EU662602.1	577333	3485.3	4356.5	4493.2	2975.6	5651.4	2960.7
AB476188.1	536599	61.8	167.2	494.7	139.7	149.9	190.3
AY197378.1	83351	406.5	75.0	1072.6	255.5	75.4	42.5
FJ535271.1	544300	29.8	59.0	954.3	54.0	59.0	18.2
EF462600.1	303123	5034.8	6065.6	3364.6	3145.4	6250.1	6347.0
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DQ394894.1	151332	284.0	350.8	799.7	350.1	247.8	199.1
AY531575.1	107689	2098.5	2011.9	5834.9	3967.7	3535.7	4691.0
AY531585.1	103824	2774.3	3027.4	1514.3	5926.1	5048.3	3017.6
AY225614.1	96015	212.2	204.8	763.9	336.1	1048.9	256.5
AB232530.1	151369	146.4	62.3	298.0	264.6	87.3	51.3
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AY531600.1	104287	45.5	46.2	33.3	51.8	63.2	30.6
AY531591.1	99285	56.6	145.6	2410.5	310.7	62.2	66.9
AY327882.1	90455	135.3	212.4	2037.1	358.2	147.7	268.0
AY225624.1	97289	825.5	1193.6	1900.9	656.7	2080.0	1313.6
AF420351.1	67787	673.7	640.4	1176.2	727.6	205.4	211.2
EU617859.1	345356	9790.2	9788.2	4819.5	7337.0	10367.7	11685.1
FJ799124.1	510696	1186.1	1425.5	2502.2	888.8	841.1	1873.3
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EF462801.1	299935	8239.6	8713.7	6653.8	9542.1	6664.7	6469.7
DQ270655.1	141448	1587.7	1395.3	389.6	351.1	497.6	316.0
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GQ167319.1	562624	1034.4	1387.0	8926.8	4486.1	441.3	1592.6
FJ535292.1	551198	385.9	376.9	770.0	701.8	350.0	420.3
AF449253.1	61855	2670.2	2643.7	2792.1	1725.8	2225.5	2442.1
AY672522.1	99252	1836.5	1594.0	2648.7	1685.3	3159.4	2170.6
DQ071276.1	140018	1180.2	385.9	3684.3	1442.2	1489.3	724.6
EF462733.1	291526	16583.2	16514.0	10017.4	14706.7	18005.8	15659.9
AY704398.1	112176	9847.6	9897.3	5857.0	8555.0	8188.1	7556.5
AB440161.1	549495	115.7	69.8	2280.4	332.5	75.9	59.2
EF462696.1	289073	7501.4	8059.9	4738.0	7631.4	7663.8	7063.3
AY531570.1	106942	1552.6	2140.5	528.5	1047.0	2479.5	1607.1
AB239758.1	149235	3520.3	4372.8	1671.0	6297.8	6147.1	5508.3
FJ535270.1	533833	241.4	483.6	2374.4	239.6	1789.5	888.7

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FJ535266.1 gg_id:569006 within iron-containing flocculent mats submarine volcanoes along Kermadec Arc iron
EU265789.1 gg_id:258893 epibiotic assemblage recently described Yeti Kiwa hirsuta (Kiwidae) surface crab hyc
AM268719.1 gg_id:232342 Fluid chemistry and microbial southern hydrothermal field (Lilliput) on Mid-Atlantic
AF154091.1 gg_id:11137 hydrocarbon seep clone BPC056
DQ071288.1 gg_id:139782 dominate filamentous sulfur mat 13 degree north field East Pacific Rise deep-sea hy
AB440162.1 gg_id:557961 Farming and harvesting filamentous vent- galatheid crab (Decapoda; Anomura) vent
GQ261779.1 gg_id:573816 shifts taxa and response localized organic loading deep sea sediment whale falls clo
EF462627.1 gg_id:297366 meta-genome level extreme microbial symbiosis dorsal surface deep sea hydrotherm
EU487914.1 gg_id:538726 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and
EF462714.1 gg_id:293356 meta-genome level extreme microbial symbiosis dorsal surface deep sea hydrotherm
AB193955.1 gg_id:108919 deep-sea vent clone Sd-EB04
EF462827.1 gg_id:292616 meta-genome level extreme microbial symbiosis dorsal surface deep sea hydrotherm
AY531571.1 gg_id:107097 Indian Ocean hydrothermal vent clone SF_C23-H10
FJ535282.1 gg_id:538493 within iron-containing flocculent mats submarine volcanoes along Kermadec Arc iron
DQ394936.1 gg_id:153573 harbor sediment clone VHS-B3-29
AB188786.1 gg_id:113953 cold seep sediment clone SB5-11
FJ497361.1 gg_id:542661 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun
AB278150.1 gg_id:177809 hydrothermal vent prokaryotes trapped 0.2- and 0.1-micro-m-filtrates obtained Mar
AF121887.1 gg_id:11128 2-bromophenol-dehalogenating consortium clone 2BP-7
FM203396.1 gg_id:423805 Biogeography filamentous and epsilonproteobacterial ectosymbionts vent shrimp e
EF061978.1 gg_id:190937 Xiamen China mangrove sediment clone XME34
AY327881.1 gg_id:88572 surface vent snail foot clone SF_C4-C4
FJ497343.1 gg_id:549911 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun
FJ497347.1 gg_id:582544 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun
GU180158.1 gg_id:537179 Impact coplanar PCBs on microbial activity anaerobic estuarine sediments sediment
EU107476.1 gg_id:343167 Identification Ectosymbiont on Hair Inhabiting Hydrothermal Vents hair Shinkaia cro
EU662505.1 gg_id:571991 Productivity- Chemolithoautotrophically Based Sulfidic Karst Systems microbial mat
EF462800.1 gg_id:293062 meta-genome level extreme microbial symbiosis dorsal surface deep sea hydrotherm
FJ497375.1 gg_id:581955 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun
GQ249549.1 gg_id:575344 Microbial anaerobic sediments Bay Cadiz (Spain) marine sediment: 12-14 cm layer c
FJ264679.1 gg_id:328542 Manganese and Iron Dependent Anaerobic Oxidation Methane methane seep sedim
EF687491.1 gg_id:284524 Biogeochemistry iron- and sulfur-precipitating microbial mats (Nile Mediterranean) s
FJ905647.1 gg_id:545620 s Tonga-Kermadec iron oxide chimney-like structure on Volcano 19 Tonga Arc clone V
AY531592.1 gg_id:99437 Indian Ocean hydrothermal vent clone SF_C23-B12_shell
FJ497326.1 gg_id:571424 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun
FJ717162.1 gg_id:554142 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United King
FJ497317.1 gg_id:574124 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun
FJ535287.1 gg_id:544443 within iron-containing flocculent mats submarine volcanoes along Kermadec Arc iron
FJ497276.1 gg_id:586842 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun
EF061975.1 gg_id:175519 Xiamen China mangrove sediment clone XME6
AY672498.1 gg_id:102927 hydrothermal vent 9 degrees North East Rise Pacific Ocean clone CH1_10_BAC_16Sr

FJ535266.1	569006	1874.1	1183.5	165.1	1017.0	1906.4	1187.5
EU265789.1	258893	47.1	72.9	637.3	123.9	112.8	50.1
AM268719.1	232342	7912.4	9365.8	7352.6	7438.1	9545.0	8464.7
AF154091.1	11137	857.9	985.4	1303.0	565.4	878.6	881.4
DQ071288.1	139782	64.2	50.9	126.6	145.5	103.9	67.0
AB440162.1	557961	39.1	67.6	99.3	70.5	95.5	36.8
GQ261779.1	573816	27.2	55.3	136.7	71.0	235.7	65.1
EF462627.1	297366	956.8	1688.4	1777.4	553.1	1134.1	1243.7
EU487914.1	538726	3189.8	1981.5	5843.5	4507.2	3528.6	3541.6
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EF462827.1	292616	4357.5	4232.7	6183.7	6517.6	4256.7	3705.0
AY531571.1	107097	3002.1	3386.7	3681.8	2666.0	2805.1	2329.7
FJ535282.1	538493	5901.5	5435.8	4041.2	6280.7	10815.8	6299.4
DQ394936.1	153573	25.2	21.1	29.4	61.1	73.2	23.1
AB188786.1	113953	4375.7	4452.6	4049.6	4723.5	10511.4	9742.9
FJ497361.1	542661	635.3	548.3	651.3	176.6	1691.5	38.2
AB278150.1	177809	163.0	167.1	207.0	201.0	110.1	120.1
AF121887.1	11128	36.7	121.7	80.6	60.1	64.9	84.2
FM203396.1	423805	84.8	115.2	122.0	102.0	90.6	66.0
EF061978.1	190937	871.0	407.4	3414.0	947.4	467.2	1063.3
AY327881.1	88572	4928.9	4863.2	2391.8	5846.8	7699.2	5639.8
FJ497343.1	549911	796.1	426.0	850.2	367.0	677.6	192.9
FJ497347.1	582544	6428.5	4763.4	4766.0	6215.1	6957.2	4078.8
GU180158.1	537179	4845.9	4241.1	7568.6	4925.7	4649.4	6206.8
EU107476.1	343167	45.0	94.2	74.0	44.1	58.6	55.4
EU662505.1	571991	69.2	169.6	1684.3	122.8	84.9	98.9
EF462800.1	293062	6165.9	7045.3	4329.2	8229.3	8036.6	6229.8
FJ497375.1	581955	5031.7	8064.7	5698.7	2124.9	1732.4	4011.2
GQ249549.1	575344	8675.1	6786.7	7737.7	8418.5	7365.8	6852.9
FJ264679.1	328542	10498.9	11088.4	9863.8	8732.0	11715.8	9987.1
EF687491.1	284524	155.1	94.9	1379.5	177.7	188.3	153.6
FJ905647.1	545620	49.0	86.4	593.8	110.9	63.7	47.4
AY531592.1	99437	3678.3	3465.1	2277.3	3128.3	4105.9	3227.8
FJ497326.1	571424	228.0	333.7	826.2	313.4	641.0	423.6
FJ717162.1	554142	520.7	177.3	4166.8	1044.3	1466.9	758.8
FJ497317.1	574124	2835.1	2576.6	4164.5	3857.4	3525.8	3599.1
FJ535287.1	544443	231.9	213.3	413.6	123.2	109.0	128.0
FJ497276.1	586842	5239.0	4632.9	3516.7	4771.3	5286.6	3548.0
EF061975.1	175519	1880.7	1433.3	3322.0	1779.5	1283.7	2148.7
AY672498.1	102927	96.6	159.4	183.1	107.4	147.9	149.0

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AF449251.1 gg_id:61858 Riftia pachyptila's tube clone R76-B78
L35520.1 gg_id:11121 Alvinella pompejana
GU369898.1 gg_id:520798 and mats vents Arc white filamentous microbial mat photic shal hydrothermal vent
AY327880.1 gg_id:88951 surface vent snail foot clone SF_C5-F8
FJ712566.1 gg_id:508922 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) K
DQ925872.1 gg_id:241522 Microbes and Thermal Gradients Temperature Hydrothermal Chimneys hydrotherm
EF462629.1 gg_id:295292 meta-genome level extreme microbial symbiosis dorsal surface deep sea hydrotherm
GQ261802.1 gg_id:543184 shifts taxa and response localized organic loading deep sea sediment whale falls clo
AF420344.1 gg_id:67793 hydrothermal sediment clone AF420344
DQ295602.2 gg_id:159750 Epsilonproteobacteria terrestrial caves and springs microbial mat sulfidic spring Drin
FJ497396.1 gg_id:542332 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun
EF462824.1 gg_id:302928 meta-genome level extreme microbial symbiosis dorsal surface deep sea hydrotherm
AB187014.1 gg_id:101863 Suiyo seamount hydrothermal vent water 0.2micro-m filterable fraction clone SSM-E
AY542550.1 gg_id:114277 Gulf Mexico seafloor sediment clone GoM GB425 02B-9
FJ902253.1 gg_id:571547 phreatic limestone sinkholes northeastern Mexico water column 32m deep cenote Ca
FJ264760.1 gg_id:339147 Manganese and Iron Dependent Anaerobic Oxidation Methane methane seep sedime
AY355304.2 gg_id:101665 epibiontic clone C11-C9
AB091292.1 gg_id:84230 Sulfurovum lithotrophicum str. 42BKT
AY672512.1 gg_id:103225 hydrothermal vent 9 degrees North East Rise Pacific Ocean clone CH3_1_BAC_16SrR
AY531604.1 gg_id:104899 Indian Ocean hydrothermal vent clone SF_C23-F6
AJ132737.1 gg_id:20059 hydrothermal vent clone Top-147
AY672506.1 gg_id:107659 hydrothermal vent 9 degrees North East Rise Pacific Ocean clone CH1_23_BAC_16Sr
EU245507.1 gg_id:252330 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M2-D1
FJ165504.1 gg_id:539775 Microbially-enhanced Dissolution Karst Carbonates microbial biofilm Sonterra #8 well
DQ295697.1 gg_id:160880 Epsilonproteobacteria terrestrial caves and springs floating microbial mat sulfidic gr
AF449236.1 gg_id:61874 Riftia pachyptila's tube clone R103-B37
AY672537.1 gg_id:105096 hydrothermal vent 9 degrees North East Rise Pacific Ocean clone CH9_6_BAC_16SrR
AJ969446.1 gg_id:158924 Microbial black smoker s Mid Atlantic Ridge ecological implications rock fragments ch
GU390848.1 gg_id:530358 Dark hot springs: structure biofilms caves Acquasanta Terme (Italy) sulfidic cave stre
AM745162.1 gg_id:292405 Impact oil er hydrocarbons on microbial and activity Gulf Mexico cold seep marine s
AF420360.1 gg_id:67780 hydrothermal sediment clone AF420360.1
AF420342.1 gg_id:67795 hydrothermal sediment clone AF420342
AB105048.1 gg_id:93761 Hydrogenimonas thermophila str. EP1-55-1%
AY261811.1 gg_id:83596 UASB reactor granular sludge clone PD-UASB-2 proteobacterium
DQ295692.1 gg_id:161262 Epsilonproteobacteria terrestrial caves and springs floating microbial mat sulfidic gr
AY531574.1 gg_id:107543 Indian Ocean hydrothermal vent clone SF_C23-G7
AB278149.1 gg_id:184732 hydrothermal vent prokaryotes trapped 0.2- and 0.1-micro-m-filtrates obtained Mar
AB175498.1 gg_id:106632 Thioreductor micantisoli str. BKB25Ts-Y
EF467531.1 gg_id:213162 situ microelectrode voltammetry sulfur-oxidizing biofilms Frasassi sulfidic cave strear
FJ497432.1 gg_id:556468 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun
EF467559.1 gg_id:211322 situ microelectrode voltammetry sulfur-oxidizing biofilms Frasassi sulfidic cave strear

AF449251.1	61858	55.2	61.3	1103.4	135.9	75.7	40.1
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GU369898.1	520798	106.4	152.6	781.1	132.3	53.8	55.6
AY327880.1	88951	4834.8	5975.9	3604.4	7777.2	8384.3	6803.6
FJ712566.1	508922	82.0	135.5	1742.2	153.4	196.0	86.4
DQ925872.1	241522	2541.1	3357.2	2740.4	2401.8	4037.1	1857.2
EF462629.1	295292	8564.5	10727.6	4100.5	9252.7	9641.6	9115.4
GQ261802.1	543184	1275.6	1368.0	3144.6	2505.6	3378.1	2301.2
AF420344.1	67793	5568.5	7477.1	2921.6	4853.9	11191.1	8052.1
DQ295602.2	159750	2840.5	2995.9	3177.8	2250.9	3554.6	2869.5
FJ497396.1	542332	532.6	507.2	2115.7	245.7	1275.6	462.1
EF462824.1	302928	8340.4	10425.7	9964.9	8737.4	6375.2	5101.5
AB187014.1	101863	64.9	45.6	252.9	88.1	91.6	87.7
AY542550.1	114277	2735.7	828.3	6520.2	2300.7	1318.7	730.4
FJ902253.1	571547	1028.5	78.2	2000.9	1553.8	79.6	62.0
FJ264760.1	339147	755.5	1376.9	2322.3	631.8	1518.6	672.1
AY355304.2	101665	274.2	270.4	1012.3	410.6	109.8	108.5
AB091292.1	84230	957.6	1944.0	1448.9	807.4	1244.4	453.8
AY672512.1	103225	13.7	14.5	16.0	39.5	42.9	14.1
AY531604.1	104899	71.7	183.2	441.1	98.0	133.7	194.4
AJ132737.1	20059	48.1	55.4	193.9	112.4	84.4	48.4
AY672506.1	107659	2137.0	2061.6	2527.7	1524.2	1972.4	1887.6
EU245507.1	252330	53.1	83.2	154.1	91.2	111.9	297.2
FJ165504.1	539775	11107.1	12405.9	7404.7	10666.8	14219.0	10734.1
DQ295697.1	160880	6216.7	6043.2	4088.5	6708.4	7646.1	7608.9
AF449236.1	61874	14.0	13.9	13.6	39.5	52.1	18.8
AY672537.1	105096	9372.1	10073.6	5479.7	6987.0	7176.2	6446.1
AJ969446.1	158924	989.5	1141.1	2704.2	1751.1	752.7	721.0
GU390848.1	530358	894.8	1323.5	2752.4	592.6	6799.0	3797.2
AM745162.1	292405	598.8	911.8	1150.8	716.1	526.2	1794.0
AF420360.1	67780	223.7	133.1	478.8	173.5	122.9	137.4
AF420342.1	67795	61.2	132.8	327.9	153.1	222.3	74.8
AB105048.1	93761	1224.4	1314.1	4712.7	2038.2	3957.7	4119.5
AY261811.1	83596	8447.5	9762.1	8001.4	8478.5	12583.6	11648.6
DQ295692.1	161262	1753.1	1713.6	2590.3	990.9	2985.5	2466.9
AY531574.1	107543	64.2	237.9	316.2	312.9	318.4	331.0
AB278149.1	184732	162.3	272.2	403.9	429.6	353.8	391.8
AB175498.1	106632	34.6	49.2	153.8	86.4	51.9	23.8
EF467531.1	213162	8921.4	8436.2	7206.2	5820.1	7052.1	7001.9
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EF467559.1	211322	1119.3	1086.4	4284.5	918.5	1344.5	774.4

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EF467581.1 gg_id:216198 situ microelectrode voltammetry sulfur-oxidizing biofilms Frasassi sulfidic cave strear
AM268717.1 gg_id:233206 Fluid chemistry and microbial southern hydrothermal field (Lilliput) on Mid-Atlantic
AY280433.1 gg_id:106294 exterior deep-sea hydrothermal vent sulfide chimney Juan de Fuca Ridge Pacific Oce
DQ295651.1 gg_id:161606 Epsilonproteobacteria terrestrial caves and springs microbial mat sulfidic cave strea
EF462765.1 gg_id:299712 meta-genome level extreme microbial symbiosis dorsal surface deep sea hydrotherm
GU196200.1 gg_id:579980 Bioaugmentation improved recovery digesters after toxicant exposure lab-scale ana
AB278151.1 gg_id:180340 hydrothermal vent prokaryotes trapped 0.2- and 0.1-micro-m-filtrates obtained Mar
AY531573.1 gg_id:107393 Indian Ocean hydrothermal vent clone SF_C23-G8
FJ799123.1 gg_id:584284 Microbial Responsible Intermediates Degradation Anaerobic Digestion System Deterr
AJ441202.1 gg_id:57475 hydrothermal vent polychaete mucous clone P. palm C 140
DQ295708.1 gg_id:160328 Epsilonproteobacteria terrestrial caves and springs microbial mat sulfidic stream Mil
EF467511.1 gg_id:215667 situ microelectrode voltammetry sulfur-oxidizing biofilms Frasassi sulfidic cave strear
FJ485355.1 gg_id:545841 microbial autonomous rover world's deepest phreatic sinkhole wall biomat El Zacator
DQ228655.1 gg_id:141137 Microbial colonizing mineral surfaces within sulfide-microbial incubator clone CH2b1
EF462722.1 gg_id:296261 meta-genome level extreme microbial symbiosis dorsal surface deep sea hydrotherm
EU234099.1 gg_id:246280 receiving river and un techniques anaerobic process WWTP treating penicillin G prod
AJ576002.1 gg_id:98839 deep sea hydrothermal vent clone T6-Ph07-983
GU390742.1 gg_id:517462 Dark hot springs: structure biofilms caves Acquasanta Terme (Italy) sulfidic cave stre
AY082468.1 gg_id:67838 neutral pH mine biofilm clone 44a-B1-40
AY280427.1 gg_id:101920 exterior deep-sea hydrothermal vent sulfide chimney Juan de Fuca Ridge Pacific Oce
EF467460.1 gg_id:205100 situ microelectrode voltammetry sulfur-oxidizing biofilms Frasassi sulfidic cave strear
AB198587.1 gg_id:135519 termite gut fluid and protists fraction clone RsC01-014
DQ295656.1 gg_id:160561 Epsilonproteobacteria terrestrial caves and springs microbial mat sulfidic cave strea
AF286053.1 gg_id:29701 Helicobacter rappini W.Tee-Yu
AY571498.1 gg_id:114816 termite gut clone RsaHf427
GU369897.1 gg_id:528299 and mats vents Arc white filamentous microbial mat photic shal hydrothermal vent
AY355299.2 gg_id:106198 epibiontic clone C11-E8
EU662478.1 gg_id:557968 Productivity- Chemolithoautotrophically Based Sulfidic Karst Systems microbial mat
AY578096.1 gg_id:105995 Helicobacter bilis str. KI900
AY251062.1 gg_id:103492 deep-sea hydrothermal biofilm Edmond vent field on Central Indian Ridge clone FT17
EF462645.1 gg_id:297781 meta-genome level extreme microbial symbiosis dorsal surface deep sea hydrotherm
AF449237.1 gg_id:61872 Riftia pachyptila's tube clone R103-B43
EF467591.1 gg_id:214381 situ microelectrode voltammetry sulfur-oxidizing biofilms Frasassi sulfidic cave strear
AY672507.1 gg_id:107804 hydrothermal vent 9 degrees North East Rise Pacific Ocean clone CH1_25_BAC_16Sr
EF462782.1 gg_id:290493 meta-genome level extreme microbial symbiosis dorsal surface deep sea hydrotherm
EU662427.1 gg_id:579840 Productivity- Chemolithoautotrophically Based Sulfidic Karst Systems microbial mat
U51874.2 gg_id:10979 Helicobacter sp. Dog-4 str. Dog-4; Eaton 1302
DQ071280.1 gg_id:140620 dominate filamentous sulfur mat 13 degree north field East Pacific Rise deep-sea hy
AY531583.1 gg_id:103545 Indian Ocean hydrothermal vent clone SF_C23-F3
GU390798.1 gg_id:516081 Dark hot springs: structure biofilms caves Acquasanta Terme (Italy) sulfidic cave stre

AY672540.1	100136	27.5	79.4	93.9	82.1	77.8	43.1
EF467581.1	216198	5547.7	5251.7	4747.3	5565.9	4744.0	3935.4
AM268717.1	233206	3894.6	3745.5	1421.2	2599.1	3554.5	3480.4
AY280433.1	106294	104.7	103.4	473.6	93.5	87.2	250.9
DQ295651.1	161606	5007.7	4182.1	4758.9	6379.3	6355.1	5602.2
EF462765.1	299712	8250.2	7514.6	2677.5	9559.1	9144.5	11296.7
GU196200.1	579980	3755.7	5285.6	2742.1	3832.6	5577.7	5815.7
AB278151.1	180340	34.5	48.5	159.5	80.1	80.4	30.5
AY531573.1	107393	77.1	89.7	279.0	119.9	75.7	105.1
FJ799123.1	584284	2650.3	2328.4	2207.3	3087.3	2819.9	2080.2
AJ441202.1	57475	14.0	19.4	20.5	31.2	36.7	8.7
DQ295708.1	160328	35.6	36.0	96.0	67.5	51.7	23.6
EF467511.1	215667	1197.6	1868.9	1719.8	1352.8	1497.1	1062.2
FJ485355.1	545841	6197.9	10051.3	4626.4	4404.1	7416.2	7013.6
DQ228655.1	141137	2742.7	2832.9	2550.7	1811.3	3182.6	2530.6
EF462722.1	296261	828.2	1549.7	2592.0	1609.8	3794.2	3643.6
EU234099.1	246280	1891.7	1827.0	1689.6	2191.5	3447.5	2063.8
AJ576002.1	98839	233.6	213.5	2047.6	213.7	236.4	552.3
GU390742.1	517462	827.5	1344.1	2602.2	421.8	1935.1	2095.1
AY082468.1	67838	7661.3	9027.9	3341.1	6688.6	2719.0	2551.4
AY280427.1	101920	71.6	73.8	128.1	67.3	51.7	27.3
EF467460.1	205100	2369.7	2414.9	7175.2	3924.6	2184.2	2207.4
AB198587.1	135519	60.3	45.3	30.8	72.7	69.0	39.8
DQ295656.1	160561	21.0	21.3	72.9	56.3	51.9	29.2
AF286053.1	29701	3285.0	2100.6	4997.8	5322.6	4676.4	2986.9
AY571498.1	114816	23.5	26.1	33.7	68.3	59.7	22.1
GU369897.1	528299	1368.9	1079.1	6014.7	2110.1	158.6	501.7
AY355299.2	106198	38.8	84.8	281.8	98.1	471.3	313.3
EU662478.1	557968	5635.7	6536.0	6676.5	6278.7	4176.9	5676.8
AY578096.1	105995	13474.4	13154.8	8266.6	12872.4	14954.4	11817.5
AY251062.1	103492	78.6	105.8	904.1	161.9	98.6	72.7
EF462645.1	297781	7341.3	8341.5	3757.2	4601.8	5918.2	6652.7
AF449237.1	61872	396.6	1183.4	760.6	459.3	234.9	236.0
EF467591.1	214381	43.6	97.9	81.7	51.6	50.8	23.9
AY672507.1	107804	2899.7	2345.8	4008.7	3607.0	2150.5	2292.2
EF462782.1	290493	2270.1	2294.2	2074.9	2766.1	2194.3	2532.5
EU662427.1	579840	42.9	64.5	27.1	49.5	941.3	210.6
U51874.2	10979	1037.8	704.0	3340.4	894.5	1078.5	1515.2
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AY531583.1	103545	5933.2	5934.5	5442.4	8421.5	7686.2	6862.5
GU390798.1	516081	5362.6	6091.9	7190.3	3906.9	7544.1	5768.1

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AY510213.1 gg_id:110174 microbial mat cave sulfidic spring clone LKC3_159.12
AY578099.1 gg_id:106472 Helicobacter bilis str. KO214
AF420347.1 gg_id:67790 hydrothermal sediment clone AF420347.1
EF467570.1 gg_id:212152 situ microelectrode voltammetry sulfur-oxidizing biofilms Frasassi sulfidic cave strear
AF420343.1 gg_id:67794 hydrothermal sediment clone AF420343
AF449232.1 gg_id:61877 Riftia pachyptila's tube clone R103-B18
GQ355026.1 gg_id:565854 structure between two geochemically distinct springs Alum Rock Park spring clone M
L35522.1 gg_id:11150 Alvinella pompejana epibiont
AJ969465.1 gg_id:157898 Microbial black smoker s Mid Atlantic Ridge ecological implications rock fragments ch
EU864466.1 gg_id:334109 structures under selection pressure levels antibiotics Xiao River receiving treated oxy
EF644836.1 gg_id:300292 genes and citrate lyase deep-sea microbial MAR Rainbow hydrothermal vent system
EF467464.1 gg_id:213273 situ microelectrode voltammetry sulfur-oxidizing biofilms Frasassi sulfidic cave strear
EF467519.1 gg_id:205825 situ microelectrode voltammetry sulfur-oxidizing biofilms Frasassi sulfidic cave strear
GU390782.1 gg_id:516622 Dark hot springs: structure biofilms caves Acquasanta Terme (Italy) sulfidic cave stre
AY766315.1 gg_id:108123 VC2.2 hydrothermal chimney Snake Pit site on mid Atlantic ridge clone 3
GU390711.1 gg_id:515047 Dark hot springs: structure biofilms caves Acquasanta Terme (Italy) sulfidic cave stre
AY280435.1 gg_id:106612 exterior deep-sea hydrothermal vent sulfide chimney Juan de Fuca Ridge Pacific Oce
NC_005090.1 gg_id:93903 Wolinella succinogenes str. DSM 1740
AF273252.1 gg_id:29152 Wolinella succinogenes str. SeR-1
AF068812.2 gg_id:11156 hydrothermal vent clone VC2.1 Bac12
AY691429.1 gg_id:106012 Caminibacter sp. str. TB-1
NR_028943.1 gg_id:571654 Caminibacter hydrogeniphilus str. AM1116; DSM 14510
AF299128.1 gg_id:40818 S17sBac34 complete clone
AF068804.2 gg_id:11155 hydrothermal vent clone VC2.1 Bac30
ABCJ01000004.1 gg_id:243079 Caminibacter mediatlanticus str. TB-2
NR_028999.1 gg_id:579615 Caminibacter profundus str. CR; DSM 15016
CP001279.1 gg_id:528797 Nautilia profundicola str. AmH
NR_025497.1 gg_id:566284 Nautilia lithotrophica str. 525; DSM 13520
AM937002.1 gg_id:260087 Nautilia abyssi str. PH1209
AP009178.1 gg_id:247747 Nitratiruptor sp. str. SB155-2
AB175499.1 gg_id:106788 Nitratiruptor tergarcus str. MI55-1
AB167820.1 gg_id:136358 Lebetimonas acidiphila str. Pd55
EF462830.1 gg_id:302768 meta-genome level extreme microbial symbiosis dorsal surface deep sea hydrotherm
AY830901.1 gg_id:109592 Acidithiobacillus thiooxidans str. OYCS3
DQ431197.1 gg_id:156297 Acidithiobacillus caldus str. YN06
FJ154522.1 gg_id:556258 Acidithiobacillus caldus str. Da
AF329205.1 gg_id:33408 Acidithiobacillus ferrooxidans str. ATCC23270
DQ646482.1 gg_id:257953 Acidithiobacillus ferrooxidans str. DX-AF-1
DQ646485.1 gg_id:238863 Acidithiobacillus ferrooxidans str. DX-AF-4
EU079375.1 gg_id:243219 Acidithiobacillus ferrooxidans str. NF-01
AB039820.1 gg_id:19750 Acidithiobacillus ferrooxidans str. NASF-1

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AY578099.1	106472	1359.5	1510.3	2962.7	1991.5	1270.4	1541.0
AF420347.1	67790	27.4	41.0	85.3	51.6	48.5	22.1
EF467570.1	212152	15481.6	15404.4	7703.7	14033.6	15427.4	15115.3
AF420343.1	67794	26.9	42.9	166.8	78.1	57.0	51.4
AF449232.1	61877	66.1	77.2	2078.3	106.3	98.6	36.3
GQ355026.1	565854	1285.4	2042.5	2610.6	927.3	1868.3	1963.4
L35522.1	11150	7553.8	9777.4	4951.0	7033.8	4542.1	5859.4
AJ969465.1	157898	56.0	81.1	446.5	261.4	77.5	49.1
EU864466.1	334109	5404.5	5720.9	2285.8	6851.3	9498.1	7641.8
EF644836.1	300292	1611.7	941.4	2182.4	1338.6	1630.6	1433.2
EF467464.1	213273	407.9	642.4	1470.6	302.4	609.6	226.0
EF467519.1	205825	7378.9	8252.3	6653.6	6833.4	6112.4	4503.8
GU390782.1	516622	4603.8	4540.6	4347.0	6544.5	5792.2	4925.7
AY766315.1	108123	55.7	74.0	39.2	243.8	135.1	88.4
GU390711.1	515047	2382.5	1809.0	3903.4	1010.5	1874.2	939.8
AY280435.1	106612	408.3	244.7	1456.5	518.7	136.0	337.5
NC_005090.1	93903	161.5	217.9	1155.9	191.5	212.8	257.2
AF273252.1	29152	5495.3	7076.4	4843.2	5119.9	7457.2	6778.9
AF068812.2	11156	2461.1	3983.1	4736.5	1604.3	4543.2	3672.3
AY691429.1	106012	1143.9	2368.5	3951.3	673.3	1981.9	1515.8
NR_028943.1	571654	783.8	1745.7	2923.0	1665.4	4190.1	4961.9
AF299128.1	40818	3848.9	4944.1	6169.4	4245.3	5848.1	7614.2
AF068804.2	11155	17729.4	17116.5	15044.5	13825.7	16116.8	15817.9
ABCJ01000004.1	243079	1338.0	2250.1	3104.4	1122.9	1877.6	3468.6
NR_028999.1	579615	486.2	1417.0	4006.6	921.3	630.8	738.2
CP001279.1	528797	6436.5	7914.4	7922.7	6325.3	9467.6	1823.8
NR_025497.1	566284	1205.0	858.9	4173.6	884.0	3860.2	2364.4
AM937002.1	260087	704.6	1267.4	5262.4	733.2	747.1	1085.8
AP009178.1	247747	120.3	229.5	364.5	169.4	244.3	343.9
AB175499.1	106788	91.1	85.9	242.9	115.7	87.5	70.1
AB167820.1	136358	385.9	256.8	246.3	428.7	856.8	969.9
EF462830.1	302768	2934.8	3870.9	6043.3	3196.3	3018.8	4045.6
AY830901.1	109592	35.4	91.2	65.6	65.3	84.7	35.8
DQ431197.1	156297	1246.4	1358.2	1620.8	2710.8	1676.9	1863.1
FJ154522.1	556258	96.6	103.6	298.3	1142.9	132.6	39.2
AF329205.1	33408	17594.0	19180.8	6438.0	12959.6	12170.9	9874.4
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DQ646485.1	238863	1205.7	1760.9	3943.3	1411.2	3537.7	4308.2
EU079375.1	243219	3587.8	3909.9	5055.7	5540.1	8593.8	5512.0
AB039820.1	19750	9219.1	9690.1	5528.9	5483.6	11027.4	8848.9

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o__Acidithiobacillales	f__Acidithiobacillaceae
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s__Acidithiobacillus ferrooxidans	3043
s__Acidithiobacillus ferrooxidans	3200
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AF362022.1 gg_id:53544 Acidithiobacillus ferrooxidans str. ATCC 19859
EF015577.1 gg_id:177741 Acidithiobacillus ferrooxidans str. SRHGR
DQ321746.1 gg_id:148463 Acidithiobacillus ferrooxidans str. yunnan1
DQ909079.1 gg_id:170265 Acidithiobacillus ferrooxidans str. c
GU167981.1 gg_id:583008 Acidithiobacillus ferrooxidans
AF359940.1 gg_id:21015 Acidithiobacillus thiooxidans str. KCTC 8929P
AJ879995.1 gg_id:127417 Acidithiobacillus ferrooxidans str. B4
DQ529311.1 gg_id:301400 Acidithiobacillus ferrooxidans str. DBS-1
EU250259.1 gg_id:241484 acid mine drainage clone GXDC-45
EF446188.1 gg_id:210453 Prokaryotic and Ecology Floating Macroscopic Filaments Extreme Acidic River Rio Tint
FJ946877.1 gg_id:567607 Acidithiobacillus ferrooxidans str. NK-16
AY552091.1 gg_id:147725 Acidithiobacillus sp. str. CASQ22
FJ890908.1 gg_id:574423 Microbial heap: implications model and control process -grade copper bioleaching he
EF612419.1 gg_id:248238 historic semiarid lead-zinc site mine tailings clone K6-C19
EF059761.1 gg_id:188237 Acidithiobacillus ferrooxidans str. CHMS
X75266.1 gg_id:7484 Acidithiobacillus ferrooxidans
FJ154519.1 gg_id:539257 Acidithiobacillus ferrooxidans str. F6
AM502930.1 gg_id:241149 Acidithiobacillus ferrooxidans str. LMT1
EU084698.1 gg_id:254158 Acidithiobacillus ferrooxidans str. DGS
DQ159176.1 gg_id:139484 Wetland System Treating Acid Coal Mine Drainage wetland clone AMD 636
EU250217.1 gg_id:253906 acid mine drainage clone GXDC-3
AJ459801.1 gg_id:66601 Thermithiobacillus tepidarius str. DSM 3134
AJ458408.1 gg_id:67017 Aeromonas encheleia str. LMG 16328
AJ458416.1 gg_id:67011 Aeromonas encheleia str. E195 = S 191
FJ940842.1 gg_id:419066 Aeromonas enteropelogenes str. CRX104
FJ940843.1 gg_id:465898 Aeromonas enteropelogenes str. CRX105
FJ940844.1 gg_id:457890 Aeromonas enteropelogenes str. CRX203
FJ940845.1 gg_id:394895 Aeromonas enteropelogenes str. CRX207
FJ966347.1 gg_id:411204 Aeromonas veronii str. 5CB1
FJ940820.1 gg_id:455969 Aeromonas veronii str. LNC205
FJ940816.1 gg_id:401894 Aeromonas jandaei str. LC208
EU770282.1 gg_id:320191 Aeromonas veronii str. IH118
AB032088.1 gg_id:9365 Aeromonas hydrophila str. Ef1L1
AF157690.1 gg_id:9454 Aeromonas media str. 86352
AY900170.1 gg_id:143274 Aeromonas hydrophila str. PCA0081
FJ940831.1 gg_id:449999 Aeromonas media str. pW28
EU488683.1 gg_id:545213 Aeromonas media str. 974a
FJ168773.1 gg_id:559246 Aeromonas media str. 480a
AF418218.1 gg_id:59117 Aeromonas media 5
GQ470996.1 gg_id:546104 Aeromonas hydrophila str. HQ070610B-1
AM262152.1 gg_id:158666 Aeromonas media str. CDC 0862-83

AF362022.1	53544	84.8	243.6	629.5	110.2	90.6	113.3
EF015577.1	177741	10098.8	10173.3	6397.4	9388.0	8933.2	8275.5
DQ321746.1	148463	2438.3	2652.0	2707.3	2262.6	3535.8	4094.4
DQ909079.1	170265	4725.2	4175.0	1805.1	7342.8	8165.8	6267.8
GU167981.1	583008	278.6	672.3	1159.1	961.5	1015.8	1350.5
AF359940.1	21015	415.0	1084.3	255.5	206.7	319.0	313.4
AJ879995.1	127417	2021.1	1929.2	1625.9	1371.2	2080.7	1558.8
DQ529311.1	301400	893.7	1296.1	1351.3	1147.0	1837.9	1234.8
EU250259.1	241484	5425.5	6866.5	3117.0	6589.0	8665.4	7630.0
EF446188.1	210453	7408.9	6019.0	7561.7	7793.6	4855.4	5871.9
FJ946877.1	567607	3620.0	4179.6	3391.0	2865.2	3738.3	3267.0
AY552091.1	147725	11334.4	12226.0	7117.4	7904.3	7235.7	7258.4
FJ890908.1	574423	962.3	980.4	1075.7	1845.1	1118.7	1304.6
EF612419.1	248238	2679.6	2796.9	2533.8	1452.9	1952.5	2849.6
EF059761.1	188237	1899.8	2705.8	2526.6	1864.3	2620.1	2334.6
X75266.1	7484	8116.9	10193.6	6658.5	5922.1	8443.8	6683.4
FJ154519.1	539257	6867.8	9607.3	6903.0	6458.9	7446.0	7929.7
AM502930.1	241149	7335.3	7740.4	6791.5	6316.1	9191.7	8263.1
EU084698.1	254158	7444.8	9384.7	6792.8	7141.9	10456.5	9471.7
DQ159176.1	139484	6314.8	5888.6	1333.3	7191.4	9006.4	7921.0
EU250217.1	253906	8773.0	10689.7	8725.6	6564.9	7788.7	6082.5
AJ459801.1	66601	243.2	567.8	418.4	331.6	1247.5	1368.1
AJ458408.1	67017	610.7	969.8	5895.1	692.5	368.7	1649.3
AJ458416.1	67011	509.3	975.2	4289.4	552.4	404.6	2416.8
FJ940842.1	419066	197.2	645.5	2045.1	236.5	195.2	831.6
FJ940843.1	465898	3581.9	2753.6	3498.5	2593.5	2915.3	4082.7
FJ940844.1	457890	113.1	252.4	973.9	150.8	259.0	733.6
FJ940845.1	394895	73.4	176.1	299.3	141.0	91.4	424.0
FJ966347.1	411204	861.3	1406.3	4432.9	1404.7	1557.0	3359.3
FJ940820.1	455969	633.8	1314.4	3659.4	626.7	497.5	2163.4
FJ940816.1	401894	250.2	541.1	1718.9	383.4	139.1	693.6
EU770282.1	320191	1523.4	1842.0	4580.9	1778.8	1052.3	3367.8
AB032088.1	9365	425.0	869.9	2372.8	638.9	958.2	1801.3
AF157690.1	9454	981.2	1189.1	3850.1	1077.0	950.3	1569.8
AY900170.1	143274	1272.0	1691.9	4517.3	1689.5	2046.0	2566.6
FJ940831.1	449999	1287.0	1650.7	4300.5	1729.8	1741.8	2497.6
EU488683.1	545213	157.1	520.5	1428.3	280.1	105.7	1079.2
FJ168773.1	559246	649.1	1219.9	2840.3	911.3	1664.2	2352.6
AF418218.1	59117	163.4	116.1	1461.1	120.3	59.1	207.8
GQ470996.1	546104	395.6	804.1	1662.9	302.6	166.9	1312.0
AM262152.1	158666	868.3	795.6	3012.6	979.3	2618.6	2081.8

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AM184282.1 gg_id:161440 Aeromonas hydrophila str. WAB1943
FJ940794.1 gg_id:423232 Aeromonas media str. 4LNC208
FJ494900.1 gg_id:424847 Aeromonas hydrophila str. B27
AF468055.1 gg_id:28522 Aeromonas hydrophila str. 45/90
EU488681.1 gg_id:543209 Aeromonas media str. 83a
AM262150.1 gg_id:157051 Aeromonas media str. V69
EU669667.1 gg_id:306838 Aeromonas hydrophila
AF468056.1 gg_id:42667 Aeromonas hydrophila str. 4AK4
GU174503.1 gg_id:583380 Aeromonas media str. 2CCH201
AY532688.1 gg_id:99610 Aeromonas molluscorum str. 93M
GQ845452.1 gg_id:592308 Aeromonas schubertii str. HYS1
GQ844302.1 gg_id:589738 Aeromonas schubertii str. HYL2
GQ844301.1 gg_id:580340 Aeromonas schubertii str. HYK1
GQ860945.2 gg_id:559436 Aeromonas simiae str. MDC 54
AF150699.1 gg_id:47441 Elbe River snow isolate Iso19neu Iso19neu_1356 snow
FJ233860.1 gg_id:313618 Aeromonas jandaei str. AE25
EF634211.1 gg_id:236518 Aeromonas bv. veronii str. 2T2C70
EF634212.1 gg_id:248791 Aeromonas bv. veronii str. 2T2C72
DQ166946.1 gg_id:153877 Aeromonas hydrophila str. S-1
AY966888.1 gg_id:115178 Aeromonas punctata str. HC960704-1
AM931169.1 gg_id:271869 Aeromonas salmonicida str. 242-Hgo
AF170914.4 gg_id:9385 Aeromonas culicicola str. MTCC 3249
EU918692.1 gg_id:347086 Pasteurella multocida str. SXXG0802
AB027005.1 gg_id:9445 Aeromonas salmonicida str. NI-441 T83-k-sw-2 IS-205
EU770278.1 gg_id:327136 Aeromonas veronii str. IH101
EU770304.1 gg_id:316400 Aeromonas veronii str. MW17
FJ940826.1 gg_id:448981 Aeromonas hydrophila str. pW14
AY987773.1 gg_id:186571 Aeromonas media str. CDC 0862-83
AY987741.1 gg_id:198899 Aeromonas hydrophila str. -32
FM999979.1 gg_id:516755 Aeromonas popoffii str. LMG 17546
EU770292.1 gg_id:328368 Aeromonas veronii str. IQ309
EU770270.1 gg_id:308207 Aeromonas veronii str. HH104
EU770296.1 gg_id:316179 Aeromonas punctata str. ME15
AY928478.1 gg_id:138908 Aeromonas veronii bv. Sobria str. A155
DQ817276.1 gg_id:170303 mouse cecum clone aaa71g08
FJ494905.1 gg_id:370966 Aeromonas veronii str. 08004
EU770309.1 gg_id:352788 Aeromonas veronii str. WS03
AY928475.1 gg_id:138989 Aeromonas veronii bv. Sobria str. CDC0437-84
FJ233858.1 gg_id:323934 Aeromonas allosaccharophila str. AE35
EU770271.1 gg_id:317346 Aeromonas veronii str. HQ103
FJ940797.1 gg_id:414411 Aeromonas punctata str. 4LNC310

AM184282.1	161440	2530.4	2656.0	5895.0	2996.9	2637.1	4231.7
FJ940794.1	423232	186.1	474.5	2627.8	713.4	206.1	706.5
FJ494900.1	424847	2076.5	1888.0	5024.5	1677.5	1987.7	3077.3
AF468055.1	28522	1246.5	1527.7	3757.9	1668.9	1707.7	2448.1
EU488681.1	543209	379.2	1109.1	2584.5	314.9	319.0	984.0
AM262150.1	157051	1439.4	1048.7	3920.7	1592.2	2445.0	2337.8
EU669667.1	306838	642.4	1074.2	2416.0	541.5	469.6	1799.1
AF468056.1	42667	7987.9	9989.2	5475.6	6011.2	12716.2	10285.9
GU174503.1	583380	1402.8	2082.3	4896.4	1135.0	1696.6	1504.5
AY532688.1	99610	784.5	1606.9	5747.3	1183.7	1396.5	3119.0
GQ845452.1	592308	811.8	1506.7	2815.4	2427.1	732.5	2794.2
GQ844302.1	589738	828.6	1578.3	3492.8	2400.6	729.6	2898.7
GQ844301.1	580340	1640.5	1560.9	4588.0	5478.8	992.2	2769.4
GQ860945.2	559436	1977.4	1617.0	1638.6	2511.9	1868.8	1724.8
AF150699.1	47441	1318.8	1155.2	5472.2	2098.5	1681.0	3375.9
FJ233860.1	313618	334.8	896.7	3833.2	525.5	271.0	1717.0
EF634211.1	236518	696.8	867.3	4711.5	1330.4	1123.9	3395.8
EF634212.1	248791	478.1	627.3	4456.3	878.9	724.8	2383.1
DQ166946.1	153877	517.7	944.8	5562.3	854.1	667.0	2346.7
AY966888.1	115178	6380.4	6652.2	8726.1	7922.0	5547.9	5829.9
AM931169.1	271869	8018.9	8732.9	7058.0	9077.4	13260.1	11432.1
AF170914.4	9385	229.6	542.1	2327.0	350.6	129.3	508.4
EU918692.1	347086	103.7	262.8	2846.5	525.5	100.9	651.3
AB027005.1	9445	1279.1	1316.2	5589.5	1630.9	2528.1	2665.3
EU770278.1	327136	1818.4	2138.0	5205.9	1856.4	1807.2	4180.4
EU770304.1	316400	1523.4	1843.5	4581.5	1903.5	1051.6	3145.3
FJ940826.1	448981	264.2	589.8	1499.1	176.8	506.3	1211.9
AY987773.1	186571	787.5	1397.4	3495.7	1112.9	1720.2	2244.0
AY987741.1	198899	118.1	300.8	651.5	144.7	155.8	427.0
FM999979.1	516755	612.4	981.3	5955.7	698.9	368.5	1790.1
EU770292.1	328368	2194.2	3348.4	3667.1	1614.3	4340.9	2926.2
EU770270.1	308207	631.5	1277.7	3769.1	1278.1	2156.7	1885.9
EU770296.1	316179	1339.7	2571.6	2605.4	1121.4	4043.8	1923.8
AY928478.1	138908	878.2	1240.8	5304.8	1570.5	2098.0	3790.1
DQ817276.1	170303	3622.4	3530.2	2146.2	1039.0	1872.4	1843.3
FJ494905.1	370966	1335.9	1439.6	4111.2	1341.8	545.2	2436.9
EU770309.1	352788	4190.2	5123.6	3216.1	1392.9	695.3	2924.6
AY928475.1	138989	337.6	879.0	5220.7	807.3	641.3	1936.3
FJ233858.1	323934	190.5	425.9	3585.9	465.3	508.8	1884.7
EU770271.1	317346	4853.7	5835.7	6094.7	4363.0	9067.7	7212.6
FJ940797.1	414411	593.1	910.4	1793.0	1075.7	1032.5	1656.5

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AY928471.1 gg_id:139267 Aeromonas veronii bv. Sobria
FJ940834.1 gg_id:445987 Aeromonas veronii str. CHS102
GU227144.1 gg_id:592870 Aeromonas hydrophila str. CDB34
EU770301.1 gg_id:334017 Aeromonas veronii str. MS14
AY987747.1 gg_id:193639 Aeromonas media str. 345
GU187060.1 gg_id:532655 Aeromonas sobria str. 2CCH202
AY827493.1 gg_id:109974 Aeromonas hydrophila str. HC010916B-1
FJ544348.1 gg_id:409049 Aeromonas punctata str. ji5
FJ940800.1 gg_id:423025 Aeromonas punctata str. 4pM02
AJ223180.1 gg_id:9389 Aeromonas popoffii str. LMG 17542
EU916707.1 gg_id:316818 Aeromonas veronii str. 3r
FJ233856.1 gg_id:307855 Aeromonas hydrophila str. AE29
GU205194.1 gg_id:544819 Aeromonas hydrophila str. JNC1203
EF634209.1 gg_id:257451 Aeromonas veronii str. 2T2C61
EU770294.1 gg_id:353489 Aeromonas veronii str. IQ321
X60417.1 gg_id:9431 Aeromonas sp str. ATCC 35941
EF669478.1 gg_id:252619 Aeromonas hydrophila str. HC060718-1
AF005256.1 gg_id:9416 Aeromonas sp. str. MR-64
AY987744.1 gg_id:177411 Aeromonas veronii bv. Sobria str. -50
GQ304779.1 gg_id:538852 Aeromonas enteropelogenes str. A3
FJ494902.1 gg_id:463706 Aeromonas veronii str. 08001
AY264937.1 gg_id:102248 Aeromonas hydrophila str. ATCC 7966
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FJ940817.1 gg_id:467491 Aeromonas veronii str. LC211
GU296671.1 gg_id:546546 Aeromonas hydrophila str. ANSE1
FJ440680.1 gg_id:543987 Aeromonas hydrophila str. ccts1
FJ940839.1 gg_id:447408 Aeromonas hydrophila str. CLX208
AF108136.1 gg_id:44568 Aeromonas salmonicida
FJ233865.1 gg_id:337058 Aeromonas bv. veronii str. AE10
FJ940835.1 gg_id:440842 Aeromonas veronii str. CHS105
AY987776.1 gg_id:179474 Aeromonas punctata str. ACVM
FJ544359.1 gg_id:388323 Aeromonas punctata str. ji22
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GQ284535.1 gg_id:576068 Aeromonas sp. str. PCSAS2-31
FJ940830.1 gg_id:371339 Aeromonas jandaei str. pW23
EF077527.1 gg_id:193001 Aeromonas hydrophila

AB211226.1	115351	8971.3	9125.7	7376.4	8624.3	9674.8	9675.8
AY928471.1	139267	663.9	920.8	4725.5	602.8	1000.4	2886.7
FJ940834.1	445987	125.3	325.7	1389.0	191.7	150.1	381.5
GU227144.1	592870	546.5	1126.1	2677.2	799.7	1452.2	2511.8
EU770301.1	334017	7312.6	10087.6	5307.1	5767.9	6357.3	4652.1
AY987747.1	193639	288.5	627.1	969.1	251.7	181.0	916.1
GU187060.1	532655	1279.6	2063.1	5426.5	1915.2	2159.3	4652.2
AY827493.1	109974	240.0	525.3	3876.4	342.5	357.8	1710.5
FJ544348.1	409049	45.6	133.8	783.9	97.9	64.8	444.6
FJ940800.1	423025	980.8	1374.2	4297.2	1831.4	350.8	2175.8
AJ223180.1	9389	6426.6	6188.0	8051.3	6504.0	5602.1	4824.5
EU916707.1	316818	1428.7	1849.0	4691.3	1783.8	1052.8	3208.7
FJ233856.1	307855	632.0	1178.0	1938.9	460.8	610.5	1997.4
GU205194.1	544819	196.7	683.8	3080.3	229.0	282.1	1010.0
EF634209.1	257451	1265.2	1242.6	4265.2	1259.4	464.9	2156.2
EU770294.1	353489	6397.7	6900.6	8137.1	7162.6	8004.0	7568.6
X60417.1	9431	2992.4	2682.8	4978.9	4737.4	1431.1	4430.9
EF669478.1	252619	134.5	445.6	3149.3	193.1	135.6	678.7
AF005256.1	9416	11176.3	12662.4	10522.5	12135.2	11815.6	11667.0
AY987744.1	177411	7528.9	7196.7	3872.1	4501.6	5868.9	6250.3
GQ304779.1	538852	12763.6	15926.7	10400.6	8669.1	14197.5	12927.8
FJ494902.1	463706	1324.2	1402.7	4304.9	1308.0	478.3	2346.5
AY264937.1	102248	257.6	473.4	2189.2	301.1	149.1	497.0
FJ940819.1	391916	1146.0	1373.7	3518.6	2097.4	995.7	1797.7
EF645799.1	237066	96.3	258.0	1397.9	132.7	98.6	282.6
GU205198.1	555360	119.1	306.7	630.3	167.2	106.6	550.4
DQ817289.1	172125	7402.4	8683.3	2027.1	2166.3	558.6	2251.6
AY538658.1	101689	8536.9	7622.8	9466.6	6577.0	10011.3	10745.0
FJ940817.1	467491	1516.2	1831.0	4422.7	1769.9	1058.4	3293.3
GU296671.1	546546	687.0	1282.2	6414.2	1629.5	1550.1	1241.0
FJ440680.1	543987	2483.1	2425.9	5913.0	2297.8	2688.4	4009.9
FJ940839.1	447408	1967.8	2109.3	4091.6	2178.4	3352.6	4376.5
AF108136.1	44568	932.4	1666.8	7305.2	1485.6	1290.6	1961.2
FJ233865.1	337058	4258.5	4420.7	4626.3	7049.1	6114.6	7077.6
FJ940835.1	440842	401.6	1064.2	3048.7	613.3	150.3	753.7
AY987776.1	179474	376.3	795.8	1519.3	627.4	347.6	1089.9
FJ544359.1	388323	101.0	275.6	495.2	107.2	96.5	373.6
GU205193.1	561913	115.5	312.3	1141.6	124.6	84.9	413.9
GQ284535.1	576068	278.7	403.5	3207.9	893.7	159.0	522.3
FJ940830.1	371339	282.6	748.8	3140.0	447.8	264.0	1055.1
EF077527.1	193001	4030.9	5870.9	7692.4	2675.0	6229.9	6102.7

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GU205201.1 gg_id:576517 Aeromonas media str. JHS07
FJ233866.1 gg_id:313306 Aeromonas schubertii str. AE2
AF418217.1 gg_id:59115 Aeromonas media 4
AM184224.1 gg_id:161336 Aeromonas veronii bv. Veronii str. WAB1882
X74674.1 gg_id:9452 Aeromonas punctata str. ATCC 15468T
AY928477.1 gg_id:151083 Aeromonas veronii bv. Sobria str. A155
FJ940796.1 gg_id:433024 Aeromonas punctata str. 4LNC309
AY987745.1 gg_id:188420 Aeromonas jandaei str. -51
FM999978.1 gg_id:531043 Aeromonas popoffii str. LMG 17545
FJ233863.1 gg_id:333045 Aeromonas bv. veronii str. AE34
GU296672.1 gg_id:591386 Aeromonas hydrophila str. ANSE2
AF427150.1 gg_id:25552 Aeromonas sp. PAR2A
FJ544354.1 gg_id:433080 Aeromonas punctata str. ji14
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EU770286.1 gg_id:340453 Aeromonas veronii str. IH325
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EU700096.1 gg_id:296747 Aeromonas hydrophila str. SWCH-6
AJ458411.1 gg_id:67014 Aeromonas eucrenophila str. LMG 17059
EU770293.1 gg_id:324097 Aeromonas veronii str. IQ318
EU488685.1 gg_id:549142 Aeromonas punctata str. 121c
EU770302.1 gg_id:315651 Aeromonas veronii str. MS15
EU488693.1 gg_id:575182 Aeromonas veronii str. 633c
EU770303.1 gg_id:334972 Aeromonas veronii str. MW15
FJ407187.1 gg_id:361976 Aeromonas punctata str. W20060720
AJ224309.1 gg_id:9396 Aeromonas encheleia str. 1881
AF418214.1 gg_id:56067 Aeromonas media 1
FJ544362.1 gg_id:411774 Aeromonas punctata str. ji31
FJ940810.1 gg_id:390498 Aeromonas veronii str. 4pW23
AB211227.1 gg_id:115297 Aeromonas salmonicida str. NKCM8904
FJ940832.1 gg_id:423276 Aeromonas jandaei str. CCC204
AY987724.1 gg_id:180428 Aeromonas veronii bv. Sobria str. AE-21
GQ262778.1 gg_id:592654 Aeromonas hydrophila str. S1
AB034761.1 gg_id:74870 Aeromonas hydrophila str. 28SA
FJ940833.1 gg_id:433791 Aeromonas hydrophila str. CHS101
DQ539497.1 gg_id:169858 Aeromonas hydrophila SBRD9
DQ816568.1 gg_id:161901 mouse cecum clone aab19g05

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GU205201.1	576517	418.2	896.3	2301.8	758.7	364.9	1237.2
FJ233866.1	313306	7920.0	8263.1	6583.9	10091.8	11878.7	13072.9
AF418217.1	59115	487.8	977.0	2957.3	469.3	931.4	1369.4
AM184224.1	161336	2394.8	2375.3	5743.8	2983.9	2224.8	4976.3
X74674.1	9452	991.6	991.8	3079.7	1123.5	982.4	1805.1
AY928477.1	151083	590.4	805.0	5300.1	988.5	1238.3	2703.8
FJ940796.1	433024	106.2	289.6	1062.9	156.4	283.5	837.8
AY987745.1	188420	291.2	356.6	1918.9	556.2	472.6	1137.4
FM999978.1	531043	846.2	1726.9	3389.4	839.2	184.4	1435.9
FJ233863.1	333045	521.9	836.3	3974.3	655.2	870.8	2436.7
GU296672.1	591386	814.7	1440.6	5227.6	1420.9	1561.8	3329.0
AF427150.1	25552	333.0	592.4	3264.4	454.7	195.5	699.6
FJ544354.1	433080	702.9	1082.8	2025.8	974.6	1865.8	2295.0
AY987739.1	191655	119.0	274.2	1062.7	158.9	287.9	892.8
AY987749.1	188082	271.6	369.7	2204.2	488.5	110.2	875.7
EU770273.1	326038	891.0	1061.4	3111.1	1293.9	886.1	1491.7
EU770286.1	340453	880.7	1343.2	5546.3	1633.3	1162.8	2971.2
FJ940804.1	372890	881.4	1304.8	2350.4	1033.2	992.0	2613.7
EU700096.1	296747	4675.8	6460.1	10153.5	5830.5	10186.5	9424.5
AJ458411.1	67014	1499.9	1918.7	4974.0	1684.4	1157.1	3585.1
EU770293.1	324097	719.5	1337.7	3881.1	1348.8	1531.0	3015.9
EU488685.1	549142	1398.6	1798.9	3913.6	1582.5	915.8	2813.0
EU770302.1	315651	7470.1	6077.9	5731.6	8079.0	6288.5	5013.6
EU488693.1	575182	2238.3	2087.2	5080.3	2909.3	2191.5	4495.7
EU770303.1	334972	917.8	1048.8	2765.5	1488.2	657.3	1412.6
FJ407187.1	361976	53.2	111.4	596.3	136.3	80.0	433.6
AJ224309.1	9396	755.0	1214.6	4861.8	733.1	417.4	2525.0
AF418214.1	56067	271.8	687.6	5212.3	528.5	349.2	1532.3
FJ544362.1	411774	59.6	132.9	229.0	96.7	69.1	284.0
FJ940810.1	390498	200.2	439.1	3566.8	330.0	101.4	813.7
AB211227.1	115297	379.7	875.2	3617.8	755.6	942.9	2175.7
FJ940832.1	423276	254.2	702.3	3032.5	405.4	272.7	617.8
AY987724.1	180428	2028.8	2247.4	5126.0	2713.4	1840.5	4624.2
GQ262778.1	592654	2328.0	2233.5	5432.0	2562.7	2090.5	3362.9
AB034761.1	74870	195.2	317.1	4001.9	401.2	157.4	1150.9
FJ940833.1	433791	2038.0	1834.3	2585.2	3951.0	1705.5	3537.4
DQ539497.1	169858	990.6	1207.7	4066.8	1087.9	953.5	1620.7
DQ816568.1	161901	395.0	414.8	257.7	268.1	994.9	400.8

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FJ026735.1 gg_id:338819 Aeromonas punctata str. ZZF071029
X71120.1 gg_id:9386 Aeromonas ichthiosmia
AF418215.1 gg_id:59123 Aeromonas media 2
EU770290.1 gg_id:326583 Aeromonas veronii str. IQ304
FJ940850.1 gg_id:425695 Aeromonas veronii str. CYJ209
EU770275.1 gg_id:350629 Aeromonas hydrophila str. IB336
GQ232759.1 gg_id:538649 Aeromonas sobria str. JY081016-1
EU770285.1 gg_id:332437 Aeromonas veronii str. IH323
EU770288.1 gg_id:353344 Aeromonas veronii str. IQ117
EU730930.1 gg_id:311549 Aeromonas eucrenophila str. 189
EU770274.1 gg_id:327072 Aeromonas hydrophila str. IB101
DQ837028.1 gg_id:162354 Aeromonas jandaei sf3-14
FJ230076.1 gg_id:587653 Aeromonas sanarellii str. A2-67
AY987723.1 gg_id:198790 Aeromonas punctata str. AE-11
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FJ940825.1 gg_id:387302 Aeromonas veronii str. pM05
FJ976606.1 gg_id:545344 Aeromonas hydrophila
EF446897.1 gg_id:215466 Aeromonas veronii str. Philippines-An11
FJ544406.1 gg_id:447507 Aeromonas punctata str. w4
AY987733.1 gg_id:192245 Aeromonas hydrophila str. AE-55
EU770289.1 gg_id:343054 Aeromonas veronii str. IQ120
FJ947060.1 gg_id:508769 Aeromonas punctata str. nA3
AJ223181.1 gg_id:9390 Aeromonas popoffii str. LMG 17543
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EU696781.1 gg_id:292266 Aeromonas hydrophila str. BJ
FJ940828.1 gg_id:377570 Aeromonas veronii str. pW18
AF418216.1 gg_id:59119 Aeromonas media 3
FJ940811.1 gg_id:395273 Aeromonas veronii str. BC104
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FJ940815.1 gg_id:413385 Aeromonas jandaei str. LC206
EU021049.1 gg_id:255922 Aeromonas salmonicida str. 04/3244-4k
FJ230077.1 gg_id:589204 Aeromonas taiwanensis str. A2-50
AY987726.1 gg_id:190833 Aeromonas enteropelogenes str. AE-31
AM184294.1 gg_id:159899 Aeromonas punctata str. WAB1955
GQ401237.1 gg_id:583416 Aeromonas punctata str. VITSCA01
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GU205196.1 gg_id:585209 Aeromonas popoffii str. JW08
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AY928480.1	139256	854.1	1499.0	4788.4	1007.1	629.9	2655.7
DQ814455.1	168069	6297.7	7173.4	7051.0	8146.6	9002.7	9011.8
FJ026735.1	338819	1291.0	1886.3	5588.4	1266.5	1809.5	2483.7
X71120.1	9386	1148.9	1594.1	2711.0	1804.1	1307.3	3088.2
AF418215.1	59123	184.8	615.7	2126.4	248.5	147.6	546.2
EU770290.1	326583	2116.0	2335.4	4456.9	2947.4	1984.3	3155.3
FJ940850.1	425695	678.9	798.3	2765.7	494.1	1110.8	2007.8
EU770275.1	350629	4214.9	4669.5	2996.6	2396.8	5205.0	4526.4
GQ232759.1	538649	667.4	1045.1	4461.5	1122.9	913.8	2961.6
EU770285.1	332437	259.3	701.7	1489.1	280.5	89.9	1033.6
EU770288.1	353344	1155.8	1384.4	3776.6	2090.1	994.4	1819.4
EU730930.1	311549	266.1	584.8	4316.5	369.5	351.4	1806.2
EU770274.1	327072	237.3	794.0	3668.3	276.6	424.8	1110.7
DQ837028.1	162354	985.2	1196.5	1849.4	1795.0	1238.7	2762.4
FJ230076.1	587653	131.6	347.3	1248.7	161.6	94.8	429.2
AY987723.1	198790	501.4	301.0	934.9	282.3	477.0	590.1
FJ940822.1	389565	965.9	1520.0	5159.9	1642.7	1632.9	3452.6
FJ940825.1	387302	2148.6	3393.5	5697.2	2200.8	6772.2	6250.0
FJ976606.1	545344	96.9	333.1	1611.8	168.3	93.7	674.2
EF446897.1	215466	2262.2	2117.7	2206.1	1505.7	2146.0	1523.6
FJ544406.1	447507	173.1	386.8	1407.7	278.1	153.2	526.3
AY987733.1	192245	2566.3	3298.1	5239.2	2978.5	3230.1	4850.0
EU770289.1	343054	6538.8	6577.0	8615.1	6362.7	6118.4	5641.8
FJ947060.1	508769	187.2	406.6	1710.2	284.0	154.0	612.8
AJ223181.1	9390	855.7	1417.7	4644.9	1861.0	1776.4	3826.8
AF418219.1	59116	125.9	416.1	2025.0	173.7	109.7	387.7
EU696781.1	292266	434.9	1024.2	4255.5	384.1	949.3	1563.0
FJ940828.1	377570	11051.2	11487.8	7117.7	8942.2	13088.6	11758.0
AF418216.1	59119	214.3	665.4	2322.3	300.4	164.9	757.6
FJ940811.1	395273	833.3	1208.4	3957.6	1375.8	1563.4	3257.2
AM184219.1	161149	2500.3	2430.0	5162.2	2969.9	2644.0	4129.7
FJ940815.1	413385	1946.8	1292.7	3173.6	3788.0	1969.0	2809.9
EU021049.1	255922	138.0	347.7	3623.8	315.1	152.9	719.4
FJ230077.1	589204	254.0	594.5	2671.2	275.0	123.8	854.1
AY987726.1	190833	814.1	438.0	1147.6	787.6	146.2	644.2
AM184294.1	159899	571.0	989.7	2220.9	782.0	1462.7	2476.1
GQ401237.1	583416	1136.3	1383.6	3432.9	1627.4	1592.0	2841.9
DQ095911.1	136342	7089.9	6196.4	7271.8	5684.3	7025.5	6027.8
GU205196.1	585209	1039.9	1401.8	4870.4	1737.6	1359.5	3391.8
GU205192.1	534484	963.9	1646.2	5385.0	1659.6	2811.0	4282.3

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EU770305.1 gg_id:306230 Aeromonas veronii str. WE02
AM945539.1 gg_id:554884 Aeromonas hydrophila ayu-Ah0201
DQ814092.1 gg_id:162823 zebrafish digestive tract clone aab59f09
AY347679.1 gg_id:110092 Aeromonas culicicola str. 03037TRG
FJ966348.1 gg_id:411481 Aeromonas veronii str. QB205
EF371904.1 gg_id:208133 Aeromonas veronii str. TF15
AY987759.1 gg_id:189821 Aeromonas punctata str. RK 25447
AF094724.1 gg_id:73145 Oceanimonas doudoroffii str. ATCC 27123
AB019390.1 gg_id:9401 Oceanimonas doudoroffii str. MBIC1298 (=ATCC27123)
DQ416806.1 gg_id:263963 Oceanimonas sp. G2DM-26
AY562194.1 gg_id:113893 Oceanimonas sp. str. Be07
GU183679.1 gg_id:567474 Marinomonas sp. str. H1693
EU530640.1 gg_id:270644 Oceanimonas sp. str. GK1
AJ550470.1 gg_id:84842 Oceanisphaera litoralis str. DSM 15406
CP001616.1 gg_id:526816 Tolumonas auensis str. DSM 9187
EU569287.1 gg_id:274900 Zobellella denitrificans str. MW1
EU109731.1 gg_id:237124 Shewanella sp. str. NH21
FJ230836.1 gg_id:346053 Serratia sp. str. AN4
DQ195676.1 gg_id:140125 Zobellella taiwanensis str. ZT1T
NR_026075.1 gg_id:560865 Anaerobiospirillum succiniciproducens str. S411; ATCC 29305
EF428122.1 gg_id:206236 Anaerobiospirillum sp. str. 78/9/02
GQ867410.1 gg_id:538586 and prevalence blaTEM genes Arctic seals colon content clone S7_13
GQ867419.1 gg_id:587570 and prevalence blaTEM genes Arctic seals colon content clone S7_31
EU776462.1 gg_id:320643 Red Kangaroo feces clone KO2_aai17h02
EU794084.1 gg_id:309826 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_E16
GU303104.1 gg_id:577587 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium
AB004908.1 gg_id:9350 Ruminobacter amylophilus str. NIAH-3 Bovine rumen
FJ684530.1 gg_id:511689 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ673136.1 gg_id:513301 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ681014.1 gg_id:514935 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ678936.1 gg_id:529684 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ680138.1 gg_id:514703 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ673291.1 gg_id:522804 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ681705.1 gg_id:517924 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ680474.1 gg_id:517852 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU532009.1 gg_id:259131 Predominant role host genetics controlling gut microbiota FMF remission stool clone
FJ680476.1 gg_id:521800 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ679937.1 gg_id:525643 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ676890.1 gg_id:530694 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ681292.1 gg_id:530658 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee

EF428988.1	205966	462.8	796.6	2231.0	514.0	159.0	1364.5
EU770305.1	306230	1923.3	2509.0	6684.3	4443.6	2573.8	4469.7
AM945539.1	554884	2336.9	3226.4	6705.6	4018.6	3172.8	5074.1
DQ814092.1	162823	4562.9	4248.5	3592.8	3024.6	3872.0	4267.4
AY347679.1	110092	982.6	1539.0	5413.0	1718.2	1833.8	3704.4
FJ966348.1	411481	1010.3	1863.2	3064.5	1197.0	1718.8	2437.0
EF371904.1	208133	9430.5	9427.5	9472.6	8979.8	11781.7	11009.7
AY987759.1	189821	658.2	1392.9	3116.7	873.6	397.9	1993.3
AF094724.1	73145	12571.1	11355.7	11261.3	8509.7	12174.1	11152.5
AB019390.1	9401	77.9	145.8	997.3	79.6	75.6	239.7
DQ416806.1	263963	663.6	717.6	1150.3	1225.0	1985.6	2371.7
AY562194.1	113893	1856.6	1352.1	889.5	1154.2	4488.7	4890.2
GU183679.1	567474	2372.2	1809.1	2266.5	1117.8	1173.0	2317.0
EU530640.1	270644	111.9	106.2	207.5	72.2	64.8	46.3
AJ550470.1	84842	24.2	53.0	178.4	63.9	53.8	36.2
CP001616.1	526816	2342.0	2001.1	7546.9	5078.3	5986.4	4034.0
EU569287.1	274900	254.5	245.3	3208.5	488.3	276.6	693.5
EU109731.1	237124	683.6	960.4	1682.9	860.8	1917.2	1381.4
FJ230836.1	346053	173.0	304.5	1251.4	202.1	103.5	706.2
DQ195676.1	140125	2222.8	2434.0	3360.8	3026.6	1319.5	1834.7
NR_026075.1	560865	2853.9	2094.6	3152.6	1771.6	5102.9	3064.5
EF428122.1	206236	1473.2	1405.6	239.1	437.4	941.5	787.1
GQ867410.1	538586	3037.8	1675.5	3693.5	2834.3	3938.3	3463.0
GQ867419.1	587570	1582.3	1694.5	2532.8	835.4	1303.9	847.2
EU776462.1	320643	7274.0	7802.6	7566.1	8263.9	10949.4	10481.9
EU794084.1	309826	6733.6	7831.3	4753.7	7222.5	11805.0	9455.2
GU303104.1	577587	940.7	1153.7	2722.9	4259.4	416.1	1810.8
AB004908.1	9350	41.9	488.5	73.1	183.3	762.0	659.2
FJ684530.1	511689	2943.3	3887.3	5084.7	3576.3	2715.3	3720.4
FJ673136.1	513301	1076.3	1689.9	2659.3	1829.9	2832.0	4343.2
FJ681014.1	514935	5586.2	7320.4	6552.1	4378.1	7362.2	8965.3
FJ678936.1	529684	4785.3	4209.1	6157.1	4834.8	6158.2	4546.8
FJ680138.1	514703	12808.7	14593.0	14590.0	9764.1	14893.6	11512.9
FJ673291.1	522804	8326.3	11181.2	9132.5	8980.8	15320.9	13135.7
FJ681705.1	517924	8535.4	9018.1	7750.5	7432.6	9037.1	9713.9
FJ680474.1	517852	9314.9	8850.3	6238.1	12789.0	16237.2	12185.8
EU532009.1	259131	6239.1	7041.7	4754.1	6987.5	11646.6	10790.4
FJ680476.1	521800	19237.0	20968.5	16549.9	14880.8	21078.4	15495.9
FJ679937.1	525643	10434.4	7928.3	4298.2	11693.4	10475.3	10147.7
FJ676890.1	530694	4127.1	4354.2	4934.9	5545.9	6414.5	3964.9
FJ681292.1	530658	6485.9	8046.9	7388.3	7777.4	12497.7	10083.6

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FJ681318.1 gg_id:519035 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ673806.1 gg_id:519747 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ685189.1 gg_id:515645 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ683080.1 gg_id:526775 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ678755.1 gg_id:524387 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ685307.1 gg_id:526414 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ673228.1 gg_id:521876 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ681105.1 gg_id:518112 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ678694.1 gg_id:532412 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ684018.1 gg_id:529769 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ682802.1 gg_id:522494 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ681900.1 gg_id:523612 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ678730.1 gg_id:531116 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ683575.1 gg_id:516087 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ673346.1 gg_id:514406 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ673002.1 gg_id:524997 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ678905.1 gg_id:530101 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ684508.1 gg_id:525389 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ673381.1 gg_id:516159 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ680565.1 gg_id:519066 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ679553.1 gg_id:531893 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ676324.1 gg_id:517601 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ679041.1 gg_id:530617 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ904673.1 gg_id:163857 human fecal clone 001-d11
FJ680750.1 gg_id:518347 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ678215.1 gg_id:520650 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ679230.1 gg_id:520332 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ676809.1 gg_id:530331 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ673289.1 gg_id:513756 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ679155.1 gg_id:528625 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ683157.1 gg_id:521108 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ678890.1 gg_id:521551 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ679040.1 gg_id:528737 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ672134.1 gg_id:518385 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
FJ673998.1 gg_id:532469 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ682525.1 gg_id:521818 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ681785.1 gg_id:531974 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ676261.1 gg_id:529152 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ678600.1 gg_id:524710 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EF445277.1 gg_id:205408 dairy cow rumen clone NED4F7

FJ679295.1	511528	4856.6	5038.2	7488.1	6824.1	8242.0	6814.5
FJ681318.1	519035	3679.6	4643.9	4051.8	4339.3	9651.0	5762.8
FJ673806.1	519747	5022.9	7700.7	7303.6	5037.2	8756.0	9643.1
FJ685189.1	515645	3413.9	4650.7	6078.7	4822.7	5731.2	4728.7
FJ683080.1	526775	12237.4	13024.2	6203.0	8256.8	10200.3	7609.4
FJ678755.1	524387	6529.7	7303.6	5513.5	8237.9	9986.4	9221.4
FJ685307.1	526414	2083.1	2976.9	2946.6	2030.1	4046.1	6151.9
FJ673228.1	521876	8309.8	6698.3	8955.7	10249.6	8959.0	7745.3
FJ681105.1	518112	4138.6	3809.3	3671.5	5914.6	7495.5	5717.9
FJ678694.1	532412	7659.3	8629.1	5136.4	6050.0	7373.2	6763.2
FJ684018.1	529769	3947.9	3534.7	3194.3	4492.1	4457.5	5840.0
FJ682802.1	522494	3002.9	3873.2	5949.1	3064.3	7398.3	4530.8
FJ681900.1	523612	7124.2	4816.1	6290.4	9339.0	10942.0	7734.8
FJ678730.1	531116	5959.2	6099.3	3005.4	6338.3	10138.1	7778.2
FJ683575.1	516087	2446.9	2394.2	5246.1	3435.6	1991.8	3472.8
FJ673346.1	514406	6078.3	6220.2	4472.0	4517.6	7491.8	6214.0
FJ673002.1	524997	2748.3	5366.3	3581.0	3031.0	10353.0	11523.6
FJ678905.1	530101	3098.8	3088.5	4920.6	6988.2	3383.0	4287.6
FJ684508.1	525389	1586.8	3119.6	1452.6	1173.8	11344.5	6588.2
FJ673381.1	516159	9322.1	11169.1	5710.7	8317.2	12324.9	12029.1
FJ680565.1	519066	4411.8	6594.6	9410.0	5431.0	15359.3	11064.6
FJ679553.1	531893	7665.9	7180.8	3220.7	8344.4	8413.1	7572.7
FJ676324.1	517601	10969.3	10509.6	9207.6	11387.2	10544.2	10052.0
FJ679041.1	530617	4737.9	4542.2	4698.6	3936.4	8895.8	6804.3
DQ904673.1	163857	8809.0	10231.8	6455.6	9677.2	15270.4	12055.2
FJ680750.1	518347	8402.7	9467.7	4406.2	9209.1	14806.8	11140.2
FJ678215.1	520650	4377.1	5860.4	3804.2	4999.2	9533.8	8309.5
FJ679230.1	520332	8753.7	8213.3	5454.8	8148.7	9967.3	7843.0
FJ676809.1	530331	2234.3	2790.9	3707.2	2805.2	3728.1	4800.2
FJ673289.1	513756	3520.4	3480.3	4677.0	4555.6	4492.1	3964.1
FJ679155.1	528625	4937.6	3947.4	4213.9	6938.8	6658.1	5335.7
FJ683157.1	521108	435.1	1678.3	3806.5	1738.5	2087.3	1652.2
FJ678890.1	521551	4456.7	4790.3	4987.7	6113.8	7544.1	5654.9
FJ679040.1	528737	14271.7	14930.1	10047.2	11966.7	16406.2	14127.0
FJ672134.1	518385	452.3	632.8	1771.6	467.8	677.2	979.6
FJ673998.1	532469	3622.0	3263.1	11220.0	7341.5	8792.8	4299.1
FJ682525.1	521818	10667.1	10006.4	6795.1	8201.0	9823.8	8252.7
FJ681785.1	531974	7246.4	5405.4	10106.5	8045.8	6840.4	6420.0
FJ676261.1	529152	7926.4	7654.4	4039.6	7740.0	14060.0	11130.6
FJ678600.1	524710	9468.4	10954.4	7352.3	9152.8	9428.3	6856.2
EF445277.1	205408	2418.7	3741.6	3838.0	2976.5	5639.8	5422.3

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s__unclassified	1312

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FJ679573.1 gg_id:530904 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU794184.1 gg_id:344867 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_B23
FJ679565.1 gg_id:527828 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ679188.1 gg_id:520121 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ673005.1 gg_id:530535 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
Y17599.1 gg_id:9351 Succinimonas amylolytica str. DSM 2873
EF445219.1 gg_id:207757 dairy cow rumen clone NED4C12
FJ440064.1 gg_id:511871 Megamonas hypermegale colonization correlates Campylobacter jejuni exclusion pou
AJ420985.1 gg_id:29865 Anaerobiospirillum thomasii str. DSM 11806T
FJ832419.1 gg_id:577393 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P1Q401_75C10
GU303829.1 gg_id:539467 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c
AF018457.1 gg_id:9354 Aeromonas subgroup subdivision clone 12-11
FJ832403.1 gg_id:548716 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P1Q401_45E06
FJ832430.1 gg_id:559309 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P1Q401_91C12
DQ456106.1 gg_id:158543 pre-adolescent turkey cecum clone CFT114E2
EU381934.1 gg_id:271179 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase
FJ952818.1 gg_id:443894 Alteromonas sp. str. 2tb4
GQ391974.1 gg_id:519442 Aestuariibacter sp. str. PaD1.02
AB076557.1 gg_id:60317 Agarivorans albus str. MKT 82
GQ200591.1 gg_id:544653 Agarivorans sp. str. WH0801
DQ416550.1 gg_id:153331 s1cb18
AF290480.1 gg_id:27315 cf. Alishewanella fetalis clone Llangefni 75 mite
AF144407.1 gg_id:33192 Alishewanella fetalis str. CCUG 30811
AY093457.1 gg_id:55811 deep marine sediment clone MB-A2-102
DQ256339.1 gg_id:142481 subsurface water clone EV818BHEB5102702SAS10
AY820719.1 gg_id:109054 drilling fluid clone CCSD_DF2030_B15
FJ040187.1 gg_id:347660 Alteromonas genoviensis str. I96
EU189225.1 gg_id:239877 Alteromonas marina str. MB 3
AY881234.1 gg_id:145384 Alteromonas marina SCH0402
AF288360.1 gg_id:71626 Alteromonas alvinellae str. HY757
AF386742.1 gg_id:44702 Alteromonas sp. str. 4BT
AJ319537.1 gg_id:71568 Alteromonas macleodii subsp. abyssi str. HYD657 subsp.
AM931040.1 gg_id:239418 Alteromonas sp. str. BUS 07-8
DQ836766.1 gg_id:163484 Alteromonas simiduii str. BCRC 17572
AF114499.1 gg_id:8878 attached marine recovered surface clone 17 proteobacterium
EF061429.1 gg_id:190836 Alteromonas sp. NJSX37
EU982324.1 gg_id:322486 Alteromonas sp. str. UST010723-013
FJ210814.1 gg_id:309174 Alteromonas sp. str. QDHT-19
DQ486510.1 gg_id:227411 Alteromonas sp. str. DG1302
AF114505.1 gg_id:8883 attached marine recovered deep chlorophyll maximum depth clone 2 proteobacterium

FJ680116.1	526488	8572.0	7576.9	5252.9	9054.2	7908.4	8888.3
FJ679573.1	530904	10175.3	9431.2	7861.4	11566.5	13598.9	11617.5
EU794184.1	344867	2778.9	2843.0	2756.2	1734.3	4899.0	6884.4
FJ679565.1	527828	4404.1	4802.9	2698.0	2812.8	4875.5	3869.5
FJ679188.1	520121	3517.9	3319.4	6593.5	3976.0	4798.7	4051.3
FJ673005.1	530535	11566.4	10450.1	4688.9	11482.2	10961.4	10790.8
Y17599.1	9351	969.7	1926.3	4528.8	870.3	6066.1	2388.9
EF445219.1	207757	6350.5	7615.7	2736.6	6577.7	6480.0	7350.8
FJ440064.1	511871	8615.3	9644.6	3305.7	5916.4	5336.1	5907.3
AJ420985.1	29865	394.1	479.9	954.7	728.6	183.4	373.9
FJ832419.1	577393	3470.2	4057.4	7527.2	4821.2	9753.4	7311.6
GU303829.1	539467	614.8	582.5	1025.3	2950.3	1132.5	2010.6
AF018457.1	9354	2854.4	3422.7	2513.2	3993.6	2495.8	3133.0
FJ832403.1	548716	2780.1	2981.4	4913.6	3956.5	5327.3	3514.2
FJ832430.1	559309	3661.1	3070.8	3266.0	2854.8	8570.4	6199.1
DQ456106.1	158543	385.2	766.2	1872.4	263.3	2013.9	565.3
EU381934.1	271179	1842.7	2226.9	642.4	1597.0	1523.4	1330.3
FJ952818.1	443894	258.8	361.6	670.3	320.6	534.2	242.7
GQ391974.1	519442	550.7	993.5	1322.4	1327.7	4507.5	1612.0
AB076557.1	60317	1005.7	873.9	3501.1	1701.3	588.6	1192.0
GQ200591.1	544653	2107.6	3296.3	3054.9	3100.3	4484.1	5918.6
DQ416550.1	153331	4992.6	3947.7	5193.8	5882.9	5988.6	6591.5
AF290480.1	27315	2530.2	1065.7	749.7	2021.7	278.8	829.2
AF144407.1	33192	1046.3	941.4	1609.1	1157.7	2493.6	2076.7
AY093457.1	55811	1922.5	2599.2	4836.5	2196.2	6352.5	5750.1
DQ256339.1	142481	5528.8	6912.2	1870.9	4288.4	3919.1	4341.5
AY820719.1	109054	6542.7	5071.9	4287.9	8091.7	15276.6	10488.8
FJ040187.1	347660	108.6	136.2	54.8	128.0	173.3	130.1
EU189225.1	239877	787.5	762.1	1351.4	1072.1	3201.0	2211.2
AY881234.1	145384	806.5	776.0	872.0	976.7	2603.3	904.4
AF288360.1	71626	31.7	47.9	61.9	92.3	107.1	85.9
AF386742.1	44702	10278.2	9035.2	1399.2	3332.6	6066.0	6589.5
AJ319537.1	71568	288.6	299.6	799.3	514.8	2396.4	702.2
AM931040.1	239418	691.7	635.4	892.2	555.7	2548.4	773.3
DQ836766.1	163484	644.2	613.4	851.7	555.7	2405.7	870.0
AF114499.1	8878	88.0	270.5	53.2	158.0	818.1	185.2
EF061429.1	190836	905.3	904.7	317.6	682.3	777.0	479.9
EU982324.1	322486	415.9	271.5	177.4	835.8	465.7	518.4
FJ210814.1	309174	775.9	349.8	731.4	692.7	925.9	512.5
DQ486510.1	227411	758.3	521.8	649.7	873.4	3278.6	710.7
AF114505.1	8883	5454.6	6284.4	5369.7	4836.4	11264.3	5202.1

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AF114498.1 gg_id:8877 attached marine recovered surface clone 14 proteobacterium
AF114504.1 gg_id:8882 attached marine recovered depth 400m clone 25 proteobacterium
AF114508.1 gg_id:8886 attached marine recovered surface clone 8
AY428573.1 gg_id:105550 Alteromonas litorea str. TF-22
Y18232.1 gg_id:19130 Alteromonas macleodii str. CH-518
AY344429.1 gg_id:91492 Lake Kauhako 30 m clone K2-30-18
AM885869.1 gg_id:240896 Alteromonas macleodii R-28696
AF114501.1 gg_id:8880 attached marine recovered surface clone 18 proteobacterium
AF114496.1 gg_id:8875 attached marine recovered deep chlorophyll maximum depth clone proteobacterium
EF574195.1 gg_id:228587 site S25 near Coco's Island marine clone S25_539
DQ071162.1 gg_id:136631 marine surface water clone Surf1.42
AM882576.1 gg_id:311934 Structure along hydrocarbon contamination coastal sediment oil polluted water pet
AY165578.1 gg_id:81399 Antarctic pack ice Lasarev Sea Southern Ocean clone ANTXI/4_14-11
AF468279.1 gg_id:80086 Arctic pack ice; northern Fram Strait; 80 31.1 N; 01 deg 59.7 min E clone ARKIA-118
CP000388.1 gg_id:160590 Pseudoalteromonas atlantica str. T6c
AY697880.1 gg_id:104267 Antarctica clone F2C28
U85854.1 gg_id:8873 Glaciecola pallidula str. ACAM 615T IC079
AY167284.2 gg_id:81210 Glaciecola sp. str. ANT9142
AB238790.1 gg_id:140832 Glaciecola sp. #105
AM941178.1 gg_id:284078 Microbes enriched seawater after addition coral mucus and reef waters mixture1-8
AM913910.1 gg_id:439090 antibiotic-active brown alga Laminaria saccharina Baltic Sea Saccharina latissima
AJ240915.1 gg_id:73940 5' clone CHAB-XII-8
AY771709.1 gg_id:108683 Glaciecola mesophila str. S2-38
AJ488501.1 gg_id:65357 Glaciecola mesophila str. KMM 241
Y18230.1 gg_id:202397 macleodii- and cellular rDNAs Mediterranean seawater mesocosm experiment Alterom
AJ548479.1 gg_id:89023 Glaciecola mesophila str. LMG 21855
AF173965.1 gg_id:71399 Alteromonas macleodii str. KT1113
AY349463.1 gg_id:91221 Glaciecola sp. WHOI JT-6b
U73724.1 gg_id:8898 gas vacuolate str. 214.6
AJ293820.1 gg_id:39858 Glaciecola polaris str. LMG 21857
DQ784575.1 gg_id:162089 Glaciecola agarolytica str. NO2
AY553295.1 gg_id:106840 Salinimonas chungwhensis str. BH030046
EU583725.1 gg_id:272031 Alteromonas sp. str. JSM 073008
AJ240916.1 gg_id:74015 5' clone CHAB-V-29
AB040465.1 gg_id:38060 Alteromonas sp. str. K
FJ024319.1 gg_id:368249 Prokaryotic and their role biogeochemical cycling marine basalts basalt Juan de Fuca I
AB473549.1 gg_id:419632 Aestuariibacter sp. NT-2008 str. Sd 2-38 (= KMM 3894)
AY207502.1 gg_id:84007 Aestuariibacter salexigens str. JC2042
AY207503.1 gg_id:83231 Aestuariibacter halophilus str. JC2043
AB040466.1 gg_id:45496 Alteromonas sp. str. D
FJ202664.1 gg_id:350427 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k

AF114498.1	8877	739.7	278.4	918.7	1457.5	404.4	866.8
AF114504.1	8882	191.2	251.0	410.3	243.6	248.7	240.2
AF114508.1	8886	76.2	150.5	246.0	117.3	593.4	328.9
AY428573.1	105550	482.5	657.8	807.5	852.4	3075.5	1256.0
Y18232.1	19130	2948.0	3543.5	4796.0	596.9	7695.7	4926.4
AY344429.1	91492	793.0	1318.1	568.8	1428.1	2133.7	1131.4
AM885869.1	240896	662.8	499.3	241.9	559.3	370.0	297.6
AF114501.1	8880	7198.2	7658.7	5368.8	5482.7	5624.8	5198.2
AF114496.1	8875	1149.1	1624.2	640.2	1947.1	2697.4	1492.3
EF574195.1	228587	1708.9	2955.8	2356.2	1361.7	3866.9	1778.5
DQ071162.1	136631	2703.7	4624.8	6494.3	3512.4	6068.4	3394.2
AM882576.1	311934	665.1	831.5	3003.8	345.1	5545.1	578.6
AY165578.1	81399	2199.4	1779.7	2035.4	2733.0	3657.0	1665.4
AF468279.1	80086	1194.4	843.0	1639.1	1008.0	3010.4	1585.9
CP000388.1	160590	3531.7	3066.7	2966.8	3146.3	3377.1	3087.7
AY697880.1	104267	4945.3	4413.0	4080.6	4123.8	4643.2	5618.2
U85854.1	8873	64.5	105.7	254.6	67.0	63.1	48.6
AY167284.2	81210	3528.5	2050.1	2166.6	3779.6	2770.1	3843.6
AB238790.1	140832	8999.7	9744.3	8811.9	8290.2	10772.5	11982.6
AM941178.1	284078	2646.6	3175.5	5024.0	3874.5	8718.8	4902.9
AM913910.1	439090	1979.3	2111.2	3648.5	1380.4	3858.3	3425.2
AJ240915.1	73940	8774.5	8906.1	7442.0	7948.2	9250.9	9160.5
AY771709.1	108683	2511.4	1658.6	1172.6	1672.2	2665.6	3890.7
AJ488501.1	65357	3689.7	3510.8	3060.4	3193.3	3542.4	3178.0
Y18230.1	202397	952.2	1054.9	1954.2	1173.0	917.6	1736.2
AJ548479.1	89023	3946.7	3474.8	2777.5	3135.6	3322.9	3076.6
AF173965.1	71399	142.2	320.5	287.8	74.9	1729.1	306.9
AY349463.1	91221	1628.0	1774.8	3165.4	3167.8	5982.3	3528.2
U73724.1	8898	124.1	231.5	385.7	322.4	425.0	281.9
AJ293820.1	39858	149.4	114.7	226.3	265.9	1407.4	2730.3
DQ784575.1	162089	448.1	558.6	697.1	556.6	2876.3	897.9
AY553295.1	106840	32.8	42.6	75.7	55.5	72.1	44.4
EU583725.1	272031	1244.7	940.8	2532.6	1764.0	687.7	843.9
AJ240916.1	74015	380.3	318.4	252.8	199.2	86.5	65.3
AB040465.1	38060	2359.6	2981.7	1064.7	3402.4	3168.2	3434.5
FJ024319.1	368249	70.6	107.0	142.2	90.5	299.0	139.3
AB473549.1	419632	2901.8	2860.0	3399.2	4678.8	5278.8	4276.2
AY207502.1	84007	1674.9	473.3	960.0	613.5	377.3	755.3
AY207503.1	83231	3047.7	2003.6	2479.6	1886.6	5903.8	2699.4
AB040466.1	45496	867.1	1548.3	1570.9	1644.5	469.0	1996.0
FJ202664.1	350427	110.9	259.6	1088.5	446.5	411.5	338.7

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s__Colwellia psychrerythraea	1002
s__Colwellia psychrerythraea	131

EU188146.1 gg_id:347006 Uncultivated oceanic unicellular N2-fixing cyanobacteria are picoplankton unusual 7(
FJ425616.1 gg_id:366875 communnities healthy and diseased colonies Caribbean coral Montastrea faveolata A
GU289642.1 gg_id:552344 Alteromonas sp. str. MEBiC06033
EU907922.1 gg_id:304111 Alteromonas sp. str. SKUK MB1007
DQ343294.1 gg_id:149488 Bowmanella denitrificans str. BD1
EF092177.1 gg_id:275572 Persistent Axinella corrugata Alteromonas clone AC3_H2
AJ295715.1 gg_id:73259 Alteromonas stellipolaris str. LMG 21861
AM882575.1 gg_id:316071 Structure along hydrocarbon contamination coastal sediment oil polluted water pet
EU287412.1 gg_id:256595 Pacific arctic surface sediment clone S26-112
AM990642.1 gg_id:277954 Alteromonas sp. MOLA 365
AY926461.1 gg_id:113825 Alteromonas hispanica str. B-35
AB040464.1 gg_id:137101 Alteromonas sp. str. S
AB526336.1 gg_id:573848 Alteromonas sp. str. JAM-GA13
Y18233.1 gg_id:8895 Alteromonas macleodii str. CH-460
EU188189.1 gg_id:317008 Uncultivated oceanic unicellular N2-fixing cyanobacteria are picoplankton unusual 7(
GQ495024.1 gg_id:581173 Pseudoalteromonas sp. str. W-14-2
AM183347.1 gg_id:155988 Alishewanella baltica str. BA131
EU841485.1 gg_id:310357 Alishewanella sp. str. 205
AB295494.1 gg_id:216998 Alteromonas sp. str. A14
NR_027234.1 gg_id:540876 Algicola sagamiensis str. B-10-31; DSM 14643
GU108538.1 gg_id:591045 active chemolithoautotrophic prokaryotes sulfidic zone Black pelagic redoxcline dete
EU714266.1 gg_id:332103 Alteromonas sp. str. BG20
DQ913886.1 gg_id:276341 Celerinatantimonas diazotrophica J-G1-2
AJ002006.1 gg_id:8823 Rheinheimera baltica str. OS140 Baltic # 166
DQ985066.1 gg_id:177157 Rheinheimera sp. str. JL1145
GQ009534.1 gg_id:500133 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw77
GQ280117.1 gg_id:570209 Rheinheimera aquimaris str. JS-47
FJ170027.1 gg_id:325282 Rheinheimera sp. str. CF12-10
FJ821606.1 gg_id:569335 Rheinheimera sp. str. TPS16
DQ298025.2 gg_id:143812 Rheinheimera chironomi str. K19414
FJ902308.1 gg_id:509338 phreatic limestone sinkholes northeastern Mexico biomat rock outcrop cenote La Pal
AM117933.1 gg_id:143326 marine boreal sponge Geodia baretti Norway:Korsfjord
GQ240227.1 gg_id:576918 Rheinheimera sp. str. BZ19
EU662623.1 gg_id:594183 Productivity- Chemolithoautotrophically Based Sulfidic Karst Systems floating microb
GQ130023.1 gg_id:440958 Genetic inventory 'JPL-SAF' during MSL mission spacecraft assembly clean room floc
AY887010.1 gg_id:114447 fresh water clone 1.34.5
FJ902639.1 gg_id:593719 phreatic limestone sinkholes northeastern Mexico biofilm 1m deep hydrothermal ver
AY701891.1 gg_id:140048 Rheinheimera texana str. A62-14B
GU108532.1 gg_id:548750 active chemolithoautotrophic prokaryotes sulfidic zone Black pelagic redoxcline dete
FN397813.1 gg_id:405654 geomicrobiological investigation sediments Gulf Cadiz GeoB 9072-1 anoxic sub-surfa
AY167340.1 gg_id:81146 Psychrobacter sp. str. ARK10133

EU188146.1	347006	2426.0	2011.6	2081.1	743.1	3462.5	4084.7
FJ425616.1	366875	1718.4	1537.6	2871.0	3275.4	3686.7	2555.4
GU289642.1	552344	633.8	743.2	311.2	643.3	3460.1	1089.5
EU907922.1	304111	1457.0	966.0	1566.8	1636.7	2363.5	1279.4
DQ343294.1	149488	85.1	52.9	27.6	112.3	66.8	85.9
EF092177.1	275572	1877.2	1315.6	2777.5	2303.3	3838.6	2824.9
AJ295715.1	73259	3823.7	1989.5	5100.8	4031.1	8464.3	4675.5
AM882575.1	316071	1317.2	1551.0	3560.4	3284.2	4745.0	2300.0
EU287412.1	256595	1273.6	1749.1	4185.2	2029.6	5570.8	3361.3
AM990642.1	277954	120.8	280.4	736.4	359.1	1581.4	592.3
AY926461.1	113825	1559.7	709.1	910.7	1824.5	2957.5	797.1
AB040464.1	137101	52.2	55.6	56.3	81.9	86.1	40.8
AB526336.1	573848	1704.6	766.6	7117.8	6631.1	2689.2	1335.3
Y18233.1	8895	238.9	261.1	299.5	303.6	541.2	175.1
EU188189.1	317008	4780.9	2349.8	8021.5	6195.1	6034.4	3531.0
GQ495024.1	581173	157.8	267.2	225.3	179.6	1517.4	204.9
AM183347.1	155988	5293.7	5569.0	4274.6	5059.6	8884.5	6881.3
EU841485.1	310357	2480.6	3050.4	1967.4	2389.1	2415.8	3212.7
AB295494.1	216998	486.5	260.3	367.9	412.1	1370.2	270.7
NR_027234.1	540876	96.8	123.2	117.4	81.2	121.6	61.1
GU108538.1	591045	5762.7	5305.6	4594.0	5669.4	8171.8	6046.1
EU714266.1	332103	422.0	459.0	1310.8	626.6	1015.7	1170.4
DQ913886.1	276341	2094.8	2994.7	2348.2	2457.1	4110.5	3457.5
AJ002006.1	8823	12111.2	10724.4	10762.1	11291.2	12790.5	11482.2
DQ985066.1	177157	2734.5	3616.4	5534.2	3541.9	6313.8	6325.1
GQ009534.1	500133	453.5	279.9	385.1	255.5	188.3	1242.1
GQ280117.1	570209	5181.2	4576.1	5517.9	5417.2	7729.1	5903.2
FJ170027.1	325282	4115.2	3847.3	3758.3	4361.2	5659.2	4734.5
FJ821606.1	569335	2948.0	1599.3	3043.7	3086.1	2729.8	3451.4
DQ298025.2	143812	2133.4	1191.3	1976.2	1931.9	1146.4	3624.0
FJ902308.1	509338	10831.6	7013.8	7963.6	11726.7	9593.7	8468.1
AM117933.1	143326	2667.0	2205.0	2731.7	2501.7	1515.6	2552.9
GQ240227.1	576918	2252.1	2862.6	4184.4	3146.9	1363.6	4022.9
EU662623.1	594183	3762.2	2519.0	6036.3	4721.0	3819.7	4040.9
GQ130023.1	440958	5642.5	4403.6	6025.0	6844.9	5645.2	6285.7
AY887010.1	114447	8476.4	9630.0	3087.9	3929.3	4696.9	6242.1
FJ902639.1	593719	4346.3	3849.6	3941.8	2348.2	4460.6	7792.1
AY701891.1	140048	2715.7	2697.9	5648.5	8378.5	3122.8	5303.7
GU108532.1	548750	1328.0	1788.5	2518.0	1366.1	2219.3	2213.3
FN397813.1	405654	2668.6	2607.9	3393.6	2221.2	3785.6	4279.4
AY167340.1	81146	3710.7	6397.4	4563.8	3548.6	8131.1	9476.1

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o__Alteromonadales	f__Colwelliaceae
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s__Colwellia psychrerythraea	1575
s__Colwellia psychrerythraea	2018
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s__Colwellia psychrerythraea	369
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s__Colwellia psychrerythraea	968
s__Colwellia rossensis	852
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s__unclassified	1060
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s__unclassified	2158
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s__unclassified	510
s__unclassified	523
s__unclassified	610
s__unclassified	69
s__unclassified	738
s__unclassified	95
s__unclassified	990
s__Thalassomonas agarivorans	1374

AF173964.1 gg_id:36120 Colwellia psychrerythraea str. KT0919
EU236321.1 gg_id:299112 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg1bG1
AB011364.1 gg_id:8843 Colwellia psychrerythraea str. ATCC27364
FN397812.1 gg_id:392867 geomicrobiological investigation sediments Gulf Cadiz GeoB 9072-1 anoxic sub-surfa
GU061308.1 gg_id:560509 Evaluation culturing methods cultivate previously Yel Sea intertidal beach seawater
U85841.1 gg_id:8840 Colwellia psychrerythraea str. ACAM 604
AF001375.1 gg_id:8836 Colwellia psychrerythraea str. ATCC27364; ACAM 550T
AF530145.1 gg_id:61116 Colwellia psychrerythraea str. MGP-41
AY167332.1 gg_id:82309 Colwellia rossensis str. ANT9271
AY167269.1 gg_id:82300 Colwellia rossensis str. ANT8283
FJ905674.1 gg_id:560989 s Tonga-Kermadec iron oxide chimney-like structure on Volcano 19 Tonga Arc clone V
DQ027051.1 gg_id:130223 Colwellia sp. str. MT41
EF551378.1 gg_id:225725 Colwellia sp. str. BSw20516
EU050773.1 gg_id:257619 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_01_78
DQ837294.1 gg_id:235556 Archaeal and pristine National Park Spain Donana coastal aquifer clone 49S1_1B_55
DQ490038.1 gg_id:158539 Microbial life ridge flank crustal fluids clone ODP-70B-02
AY167330.1 gg_id:81643 Colwellia sp. str. ANT9407
DQ351740.1 gg_id:146764 Microbial Adherent Sediment Particles Heavy Metal Contaminated North Sea Surfac
GQ350647.1 gg_id:559927 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
GQ848466.1 gg_id:581903 Microbial sediments vents along East Lau Spreading Centre deep sea hydrothermal
L10950.1 gg_id:8854 marine snow clone agg53
AY829231.2 gg_id:179606 Colwellia sp. IE7-5
EU394582.1 gg_id:309555 Coccolithophore bloom dynamics shape (NE-Atl) northern Bay Biscay pelagic particle
DQ027052.1 gg_id:131520 Colwellia sp. str. KT27
GU391219.1 gg_id:531807 Thalassomonas sp. str. JYr2
AY165571.1 gg_id:81437 Antarctic pack ice Lasarev Sea Southern Ocean clone ANTXI/4_14-151 sea
AB094412.1 gg_id:97603 Colwellia piezophila str. Y223G
AF419350.1 gg_id:74479 Colwellia sp. str. Ant5-9
EU491932.1 gg_id:271119 Abundance and microbial life ocean crust deep seawater East Pacific Rise clone EPR4
EU599214.3 gg_id:319654 Colwellia sp. str. KMD002
EU491916.1 gg_id:258657 Abundance and microbial life ocean crust deep seawater East Pacific Rise clone EPR4
DQ492707.1 gg_id:158794 Colwellia sp. str. BSi20061
NR_024635.1 gg_id:548903 Colwellia maris str. ABE-1
EU491896.1 gg_id:259552 Abundance and microbial life ocean crust deep seawater East Pacific Rise clone EPR4
AY165566.1 gg_id:81127 Antarctic pack ice Lasarev Sea Southern Ocean clone ANTXI/13-90 sea
AF530146.1 gg_id:103969 Colwellia sp. str. MGP-59
GU108544.1 gg_id:589927 active chemolithoautotrophic prokaryotes sulfidic zone Black pelagic redoxcline dete
AY167264.1 gg_id:81818 Colwellia sp. str. ANT8203
DQ923440.1 gg_id:179604 Alteromonas sp. W-6
DQ228659.1 gg_id:141317 Microbial colonizing mineral surfaces within sulfide-microbial incubator clone CH2b7
DQ212914.1 gg_id:140089 Thalassomonas agarivorans str. TMA1

AF173964.1	36120	210.3	246.6	229.2	185.1	75.0	150.2
EU236321.1	299112	265.8	257.6	337.0	207.7	228.3	368.5
AB011364.1	8843	6084.1	4473.8	3950.0	5825.1	5699.1	4166.5
FN397812.1	392867	14215.7	14219.4	13463.1	10665.7	13504.0	13512.6
GU061308.1	560509	3105.6	5667.3	2378.9	1978.0	1450.5	1874.1
U85841.1	8840	80.0	75.0	59.7	102.5	65.9	44.1
AF001375.1	8836	1046.5	1417.7	1257.8	1500.6	836.6	1385.8
AF530145.1	61116	6777.3	7945.1	6159.4	5920.8	8277.4	7082.4
AY167332.1	82309	3266.1	2143.5	1132.6	4240.0	3515.8	3371.5
AY167269.1	82300	165.8	150.9	109.3	187.9	101.7	176.2
FJ905674.1	560989	6739.6	5761.6	5363.4	6478.3	8945.5	6660.2
DQ027051.1	130223	226.9	323.4	1938.4	260.9	885.7	974.6
EF551378.1	225725	363.8	300.1	1181.2	459.3	914.8	312.6
EU050773.1	257619	572.7	588.1	3165.2	952.5	3216.7	1586.3
DQ837294.1	235556	1002.3	1032.3	389.3	517.3	645.0	561.1
DQ490038.1	158539	1877.3	2440.8	3202.8	1051.2	2828.6	2512.4
AY167330.1	81643	1273.3	933.6	2267.5	944.1	1244.0	1168.8
DQ351740.1	146764	1726.8	939.9	1052.3	1054.4	1575.0	1478.9
GQ350647.1	559927	909.1	1160.5	658.0	1118.3	798.6	666.1
GQ848466.1	581903	4521.7	3110.2	3200.2	5590.5	4413.0	3588.3
L10950.1	8854	22.1	42.3	39.7	58.4	63.0	38.2
AY829231.2	179606	3206.6	2921.2	3748.0	4414.1	2018.5	3270.8
EU394582.1	309555	102.2	127.6	53.4	166.7	1290.0	219.7
DQ027052.1	131520	3454.3	3148.2	2464.0	2203.1	3903.1	2960.5
GU391219.1	531807	242.1	362.4	2210.9	620.1	2749.8	878.1
AY165571.1	81437	5606.5	4370.4	2682.1	3265.4	1823.0	3053.9
AB094412.1	97603	2545.2	2464.9	2694.2	2793.9	5765.4	2753.5
AF419350.1	74479	5045.9	4754.2	6010.8	3441.2	4423.4	4535.6
EU491932.1	271119	271.5	349.6	512.4	483.6	89.4	675.9
EU599214.3	319654	1385.5	1120.3	1807.6	1623.4	1574.6	1297.5
EU491916.1	258657	3141.2	2418.2	1987.8	1036.1	2836.3	2303.6
DQ492707.1	158794	1380.1	1508.4	3801.8	2473.9	3765.7	1686.9
NR_024635.1	548903	303.5	251.9	274.2	241.5	60.4	148.8
EU491896.1	259552	5106.9	4807.9	6939.6	5007.3	7618.5	4653.5
AY165566.1	81127	203.0	426.7	611.5	384.1	852.0	1184.2
AF530146.1	103969	9716.0	12982.4	6300.5	6625.8	8719.8	6540.5
GU108544.1	589927	4843.6	5715.0	5891.8	5424.9	6667.1	4440.5
AY167264.1	81818	285.3	355.2	339.9	521.8	410.8	588.4
DQ923440.1	179604	400.1	1547.3	1750.1	433.0	766.3	842.1
DQ228659.1	141317	2450.5	2398.8	1798.9	907.7	2010.5	1541.9
DQ212914.1	140089	2432.7	1603.2	3304.6	3865.5	1830.2	1092.3

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GQ848478.1 gg_id:584370 Microbial sediments vents along East Lau Spreading Centre deep sea hydrothermal
FJ717227.1 gg_id:553622 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United King
FJ202297.1 gg_id:322290 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k
GU230351.1 gg_id:594414 Multilevel approach along Rio de la Plata-South Atlantic Ocean coastal sediment clo
FJ203045.1 gg_id:322845 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c
AY643537.2 gg_id:131602 White plague like disease Eilat coral reef
AY194066.1 gg_id:81968 Thalassomonas ganghwensis str. JC2041
FJ203217.1 gg_id:306276 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c
EU491328.1 gg_id:269454 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak
U15115.1 gg_id:8864 hydrothermal vent clone PVB_OTU_12
FJ791872.1 gg_id:513615 Unexpectedly archaeal species shift between rare and dominant over thousand year
FJ203091.1 gg_id:324976 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c
AJ294747.1 gg_id:26868 Thalassomonas viridans str. XOM5 CECT 5082 DSM 13753
AY770724.1 gg_id:110997 sea urchin Paracentrotus lividus clone PlS53
FJ952826.1 gg_id:382239 Colwellia sp. str. 1tb5
AB193748.1 gg_id:111458 Ferrimonas marina str. A2A-30
AB252733.1 gg_id:243052 Paraferrimonas sedimenticola str. Mok-142
GU391222.1 gg_id:528038 Ferrimonas sp. str. JYr13
FJ203654.1 gg_id:341133 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h
EU620413.1 gg_id:278677 Ferrimonas balearica str. S8-05
AB193752.1 gg_id:112098 Ferrimonas balearica str. A2A-18
AB193755.1 gg_id:111912 Ferrimonas sp. str. A3B-58
NR_027560.1 gg_id:549106 Idiomarina baltica OS145 str. OS145; DSM 15154
NC_006512.1 gg_id:128686 Idiomarina loihiensis str. L2TR
AE017340.1 gg_id:128915 Idiomarina loihiensis str. L2TR
AY092077.1 gg_id:67499 Idiomarina loihiensis str. 53
AY635468.1 gg_id:107632 Idiomarina seosinensis str. CL-SP19
EU603445.1 gg_id:275762 Idiomarina seosinensis str. PTG4-5
AY553081.1 gg_id:107227 Idiomarina loihiensis str. GSP41
NR_029115.1 gg_id:557590 Idiomarina fontislapidosi str. F23; LMG 22169
EU440964.1 gg_id:311612 Idiomarina seosinensis str. PR58-8
DQ235566.1 gg_id:142194 biofilm water pipeline biofilms steel pipelines Gulf Mexico clone 20
AY526862.1 gg_id:102489 Idiomarina ramblicola str. R22
AY505529.1 gg_id:101950 Idiomarina loihiensis str. GSP13
FM877003.1 gg_id:574998 Idiomarina sp. IT-2008 str. CVS-6
DQ234155.2 gg_id:144284 determined library mangrove clone DS071
EF486355.1 gg_id:222466 Idiomarina salinae str. ISL-52
GQ180187.1 gg_id:591011 Pseudidiomarina sp. str. SW5
GQ246209.1 gg_id:577128 Pseudidiomarina sp. str. YCSA4
DQ416777.1 gg_id:268666 Idiomarina sp. G2DM-8
DQ118948.1 gg_id:131585 Pseudoidiomarina taiwanensis str. PIT1

GQ848478.1	584370	3340.1	2070.4	5241.1	2641.2	2750.2	3641.2
FJ717227.1	553622	7683.4	7498.5	5741.0	6815.4	8228.0	6283.5
FJ202297.1	322290	2892.9	2297.9	1071.2	514.7	1986.3	1259.9
GU230351.1	594414	3115.5	2459.2	2593.4	2651.7	2613.4	2562.9
FJ203045.1	322845	5027.1	2414.2	1646.8	1313.3	595.8	869.0
AY643537.2	131602	1466.0	1040.0	1394.6	1042.4	213.7	566.3
AY194066.1	81968	2826.1	1928.7	5056.6	2367.1	4140.1	3358.3
FJ203217.1	306276	8150.8	8240.5	8610.8	8343.6	14239.8	12696.5
EU491328.1	269454	5374.1	4960.6	4209.0	4523.4	7520.5	5888.6
U15115.1	8864	110.3	139.6	338.4	124.4	127.2	105.7
FJ791872.1	513615	2868.1	3162.8	3629.7	3024.3	2829.3	2468.5
FJ203091.1	324976	7089.9	4869.1	2859.8	8061.2	7459.1	6250.1
AJ294747.1	26868	113.3	165.7	124.4	108.7	75.0	253.2
AY770724.1	110997	32.1	38.3	16.5	45.6	50.5	26.1
FJ952826.1	382239	1111.2	1956.3	2890.2	1143.4	2648.4	2073.4
AB193748.1	111458	197.2	228.6	492.0	195.0	199.4	74.4
AB252733.1	243052	1165.6	760.5	2433.4	1947.7	687.8	1041.1
GU391222.1	528038	148.2	45.3	260.9	54.1	160.5	133.6
FJ203654.1	341133	4079.4	3932.9	1294.6	5474.8	6064.3	4830.9
EU620413.1	278677	213.3	203.5	2128.5	346.8	305.1	280.1
AB193752.1	112098	888.7	486.4	2190.5	1463.6	1042.1	1149.9
AB193755.1	111912	418.9	822.5	2537.4	1215.1	399.9	503.1
NR_027560.1	549106	462.2	865.9	2293.1	542.6	930.3	684.5
NC_006512.1	128686	887.7	1683.3	1245.2	833.5	2754.9	1377.1
AE017340.1	128915	1628.4	1802.8	2876.1	1168.5	4945.0	2578.6
AY092077.1	67499	788.7	1335.5	1178.0	621.1	880.1	982.6
AY635468.1	107632	4623.9	5818.4	2578.9	2152.5	3969.9	2432.8
EU603445.1	275762	850.2	1401.7	2178.3	1502.0	785.5	1358.7
AY553081.1	107227	1549.7	1915.2	4304.8	1345.0	8458.7	2442.3
NR_029115.1	557590	582.7	1501.0	3316.6	1076.7	1198.5	2046.9
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DQ235566.1	142194	4459.9	4436.2	2870.8	4927.7	7565.9	4942.4
AY526862.1	102489	1849.1	2033.2	4613.0	1422.1	5366.5	2601.0
AY505529.1	101950	449.2	694.1	834.4	333.0	1474.3	866.6
FM877003.1	574998	46.5	123.9	275.3	102.9	242.3	618.0
DQ234155.2	144284	74.9	60.6	106.7	112.8	99.1	62.1
EF486355.1	222466	248.5	549.3	470.3	169.7	1777.4	707.4
GQ180187.1	591011	258.0	419.3	490.3	359.2	449.4	312.0
GQ246209.1	577128	537.3	900.8	1243.2	406.6	1607.2	1707.2
DQ416777.1	268666	182.5	219.9	670.2	272.8	1142.3	826.5
DQ118948.1	131585	347.7	688.5	1827.6	471.4	419.3	346.9

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EF212001.1 gg_id:214514 Pseudidiomarina sp. str. c121
EU600202.2 gg_id:260949 Pseudidiomarina sp. str. 8C
EU722654.1 gg_id:327394 Microbial athalassohaline Tirez lagoon (Spain) sediment clone SB43
EF554907.1 gg_id:222862 Idiomarina sp. str. G-He8
GU458902.1 gg_id:562858 microbiota human male female forehead forearm and influence make-up skin clone
X92129.1 gg_id:44150 Crater Lake isolate 11C1
GU471247.1 gg_id:517013 Idiomarina sp. str. 10-D-4
EF554896.1 gg_id:226059 Idiomarina sp. str. JK38
FJ152984.1 gg_id:347471 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX4CI
EF554906.1 gg_id:223511 Idiomarina sp. str. G-He7
X92128.1 gg_id:32525 Lake Nakuru isolate 20N1
D21224.1 gg_id:8975 Moritella japonica str. DSK1
AF530133.1 gg_id:70982 Moritella sp. str. MGP-6
AJ132226.1 gg_id:8977 Moritella viscosa str. NVI 88/478T
AB189343.1 gg_id:112983 cold seep sediment clone JT58-18
AJ297540.1 gg_id:48310 Moritella marina str. NCIMB 2263
AY700605.1 gg_id:109434 Australia: Great Barrier Reef clone PDA-OTU7
AB183504.1 gg_id:105913 Moritella sp. str. 47A1
AB008797.1 gg_id:8989 Moritella yayanosii str. DB21MT-5
AY382585.1 gg_id:96373 Moritella sp. str. 2-2-2-1
AB038033.1 gg_id:33284 Moritella marina str. ATCC15381T
NR_025380.1 gg_id:573974 Moritella abyssi str. 2693; JCM 11436
AJ252023.2 gg_id:72172 Moritella profunda str. 2674
AB183499.1 gg_id:101616 Moritella sp. str. 38C1
AB183496.1 gg_id:101122 Moritella sp. str. 36C1
AB013841.1 gg_id:8993 Moritella sp. 9-11.F
AB013842.1 gg_id:8994 Shewanella sp. 7-1.E
AB040467.1 gg_id:20333 Pseudoalteromonas sp. str. R
DQ349123.1 gg_id:147282 Pseudoalteromonas aurantia
CR954246.1 gg_id:140486 Pseudoalteromonas haloplanktis str. TAC125
CR954246.1 gg_id:140406 Pseudoalteromonas haloplanktis str. TAC125
AY040230.1 gg_id:21879 Pseudoalteromonas translucida str. KMM520
AF316144.1 gg_id:52879 Pseudoalteromonas issachenkonii str. KMM 3549; F13
EU880522.1 gg_id:351145 Pseudoalteromonas elyakovii str. P18
AF316142.1 gg_id:37455 Pseudoalteromonas issachenkonii str. KMM 3558; F2
FJ457238.1 gg_id:568943 Pseudoalteromonas luteoviolacea str. S4060
FJ952795.1 gg_id:446774 Pseudoalteromonas sp. str. 1tc11
FJ200646.1 gg_id:308744 Pseudoalteromonas haloplanktis str. I 6
EF584051.1 gg_id:228654 Pseudoalteromonas sp. str. GAS9
EF584064.1 gg_id:227631 Pseudoalteromonas sp. str. LS3

FJ581032.1	541977	2815.2	2350.6	2545.6	5120.6	4128.1	3651.1
EF212001.1	214514	2891.1	4679.1	1049.5	920.9	1130.2	532.4
EU600202.2	260949	78.3	223.9	519.1	162.1	267.3	711.3
EU722654.1	327394	959.2	1023.9	1563.6	469.0	2006.2	1725.6
EF554907.1	222862	2828.6	3728.3	6008.6	3533.7	6577.3	5721.4
GU458902.1	562858	7384.9	7527.8	6138.0	6689.1	9214.2	9823.9
X92129.1	44150	70.7	192.2	250.7	158.1	733.5	439.5
GU471247.1	517013	616.9	670.9	843.5	508.9	547.4	686.6
EF554896.1	226059	421.0	469.9	1696.0	733.8	2111.5	1926.3
FJ152984.1	347471	924.1	970.4	2486.7	1387.5	5299.2	2506.7
EF554906.1	223511	532.9	1430.3	1884.8	365.7	1275.7	948.1
X92128.1	32525	54.3	73.7	64.3	112.8	141.8	85.7
D21224.1	8975	3257.3	3772.2	3378.5	2648.0	2473.8	3888.9
AF530133.1	70982	3172.3	2740.2	1060.3	2080.9	2860.9	2383.7
AJ132226.1	8977	1231.6	2309.4	1408.2	1279.6	6462.0	3643.1
AB189343.1	112983	3539.5	5011.5	2082.8	3624.7	4255.9	5166.8
AJ297540.1	48310	7888.7	8102.8	4005.2	7896.4	6410.0	6445.8
AY700605.1	109434	4592.5	4262.0	2662.7	4130.9	4999.9	5065.2
AB183504.1	105913	4350.5	2461.4	2544.7	3831.6	3279.0	3268.1
AB008797.1	8989	3659.4	3719.9	2751.2	2436.0	2683.3	3955.8
AY382585.1	96373	7721.8	8710.2	7144.4	7769.2	10282.9	9262.5
AB038033.1	33284	3105.1	3321.2	2854.8	1964.1	2114.8	3025.9
NR_025380.1	573974	3370.0	3469.8	2858.1	2198.9	2116.4	3614.0
AJ252023.2	72172	1199.6	1560.3	928.9	325.9	5860.3	2973.8
AB183499.1	101616	1650.4	1385.9	628.9	1011.5	1186.5	1181.0
AB183496.1	101122	883.6	557.4	1044.2	1108.7	307.4	1922.5
AB013841.1	8993	4145.6	1817.7	803.9	1072.9	1000.0	1124.4
AB013842.1	8994	1766.2	996.4	754.1	710.1	1250.2	804.3
AB040467.1	20333	422.0	777.1	898.7	649.1	1366.2	2748.8
DQ349123.1	147282	338.6	275.8	259.4	337.1	142.5	372.2
CR954246.1	140486	304.8	469.9	434.6	100.2	754.4	733.7
CR954246.1	140406	34.4	38.4	110.3	67.4	230.8	45.6
AY040230.1	21879	129.8	213.3	486.9	224.0	1486.8	694.1
AF316144.1	52879	1673.8	1884.5	2004.2	2750.3	5609.4	2683.9
EU880522.1	351145	264.8	480.4	891.8	334.7	2876.3	1245.2
AF316142.1	37455	816.6	1654.2	1766.4	1637.2	5270.1	3713.9
FJ457238.1	568943	56.0	75.7	59.8	197.6	131.6	61.1
FJ952795.1	446774	14618.7	19582.8	18002.7	9092.2	28532.3	23793.8
FJ200646.1	308744	960.2	1209.8	1241.3	915.1	3348.6	1477.1
EF584051.1	228654	695.3	423.2	1025.1	530.4	110.1	263.8
EF584064.1	227631	506.7	295.6	883.1	675.3	330.6	202.5

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AY621063.1 gg_id:107053 Pseudoalteromonas sp. str. NJ6-3-1
FJ362488.1 gg_id:360655 Pseudoalteromonas sp. str. 4-9-11-2
FJ200651.1 gg_id:309736 Pseudoalteromonas porphyrae str. I 85
AF475096.1 gg_id:42828 Pseudoalteromonas porphyrae str. Q-1-6
DQ531952.1 gg_id:161487 Pseudoalteromonas sp. str. MJ5322
X82147.1 gg_id:8972 Pseudoalteromonas rubra str. ATCC 29570T
FJ457188.1 gg_id:539701 Pseudoalteromonas rubra str. S2676
FJ457197.1 gg_id:559457 Pseudoalteromonas ruthenica str. S2756
NZ_AAOH01000015.1 gg_id:156459 Pseudoalteromonas tunicata str. D2
AF295593.1 gg_id:19424 Pseudoalteromonas sp. str. ACEM-4
Z25522.1 gg_id:8973 Pseudoalteromonas tunicata str. D2
FJ497712.1 gg_id:590855 Pseudoalteromonas sp. str. VS-105
EU330355.1 gg_id:238270 Pseudoalteromonas sp. str. BSi20440
EU330364.1 gg_id:249895 Pseudoalteromonas sp. str. BSi20654
AJ874344.1 gg_id:110410 Pseudoalteromonas atlantica str. 01/110
EF673282.1 gg_id:249648 Pseudoalteromonas sp. str. BSi20628
U85855.1 gg_id:8913 Pseudoalteromonas prydzensis str. MB8-11
FJ952812.1 gg_id:419834 Pseudoalteromonas sp. str. 2ta8
DQ218321.1 gg_id:139718 Pseudoalteromonas sp. str. EBD
DQ492780.1 gg_id:157463 Pseudoalteromonas sp. str. BSi20598
AF366042.1 gg_id:27905 marine str. BB2AT2
DQ520891.1 gg_id:161179 Pseudoalteromonas sp. str. BSi20526
DQ985065.1 gg_id:177202 Pseudoalteromonas sp. str. JL1130
AF529062.1 gg_id:60988 Pseudoalteromonas citrea str. CIP 105339
AM111083.1 gg_id:140836 Pseudoalteromonas sp. str. 8049
X82139.1 gg_id:8918 Pseudoalteromonas tetraodonis str. IAM 14160T
EF551372.1 gg_id:220500 Pseudoalteromonas sp. str. BSw20508
FJ457152.1 gg_id:546070 Pseudoalteromonas sp. str. S1610
FJ200640.1 gg_id:341432 Pseudoalteromonas agarivorans str. C 36
AB231330.1 gg_id:137602 Pseudoalteromonas viridis str. G-1387 (=MBIC03135)
EF584014.1 gg_id:233255 Pseudoalteromonas sp. str. AS1
AM180744.1 gg_id:150838 Pseudoalteromonas citrea UL34
DQ537514.1 gg_id:161414 Pseudoalteromonas haloplanktis str. BSi20545
AM111018.1 gg_id:140829 Pseudoalteromonas sp. str. 7016
AM111094.1 gg_id:140955 Pseudoalteromonas sp. str. 8060
AB457045.1 gg_id:309901 Pseudoalteromonas sp. str. SB-A1
AM111086.1 gg_id:140902 Pseudoalteromonas sp. str. 8052
AM691088.1 gg_id:221420 Pseudoalteromonas carrageenovora str. EG27
AF539773.1 gg_id:84384 Pseudoalteromonas sp. str. E36
AF144036.1 gg_id:8967 Pseudoalteromonas maricaloris str. KMM636; LMG 19692; CIP 106859

DQ005864.1	131493	508.3	280.9	944.4	685.7	329.8	201.6
AY621063.1	107053	317.8	186.3	560.5	420.3	140.1	147.7
FJ362488.1	360655	1573.3	1300.9	1073.2	1764.4	2948.3	1934.6
FJ200651.1	309736	6690.3	8474.5	2661.6	7579.8	8324.0	8063.6
AF475096.1	42828	624.2	1078.7	586.0	456.4	1542.8	2534.3
DQ531952.1	161487	592.2	859.2	606.5	527.3	1549.6	591.2
X82147.1	8972	1422.6	1851.8	1063.1	1286.0	2084.1	1526.1
FJ457188.1	539701	1341.4	1786.5	1191.0	1259.0	3135.0	1542.8
FJ457197.1	559457	177.1	340.0	327.5	237.2	145.6	157.4
NZ_AAOH01000015.1	156459	184.5	292.5	393.7	261.1	171.3	410.6
AF295593.1	19424	2787.5	3882.6	2321.4	4833.6	4785.1	3815.3
Z25522.1	8973	4316.0	6756.2	4419.3	6056.3	9761.1	7188.1
FJ497712.1	590855	139.9	267.1	528.6	207.6	729.0	679.8
EU330355.1	238270	4349.9	5083.6	5670.9	3577.4	7962.5	6227.3
EU330364.1	249895	1922.5	1264.0	2001.1	4105.3	1401.5	1637.4
AJ874344.1	110410	4114.1	4090.4	4810.7	3879.7	7053.3	5806.1
EF673282.1	249648	120.9	261.5	141.0	190.6	2540.1	720.6
U85855.1	8913	5248.8	9394.4	7450.9	6114.8	10829.4	10308.4
FJ952812.1	419834	1344.7	1799.1	1219.4	1259.1	3136.5	1585.4
DQ218321.1	139718	266.8	491.3	922.1	326.5	3157.7	1316.1
DQ492780.1	157463	184.4	312.5	1078.4	347.2	2512.5	1427.2
AF366042.1	27905	2388.1	3293.0	2760.1	2617.2	3212.9	3748.7
DQ520891.1	161179	51.4	65.8	53.1	78.4	88.8	55.8
DQ985065.1	177202	88.2	151.8	1178.5	93.5	198.0	24.7
AF529062.1	60988	102.8	167.8	238.5	165.8	1489.8	387.8
AM111083.1	140836	5886.6	5635.9	3809.0	3992.2	5502.1	4344.6
X82139.1	8918	554.3	768.1	1428.1	852.8	1524.4	1581.6
EF551372.1	220500	2677.2	2703.9	1806.9	1841.6	8493.7	4762.5
FJ457152.1	546070	325.6	524.6	192.1	101.7	1125.2	714.6
FJ200640.1	341432	11290.4	12423.9	4014.2	11936.2	14624.7	13337.3
AB231330.1	137602	5769.8	6596.5	5596.7	4988.2	10026.7	6289.6
EF584014.1	233255	1143.7	1095.9	237.0	1438.8	2110.1	1133.9
AM180744.1	150838	329.2	456.4	216.3	101.2	1256.1	701.4
DQ537514.1	161414	1062.3	823.0	1713.5	1236.9	1840.0	472.4
AM111018.1	140829	2607.7	2356.7	1967.6	1123.8	3790.5	2430.6
AM111094.1	140955	3634.3	4135.1	3387.9	5781.6	6985.7	4545.6
AB457045.1	309901	20268.8	19648.3	11319.1	18066.0	17659.3	18333.4
AM111086.1	140902	4878.7	5769.5	4995.7	5251.3	9293.7	8497.4
AM691088.1	221420	650.7	877.1	2237.8	1255.6	4783.2	2122.6
AF539773.1	84384	64.3	135.1	52.5	49.3	99.7	79.1
AF144036.1	8967	304.6	287.0	578.7	518.3	1045.4	646.5

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AF082564.1 gg_id:8947 Pseudoalteromonas distincta str. KMM638T
X98336.1 gg_id:8944 Pseudoalteromonas antarctica str. CECT 4664 NF3
FJ457157.1 gg_id:566474 Pseudoalteromonas sp. str. S1688
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DQ492778.1 gg_id:158463 Pseudoalteromonas sp. str. BSi20595
EU807989.1 gg_id:310988 Pseudoalteromonas haloplanktis str. AFMB-008041
DQ492753.1 gg_id:157167 Pseudoalteromonas sp. str. BSi20333
AB457046.1 gg_id:347435 Pseudoalteromonas sp. str. SB-A2
EU330377.1 gg_id:249390 Pseudoalteromonas sp. str. BSw20050
FJ937921.1 gg_id:512210 Pseudoalteromonas sp. str. LS169
DQ173044.1 gg_id:139222 Pseudoalteromonas sp. str. YASM-6
FJ040186.1 gg_id:308609 Pseudoalteromonas haloplanktis str. I2
DQ537512.1 gg_id:160870 Pseudoalteromonas elyakovii str. BSi20539
AF218245.1 gg_id:23171 Pseudoalteromonas sp
EU365506.1 gg_id:266144 Pseudoalteromonas sp. str. BSs20004
AB100883.1 gg_id:80048 Pseudoalteromonas atlantica str. H6-2-4
FN377708.1 gg_id:591491 Pseudoalteromonas sp. KBO-3
GQ406774.1 gg_id:526534 Pseudoalteromonas sp. str. PaH3.10
FJ457122.1 gg_id:511161 Pseudoalteromonas marina str. S186
FJ200650.1 gg_id:312090 Pseudoalteromonas elyakovii str. I 84
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EF673279.1 gg_id:251916 Pseudoalteromonas sp. str. BSi20518
AF081498.1 gg_id:8969 Pseudoalteromonas piscicida str. Cura-d
FJ494890.1 gg_id:419752 Pseudoalteromonas sp. str. B10
DQ492719.1 gg_id:158083 Pseudoalteromonas sp. str. BSi20121
DQ517866.1 gg_id:161247 Pseudoalteromonas elyakovii str. BSi20428
FJ196018.1 gg_id:337457 Pseudoalteromonas sp. str. ZS4-11
DQ537520.1 gg_id:160149 Pseudoalteromonas elyakovii str. BSi20610
AF539778.1 gg_id:84701 Pseudoalteromonas sp. str. RE2-11
FJ497708.1 gg_id:570045 Pseudoalteromonas sp. str. VS-1
AF116188.1 gg_id:8932 Pseudoalteromonas elyakovii str. O22
AF297959.1 gg_id:39091 Pseudoalteromonas piscicida str. IAM12932T
DQ537517.1 gg_id:161333 Pseudoalteromonas haloplanktis str. BSi20585
AJ704790.1 gg_id:103112 Pseudoalteromonas sp. str. ws17
EU240534.1 gg_id:349996 Pseudoalteromonas viridis str. P1
AJ417594.1 gg_id:46753 Pseudoalteromonas agarivorans str. KMM 255
X82134.1 gg_id:8912 Pseudoalteromonas atlantica str. IAM 12927T
DQ537518.1 gg_id:161195 Pseudoalteromonas haloplanktis str. BSi20594

AF007286.1	8968	13403.8	11920.4	11297.8	12742.5	17156.3	14301.0
AF082564.1	8947	52.5	69.1	93.7	72.3	303.1	89.2
X98336.1	8944	19.9	24.2	38.4	69.3	54.7	129.1
FJ457157.1	566474	246.3	421.5	859.8	245.7	1949.0	1126.4
DQ520896.1	159738	3341.7	2846.0	2612.5	7633.0	2798.0	2862.2
DQ492778.1	158463	1399.4	1375.5	1754.9	2711.3	3949.4	1812.5
EU807989.1	310988	98.0	42.0	47.2	106.5	630.1	67.6
DQ492753.1	157167	719.6	557.5	1306.1	892.2	1507.3	325.0
AB457046.1	347435	19050.7	19188.0	14031.9	15049.8	22645.1	19190.8
EU330377.1	249390	2239.0	2636.0	2566.2	3647.0	7318.3	6439.6
FJ937921.1	512210	2485.8	1682.9	5396.5	4567.4	3232.9	2074.8
DQ173044.1	139222	8229.9	6751.3	4692.5	9182.7	17176.0	12144.8
FJ040186.1	308609	4181.7	4167.7	4200.9	3177.3	7369.7	3836.1
DQ537512.1	160870	36.6	39.2	34.7	77.5	61.5	50.0
AF218245.1	23171	3275.9	2312.7	747.4	1358.1	3656.8	2251.5
EU365506.1	266144	6435.4	7505.6	6250.3	5275.1	11697.5	8254.0
AB100883.1	80048	2641.8	1694.5	2344.6	1962.0	2060.8	2275.4
FN377708.1	591491	575.1	899.8	1902.3	950.6	3584.5	3491.7
GQ406774.1	526534	447.6	363.1	896.3	531.0	396.9	654.2
FJ457122.1	511161	1963.8	1728.0	2437.4	1749.7	3928.1	2752.4
FJ200650.1	312090	70.1	94.6	105.3	137.1	974.4	162.4
AY646432.1	99368	187.4	186.0	614.5	531.1	1514.7	253.2
EF375559.1	205894	8350.7	9316.9	5081.1	5285.7	10517.0	9748.2
DQ517869.1	160295	260.1	487.9	922.3	314.4	3159.1	1307.8
EF673279.1	251916	94.7	176.6	72.8	103.1	1327.1	566.4
AF081498.1	8969	2935.7	3276.4	1233.5	2296.8	4075.9	3148.3
FJ494890.1	419752	3778.8	4197.5	3445.5	5996.1	8054.0	6710.2
DQ492719.1	158083	373.4	326.5	875.9	397.9	2671.2	471.0
DQ517866.1	161247	18.3	22.9	19.1	36.4	60.6	27.9
FJ196018.1	337457	1009.9	1216.1	591.4	1072.9	4241.0	3675.2
DQ537520.1	160149	170.4	281.6	234.3	130.4	1704.7	1362.8
AF539778.1	84701	3252.1	3380.8	3143.4	2622.5	2346.9	2907.8
FJ497708.1	570045	10768.7	11108.6	5243.6	9969.9	12443.2	10268.5
AF116188.1	8932	8745.6	9505.0	1229.9	3377.0	5866.9	4750.3
AF297959.1	39091	1840.1	1757.7	1874.7	1376.5	3512.8	2279.0
DQ537517.1	161333	547.7	749.8	1481.2	984.1	5130.3	1946.2
AJ704790.1	103112	11655.3	8128.8	8330.4	7415.7	9103.1	9576.2
EU240534.1	349996	102.0	202.0	233.6	216.7	1851.5	421.2
AJ417594.1	46753	5139.0	5910.7	3058.0	5284.0	8777.9	7227.7
X82134.1	8912	1735.6	2123.5	2773.8	1697.0	5060.5	3224.2
DQ537518.1	161195	12168.7	9078.6	12067.0	8229.7	11462.3	9324.6

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FJ457185.1 gg_id:542853 Pseudoalteromonas rubra str. S2472
AF038846.1 gg_id:8907 Pseudoalteromonas gracilis str. B9
X82136.1 gg_id:8908 Pseudoalteromonas carrageenovora str. ATCC 12662T
FJ200644.1 gg_id:336893 Pseudoalteromonas elyakovii str. C 102
AY771728.1 gg_id:141235 Pseudoalteromonas nigrifaciens S3-28
DQ492775.1 gg_id:158978 Pseudoalteromonas sp. str. BSi20576
EF584090.1 gg_id:234336 Pseudoalteromonas sp. str. VHOS1
AM110980.1 gg_id:140920 Pseudoalteromonas sp. str. 3025
AF354597.1 gg_id:19398 marine clone Arctic96B-17
DQ005900.1 gg_id:130450 Pseudoalteromonas rubra str. C312
AY864628.1 gg_id:111346 Pseudoalteromonas sp. str. U50
DQ665793.1 gg_id:173097 Pseudoalteromonas elyakovii str. BSi20460
NC_007481.1 gg_id:140750 Pseudoalteromonas haloplanktis str. TAC125
AM111017.1 gg_id:140854 Pseudoalteromonas sp. str. 7015
AF218246.1 gg_id:25530 Pseudoalteromonas sp
NR_025032.1 gg_id:573650 Pseudoalteromonas ulvae str. UL12; UNSW 095600
EF551371.1 gg_id:221998 Pseudoalteromonas sp. str. BSw20507
AM111034.1 gg_id:140870 Pseudoalteromonas sp. str. 7038
FJ200648.1 gg_id:350574 Pseudoalteromonas marina str. I 17
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AB257325.2 gg_id:180592 Pseudoalteromonas tetraodonis str. Do-17
EU849123.1 gg_id:348634 Pseudoalteromonas sp. str. LP621
AY682201.1 gg_id:107552 Pseudoalteromonas chazhmella str. R10SW10
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DQ923439.1 gg_id:187538 Pseudoalteromonas sp. W-5
AB257336.2 gg_id:182468 Pseudoalteromonas mariniglutinosa str. Do-52
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EU330366.1 gg_id:235804 Pseudoalteromonas sp. str. BSi20411
AM111090.1 gg_id:140875 Pseudoalteromonas sp. str. 8056
AM110975.1 gg_id:140860 Pseudoalteromonas sp. str. 3020
NR_026222.1 gg_id:543735 Pseudoalteromonas nigrifaciens str. NCIMB 8614
AF045560.1 gg_id:8946 Pseudoalteromonas antarctica str. N-1
AB457051.1 gg_id:346476 Pseudoalteromonas sp. str. SB-E1
FJ200643.1 gg_id:320146 Pseudoalteromonas marina str. C 90
AJ507251.1 gg_id:59526 Pseudoalteromonas mariniglutinosa str. KMM 3635
FJ172090.1 gg_id:348422 Pseudoalteromonas sp. str. SBC7

DQ492772.1	158527	160.4	357.0	187.4	154.5	1854.7	1180.8
DQ011289.1	124110	439.9	310.0	540.6	195.7	728.3	238.7
FJ457185.1	542853	2471.6	3970.8	2089.5	2347.3	5010.7	2822.0
AF038846.1	8907	18.0	22.5	22.9	33.3	52.5	21.2
X82136.1	8908	1866.4	1940.6	2594.7	1700.2	4824.1	3213.7
FJ200644.1	336893	329.2	236.1	233.7	109.5	1244.1	1223.9
AY771728.1	141235	459.9	296.9	526.3	333.9	140.9	152.1
DQ492775.1	158978	3273.5	3780.0	4462.1	3211.1	7914.5	5956.1
EF584090.1	234336	211.6	207.8	571.5	248.7	196.0	155.7
AM110980.1	140920	104.4	122.6	113.3	116.9	354.2	448.1
AF354597.1	19398	2804.7	2090.9	2643.4	3971.4	2528.1	4330.4
DQ005900.1	130450	6180.5	7253.2	3782.3	7583.6	6947.1	5062.8
AY864628.1	111346	2980.4	5147.0	785.0	2571.8	3387.9	3081.9
DQ665793.1	173097	618.9	400.8	1277.0	910.6	977.9	232.3
NC_007481.1	140750	499.5	582.9	745.3	521.1	4743.0	1536.4
AM111017.1	140854	5498.2	8060.5	5292.5	5617.7	10098.3	8377.9
AF218246.1	25530	2612.9	2313.5	2579.9	2374.7	4273.6	4345.5
NR_025032.1	573650	339.7	454.1	1208.9	756.1	959.2	617.8
EF551371.1	221998	3901.9	5852.9	4929.8	4125.0	9252.8	7268.0
AM111034.1	140870	52.2	130.0	260.5	165.7	125.7	154.9
FJ200648.1	350574	8134.2	9223.3	6496.2	5560.9	11984.3	6817.8
DQ492816.1	157558	1816.1	1991.1	2788.8	2675.3	3845.8	2778.6
AB257325.2	180592	404.4	507.4	1187.4	539.1	2191.9	1076.1
EU849123.1	348634	1568.2	1802.5	1213.5	2063.9	3323.9	2095.5
AY682201.1	107552	2308.6	2025.7	2685.1	2204.9	4209.6	4578.2
DQ517879.1	161373	340.9	447.1	643.9	225.6	3776.0	1297.8
AB518970.1	543117	413.7	507.6	3080.1	3879.5	1184.6	1160.7
DQ492738.1	158140	3216.8	3844.2	2154.4	4128.2	5807.3	6139.0
AF313497.1	111481	850.9	431.0	867.5	636.1	909.3	513.3
DQ923439.1	187538	4672.6	2806.8	3706.4	5066.1	2724.5	4738.7
AB257336.2	182468	30.3	44.2	24.6	53.4	49.7	30.8
AM110978.1	140823	258.4	400.8	579.5	403.5	1025.0	1122.4
EU330366.1	235804	1244.2	1336.5	621.2	956.6	4153.6	1484.5
AM111090.1	140875	7898.7	6359.1	3369.0	4862.6	5662.6	4314.8
AM110975.1	140860	1272.2	1389.1	884.8	2140.3	3214.2	1297.8
NR_026222.1	543735	39.5	47.4	201.0	68.4	184.1	56.6
AF045560.1	8946	12861.8	11339.5	9286.8	9720.8	16758.5	11493.5
AB457051.1	346476	826.5	937.4	927.7	659.9	299.4	1252.2
FJ200643.1	320146	16660.8	18323.8	7585.2	10415.3	13520.2	9643.8
AJ507251.1	59526	2507.7	3043.1	2706.5	4498.7	5235.8	2718.8
FJ172090.1	348422	12.8	19.0	18.7	35.4	57.5	20.8

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DQ492784.1 gg_id:158866 Pseudoalteromonas sp. str. BSi20612
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AB049728.1 gg_id:51317 Pseudoalteromonas atlantica str. AR06
DQ011614.1 gg_id:125030 Pseudoalteromonas ganghwensis str. FR1302
FN554588.1 gg_id:566577 Pseudoalteromonas sp. str. HL4
AM111074.1 gg_id:140761 Pseudoalteromonas sp. str. 8039
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AF173963.1 gg_id:18661 Pseudoalteromonas atlantica str. KT0910
DQ787199.1 gg_id:165819 Pseudoalteromonas arctica str. 37-1-2
DQ492758.1 gg_id:157718 Pseudoalteromonas sp. str. BSi20343
AM111078.1 gg_id:140967 Pseudoalteromonas sp. str. 8043
AF043742.1 gg_id:22902 Pseudoalteromonas distincta str. KMM 638T; ATCC700518
FJ202088.1 gg_id:326316 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k
EU050781.1 gg_id:246147 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_02_66
FJ403097.1 gg_id:359108 Disease- changes healthy and diseased colonies Caribbean coral Montastrea faveolat
EU930871.1 gg_id:342076 Pseudoalteromonas sp. str. KDW4
EF101548.1 gg_id:192719 Psychromonas arctica str. KOPRI24930
AB365349.1 gg_id:275002 Psychromonas heitensis str. 04HE-4-40 (= MBIC 08331)
NZ_AAQS01000017.1 gg_id:160611 Psychromonas ingrahamii str. 37
U14582.1 gg_id:9115 gas vacuolate str.90-P<gv>1
AJ969456.1 gg_id:157483 Microbial black smoker s Mid Atlantic Ridge ecological implications rock fragments ch
AF374385.1 gg_id:38990 Psychromonas arctica str. Pull 5.3
AY548987.2 gg_id:99098 marine bone clone sacC3D3
U85849.1 gg_id:9117 Psychromonas sp. str. IC004
AB304804.1 gg_id:236309 Psychromonas sp. str. JAMM 0394
DQ009471.1 gg_id:126016 bacterioplankton clone SPOTSMAY03_890m29
AB374544.1 gg_id:264272 Psychromonas sp. str. J42-3A
U73722.1 gg_id:9120 gas vacuolate str. 174
DQ027056.1 gg_id:133700 Psychromonas sp. str. CNPT3
AB304807.1 gg_id:252707 Psychromonas sp. str. JAMM 0700
AY167326.1 gg_id:81340 Psychromonas sp. str. ANT9265
AJ519627.1 gg_id:76528 uranium mill tailings soil clone Sh765B-TzT-48
AF235108.1 gg_id:71948 Alteromonas sp. str. KT1114
DQ530480.1 gg_id:166114 Psychromonas sp. str. gape-82
AJ416756.1 gg_id:25724 Psychromonas profunda str. 2825
FM994680.1 gg_id:561093 gill and deep-sea limpet Pectinodonta sp. digestive tract host on sunken wood deptl
EF542799.1 gg_id:224364 Shewanella algae str. YJ06114

DQ642828.1	159691	59.2	101.6	58.1	84.9	658.2	127.4
DQ665792.1	163917	391.1	404.7	433.7	302.7	2802.0	792.6
AM913936.1	403449	164.8	270.4	494.5	474.6	2346.1	806.5
EU330363.1	252092	715.0	496.6	280.2	856.1	563.6	776.8
DQ492784.1	158866	312.5	650.8	297.0	183.3	3358.9	1243.9
AY563031.1	100315	4584.7	4736.6	4806.1	3817.7	6648.4	5133.2
AB049728.1	51317	1752.8	1654.8	2003.6	1507.5	3838.0	2415.6
DQ011614.1	125030	2503.1	1863.9	1662.3	2119.3	3378.6	2010.7
FN554588.1	566577	9048.0	9638.3	3100.7	6854.5	6171.8	4744.1
AM111074.1	140761	9898.3	9500.9	10333.8	8555.6	9312.9	11359.7
FJ425222.1	367067	1083.1	1275.9	2428.0	1072.1	2416.0	2442.8
AF173963.1	18661	3960.3	2848.7	4023.2	2950.5	9448.9	5697.7
DQ787199.1	165819	577.6	733.9	787.7	263.8	4508.4	2095.4
DQ492758.1	157718	116.1	250.5	128.9	172.6	2420.7	685.1
AM111078.1	140967	162.6	266.2	293.6	654.1	568.9	1744.2
AF043742.1	22902	975.6	446.6	1745.6	1064.9	786.7	238.7
FJ202088.1	326316	16.2	21.3	39.4	61.2	59.6	26.2
EU050781.1	246147	5497.0	5382.3	7959.6	8995.6	13589.1	8867.3
FJ403097.1	359108	296.6	201.6	1083.5	416.4	165.5	248.9
EU930871.1	342076	72.1	86.1	227.5	408.2	91.2	57.3
EF101548.1	192719	8761.4	7182.1	5481.3	5011.9	2755.3	4306.8
AB365349.1	275002	4696.9	4902.1	5142.8	4945.3	5954.9	7222.2
NZ_AAQS01000017.1	160611	1553.1	1654.6	3883.3	1403.4	1143.3	1397.2
U14582.1	9115	1471.1	1392.4	1948.8	1014.3	2156.4	1562.0
AJ969456.1	157483	4145.5	4536.6	3414.2	4618.7	5051.3	2225.1
AF374385.1	38990	1146.6	1071.3	1486.0	1212.5	1030.7	1956.3
AY548987.2	99098	8260.2	8712.9	1824.0	1203.6	1155.7	1163.3
U85849.1	9117	3617.4	5422.6	3721.8	6460.1	2420.4	2988.1
AB304804.1	236309	446.5	458.3	3872.4	1597.0	212.3	396.1
DQ009471.1	126016	4869.2	6780.5	4829.8	5329.8	9449.3	7016.6
AB374544.1	264272	2538.6	2198.1	3486.4	2895.3	3392.9	3074.8
U73722.1	9120	2486.9	2536.4	2633.3	2790.4	3093.8	1682.2
DQ027056.1	133700	1262.8	1233.0	1777.3	905.5	3339.5	3143.7
AB304807.1	252707	3339.1	4308.7	4918.5	3287.1	9289.6	7228.0
AY167326.1	81340	6208.6	9429.5	4951.9	5682.2	4717.9	8068.8
AJ519627.1	76528	5827.7	6778.0	8039.7	4698.9	8205.5	7563.1
AF235108.1	71948	3178.1	2064.5	4742.8	3736.7	2798.4	3354.1
DQ530480.1	166114	4560.2	1845.5	1821.3	3982.9	1346.1	1811.3
AJ416756.1	25724	1473.3	2220.0	2991.7	2341.1	7617.1	5490.0
FM994680.1	561093	3876.8	4475.3	4904.7	2610.3	2909.1	3215.1
EF542799.1	224364	670.3	825.5	1457.9	1691.3	922.8	1132.6

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s__Shewanella sediminis	7355
s__Shewanella sp. ANA-3	6646
s__Shewanella woodyi	6637

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AB205568.1 gg_id:114235 Shewanella colwelliana str. Q14
NR_028672.1 gg_id:545987 Shewanella amazonensis str. SB2B; ATCC 700329
CP000507.1 gg_id:197258 Shewanella amazonensis str. SB2B
NC_009665.1 gg_id:255230 Shewanella baltica str. OS185
AJ006084.1 gg_id:9079 Shewanella massilia
AJ000215.1 gg_id:9075 Shewanella baltica OS155
CP000753.1 gg_id:243101 Shewanella baltica str. OS185
CP001252.1 gg_id:527695 Shewanella baltica str. OS223
NC_009997.1 gg_id:238077 Shewanella baltica str. OS195
CP000753.1 gg_id:243102 Shewanella baltica str. OS185
NC_009665.1 gg_id:255225 Shewanella baltica str. OS185
CP000563.1 gg_id:216084 Shewanella baltica str. OS155
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AJ000216.1 gg_id:9076 Shewanella baltica OS195
CP000563.1 gg_id:216083 Shewanella baltica str. OS155
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AB183498.1 gg_id:101453 Shewanella sp. str. T3607
AJ567615.1 gg_id:88337 deep-sea sediment clone MBAE94
AB183512.1 gg_id:101788 Shewanella sp. str. T5302
AB183493.1 gg_id:100644 Shewanella sp. str. 33H2
CP000302.1 gg_id:156979 Shewanella denitrificans str. OS217
AY771713.1 gg_id:137368 Shewanella frigidimarina str. S2-60
CP000447.1 gg_id:170610 Shewanella frigidimarina str. NCIMB 400
CP000931.1 gg_id:270485 Shewanella halifaxensis str. HAW-EB4
DQ011269.1 gg_id:119691 Shewanella hanedai str. ATCC 33224
AB201780.1 gg_id:138170 Shewanella kaireiae str. c952
NC_009092.1 gg_id:212575 Shewanella loihica str. PV-4
NC_009092.1 gg_id:212572 Shewanella loihica str. PV-4
AB081762.1 gg_id:55880 Shewanella sairae str. SM2-1
NC_004347.1 gg_id:141355 Shewanella oneidensis str. MR-1
NC_004347.1 gg_id:141641 Shewanella oneidensis str. MR-1
AF145921.1 gg_id:9077 Shewanella japonica str. KMM 3299
CP000851.1 gg_id:249615 Shewanella pealeana str. ATCC 700345
NC_011566.1 gg_id:360003 Shewanella piezotolerans str. WP3
NC_011566.1 gg_id:360008 Shewanella piezotolerans str. WP3
AB081761.1 gg_id:60926 Shewanella schlegeliana str. HRKC24
CP000821.1 gg_id:253801 Shewanella sediminis str. HAW-EB3
NC_009831.1 gg_id:246709 Shewanella sediminis str. HAW-EB3
AF136392.1 gg_id:137029 Shewanella sp. str. ANA-3
NZ_AAUO01000015.1 gg_id:183742 Shewanella woodyi str. ATCC 51908

DQ883817.1	164354	2510.5	2570.4	3322.7	3393.3	6347.1	3332.1
AB205568.1	114235	2703.7	2412.0	3760.4	2190.6	4917.0	5099.8
NR_028672.1	545987	5792.3	5944.6	4113.9	6396.0	6766.0	7008.3
CP000507.1	197258	725.7	850.6	2058.1	515.9	2875.9	2380.7
NC_009665.1	255230	517.7	652.2	2437.8	1360.9	858.0	1130.6
AJ006084.1	9079	114.6	160.5	759.5	247.9	67.6	255.3
AJ000215.1	9075	196.0	268.4	1352.8	250.7	95.8	370.5
CP000753.1	243101	753.1	532.6	1752.8	267.1	84.0	985.7
CP001252.1	527695	2091.9	2252.2	6105.4	2812.9	1662.0	2597.0
NC_009997.1	238077	1785.6	1680.7	3696.1	2636.4	1368.4	1775.7
CP000753.1	243102	3076.8	3321.5	6893.8	4797.7	4360.6	4380.0
NC_009665.1	255225	311.5	403.0	1441.0	868.8	291.2	618.6
CP000563.1	216084	537.9	658.3	3186.2	1430.5	823.9	1163.8
CP000753.1	243099	2106.0	2288.5	6466.6	2902.4	1633.5	2649.8
AJ000216.1	9076	1812.6	1678.4	3564.4	2715.1	1220.2	1672.1
CP000563.1	216083	618.4	944.0	2779.5	947.5	659.9	1369.5
NZ_AAIO01000004.1	131070	616.8	943.7	2967.4	1009.2	685.1	1347.4
AB183498.1	101453	308.4	436.8	232.2	169.5	242.5	288.8
AJ567615.1	88337	2907.1	5185.4	1740.3	2199.0	2765.5	2917.7
AB183512.1	101788	12880.8	15572.3	17527.9	11446.7	16870.9	15460.2
AB183493.1	100644	806.0	297.6	716.7	312.5	1444.3	396.4
CP000302.1	156979	414.3	219.9	216.1	250.1	119.1	272.3
AY771713.1	137368	1074.8	726.8	2215.2	2103.4	823.2	1432.0
CP000447.1	170610	1236.1	1012.6	2794.7	2636.0	994.7	1634.8
CP000931.1	270485	1718.0	1433.5	1726.6	2824.0	1117.9	2009.9
DQ011269.1	119691	1706.1	2035.2	2546.5	2455.1	3760.7	3145.7
AB201780.1	138170	587.8	483.5	1517.8	1275.2	985.2	1620.5
NC_009092.1	212575	2885.1	1992.6	2392.1	1867.8	2189.8	3118.6
NC_009092.1	212572	3638.0	2683.0	3741.7	1856.8	3093.6	3035.2
AB081762.1	55880	2897.7	2108.3	2904.4	4376.8	1665.3	2591.6
NC_004347.1	141355	2963.8	2656.0	4903.3	4300.2	2513.6	3130.2
NC_004347.1	141641	1343.4	1334.6	2448.8	1931.5	368.3	1672.0
AF145921.1	9077	1404.1	2006.9	1617.8	1227.8	1668.0	2823.2
CP000851.1	249615	2674.1	2166.1	2591.0	5253.9	876.1	2062.9
NC_011566.1	360003	756.4	807.5	1423.1	1260.7	2597.8	2277.5
NC_011566.1	360008	1790.8	2144.0	3084.0	1142.1	4371.8	2989.7
AB081761.1	60926	70.8	79.3	627.7	261.4	370.7	417.2
CP000821.1	253801	1473.2	1963.2	3628.0	1958.7	1461.2	2778.0
NC_009831.1	246709	2719.6	3155.4	5764.3	5935.4	3004.4	6117.1
AF136392.1	137029	6880.3	5649.3	6043.6	5798.9	6631.1	7391.4
NZ_AAUO01000015.1	183742	1080.6	1652.5	1497.6	570.7	5022.6	3776.8

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U91551.1 gg_id:9106 Shewanella putrefaciens str. NCIMB 12577
AF530149.1 gg_id:61112 Shewanella gelidimarina str. MGP-71
AF005255.1 gg_id:9108 Shewanella putrefaciens str. MR-30
AF170300.1 gg_id:70300 Shewanella putrefaciens str. IR-1
DQ010165.1 gg_id:119545 Shewanella sp. str. HN-41
FJ952791.1 gg_id:372983 Shewanella sp. str. 3tb16
AF039055.1 gg_id:9060 Shewanella oneidensis str. SP-22
AY902211.1 gg_id:113783 Shewanella sp. str. BR2
AM269901.1 gg_id:159850 Shewanella sp. str. ES-5
AM180742.1 gg_id:146524 Shewanella gaetbuli UL19
DQ537513.1 gg_id:161502 Shewanella frigidimarina str. BSi20544
NR_025794.1 gg_id:561965 Shewanella aquimarina str. SW-120; KCCM 41821
NC_009831.1 gg_id:246711 Shewanella sediminis str. HAW-EB3
DQ325517.1 gg_id:148004 Shewanella sp. str. 62
EF105398.1 gg_id:175874 Shewanella sp. str. IE9-3
AF022402.1 gg_id:9027 Shewanella sp. ANG.209 str. ANG.strain 209 ANG.209
DQ677025.1 gg_id:173087 Shewanella sp. Iso-W8
AB205571.1 gg_id:113604 Shewanella putrefaciens str. T147
EF584058.1 gg_id:234701 Shewanella sp. str. HE5
AF189696.1 gg_id:111615 Shewanella sp. str. BC47
DQ665797.1 gg_id:173544 Shewanella frigidimarina str. BSi20542
EU979479.1 gg_id:352968 Shewanella sp. str. CR07-A1
AF039056.1 gg_id:9061 Shewanella oneidensis str. SP-32
FJ497707.1 gg_id:589412 Shewanella sp. str. VS-7
AY170369.1 gg_id:69583 Shewanella fidelis str. KMM 3589
DQ307731.1 gg_id:147165 Shewanella putrefaciens str. Hac411
AF387347.1 gg_id:33931 Shewanella oneidensis str. DML7
U91553.1 gg_id:9071 Shewanella putrefaciens str. NCTC 10695
FJ456679.1 gg_id:581729 microbiota two Antarctic notothenioid fish species intestinal flora clone A221_NCI
U85903.1 gg_id:128222 Shewanella frigidimarina str. ACAM 591T ICP1
AB205567.1 gg_id:114271 Shewanella colwelliana str. Q-06
AB205578.1 gg_id:114304 Shewanella baltica str. W145
GU329909.1 gg_id:549987 Shewanella putrefaciens str. WST
NC_009052.1 gg_id:205508 Shewanella baltica str. OS155
NZ_AATK01000145.1 gg_id:166958 Shewanella baltica str. OS195
NR_029070.1 gg_id:575480 Shewanella gaetbuli str. TF-27; JCM 11814
FJ210800.1 gg_id:328373 Shewanella algae str. QDHT-04
AF132874.1 gg_id:113095 Shewanella frigidimarina str. ACAM 517
AY485224.1 gg_id:106352 Shewanella marisflavi str. SW-117
AF500079.1 gg_id:88004 Shewanella japonica KMM 3582

NZ_AAUO01000025.1	174000	2339.1	2486.6	4849.2	3081.3	2478.5	4242.4
U91551.1	9106	325.7	344.7	812.3	598.7	364.3	506.1
AF530149.1	61112	1214.9	1208.4	1062.8	819.3	5093.8	1944.1
AF005255.1	9108	5597.5	5445.3	2185.1	5974.0	7968.3	6151.5
AF170300.1	70300	2161.1	1645.9	3112.5	2874.3	3752.7	2125.9
DQ010165.1	119545	4354.8	4009.5	6550.3	5182.4	11583.4	5590.0
FJ952791.1	372983	4090.7	4276.2	5591.9	3540.9	8408.8	6637.0
AF039055.1	9060	48.4	73.9	145.9	138.2	68.8	89.9
AY902211.1	113783	2289.0	1759.3	3866.7	2108.5	2264.2	2425.8
AM269901.1	159850	679.0	996.4	3850.8	1234.0	664.6	1453.8
AM180742.1	146524	446.8	273.9	1027.9	431.0	456.3	818.1
DQ537513.1	161502	1897.7	1351.8	2939.0	3191.4	1538.1	2228.2
NR_025794.1	561965	2912.0	2143.9	2863.4	1903.3	2379.4	3373.0
NC_009831.1	246711	2376.2	2456.6	5277.7	5184.3	2423.0	4819.8
DQ325517.1	148004	390.0	670.4	562.1	904.4	1540.7	728.4
EF105398.1	175874	16.6	20.9	176.2	85.6	59.6	18.6
AF022402.1	9027	105.1	245.3	751.1	311.3	2679.3	304.1
DQ677025.1	173087	1623.6	1606.5	2933.0	2791.8	3373.9	3878.0
AB205571.1	113604	2729.7	2184.4	3893.8	2905.7	3057.7	1768.3
EF584058.1	234701	3909.8	2824.4	3767.0	2172.1	6065.3	3167.6
AF189696.1	111615	6817.2	4829.0	7465.2	7679.6	4086.1	4060.3
DQ665797.1	173544	3872.6	6164.6	1552.2	2874.1	3004.7	3485.1
EU979479.1	352968	115.3	325.0	2427.4	633.7	550.1	675.3
AF039056.1	9061	633.1	1066.5	2686.5	1077.1	1807.3	758.4
FJ497707.1	589412	5679.1	5961.8	6704.8	7446.4	9729.7	8751.3
AY170369.1	69583	74.7	117.9	209.6	117.3	682.7	340.3
DQ307731.1	147165	151.4	143.9	1448.9	318.7	79.7	371.5
AF387347.1	33931	2438.0	2081.0	4537.8	3763.2	2205.1	2645.3
U91553.1	9071	242.1	334.0	728.9	931.4	285.3	629.6
FJ456679.1	581729	7882.8	6827.3	4256.9	7610.2	6576.4	5658.6
U85903.1	128222	4043.9	2899.5	4730.0	6929.5	7878.7	3476.7
AB205567.1	114271	9618.3	7526.9	11672.6	7593.6	12550.5	10552.2
AB205578.1	114304	81.5	50.1	258.7	185.5	70.3	117.3
GU329909.1	549987	888.5	770.1	991.2	1258.7	754.1	1195.1
NC_009052.1	205508	2117.1	1856.1	5626.0	3088.4	2235.6	2694.2
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NR_029070.1	575480	192.7	256.7	766.0	265.9	1402.2	314.7
FJ210800.1	328373	537.2	810.9	1253.3	2186.6	1728.2	1566.4
AF132874.1	113095	948.2	728.1	1634.6	2623.7	667.4	1320.4
AY485224.1	106352	2760.4	2871.5	4792.3	5821.7	5635.0	6729.3
AF500079.1	88004	1499.5	1038.4	2692.7	370.7	2083.4	421.7

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AB204519.1 gg_id:137352 Shewanella pneumatophori str. SCRC-2738
AF132878.1 gg_id:38945 Shewanella frigidimarina str. ACAM 557
EU290154.1 gg_id:256999 Shewanella marinus str. C4
DQ167234.1 gg_id:139040 Shewanella sp. str. HJ039
DQ520894.1 gg_id:159825 Shewanella frigidimarina str. BSi20531
EF105397.1 gg_id:179131 Shewanella sp. str. IE9-1
AJ288152.1 gg_id:22553 Shewanella sp. Bok-1-30-2
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CP001252.1 gg_id:527693 Shewanella baltica str. OS223
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FM887036.1 gg_id:459403 Shewanella sp. str. JC19
U85905.1 gg_id:137215 Shewanella frigidimarina str. ACAM 588 ICP4
AJ288153.1 gg_id:19933 Shewanella sp. SK-3-30-1
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AB201782.1 gg_id:137622 Shewanella sedimentalis str. d943
NC_009997.1 gg_id:238071 Shewanella baltica str. OS195
FJ154999.1 gg_id:320502 seasonal fluctuation coastal Bohai Bay sequencing and RFLP soil clone G5
U91552.1 gg_id:9070 Shewanella putrefaciens str. F137
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CP000931.1 gg_id:270483 Shewanella halifaxensis str. HAW-EB4
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EU073095.1 gg_id:335676 Shewanella sp. str. TS29
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EU434392.1 gg_id:260399 Shewanella putrefaciens str. a324
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EU543691.1 gg_id:268317 Shewanella putrefaciens str. DL4
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AF295592.1 gg_id:52642 Shewanella olleyana str. ACEM-9
AB306516.1 gg_id:247972 Shewanella sp. str. MIB015
AM990834.1 gg_id:278789 Shewanella sp. MOLA 59
AY170366.1 gg_id:69757 Shewanella waksmanii str. KMM 3823
EU000237.1 gg_id:309277 Shewanella donghaensis str. KOPRI_22224
EF584057.1 gg_id:234216 Shewanella sp. str. HE4

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DQ514298.1	160423	6441.8	10187.4	4172.7	6439.2	12545.9	13341.9
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DQ167234.1	139040	3676.2	2979.2	4979.5	4907.6	3215.2	3667.9
DQ520894.1	159825	1148.1	712.7	2392.2	2457.2	825.2	1115.8
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AJ288152.1	22553	10824.7	14805.7	8080.3	10958.9	15860.9	13514.9
DQ351772.1	147472	772.2	830.8	2111.6	1283.5	826.1	1183.2
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EU543691.1	268317	770.4	588.4	2462.5	1165.6	388.0	742.0
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AB306516.1	247972	5265.7	5448.0	6860.2	4202.8	3408.7	2940.2
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s__Nitrosococcus oceani	2440

U91554.1 gg_id:9107 Shewanella putrefaciens str. 189 tr
AF173966.1 gg_id:54246 Shewanella baltica str. KT0246
AB094597.1 gg_id:83672 Shewanella surugaensis str. c959
AY445591.1 gg_id:103376 Shewanella profunda str. LT13a
NC_009665.1 gg_id:255224 Shewanella baltica str. OS185
AF132873.1 gg_id:37061 Shewanella frigidimarina str. ACAM 516
Y13699.1 gg_id:9053 Shewanella frigidimarina str. NCIMB 400
AY351983.1 gg_id:92948 Shewanella affinis str. KMM 3587
GQ869534.1 gg_id:569132 Shewanella sp. str. KCCM 42936
NC_009831.1 gg_id:246705 Shewanella sediminis str. HAW-EB3
AB013839.1 gg_id:9017 Shewanella sp. 3-8.C
NR_025934.1 gg_id:540854 Cardiobacterium hominis str. 6573; ATCC 15826
AY596470.1 gg_id:104981 Cardiobacterium valvarum str. CCUG12990
DQ645464.1 gg_id:160756 Cardiobacterium valvarum VA1941
CP000513.1 gg_id:226003 Dichelobacter nodosus str. VCS1703A
AJ717394.1 gg_id:149350 Suttonella ornithocola str. B6/99/2
X92131.1 gg_id:46026 Lake Elmenteita isolate 2E1
AF384209.1 gg_id:25151 Chromatium sp. str. NZ
AM712619.1 gg_id:237043 Allochromatium phaeobacterium str. JA144
FJ716332.1 gg_id:508808 Chlorobi dominate shal chemocline Bahamas Sawmill Sink column 10.3 m water dept
AF384208.1 gg_id:22729 Chromatium sp. str. NM2
NR_025315.1 gg_id:559119 Chromatium okenii str. DSM 169
FJ437816.1 gg_id:541203 Benthic okenone production Fayetteville New York Green Lake chemocline 20.5 m wa
AB478662.1 gg_id:548000 SSU sequences Alps Cadagno di Fuori submerged biofilm mats montane wetland clo
DQ330802.1 gg_id:159452 Guerrero Negro hypersaline microbial mat clone 02D2Z45
AJ223235.1 gg_id:7564 Lamprocystis purpurea str. DSM 4197
AM941378.1 gg_id:344367 Marichromatium indicum str. JA122
AM941379.1 gg_id:304631 Marichromatium indicum str. JA210
AM179449.1 gg_id:190862 Marichromatium imhoffii str. JA120 1
AM941377.1 gg_id:325577 Marichromatium indicum str. JA214
AM941046.1 gg_id:369706 Marichromatium indicum JA347
AJ889020.1 gg_id:112951 Marichromatium chilcum str. CH8
FJ376391.1 gg_id:360805 Marichromatium purpuratum str. DSM 1711
FM177512.1 gg_id:344391 Marichromatium indicum str. JA290
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AF294030.1 gg_id:135580 Marichromatium purpuratum str. TAR
FM177510.1 gg_id:333563 Marichromatium bheemlicum str. JA284
EU850807.1 gg_id:342759 Marichromatium purpuratum str. DSM 1591
AM180952.1 gg_id:148217 Marichromatium bheemlicum str. JA124
AJ543328.1 gg_id:111805 Marichromatium indicum str. JA100
AF508991.1 gg_id:71278 Nitrosococcus oceani str. SWC19

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AB094597.1	83672	348.9	349.6	681.9	595.6	1733.5	1118.1
AY445591.1	103376	230.6	464.7	2830.1	687.9	317.6	870.5
NC_009665.1	255224	1592.0	1975.6	7023.2	2334.9	1202.5	2357.1
AF132873.1	37061	396.3	553.7	1305.6	1068.6	538.4	867.9
Y13699.1	9053	1157.0	822.3	2526.6	2494.2	814.4	1411.6
AY351983.1	92948	1332.2	1197.5	1904.3	2828.2	1307.0	2309.2
GQ869534.1	569132	5358.8	7311.0	5298.1	8649.9	9442.1	13586.1
NC_009831.1	246705	1027.9	1574.8	2743.5	3618.8	1649.6	3558.3
AB013839.1	9017	1826.8	2669.0	2212.2	1969.2	1613.7	3606.0
NR_025934.1	540854	274.5	250.5	243.9	192.2	139.5	115.2
AY596470.1	104981	3504.7	4508.4	4598.1	1387.7	2662.5	7826.9
DQ645464.1	160756	1895.3	512.0	2429.3	1295.2	3243.0	1593.4
CP000513.1	226003	5324.8	9401.8	8722.2	6523.8	8811.6	7340.8
AJ717394.1	149350	2803.2	4104.1	4445.7	5230.8	5954.4	5195.0
X92131.1	46026	300.1	113.2	150.1	62.4	64.5	799.8
AF384209.1	25151	904.7	134.5	127.7	130.6	943.6	66.4
AM712619.1	237043	5666.4	6310.1	3980.9	6290.5	10007.5	8694.0
FJ716332.1	508808	5146.6	5420.8	6446.4	4693.0	7306.7	6403.1
AF384208.1	22729	422.4	713.4	227.5	135.4	759.5	280.5
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FJ437816.1	541203	3648.1	4592.2	3424.4	3941.0	4683.2	4500.9
AB478662.1	548000	8287.8	7888.7	10287.3	8852.2	12712.1	9783.8
DQ330802.1	159452	493.1	826.7	2351.8	892.1	3827.7	2024.0
AJ223235.1	7564	64.7	71.7	243.5	193.5	82.4	34.5
AM941378.1	344367	2067.8	2646.7	4217.8	3128.0	3507.6	2901.0
AM941379.1	304631	771.5	991.8	1578.5	1109.4	1491.5	961.3
AM179449.1	190862	963.2	965.3	1991.7	1266.4	1886.7	983.1
AM941377.1	325577	1089.1	1488.3	2187.6	2368.6	2378.4	2476.6
AM941046.1	369706	1675.9	1368.8	1971.9	715.0	624.9	1733.3
AJ889020.1	112951	1146.5	1424.3	1938.4	1626.7	1284.2	2156.5
FJ376391.1	360805	955.1	898.5	1221.0	892.8	926.4	1213.2
FM177512.1	344391	777.1	1000.7	1923.3	1277.8	1038.0	1051.0
AM179448.1	191066	1120.6	1411.9	2085.1	2343.0	3060.5	2200.4
AF294030.1	135580	6831.0	9527.9	6802.2	8972.8	10157.8	11118.3
FM177510.1	333563	552.6	1419.8	2483.1	1154.0	687.0	2023.5
EU850807.1	342759	592.7	541.9	871.2	468.0	587.9	805.3
AM180952.1	148217	1920.6	3772.2	4727.9	3975.9	2554.8	4242.4
AJ543328.1	111805	4171.8	5608.9	5702.4	5317.8	5514.8	5909.9
AF508991.1	71278	11714.1	14652.7	10049.7	8782.3	10511.7	11030.8

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g__Nitrosococcus
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s__Nitrosococcus oceani	3202
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s__Thiocystis gelatinosa	2726
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s__Thiorhodovibrio winogradskyi	3009
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s__unclassified	1289

AF508990.1 gg_id:73060 Nitrosococcus oceani str. AFC5P
AF508992.1 gg_id:56278 Nitrosococcus oceani str. AFC3
AJ298748.1 gg_id:77717 Nitrosococcus halophilus
NR_025356.1 gg_id:573506 Thiocapsa litoralis str. BM5; ATCC 700894
AF112999.1 gg_id:7533 Thiocapsa roseopersicina str. M11
AM779060.1 gg_id:261543 Thiocapsa subramanianii str. JA146
AJ581994.1 gg_id:141744 Thiocapsa marina str. BM-3
AF112998.1 gg_id:7532 Thiocapsa roseopersicina str. 5811
EF581005.1 gg_id:278653 Thiocapsa roseopersicina str. KS1
AJ277022.1 gg_id:71426 Thiococcus sp. str. A31
Y12373.3 gg_id:71248 Thiococcus pfennigii str. 4250
FN293055.1 gg_id:570678 Thiococcus pfennigii str. 4252 = DSM 228
FN293058.1 gg_id:536936 Thiocystis gelatinosa str. 4310 = DSM 215
D50655.1 gg_id:7517 Thiocystis gelatinosa
AJ224438.1 gg_id:7518 Thiocystis violascens str. DSM 168T
EF149014.1 gg_id:188673 Thiocystis sp. str. Mog3
AM086640.1 gg_id:139588 Thiocystis sp. str. 448.10
AJ971090.1 gg_id:172979 Thiorhodococcus mannitophagus str. WS
Y11316.1 gg_id:7526 Thiorhodococcus minor str. CE2203
AM748925.1 gg_id:245986 Thiophaeococcus mangrovi str. JA304
AB016986.1 gg_id:7570 Thiorhodovibrio winogradskyi str. MBIC2776T
AB294924.1 gg_id:225518 -dependent & analyses hydrothermal system off Taketomi Island Japan microbial ma
DQ867045.1 gg_id:196530 Microbial and methanogenic potential temperature water Japan natural gas field clc
FJ535065.1 gg_id:545461 microbial colonizing walls Karstic Slovenia cave wall biofilm clone 2PJM13
AF420353.1 gg_id:55790 hydrothermal sediment clone AF420353
DQ811841.1 gg_id:166871 mangrove soil clone MSB-4C11
DQ395021.1 gg_id:152376 harbor sediment clone VHS-B5-48
FJ712412.1 gg_id:516020 and Archaea Gas Hydrate Sediments (East Sea) Kazan Mud Volcano Anaximander Mo
AY225634.1 gg_id:95183 Mid-Atlantic Ridge hydrothermal sediment clone AT-s26
EU373841.1 gg_id:265007 southern Cretan margin (eastern Mediterranean Sea) canyon and slope sediment clc
AM882514.1 gg_id:309379 Structure along hydrocarbon contamination coastal sediment oil polluted water pet
GU369919.1 gg_id:524281 and mats vents Arc white microbial film on pebble aphotic zone shal hydrothermal v
FJ203535.1 gg_id:340951 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h
EU617747.1 gg_id:337743 Seasonal variation microbial Yel Sea sediment clone C13S-68
FM877665.1 gg_id:362822 Microbial several mining wastes Bulgaria vicinity uranium mine Sliven clone Sliv-109
DQ499304.1 gg_id:159535 acidic cave snottite biofilm clone CV55
EU050785.1 gg_id:254811 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_01_66
GU061986.1 gg_id:593500 and function microbial mesoscale eddy perturbations South China Sea clone S-DCM-
AY225631.1 gg_id:96909 Mid-Atlantic Ridge hydrothermal sediment clone AT-s2-13
EU652572.1 gg_id:278349 Seasonal variation microbial Yel Sea sediment clone B8S-132
DQ269059.1 gg_id:182899 marine macro-alga surface clone UA09

AF508990.1	73060	11423.0	14909.0	8958.6	10086.2	14526.2	12744.7
AF508992.1	56278	6742.1	10723.7	11536.9	6906.4	10870.7	9086.3
AJ298748.1	77717	166.3	154.8	225.3	247.9	115.9	35.8
NR_025356.1	573506	9213.8	10399.4	9976.5	9586.9	11273.5	8849.4
AF112999.1	7533	4920.4	5496.2	3427.5	4541.6	1847.2	5445.3
AM779060.1	261543	10344.4	10754.2	5337.0	7615.4	13539.3	9729.3
AJ581994.1	141744	1256.0	1750.8	5038.3	1642.8	897.7	1308.1
AF112998.1	7532	934.1	1839.5	2577.5	590.6	442.3	950.2
EF581005.1	278653	2825.2	3675.4	5152.4	2589.7	4734.5	3494.0
AJ277022.1	71426	106.2	143.1	161.0	165.6	1034.6	229.9
Y12373.3	71248	689.2	2148.6	2538.4	568.4	2585.0	4023.8
FN293055.1	570678	2014.9	2252.4	2791.0	771.5	474.5	685.8
FN293058.1	536936	1608.4	965.1	848.3	2303.7	1594.4	1320.9
D50655.1	7517	6743.2	6665.4	3447.1	6871.3	5637.1	5175.8
AJ224438.1	7518	11721.9	13420.6	6561.1	7646.4	12745.9	11057.0
EF149014.1	188673	737.3	1087.6	496.6	173.9	1428.9	639.6
AM086640.1	139588	896.0	556.8	2573.5	699.2	6054.8	1368.6
AJ971090.1	172979	1815.3	2970.7	4378.7	1868.7	2334.4	2484.1
Y11316.1	7526	1137.2	1801.7	2642.6	1122.7	1461.7	1767.8
AM748925.1	245986	3559.1	4041.3	2734.0	1580.6	4671.2	2289.3
AB016986.1	7570	68.2	77.8	175.5	127.9	88.2	51.1
AB294924.1	225518	4197.7	2081.7	3926.0	3015.5	925.4	2336.9
DQ867045.1	196530	124.1	327.5	560.2	215.6	253.6	222.3
FJ535065.1	545461	2833.3	2769.5	5443.4	5178.1	5159.8	6544.5
AF420353.1	55790	9862.9	11547.1	5933.8	7812.9	8605.5	6670.6
DQ811841.1	166871	1136.5	1680.6	4810.3	983.2	1903.6	1273.2
DQ395021.1	152376	411.9	472.5	1754.1	4963.2	932.6	699.4
FJ712412.1	516020	5850.1	5338.6	10034.0	8570.8	3130.7	4037.4
AY225634.1	95183	6111.2	6854.6	9127.8	8055.3	8525.1	6750.0
EU373841.1	265007	2748.1	3146.3	3047.4	3663.6	7649.0	6085.3
AM882514.1	309379	2514.5	1508.5	2785.5	1596.7	926.5	2519.5
GU369919.1	524281	127.2	217.3	258.2	322.2	488.2	506.3
FJ203535.1	340951	2842.5	4573.6	5327.2	2127.3	4502.5	4398.8
EU617747.1	337743	5871.3	4579.2	4752.4	7070.7	6051.5	6313.4
FM877665.1	362822	5162.1	5332.0	3343.0	7499.9	5963.5	6006.9
DQ499304.1	159535	2074.0	758.6	1786.2	2535.2	493.9	867.6
EU050785.1	254811	3243.0	2322.4	1410.0	3226.9	738.8	5663.4
GU061986.1	593500	5055.6	3095.7	4206.7	8119.3	7345.6	7015.7
AY225631.1	96909	205.5	496.8	1585.8	259.7	1459.8	738.7
EU652572.1	278349	1504.0	3031.2	4002.4	2250.7	9012.3	3738.0
DQ269059.1	182899	1351.7	1417.7	2110.9	2654.7	2393.6	1984.0

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AY592343.1 gg_id:99715 deep-sea mud volcano clone Amsterdam-1B-40; BC20-1B-40
FJ712551.1 gg_id:519028 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) K
AY796036.1 gg_id:108755 gold mine bore hole clone 47mm23
EU700150.1 gg_id:298462 Study on Shantou Bay Marine Sediments Microorganisms sediment clone STU8
FJ545527.1 gg_id:533202 Diveristy Seawater and Sediment Northern North Yel Sea seawater clone W1-36
DQ289941.1 gg_id:173031 Microbial Carbon and Nitrogen Cycling Sediments South Atlantic Bight Permeable Sh
AY225628.1 gg_id:96854 Mid-Atlantic Ridge hydrothermal sediment clone AT-s3-68
EF644798.1 gg_id:299470 genes and citrate lyase deep-sea microbial MAR Logatchev hydrothermal vent syster
EU491553.1 gg_id:268415 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR4C
DQ303270.1 gg_id:141619 Microbial ecology macroscopic filaments extreme Tinto River acidic river clone fa7
GU061300.1 gg_id:574531 Evaluation culturing methods cultivate previously Yel Sea intertidal beach seawater
DQ394966.1 gg_id:153375 harbor sediment clone VHS-B3-85
FN396767.1 gg_id:555049 constant flux thermophilic cold seabed Arctic marine surface sediment clone s5_8_I_
FJ484458.1 gg_id:553048 microbial autonomous rover world's deepest phreatic sinkhole wall biomat El Zacator
DQ351781.1 gg_id:147516 Microbial Adherent Sediment Particles Heavy Metal Contaminated North Sea Surfac
AM040135.1 gg_id:145316 sandy sediments clone Sylt 39
GQ351146.1 gg_id:586541 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Eastern
EF646139.1 gg_id:247661 Potential interactions particle- anammox and archaeal partners namibian Namibian u
FJ205341.1 gg_id:551312 Prokaryotic deep-sea hydrothermal region East Lau Spreading Centre deep marine se
AM889168.1 gg_id:584938 structure superficial sediments Bizerte (Tunisia) southern Mediterranean coastal an
FM877664.1 gg_id:367915 Microbial several mining wastes Bulgaria vicinity uranium mine Sliven clone Sliv-80
FJ529318.1 gg_id:512678 Evidence vertical transmission symbionts adult embryo Caribbean sponge Svenzea ze
AB099937.1 gg_id:79212 inactive deep-sea hydrothermal vent chimneys clone IheB2-13
DQ469234.1 gg_id:158638 Microbial and ecology water Zhong Tiaoshan mine Shanxi province China AMD clone
GU118309.1 gg_id:589714 Threatened Corals Provide Microbial Habitats clone Dstr_I04
EU801093.1 gg_id:336892 It's all ranking aquatic Delaware Bay NJ clone 2C229409
FJ205285.1 gg_id:564511 Prokaryotic deep-sea region East Lau Spreading Centre active hydrothermal field sedi
DQ833482.1 gg_id:164256 detected analyses depth sediment Guanting Reservoir clone 35-8
AJ536881.1 gg_id:78477 uranium waste soil clone JG30-KF-AS32
DQ234241.2 gg_id:143226 determined library mangrove clone DS159
EF613006.1 gg_id:234358 acid mine drainage clone YSK16S-43
FJ535355.1 gg_id:556389 Granulosicoccus sp. str. Z271
EU394558.1 gg_id:342967 Coccolithophore bloom dynamics shape (NE-Atl) northern Bay Biscay pelagic free-livi
EU439003.1 gg_id:540861 symbiont
FJ228294.1 gg_id:324503 sulfate-reducing enriched during bioremediation experiment sediments (Brandenburg
DQ070793.1 gg_id:147722 Prokaryotic Structures Seafloor Basalts Varying Age and Juan de Fuca Ridge basalt gl
DQ396312.1 gg_id:154441 deep-sea octacoral clone ctg_NISA188
EU491600.1 gg_id:270104 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39
EU617752.1 gg_id:341837 Seasonal variation microbial Yel Sea sediment clone C13S-45
EU491687.1 gg_id:276375 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39

EU799991.1	341773	1425.3	1274.7	2750.5	2527.8	2313.3	2104.3
AY592343.1	99715	12519.9	14237.2	16984.0	13436.0	13195.9	12177.6
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EU700150.1	298462	2560.7	3765.0	4835.6	1643.0	2378.8	3680.1
FJ545527.1	533202	5876.9	6013.0	5853.9	5700.8	11283.5	10290.2
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EF644798.1	299470	1565.6	2514.6	4000.2	3363.2	2239.8	2324.5
EU491553.1	268415	582.1	263.2	680.3	355.3	666.1	454.1
DQ303270.1	141619	862.9	1352.4	1809.3	971.8	3254.9	1528.5
GU061300.1	574531	3762.4	4828.5	5913.9	4626.1	5859.7	4431.9
DQ394966.1	153375	5384.1	6892.2	9061.4	6933.0	12595.9	10314.1
FN396767.1	555049	603.2	447.4	1238.5	709.6	986.2	1098.1
FJ484458.1	553048	6992.0	5811.8	7321.8	5736.8	4965.9	4414.5
DQ351781.1	147516	4078.5	2286.4	4384.1	6907.9	6925.7	5143.4
AM040135.1	145316	1787.2	1994.5	1267.1	1666.7	1828.9	1499.3
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EF646139.1	247661	7182.1	5843.4	4120.6	6064.5	8339.1	5216.1
FJ205341.1	551312	6539.1	6077.3	6633.4	9826.1	6831.0	8717.9
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AB099937.1	79212	110.8	137.8	127.3	91.5	149.8	188.8
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DQ833482.1	164256	1659.9	2870.0	6170.3	2360.3	4813.8	4768.5
AJ536881.1	78477	1215.6	1820.0	1608.4	1376.6	2420.4	2712.1
DQ234241.2	143226	28.8	67.4	146.4	68.1	132.7	31.2
EF613006.1	234358	209.0	211.4	298.4	225.2	215.0	178.0
FJ535355.1	556389	203.5	162.0	136.2	163.3	119.6	512.7
EU394558.1	342967	2914.6	4026.9	1643.7	4222.6	6490.1	5809.4
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EU035934.2 gg_id:316421 Insight microbial structure Norwegian deep-water Desmacidon sponge deep-sea cor
GU208368.1 gg_id:577626 Study on Sediment Dongping Lake sediment clone Td1-10
FM213426.1 gg_id:354483 Chemosynthetic Bivalvia species mud volcanoes Gulf Cadiz host gill tissue clone Mer
EU491699.1 gg_id:268263 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39
EU491199.1 gg_id:275872 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak
DQ396273.1 gg_id:156456 deep-sea octacoral clone ctg_NISA021
AJ567545.1 gg_id:89831 deep-sea sediment clone MBMPE27
AM882524.1 gg_id:313486 Structure along hydrocarbon contamination coastal sediment oil polluted water pet
EF540405.1 gg_id:220661 oil-shale semi-coke solid waste clone 4_4MK
GQ351258.1 gg_id:570178 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Eastern
EU491112.1 gg_id:258311 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak
DQ070809.1 gg_id:149398 Prokaryotic Structures Seafloor Basalts Varying Age and Juan de Fuca Ridge basalt gl
DQ289928.1 gg_id:168507 Microbial Carbon and Nitrogen Cycling Sediments South Atlantic Bight Permeable Sh
EU491667.1 gg_id:262608 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39
AY328730.1 gg_id:89553 drinking water system simulator clone DSSD31
AY532575.1 gg_id:106089 uranium-contaminated aquifer clone 1013-28-CG34
EF612420.1 gg_id:244634 historic semiarid lead-zinc site mine tailings clone K6-C62
EU246808.1 gg_id:241908 polyphasic description Pocillopora meandrina Palmyra Atoll Calcinus obscurus abdon
EU735667.1 gg_id:307033 archaeal structures oil contaminated and soils China pristine soil Jidong Oilfield clone
FJ535071.1 gg_id:571233 microbial colonizing walls Karstic Slovenia cave wall biofilm clone 3PJM14
DQ811846.1 gg_id:165797 mangrove soil clone MSB-4G2
GQ348058.1 gg_id:533527 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
FM877661.1 gg_id:357872 Microbial several mining wastes Bulgaria vicinity uranium mine Sliven clone Sliv-13
EU491253.1 gg_id:274139 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak
AB252438.1 gg_id:154019 Microbial extremely CO2 rich deep-sea sediment Marine sediments Yonaguni Knoll I'
GU198380.1 gg_id:546867 Metagenomic denitrifying sulfur-oxidizing consortium enriched marine sediment clo
FJ205202.1 gg_id:563890 Prokaryotic deep-sea region East Lau Spreading Centre inactive hydrothermal field se
GQ397041.1 gg_id:539039 Functional unvegetated perhumid recently-deglaciated soils do not correlate shifts s
FJ529263.1 gg_id:590516 Evidence vertical transmission symbionts adult embryo Caribbean sponge Svenzea ze
DQ925902.1 gg_id:255109 Microbes and Thermal Gradients Temperature Hydrothermal Chimneys hydrotherm
DQ269101.1 gg_id:180233 marine macro-alga surface clone DPC112
GQ495417.1 gg_id:575230 terrestrial volcanic rocks Iceland Hnausahraun lava f clone Bas-7-60
GU230383.1 gg_id:561498 Multilevel approach along Rio de la Plata-South Atlantic Ocean coastal water clone A
DQ334625.1 gg_id:186898 Impact metals on sediments heavy metal polluted marine sediment clone HB2-20-8
EU700176.1 gg_id:296708 Study on Shantou Bay Marine Sediments Microorganisms sediment clone STU34
EU800034.1 gg_id:307663 It's all ranking aquatic Newport Harbour RI clone 1C227721
GU118033.1 gg_id:579643 Threatened Corals Provide Microbial Habitats clone Apal_F02
GQ263152.1 gg_id:541400 Structure Simulated Level Waste Site simulated level waste site clone F3_08X
AF223298.1 gg_id:37006 marine sediment clone B2M54
FJ712427.1 gg_id:519729 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) K
DQ836756.1 gg_id:172425 attached biomass denitrifying bioreactor clone DB-47

EU035934.2	316421	5854.3	6995.0	9793.9	6764.9	10624.1	7329.4
GU208368.1	577626	6529.3	9747.0	10667.1	7785.7	12175.4	10111.7
FM213426.1	354483	35.0	48.6	134.4	87.2	105.1	45.5
EU491699.1	268263	2611.7	1930.3	2421.8	3253.1	2187.7	2458.3
EU491199.1	275872	3015.1	2217.8	3307.2	4829.6	5442.5	2955.1
DQ396273.1	156456	5477.8	7482.3	6542.1	7501.4	15689.8	7253.0
AJ567545.1	89831	416.6	839.6	1507.3	2093.2	3556.3	2822.0
AM882524.1	313486	2981.9	4230.8	6331.9	3104.5	9968.6	6824.0
EF540405.1	220661	7826.8	7378.7	8532.8	9812.2	8703.4	7978.9
GQ351258.1	570178	51.9	112.1	115.5	73.1	89.9	48.8
EU491112.1	258311	2581.5	2275.5	4222.8	4974.0	2719.9	3214.4
DQ070809.1	149398	11404.9	9639.1	11039.3	8415.0	11004.5	8993.2
DQ289928.1	168507	70.8	150.1	531.3	170.4	154.0	367.7
EU491667.1	262608	10183.3	11319.4	4181.0	11086.6	9274.1	9356.0
AY328730.1	89553	1713.7	1717.5	3311.0	1819.4	4528.8	2600.9
AY532575.1	106089	1429.2	2953.1	8222.5	3199.7	5302.8	3969.1
EF612420.1	244634	3576.3	3323.7	7039.7	7419.5	5477.6	3651.0
EU246808.1	241908	4686.0	4419.2	4237.6	5369.8	5881.1	4881.5
EU735667.1	307033	273.7	542.2	1165.7	582.4	283.2	490.9
FJ535071.1	571233	1697.6	1619.2	3582.2	2954.3	3071.7	2341.0
DQ811846.1	165797	531.7	444.1	1409.8	1350.7	158.6	430.8
GQ348058.1	533527	9460.8	13257.3	5750.8	9369.1	8170.3	8109.1
FM877661.1	357872	7166.4	7934.2	9954.9	8072.4	11844.8	8833.1
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DQ925902.1	255109	3227.1	3780.7	2151.1	1940.5	5534.6	5591.5
DQ269101.1	180233	40.2	360.9	59.1	94.2	78.0	38.6
GQ495417.1	575230	720.6	1661.4	1011.6	1424.9	2288.9	1998.9
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DQ334625.1	186898	23.8	42.1	92.5	53.0	75.9	131.4
EU700176.1	296708	639.9	957.9	2343.3	636.4	1367.8	1151.6
EU800034.1	307663	5478.4	6114.8	4700.0	4569.9	5740.7	5454.5
GU118033.1	579643	2148.3	2666.2	3025.1	1583.5	3338.5	3155.5
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DQ836756.1	172425	66.9	229.5	140.0	109.7	281.6	291.3

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GU302446.1 gg_id:538297 Spatial structure and activity sedimentary microbial underlying Beggiatoa spp. mat h
EU286994.1 gg_id:254165 Pacific arctic surface sediment clone B78-30
EU491103.1 gg_id:271777 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak
DQ328618.1 gg_id:148733 microorganisms populating site extreme acid mine drainage sediment clone H6
GQ262946.1 gg_id:511219 Structure Simulated Level Waste Site simulated level waste site clone F1_84X_2
AM997814.1 gg_id:543652 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A
GQ348554.1 gg_id:554477 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
GQ866093.1 gg_id:553108 Seasonal changes Norway lobster (Nephrops norvegicus) gut clone F1-2
FM178271.1 gg_id:310885 Thiolamprovum pedioforme str. 4470 = DSM 3802(T)
GQ346946.1 gg_id:555763 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
FJ497646.1 gg_id:587676 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun
DQ394927.1 gg_id:155515 harbor sediment clone VHS-B3-4
DQ070817.1 gg_id:149753 Prokaryotic Structures Seafloor Basalts Varying Age East Pacific Rise and Ridge basal
AB294934.1 gg_id:217304 -dependent & analyses hydrothermal system off Taketomi Island Japan microbial ma
FM242262.1 gg_id:329501 sequences sediment clone 93 T0h-oil
EU491843.1 gg_id:260428 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39
AM882535.1 gg_id:316871 Structure along hydrocarbon contamination coastal sediment oil polluted water pet
FJ152611.1 gg_id:355416 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX1A_
AM086641.1 gg_id:139719 Thiocystis sp. str. H1.1
EF644807.1 gg_id:297894 genes and citrate lyase deep-sea microbial MAR Logatchev hydrothermal vent syster
DQ431906.1 gg_id:213821 microorganisms catalyzing nitrogen removal and organic matter metabolism perme
FN397816.1 gg_id:429948 geomicrobiological investigation sediments Gulf Cadiz GeoB 9072-1 anoxic sub-surfa
GQ246407.1 gg_id:551973 Temporal and spatial China North Yel Sea sediments clone Ld1-12
AM882545.1 gg_id:347412 Structure along hydrocarbon contamination coastal sediment oil polluted water pet
AM997582.1 gg_id:542870 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A
AM882565.1 gg_id:312010 Structure along hydrocarbon contamination coastal sediment oil polluted water pet
FJ437960.1 gg_id:512465 Benthic okenone production Fayetteville New York Green Lake surface sediments 16.
GU454932.1 gg_id:530809 Understanding short-chain fatty acids accumulation enhanced alkaline digestion: kir
DQ498828.1 gg_id:160903 Thiocapsa sp. str. SC5
EF125462.1 gg_id:177523 mangrove soil clone MSB-2H6
EU491333.1 gg_id:261470 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak
FJ535330.1 gg_id:511313 within iron-containing flocculent mats submarine volcanoes along Kermadec Arc sedi
EF999348.1 gg_id:250082 Vertical and Methanotrophs Estuarine Sediments Pearl River Estuary sediments 6cm
FJ745203.1 gg_id:553528 Transporter genes expressed coastal response dissolved organic carbon surface wate
GQ495440.1 gg_id:543963 terrestrial volcanic rocks Iceland Hnausahraun lava f clone Bas-7-84
EU050786.1 gg_id:245663 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_07_19
FJ712524.1 gg_id:513647 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) k
AF406546.1 gg_id:60630 bacterioplankton clone AEGEAN_245
FJ497635.1 gg_id:558137 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun
FM242359.1 gg_id:317250 sequences sediment clone 16 T9d+oil
FJ717238.1 gg_id:538780 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United Kingc

GU302446.1	538297	1054.9	765.0	2526.2	1256.0	1000.1	1772.6
EU286994.1	254165	3073.4	2900.3	2005.5	3621.9	2354.7	2171.2
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DQ328618.1	148733	4745.7	5803.4	315.4	115.1	8615.2	4586.2
GQ262946.1	511219	6585.3	6884.0	11449.9	8231.1	9771.9	9258.1
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GQ866093.1	553108	5998.0	4222.0	4627.8	6189.0	2893.2	3104.1
FM178271.1	310885	4626.6	6502.7	4327.0	3689.2	3486.6	4453.1
GQ346946.1	555763	3076.9	2374.3	3776.0	1939.0	5918.4	4758.2
FJ497646.1	587676	1590.4	2967.4	916.0	1447.6	1505.6	2053.1
DQ394927.1	155515	5511.1	6594.7	8178.8	8255.3	3740.3	7350.8
DQ070817.1	149753	194.6	486.4	646.3	467.6	1097.4	893.4
AB294934.1	217304	5366.6	3709.8	2512.6	2858.7	3846.4	5238.6
FM242262.1	329501	1763.2	1576.7	3431.1	3737.1	5409.3	3502.0
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AM882535.1	316871	1578.4	1701.8	2923.9	1515.8	1123.4	933.0
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FN397816.1	429948	9821.3	8338.4	6769.3	9066.0	10017.1	10155.0
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AM882545.1	347412	1004.2	1033.5	1485.9	838.2	2095.6	902.1
AM997582.1	542870	430.2	844.3	2073.6	1194.8	6722.2	3914.2
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DQ498828.1	160903	1073.3	1307.1	1738.1	1169.3	681.1	967.7
EF125462.1	177523	184.4	179.8	532.7	588.9	122.6	118.1
EU491333.1	261470	514.5	651.6	1232.7	1505.9	429.5	1115.4
FJ535330.1	511313	7517.0	6795.7	7289.0	6999.9	9376.7	7572.2
EF999348.1	250082	470.9	1230.5	1377.1	375.4	519.0	189.0
FJ745203.1	553528	2308.4	2781.8	2992.7	4346.8	3247.4	3397.3
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EU050786.1	245663	873.7	1024.6	3625.5	1240.2	4974.3	1810.3
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AF406546.1	60630	1505.6	958.1	908.0	1412.8	1021.5	2350.4
FJ497635.1	558137	5144.4	5532.8	4424.9	4993.3	7615.2	10169.1
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FM210274.1 gg_id:528855 Marichromatium fluminis str. JA418
GQ141761.1 gg_id:435569 Microbial thriving -pH Rincon de la Vieja Volcano National Park Costa Rica superficia
EF076070.1 gg_id:256660 Sponge- microorganisms: ecology and biotechnological potential Bahamas: Little San
AB426192.1 gg_id:267544 -situ identification study benzene-degrading s under methanogenic condition anaerc
DQ925905.1 gg_id:254195 Microbes and Thermal Gradients Temperature Hydrothermal Chimneys hydrotherm
GQ406158.1 gg_id:593544 Benthic submerged sinkhole ecosystems sediment clone TS-45-9
EF654696.1 gg_id:242116 mixed granule anammox reactor clone KIST-JJY027
U24110.1 gg_id:7550 Gamma-proteobacterial endosymbiont
DQ408758.1 gg_id:241921 endosymbionts gutless marine nematode Astomonema sp. sediments coral reef sed
EU555131.1 gg_id:265444 Microbial Sulfide Hydrothermal Vent Field Juan de Fuca Ridge Dudley hydrothermal
DQ925881.1 gg_id:242627 Microbes and Thermal Gradients Temperature Hydrothermal Chimneys hydrotherm
EF125401.1 gg_id:193004 soil naked tidal flat sediment near mangrove clone MSB-1D8
AB100006.1 gg_id:79132 inactive deep-sea hydrothermal vent chimneys clone IndB3-17
AM882566.1 gg_id:314376 Structure along hydrocarbon contamination coastal sediment oil polluted water pet
EU050809.1 gg_id:253074 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_01_83
AJ006212.1 gg_id:7572 Lamprocystis purpurea str. ML1
AB252426.1 gg_id:153466 Microbial extremely CO2 rich deep-sea sediment Marine sediments Yonaguni Knoll I'
EU491139.1 gg_id:272596 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak
AB294972.1 gg_id:225408 -dependent & analyses hydrothermal system off Taketomi Island Japan microbial ma
DQ458038.1 gg_id:157435 acid mine drainage clone DX41
AM282561.1 gg_id:193170 Thiorhodococcus kakinadaii str. JA130
AACY01032263.1 gg_id:105207 Sargasso Sea
EU491349.1 gg_id:260349 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X3 clone
DQ676419.1 gg_id:223736 Archaeal and plankton freshwater pond suboxic freshwater-pond sediment clone M
AM997970.1 gg_id:541611 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A
EU491101.1 gg_id:271612 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak
EF208706.1 gg_id:202468 Vertical and horizontal structure microbial sandy carbonate sediment clone CI75cm.2
EU617749.1 gg_id:332804 Seasonal variation microbial Yel Sea sediment clone D13S-16
NR_029333.1 gg_id:589849 Thiocystis violacea str. N. Pfennig 2711; DSM 207
DQ676383.1 gg_id:219789 Archaeal sediment and plankton freshwater pond suboxic freshwater-pond clone M
EU491810.1 gg_id:261375 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39
AM491592.1 gg_id:274061 Thiohalocapsa marina str. JA142
AJ002796.2 gg_id:7556 Thiohalocapsa halophila str. SG3202
DQ330805.1 gg_id:159272 Guerrero Negro hypersaline microbial mat clone 02D2Z63
EU236358.1 gg_id:295840 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg91C2
FM242313.1 gg_id:328728 sequences sediment clone 25 T9d-oil
FJ264656.1 gg_id:346479 Manganese and Iron Dependent Anaerobic Oxidation Methane methane seep sedime
AF328856.1 gg_id:43810 Olavius algarvensis sulfur-oxidizing endosymbiont sulfur-oxidizing
AJ620507.1 gg_id:108086 Olavius crassitunicatus endosymbiont
AM934861.1 gg_id:560973 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
AY953181.1 gg_id:114439 anaerobic swine lagoon clone B-1O

FM210274.1	528855	2358.2	3194.1	2311.8	1929.5	5106.7	3817.1
GQ141761.1	435569	9202.0	7393.7	7727.9	7692.7	9613.3	9598.1
EF076070.1	256660	9486.8	9352.4	7063.5	7029.0	7851.9	5507.5
AB426192.1	267544	1539.7	1525.6	2144.9	968.7	3034.6	1610.6
DQ925905.1	254195	3249.3	2885.7	2498.1	3717.1	5111.7	3541.1
GQ406158.1	593544	4506.5	5032.6	3032.2	1511.2	3622.9	3464.9
EF654696.1	242116	2216.8	2754.5	3092.3	3633.8	7276.4	5919.4
U24110.1	7550	1883.3	2896.5	2545.9	768.8	6104.5	4260.3
DQ408758.1	241921	1664.1	1627.6	1091.4	1630.2	2624.6	2267.5
EU555131.1	265444	2575.5	2786.4	3891.8	1820.5	4019.5	5111.8
DQ925881.1	242627	7056.5	6635.1	7166.0	7925.0	10654.3	8393.2
EF125401.1	193004	532.3	981.1	3919.5	567.3	592.7	706.8
AB100006.1	79132	73.5	82.6	38.9	74.6	94.2	48.6
AM882566.1	314376	498.6	874.2	2861.0	622.5	4476.0	1094.5
EU050809.1	253074	613.2	1018.6	1446.9	1572.5	442.9	799.2
AJ006212.1	7572	2211.1	3753.5	5355.1	2621.8	6604.6	7681.4
AB252426.1	153466	3522.8	2460.5	4845.7	6391.3	1348.0	3519.0
EU491139.1	272596	1905.8	1943.2	4701.4	2666.9	2139.5	3581.2
AB294972.1	225408	61.8	124.4	151.7	108.8	946.4	168.4
DQ458038.1	157435	1636.4	1908.2	1304.5	1435.4	2442.1	2273.7
AM282561.1	193170	2791.0	3797.6	6855.8	3317.8	12475.6	5170.4
AACY01032263.1	105207	1965.0	2322.4	4232.6	2598.7	1528.0	3012.2
EU491349.1	260349	2991.2	2831.2	2635.5	4911.0	4786.7	3520.7
DQ676419.1	223736	8960.9	8907.1	2823.7	2466.9	4981.2	3615.5
AM997970.1	541611	396.5	546.2	1775.4	1013.4	1111.9	2464.7
EU491101.1	271612	871.3	772.3	988.7	650.3	508.7	2042.2
EF208706.1	202468	1820.0	2687.2	4239.5	3067.7	6276.6	6484.7
EU617749.1	332804	5315.5	5348.4	5179.0	4870.5	7641.1	4375.3
NR_029333.1	589849	619.7	1356.2	1576.1	252.7	780.7	1404.6
DQ676383.1	219789	900.7	901.5	1852.5	937.7	3295.9	1691.5
EU491810.1	261375	5918.1	4330.4	6778.5	8120.4	8209.5	7414.7
AM491592.1	274061	2825.5	4834.7	5655.0	2065.1	4039.4	4582.3
AJ002796.2	7556	134.0	196.9	77.8	102.2	110.6	119.6
DQ330805.1	159272	597.7	1135.3	4001.3	2049.1	1774.9	2442.4
EU236358.1	295840	4214.5	3586.3	6566.7	5385.3	8079.2	5604.7
FM242313.1	328728	684.9	2377.9	2679.5	868.8	2953.9	1518.9
FJ264656.1	346479	533.8	1153.7	739.5	350.8	2528.1	2988.2
AF328856.1	43810	707.0	1142.8	1790.3	805.4	4083.2	2627.5
AJ620507.1	108086	333.5	126.6	243.2	204.8	89.1	84.4
AM934861.1	560973	6546.3	6844.0	7180.5	7870.9	10284.2	8957.3
AY953181.1	114439	2191.2	3638.0	3235.0	1401.9	4512.9	3517.8

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EU491595.1 gg_id:277061 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39
AJ404006.1 gg_id:67655 Thiobaca trueperi str. BCH
AF468306.1 gg_id:80943 Arctic sea ice; northern Fram Strait clone ARKICE-74
EU035919.2 gg_id:305967 Insight microbial structure Norwegian deep-water Desmacidon sponge deep-sea cor
FM242312.1 gg_id:323358 sequences sediment clone 62 T9d-oil
AY225632.1 gg_id:98768 Mid-Atlantic Ridge hydrothermal sediment clone AT-s3-1
FM242217.1 gg_id:352618 sequences sediment clone 9 T0h-oil
GU061223.1 gg_id:560363 Evaluation culturing methods cultivate previously Yel Sea intertidal beach seawater
AM176876.1 gg_id:160373 Recovery mangrove sediment clone SZB80
EF157171.1 gg_id:246738 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon
FM242216.1 gg_id:315780 sequences sediment clone 328 T0h-oil
AM942764.1 gg_id:259432 Thiorhodococcus kakinadensis str. JA326
AB247483.1 gg_id:149328 lab-scale EBPR sludge clone Run-SP84
DQ834966.1 gg_id:239144 Methylohalomonas lacustra
GU061216.1 gg_id:561480 Evaluation culturing methods cultivate previously Yel Sea intertidal beach seawater
EF644813.1 gg_id:288087 genes and citrate lyase deep-sea microbial MAR Logatchev hydrothermal vent syster
EU734910.1 gg_id:313480 assemblages sediment station DBSE Northern Bering Sea clone 001A1
AJ620498.1 gg_id:353788 Olavius 1 endosymbiont O. ilvae Individual 2
FJ971729.1 gg_id:415655 microbial autrotrophic denitrification granular sludge clone R1-B5
FM955329.1 gg_id:546246 nematodes marine sediment
AM282559.1 gg_id:192789 Thiorhodococcus bheemlicum str. JA132
DQ408757.1 gg_id:211956 morphological between endosymbionts and marine nematode Astomonema sp. Bal
EU617748.1 gg_id:327160 Seasonal variation microbial Yel Sea sediment clone D13S-78
FJ971740.1 gg_id:437967 microbial autrotrophic denitrification granular sludge clone R2-B11
EF999974.1 gg_id:245668 Thiodictyon bacillosum str. DSM 234T
FJ712507.1 gg_id:529626 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) K
EF999973.1 gg_id:257959 Thiodictyon elegans str. DSM 232T
AB186842.1 gg_id:103037 polychlorinated dioxin dechlorinating microcosm clone TSBX13
GQ249599.1 gg_id:509542 Microbial anaerobic sediments Bay Cadiz (Spain) marine sediment: 12-14 cm layer cl
GQ347493.1 gg_id:540052 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
AF223299.1 gg_id:31454 marine sediment clone B2M60
EU652571.1 gg_id:279434 Seasonal variation microbial Yel Sea sediment clone A8S-46
FJ358866.1 gg_id:580890 and redox-stratified sediments marine reef sandy sediment clone OX79
FJ264672.1 gg_id:348014 Manganese and Iron Dependent Anaerobic Oxidation Methane methane seep sedime
DQ867047.1 gg_id:186089 Microbial and methanogenic potential temperature water Japan natural gas field clc
GQ246364.1 gg_id:593033 Temporal and spatial China North Yel Sea sediments clone Cm1-27
GU056102.1 gg_id:571289 Biologic Techniques Applied Microbial Prospecting China: Ban 876 Gas Oil Field Bein
AB530206.1 gg_id:586045 Monitoring Suez and Tokyo bays based on analyses marine sediment clone Tokyo..B
AB530192.1 gg_id:549648 Monitoring Suez and Tokyo bays based on analyses marine sediment clone Suez..Bac
DQ269062.1 gg_id:190822 marine macro-alga surface clone DPC061
EU134786.1 gg_id:243086 tallgrass prarie soil clone FFCH2627

EU491595.1	277061	1393.2	1375.5	1658.4	2186.0	2582.2	2047.8
AJ404006.1	67655	33.8	71.2	169.2	64.2	105.5	35.3
AF468306.1	80943	452.3	689.3	1104.7	625.7	1239.2	3411.1
EU035919.2	305967	6460.3	7297.8	7863.1	8271.5	8105.5	7335.3
FM242312.1	323358	2842.8	3531.2	4804.0	2976.8	5196.3	3814.1
AY225632.1	98768	5194.7	5124.9	4252.2	6225.2	8131.8	6786.8
FM242217.1	352618	4610.8	4788.5	7075.7	3170.8	6023.8	4893.9
GU061223.1	560363	7847.7	7915.2	9744.0	7399.0	7535.0	7462.9
AM176876.1	160373	3990.5	5196.5	2849.8	2577.7	4231.3	3577.6
EF157171.1	246738	2928.2	3340.9	4371.1	2061.0	3380.7	4935.4
FM242216.1	315780	1039.0	1774.8	1604.3	674.9	2678.0	1785.8
AM942764.1	259432	2226.5	2992.2	5051.0	2823.0	4837.8	3702.8
AB247483.1	149328	79.1	40.3	48.7	53.5	288.5	40.6
DQ834966.1	239144	1915.0	2698.5	5278.1	2359.7	6217.2	6408.2
GU061216.1	561480	4282.0	3835.8	5904.8	5167.4	5173.9	8952.6
EF644813.1	288087	2566.8	4116.4	4081.1	3597.1	9709.9	9721.4
EU734910.1	313480	2592.2	2684.1	3911.6	4132.1	5935.9	3381.8
AJ620498.1	353788	3131.8	3161.5	4242.4	5521.7	5944.7	6119.6
FJ971729.1	415655	8975.7	10517.3	7248.0	8688.7	14613.8	13914.5
FM955329.1	546246	2092.0	2328.5	3823.6	2494.3	2930.2	2422.0
AM282559.1	192789	1028.1	1666.5	1662.7	627.8	1711.6	1107.5
DQ408757.1	211956	108.9	178.6	834.8	238.7	564.7	59.4
EU617748.1	327160	10695.3	12260.9	14987.1	10508.2	16811.2	17917.3
FJ971740.1	437967	5271.5	7738.9	4269.7	6356.3	8957.1	6682.2
EF999974.1	245668	417.0	740.0	1143.5	829.9	729.4	599.2
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AB186842.1	103037	458.8	1417.6	1211.9	188.7	1754.9	1136.7
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FJ264672.1	348014	2871.1	3319.1	4151.7	1828.8	4673.1	5319.3
DQ867047.1	186089	2785.2	1981.3	2129.5	2962.1	2854.2	4118.9
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AB530206.1	586045	1909.0	2796.3	4784.5	3296.2	7630.2	2467.8
AB530192.1	549648	7516.6	7208.8	6174.7	9880.7	12861.6	10691.9
DQ269062.1	190822	65.8	156.4	162.1	254.4	768.0	287.6
EU134786.1	243086	6021.4	7154.2	9342.4	5090.2	4748.4	6770.9

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AJ853601.1 gg_id:110147 landfill leachate clone GZKB108
EU236373.1 gg_id:297512 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg91G3
AY225627.1 gg_id:96329 Mid-Atlantic Ridge hydrothermal sediment clone AT-s68
FJ497388.1 gg_id:579158 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun
EF632940.1 gg_id:242102 Unique microbial contrasting aquatic altitude Andean Altiplano (northern Chile) fresh
EU491429.1 gg_id:261838 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X4 clone
DQ811847.1 gg_id:164335 mangrove soil clone MSB-5C2
DQ811843.1 gg_id:172303 mangrove soil clone MSB-4E4
EF203207.1 gg_id:207236 phylotypes sediments Lake Kastoria Greece sediment clone Kas176B
FM877666.1 gg_id:366930 Microbial several mining wastes Bulgaria vicinity uranium mine Sliven clone Sliv-112
AY225635.1 gg_id:98613 Mid-Atlantic Ridge hydrothermal sediment clone AT-s80
DQ811842.1 gg_id:171222 mangrove soil clone MSB-4D7
AY328773.1 gg_id:88634 drinking water system simulator clone DSSD75
DQ351776.1 gg_id:146277 Microbial Adherent Sediment Particles Heavy Metal Contaminated North Sea Surfac
FJ937836.1 gg_id:397082 Marine Sponge Gelliodes carnosa coastal waters Lingshui Bay Hainan Island South Ch
EU236293.1 gg_id:290042 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg9Co20
GU208274.1 gg_id:568003 Study on Sediment Dongping Lake sediment clone 6F3-6
GU118056.1 gg_id:580801 Threatened Corals Provide Microbial Habitats clone Apal_E11
AB188772.1 gg_id:114044 cold seep sediment clone SB1-7
FJ205206.1 gg_id:559269 Prokaryotic deep-sea region East Lau Spreading Centre inactive hydrothermal field se
GQ356981.1 gg_id:557781 Metal Dependent Marine Methane Oxidation methane seep sediment clone FeSO4_
GU369933.1 gg_id:527507 and mats vents Arc white microbial film on pebble aphotic zone shal hydrothermal v
EF612432.1 gg_id:244758 historic semiarid lead-zinc site mine tailings clone Fe-K6-C35
EU491147.1 gg_id:261461 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak
DQ823153.1 gg_id:167115 Techniques Microbial Studies Oregon Caves National Monument Quad 3 off trail clo
AB189342.1 gg_id:113899 cold seep sediment clone JT58-17
CP000453.1 gg_id:171890 Alkalilimnicola ehrlichei str. MLHE-1
AJ404972.1 gg_id:46869 Alkalilimnicola halodurans 34Alc
DQ217918.1 gg_id:142576 Alkalispirillum sp. str. AGDZ
DQ217919.1 gg_id:142198 Alkalispirillum sp. str. ALPs 2
EU308278.1 gg_id:358039 Arhodomonas sp. str. 50B226a_1
EU653291.1 gg_id:280943 Thiobacillus prosperus str. DSM 5130
EU653290.1 gg_id:282074 Thiobacillus prosperus str. V6
AY298904.1 gg_id:89646 Ectothiorhodosinus mongolicum str. M9
EU590916.1 gg_id:265489 Ectothiorhodospira sp. str. PHS-1
AM943124.1 gg_id:556051 Ectothiorhodospira variabilis str. WN21R
AM902494.1 gg_id:571311 Ectothiorhodospira imhoffii str. JA319
FN293051.1 gg_id:562547 Halorhodospira halophila str. 9622
AJ318525.1 gg_id:62637 Halorhodospira neutrophila str. SG 3301
FJ153016.1 gg_id:323860 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX4C
NZ_ABYM01000001.1 gg_id:349593 Thioalkalivibrio sp. str. HL-EbGR7

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EU236373.1	297512	4915.3	3841.9	6527.2	5484.6	3193.9	4983.9
AY225627.1	96329	926.1	954.7	666.0	1166.7	1855.1	1507.6
FJ497388.1	579158	291.2	768.4	598.0	258.1	781.3	1684.7
EF632940.1	242102	4888.3	4416.5	8622.1	3532.0	8675.6	3195.8
EU491429.1	261838	2528.1	1745.9	1668.9	1783.6	1367.9	1996.5
DQ811847.1	164335	657.7	513.6	754.3	1022.8	1118.2	348.7
DQ811843.1	172303	2821.9	3206.3	3142.9	1179.9	6254.4	3031.9
EF203207.1	207236	5651.2	4944.9	4145.9	3978.2	2529.9	4571.0
FM877666.1	366930	5042.0	7094.5	8285.1	7147.9	12778.4	10937.7
AY225635.1	98613	559.3	689.5	1672.2	1477.7	822.1	1767.7
DQ811842.1	171222	5368.8	4822.5	4535.2	5856.2	7083.5	6388.7
AY328773.1	88634	341.3	830.6	716.5	206.6	356.3	939.0
DQ351776.1	146277	2738.2	2898.8	3103.9	4445.9	3092.9	3044.0
FJ937836.1	397082	6658.0	7816.6	9852.0	7637.2	5375.1	6747.5
EU236293.1	290042	2589.1	1973.4	4686.3	6207.5	3882.6	5715.0
GU208274.1	568003	3445.8	4912.5	5531.3	3816.6	8239.2	6729.5
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AB188772.1	114044	7880.7	7649.9	13623.5	6952.1	11259.6	13384.7
FJ205206.1	559269	5640.6	5248.9	7177.6	4873.8	5961.0	5728.8
GQ356981.1	557781	3489.1	2946.7	3322.9	4134.1	3483.6	3042.0
GU369933.1	527507	1523.7	1771.2	2435.8	2885.8	4317.9	4645.9
EF612432.1	244758	1641.4	1815.4	2418.5	2909.4	5892.1	2579.5
EU491147.1	261461	1404.1	2352.0	3819.4	3440.8	1869.5	1958.3
DQ823153.1	167115	57.6	103.7	94.9	87.9	267.2	260.4
AB189342.1	113899	4842.5	2152.3	1973.9	4935.1	7184.9	6679.2
CP000453.1	171890	2128.1	1518.2	888.1	863.8	694.7	1206.5
AJ404972.1	46869	9649.3	10675.3	8026.9	7608.8	10336.9	10447.6
DQ217918.1	142576	1493.7	967.6	586.4	388.7	115.4	192.8
DQ217919.1	142198	10915.8	10900.1	11995.4	7666.3	9468.6	7340.5
EU308278.1	358039	6157.2	7175.6	4690.2	6493.0	6865.9	7169.8
EU653291.1	280943	2329.5	2222.3	3129.5	3411.9	3157.5	3054.0
EU653290.1	282074	961.6	1532.1	3428.6	1470.9	6137.4	3337.7
AY298904.1	89646	4529.6	5103.6	7302.0	5132.8	9759.0	6486.6
EU590916.1	265489	1117.6	783.6	1877.1	1177.0	3444.2	1380.1
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AM902494.1	571311	988.6	778.8	2336.0	937.2	4162.5	1667.1
FN293051.1	562547	2776.4	2059.1	2479.2	3634.0	2195.3	3638.1
AJ318525.1	62637	80.4	111.3	155.2	325.9	88.2	132.9
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g__Thioalkalivibrio
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s__unclassified	919
s__Thiohalospira halophila	3212
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EU709869.1 gg_id:354793 Thioalkalivibrio sp. str. ALMg14
GU083686.1 gg_id:581381 Microorganism Xiarinur soda lake sediment clone x307
DQ103664.1 gg_id:130099 hypersaline endoevaporitic microbial mat clone E2aA03
GU083688.1 gg_id:568686 Microorganism Xiarinur soda lake sediment clone x309
AF126545.1 gg_id:73895 Thialkalivibrio denitrificans
EU709878.1 gg_id:341189 Thioalkalivibrio sp. HL-EbGR7 str. HL-EbGr7
AY360060.1 gg_id:93813 Thialkalivibrio thiocyanodenitrificans str. ARhD
EU368849.1 gg_id:260942 Thiohalospira halophila str. HL18
EU169227.1 gg_id:245592 Thiohalospira alkaliphila str. ALgr 6sp
EU908045.1 gg_id:341286 Thiorhodospira sp. str. SLG
AJ006530.2 gg_id:7548 Thiorhodospira sibirica A12
EF157110.1 gg_id:244243 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon
EF105756.1 gg_id:202113 microbial two endoevaporitic salt crusts evaporitic crust Lindsey Lake New Mexico cl
DQ001657.1 gg_id:158793 Microbial seeps asphalt seep clone B91-13
AM935440.1 gg_id:539161 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
AF339744.1 gg_id:40387 thermal vent clone V3
FM209168.1 gg_id:543583 Dynamics during identified and SSU libraries pilot-scale bioremediation process hydr
AJ581598.1 gg_id:93189 soil near uranium mill tailings clone KCM-B-23
EF157167.1 gg_id:245899 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon
EU735681.1 gg_id:349780 archaeal structures oil contaminated and soils China pristine soil Jidong Oilfield clone
FM242405.1 gg_id:309866 sequences sediment clone 1 T12d-oil
FM209058.1 gg_id:541794 Dynamics during identified and SSU libraries pilot-scale bioremediation process hydr
EF157096.1 gg_id:256594 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon
AJ581597.1 gg_id:94093 soil near uranium mill tailings clone KCM-B-112
AM935143.1 gg_id:536607 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
EF105729.1 gg_id:202055 microbial two endoevaporitic salt crusts evaporitic crust Lindsey Lake New Mexico cl
FJ152988.1 gg_id:321932 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX4CE
EF157181.1 gg_id:251900 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon
FJ153022.1 gg_id:306675 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX4CE
CU467452.1 gg_id:315091 Prokaryotic Tunisian saltern Saltern solar multipond clone
EF103128.1 gg_id:186404 Natronocella acetinitrilica str. ANL 6-2
EF105732.1 gg_id:203311 microbial two endoevaporitic salt crusts evaporitic crust Lindsey Lake New Mexico cl
DQ001686.1 gg_id:157622 Microbial seeps asphalt seep clone B101-25
CU467468.1 gg_id:328117 Prokaryotic Tunisian saltern Saltern solar multipond clone
AF513947.1 gg_id:62495 Ectothiorhodospiraceae clone LA7-B9
EF157075.1 gg_id:255083 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon
AB240322.1 gg_id:142319 microbial structure Phragmites rhizosphere biofilm reed bed reactor laboratory clone
AF507818.1 gg_id:62740 Mono Lake at depth 2 m station 6 July 2000 clone ML602J-47 proteobacterium
AM936356.1 gg_id:562653 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
EF105746.1 gg_id:203128 microbial two endoevaporitic salt crusts evaporitic crust Lindsey Lake New Mexico cl
EF157092.1 gg_id:256908 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon

EU709869.1	354793	4872.7	6213.3	7518.3	6309.0	11018.9	7071.2
GU083686.1	581381	3637.1	6167.9	3818.3	1266.7	3607.6	2357.8
DQ103664.1	130099	988.0	2474.0	1581.5	1163.1	3697.8	1832.3
GU083688.1	568686	2486.5	2421.3	2384.9	1650.5	3651.7	3332.3
AF126545.1	73895	4865.1	3132.8	3863.1	7553.9	5603.4	4614.9
EU709878.1	341189	2120.1	1298.2	1724.0	1731.7	1892.5	545.5
AY360060.1	93813	2604.4	2287.3	4629.4	1538.9	6632.6	4382.5
EU368849.1	260942	12.2	57.4	33.4	46.5	67.4	32.9
EU169227.1	245592	4473.1	3674.9	6576.0	5815.5	9694.6	7029.2
EU908045.1	341286	605.2	1500.4	1795.8	364.2	1951.5	1319.9
AJ006530.2	7548	28.3	57.1	48.9	79.2	81.0	118.1
EF157110.1	244243	10552.1	12334.0	10289.0	8960.5	12530.0	13384.4
EF105756.1	202113	3350.5	5039.3	5500.6	2732.7	7032.1	5819.4
DQ001657.1	158793	10787.1	9428.5	7062.4	6056.0	8611.4	10266.4
AM935440.1	539161	3211.7	3866.7	6924.4	2610.6	6022.6	9052.2
AF339744.1	40387	6807.4	7033.6	8725.9	7887.6	9541.2	11518.6
FM209168.1	543583	10042.2	13653.8	6649.1	7515.4	6957.9	7226.3
AJ581598.1	93189	13844.0	13614.0	11841.6	10348.0	13425.2	14324.1
EF157167.1	245899	13398.9	12724.4	6033.5	10060.2	11514.8	12763.4
EU735681.1	349780	1945.2	1290.4	2061.0	3769.6	3173.2	1890.9
FM242405.1	309866	3612.4	4910.7	5646.6	3114.4	5509.8	8708.0
FM209058.1	541794	3431.7	4628.6	7466.1	2236.3	3207.8	5458.3
EF157096.1	256594	10806.5	11889.2	7769.1	7888.3	10225.4	13855.1
AJ581597.1	94093	12005.4	11412.9	8555.8	10448.5	11393.1	13063.1
AM935143.1	536607	4224.7	2827.6	3566.1	4768.5	2061.8	6508.7
EF105729.1	202055	80.0	145.4	217.6	146.8	171.0	105.6
FJ152988.1	321932	4286.3	5996.5	10448.3	3680.6	7437.5	10461.1
EF157181.1	251900	12582.3	13765.2	8521.8	11352.7	8797.2	11872.1
FJ153022.1	306675	2791.4	4538.3	2155.0	1482.9	5061.8	3518.9
CU467452.1	315091	2544.3	2261.4	3848.6	3472.6	3853.1	3888.4
EF103128.1	186404	102.4	441.5	1796.0	207.3	149.0	387.5
EF105732.1	203311	15.3	39.8	42.0	47.4	54.7	19.2
DQ001686.1	157622	1061.4	1977.6	2276.4	752.8	1321.8	5698.6
CU467468.1	328117	12486.5	11484.9	9053.2	10571.3	12973.2	10394.9
AF513947.1	62495	6195.9	6092.6	3229.2	5027.1	8078.8	5036.3
EF157075.1	255083	2422.3	4552.8	6861.8	4351.0	8927.4	8554.8
AB240322.1	142319	57.6	76.7	181.0	71.1	80.5	69.0
AF507818.1	62740	54.1	90.5	42.8	69.8	77.7	48.0
AM936356.1	562653	13475.5	12889.0	8967.9	8782.6	11996.5	12498.1
EF105746.1	203128	9233.0	9632.5	7590.4	9259.5	9430.5	8430.7
EF157092.1	256908	1502.8	3327.9	2783.3	1910.3	2993.5	5388.6

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EF157077.1 gg_id:256826 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon
AM935364.1 gg_id:548480 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
EF157150.1 gg_id:245575 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon
AM936329.1 gg_id:560668 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
DQ378188.1 gg_id:153768 oil-polluted soil clone F24_Pitesti
M90662.1 gg_id:7758 Halothiobacillus hydrothermalis str. r3
AJ294337.1 gg_id:76987 Halothiobacillus hydrothermalis HY-66
AF170419.1 gg_id:19288 Halothiobacillus kellyi str. BII-1
EU124668.1 gg_id:242036 Thioalkalibacter halophilus str. ALCO1
AF173169.1 gg_id:44985 Halothiobacillus neapolitanus str. DSM 581
EU196318.1 gg_id:239328 Halothiobacillus sp. NP37
EU245085.1 gg_id:256790 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-H1-G02
EU101029.1 gg_id:246599 Sulfide/oxygen supply ratio predicts outcome competition among sulfur-oxidizing wa
EU101026.1 gg_id:246095 Sulfide/oxygen supply ratio predicts outcome competition among sulfur-oxidizing wa
EU101090.1 gg_id:239627 Sulfide/oxygen supply ratio predicts outcome competition among sulfur-oxidizing wa
AF154088.1 gg_id:7760 hydrocarbon seep clone BPC028
EU101065.1 gg_id:238117 Sulfide/oxygen supply ratio predicts outcome competition among sulfur-oxidizing wa
EU101080.1 gg_id:251622 Sulfide/oxygen supply ratio predicts outcome competition among sulfur-oxidizing wa
GU196195.1 gg_id:587626 Bioaugmentation improved recovery digesters after toxicant exposure lab-scale ana
AM950234.1 gg_id:554439 Sulphide oxidation elemental sulphur membrane bioreactor: Performance and selec
AB473891.1 gg_id:549132 sequences Cadagno di Fuori biofilm mat alpine wetland varying conductivities clone
EU037214.1 gg_id:252299 Hot Spring Microbial Mat Khir Ganga India hot spring microbial mat clone MO20
GU390833.1 gg_id:530086 Dark hot springs: structure biofilms caves Acquasanta Terme (Italy) sulfidic cave stre
GU390794.1 gg_id:519254 Dark hot springs: structure biofilms caves Acquasanta Terme (Italy) sulfidic cave stre
GU390789.1 gg_id:517389 Dark hot springs: structure biofilms caves Acquasanta Terme (Italy) sulfidic cave stre
GU196237.1 gg_id:577717 Bioaugmentation improved recovery digesters after toxicant exposure lab-scale ana
EU101158.1 gg_id:236588 Sulfide/oxygen supply ratio predicts outcome competition among sulfur-oxidizing wa
GU390879.1 gg_id:515900 Dark hot springs: structure biofilms caves Acquasanta Terme (Italy) sulfidic cave stre
DQ354745.1 gg_id:154107 subsurface water clone MS149BH1062003_5
EU101063.1 gg_id:237262 Sulfide/oxygen supply ratio predicts outcome competition among sulfur-oxidizing wa
EF467492.1 gg_id:214022 situ microelectrode voltammetry sulfur-oxidizing biofilms Frasassi sulfidic cave strear
DQ459215.1 gg_id:160856 Microbial consortia involved anaerobic degradation unsaturated and saturated LCFA
EU101162.1 gg_id:245464 Sulfide/oxygen supply ratio predicts outcome competition among sulfur-oxidizing wa
AY493939.1 gg_id:136667 Fingerprinting aggregates soil clone 455
EU134704.1 gg_id:248771 tallgrass prarie soil clone FFCH11229
GQ264259.1 gg_id:513055 Structure Simulated Level Waste Site simulated level waste site clone WW1_b62
FJ535077.1 gg_id:584489 microbial colonizing walls Karstic Slovenia cave wall biofilm clone 3PJM60
DQ123669.1 gg_id:137171 'Division Labor' Degradation Polycyclic Aromatic Hydrocarbons Bioreactor Treating C
EU449562.1 gg_id:568421 Soil are Changed Agricultural Practices agricultural soil clone Plot4-D11
EF605262.1 gg_id:262257 Steroidobacter denitrificans str. FS
EU202849.1 gg_id:313985 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo

EF157077.1	256826	4505.4	6726.5	5959.1	6399.9	9155.9	12928.4
AM935364.1	548480	4057.2	5181.7	8010.7	4215.7	8130.1	7303.5
EF157150.1	245575	1005.1	2295.6	2377.7	1025.2	1230.2	5022.6
AM936329.1	560668	10544.2	9848.5	12135.3	8831.1	7386.3	10014.6
DQ378188.1	153768	157.1	158.6	142.9	113.7	165.1	121.4
M90662.1	7758	320.6	429.0	430.7	381.7	461.2	2376.1
AJ294337.1	76987	6809.8	6320.9	1770.8	5382.2	2765.0	2813.1
AF170419.1	19288	43.3	75.0	44.2	61.2	182.4	1996.3
EU124668.1	242036	3627.7	3065.0	3392.1	3585.1	5224.3	6699.5
AF173169.1	44985	7603.3	7590.3	6175.8	7341.4	7178.7	6890.0
EU196318.1	239328	1689.9	2391.7	1608.6	1823.4	1502.7	1403.4
EU245085.1	256790	1464.6	2082.4	2033.4	1629.8	654.6	1206.2
EU101029.1	246599	10671.0	10423.1	6885.9	9515.1	8792.8	9535.3
EU101026.1	246095	4565.4	4801.9	1861.3	4739.2	8243.5	6148.1
EU101090.1	239627	5836.5	6121.1	7706.7	4466.8	12588.9	9686.2
AF154088.1	7760	3137.5	4735.5	2459.9	1719.4	964.6	2449.0
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EU101080.1	251622	6423.4	8821.2	4326.0	7538.5	9096.7	7061.3
GU196195.1	587626	2568.8	4713.9	4718.5	5023.3	4223.5	4619.7
AM950234.1	554439	4477.7	6566.7	5270.5	4096.9	6467.6	3438.5
AB473891.1	549132	10497.4	8732.4	17971.2	14437.2	9844.8	9883.2
EU037214.1	252299	7888.3	5996.6	5851.6	7288.5	7862.4	8633.8
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DQ354745.1	154107	4768.0	4266.8	2823.7	3493.0	2510.9	3885.1
EU101063.1	237262	3257.9	4907.6	2798.8	1594.6	1392.2	3823.1
EF467492.1	214022	11118.4	9616.0	6551.1	6007.3	12936.8	9127.2
DQ459215.1	160856	6908.3	9838.8	5911.5	5511.5	11981.1	8714.5
EU101162.1	245464	10181.0	8889.6	6917.0	7063.9	11912.7	8651.3
AY493939.1	136667	3447.8	3633.4	7506.0	4042.5	5538.3	4560.7
EU134704.1	248771	1354.6	1516.5	3644.3	3570.1	9382.8	3782.2
GQ264259.1	513055	1487.4	2330.7	4098.4	1633.7	732.1	1685.3
FJ535077.1	584489	6037.3	7150.2	7607.6	7689.6	8982.1	7541.5
DQ123669.1	137171	1151.2	2258.4	3784.0	969.7	1747.5	1374.4
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EF605262.1	262257	4085.8	3896.1	3741.5	6155.2	4589.0	3663.8
EU202849.1	313985	1332.5	2331.0	4996.9	697.8	763.5	1783.4

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EU528191.1 gg_id:282600 Seasonal Dynamics Mudflat Mouth Major Kentucky Lake Reservoir Tributary sedime
GQ500734.1 gg_id:593006 Surveys Biofilms and Sediments Mammoth Cave Karst Aquifers Charon's Cascade sa
AY963465.1 gg_id:150982 structures and correlated ecological factors soils two evergreen broad-leaved forests
AB198589.1 gg_id:135836 termite gut fluid and protists fraction clone RsC01-016
EF061960.1 gg_id:182496 Xiamen China mangrove sediment clone XME35
EU542478.1 gg_id:259999 Effects chemical structure concentration on pathways microbial during dechlorinatio
EF688386.1 gg_id:254180 soil clone F6-105
GQ402680.1 gg_id:581215 Accessing microbial biodiversity and metabolic potential tropical -based approach p
EU202846.1 gg_id:326004 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo
DQ450180.1 gg_id:154435 (Uruguay) Atlantic coastal lagoon clone R7C24
DQ984544.1 gg_id:235634 Mt. Nan-Jen soil clone IFD_90
AB252886.1 gg_id:172615 Identification Shibayama lagoon Ishikawa Japan iron-oxidation biofilm clone 31
EU669610.1 gg_id:320093 soil clone S11-50
EU150278.1 gg_id:277979 acidobacteria and soil Niwot Ridge LTER clone Ni_D05_SFDN
AY963328.1 gg_id:156500 structures and correlated ecological factors soils two evergreen broad-leaved forests
AM935063.1 gg_id:544132 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
AY963375.1 gg_id:154604 structures and correlated ecological factors soils two evergreen broad-leaved forests
EU786122.1 gg_id:546319 cotton rhizosphere soil clone 3H-18
GQ094382.1 gg_id:422593 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
DQ451520.1 gg_id:156986 forest soil clone FAC81
AM934850.1 gg_id:544494 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
EU150277.1 gg_id:277971 acidobacteria and soil Niwot Ridge LTER clone Ni_B09_SFDN
DQ984567.1 gg_id:238284 Mt. Nan-Jen soil clone IFD_18
FM200868.1 gg_id:556730 and distinct induced biofilm fouling operated under conditions laboratory-scale men
EU542460.1 gg_id:258611 Effects chemical structure concentration on pathways microbial during dechlorinatio
GQ214101.1 gg_id:551472 China loess clone P830
EU037949.1 gg_id:244526 Metabolic Profiles Microbial Chlorinated Pesticides Contaminated Sites Three Geogr
EF520572.1 gg_id:232138 structure lakes: what controls ? acid-impacted lake clone ADK-MOe02-45
FJ466238.1 gg_id:563462 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea
EU150274.1 gg_id:278484 acidobacteria and soil Niwot Ridge LTER clone Ni_H9P1
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EU104062.1 gg_id:332574 Evidence Comamonadaceae determinants settling performance activated sludge clo
EU409118.1 gg_id:274454 Impacted Mine Drainage Dabaoshan Mining Area mine drainage sediment clone DBS
FJ466231.1 gg_id:508976 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea
DQ659207.1 gg_id:219056 acid mine drainage clone DBS-Clone32
GU208300.1 gg_id:544822 Study on Sediment Dongping Lake sediment clone Ftd3-4
DQ659217.1 gg_id:225165 acid mine drainage clone DBS-Clone42
EU134723.1 gg_id:255115 tallgrass prarie soil clone FFCH7151
AY221082.1 gg_id:85458 Mammoth Cave clone CCU5
EF516956.1 gg_id:222645 grassland soil clone FCPP404

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AB198589.1	135836	48.9	113.5	369.0	106.8	118.2	664.4
EF061960.1	182496	6973.4	7471.3	4949.8	7748.8	7532.1	8052.7
EU542478.1	259999	3702.3	4605.1	6469.0	2992.4	5086.9	5291.2
EF688386.1	254180	1353.5	1783.4	5639.1	2186.7	711.5	1643.5
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DQ450180.1	154435	352.8	649.2	4747.1	461.9	318.3	367.7
DQ984544.1	235634	1410.7	1316.5	2256.5	2192.8	1018.4	2039.4
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EU150278.1	277979	12392.3	11831.4	5521.0	9557.4	9632.2	8741.2
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EU409118.1	274454	3559.3	3469.4	1884.0	3192.3	3555.2	3516.2
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EU104271.1 gg_id:332476 Evidence Comamonadaceae determinants settling performance activated sludge clo
FJ612377.1 gg_id:533140 and Biogeochemistry Dongping Lake Ecosystems lake water clone DP10.3.23
FJ535074.1 gg_id:512616 microbial colonizing walls Karstic Slovenia cave wall biofilm clone 3PJM1
FJ672005.1 gg_id:516961 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
EU202845.1 gg_id:316643 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo
EU193057.1 gg_id:366851 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo
FJ478844.1 gg_id:560106 species richness estimates obtained nearly and simulated pyrosequencing-generated
AM935088.1 gg_id:545602 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
DQ297982.1 gg_id:142342 Microbial hydrocarbon contaminated soil clone UE4
AJ582039.1 gg_id:93780 soil near uranium mill tailings clone JG36-GS-61
AY963329.1 gg_id:153003 structures and correlated ecological factors soils two evergreen broad-leaved forests
EF019218.1 gg_id:209393 aspen rhizosphere clone Elev_16S_386
EU403986.1 gg_id:346948 Microbial septic tank effluent and soil biozone infiltrative surface clean water clone (
AY963404.1 gg_id:156448 structures and correlated ecological factors soils two evergreen broad-leaved forests
FJ152814.1 gg_id:327382 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX5A_
EU528221.1 gg_id:282013 Seasonal Dynamics Mudflat Mouth Major Kentucky Lake Reservoir Tributary sedime
DQ984542.1 gg_id:252012 Mt. Nan-Jen soil clone IFD_16
GU454892.1 gg_id:532025 Understanding short-chain fatty acids accumulation enhanced alkaline digestion: kir
EU134725.1 gg_id:242587 tallgrass prarie soil clone FFCH10003
EU150260.1 gg_id:278275 acidobacteria and soil Niwot Ridge LTER clone Ni_D7P1
FJ535069.1 gg_id:542880 microbial colonizing walls Karstic Slovenia cave wall biofilm clone 3PJM137
AB179525.1 gg_id:105999 sedimentary rock clone MIZ34
DQ279336.1 gg_id:142645 Dynamic during maturation Tuber magnatum Pico ascoma Xanthomonas clone TM1
EF409868.1 gg_id:206356 acid mine drainage clone YSK40-06
DQ451502.1 gg_id:156972 forest soil clone FAC63
EF516354.1 gg_id:218090 grassland soil clone FCPS764
FJ744832.1 gg_id:551627 Transporter genes expressed coastal response dissolved organic carbon surface wate
GQ264209.1 gg_id:509396 Structure Simulated Level Waste Site simulated level waste site clone WW1_a84
EU150279.1 gg_id:278427 acidobacteria and soil Niwot Ridge LTER clone Ni_D06_SFDN
EU193052.1 gg_id:369332 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo
AM176834.1 gg_id:159956 Recovery mangrove sediment clone SZB11
GU061304.1 gg_id:576363 Evaluation culturing methods cultivate previously Yel Sea intertidal beach seawater
EU491633.1 gg_id:258366 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39
EU491862.1 gg_id:269926 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39
AY221036.1 gg_id:83068 Mammoth Cave sediment clone CCD24
AM935258.1 gg_id:536028 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
EF999361.1 gg_id:252341 Vertical and Methanotrophs Estuarine Sediments Pearl River Estuary sediments 6cm
GQ264010.1 gg_id:589456 Structure Simulated Level Waste Site simulated level waste site clone WC3_08
AY907782.1 gg_id:137174 identification picoplankton contrasting waters Arabian Sea water clone A712005
FJ545453.1 gg_id:513570 Diveristy Seawater and Sediment Northern North Yel Sea sediment clone S1-23
EU491448.1 gg_id:261579 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X4 clone

EU104271.1	332476	11836.6	12010.7	13000.0	10200.1	12615.9	11966.3
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FJ535074.1	512616	3934.0	6117.6	7769.8	4863.0	5960.9	4753.4
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EU202845.1	316643	2807.0	3570.6	3869.4	1741.3	1504.4	2400.0
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FJ478844.1	560106	12682.6	13467.4	15702.2	13376.5	18418.6	15341.8
AM935088.1	545602	7658.5	6153.4	10406.3	7860.0	4522.9	5634.4
DQ297982.1	142342	3383.5	3206.5	3671.6	6327.5	6612.7	6157.2
AJ582039.1	93780	144.4	270.3	1836.0	490.2	891.9	356.8
AY963329.1	153003	1605.2	2145.8	3865.4	2925.5	1085.2	2114.4
EF019218.1	209393	9190.6	8448.3	11195.9	9035.9	7708.7	7407.1
EU403986.1	346948	876.3	1998.8	4587.0	1368.5	1552.9	1164.4
AY963404.1	156448	5693.2	3682.9	1711.4	4857.9	4764.5	3888.7
FJ152814.1	327382	753.0	2042.7	4395.8	1763.7	730.6	1796.0
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EU134725.1	242587	557.7	778.6	3397.4	855.5	2338.8	1475.7
EU150260.1	278275	5534.5	5334.7	7752.5	4743.8	4206.7	5313.7
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AB179525.1	105999	2221.0	2790.4	5828.6	4901.8	5269.0	4084.2
DQ279336.1	142645	3690.7	4202.2	2560.2	3413.6	5759.1	6089.2
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EU193052.1	369332	5495.9	7211.3	9559.0	4159.1	7444.7	6258.8
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GU061304.1	576363	3066.7	5145.4	7984.3	1717.7	2150.2	2538.9
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EU491862.1	269926	4673.5	3640.5	2671.3	4773.7	3524.3	3954.5
AY221036.1	83068	3422.0	4630.7	1825.0	5250.7	6893.2	6277.4
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EF999361.1	252341	2494.3	1295.8	3627.6	3498.3	1909.1	2790.1
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EU491043.1 gg_id:263799 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount South Rift X
GQ246317.1 gg_id:511715 Temporal and spatial China North Yel Sea sediments clone Sd1-36
EU491127.1 gg_id:276781 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak
DQ351813.1 gg_id:146081 Microbial Adherent Sediment Particles Heavy Metal Contaminated North Sea Surfac
FJ202756.1 gg_id:338034 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k
AJ567537.1 gg_id:90195 deep-sea sediment clone MBMPE11
DQ270631.1 gg_id:142048 hydrothermal carbonate chimney clone LC1446B-88
EF125454.1 gg_id:175214 mangrove soil clone MSB-2F9
EU617769.1 gg_id:336977 Seasonal variation microbial Yel Sea sediment clone C13S-11
EU491671.1 gg_id:269207 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39
EU373852.1 gg_id:265200 southern Cretan margin (eastern Mediterranean Sea) canyon and slope sediment clc
EU617762.1 gg_id:339270 Seasonal variation microbial Yel Sea sediment clone D13S-135
AB015576.1 gg_id:7632 deep-sea sediment clone BD6-6
EU617760.1 gg_id:353103 Seasonal variation microbial Yel Sea sediment clone D13S-8
FM242213.1 gg_id:305299 sequences sediment clone 305 T0h-oil
FJ203584.1 gg_id:324521 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h
DQ351767.1 gg_id:145747 Microbial Adherent Sediment Particles Heavy Metal Contaminated North Sea Surfac
FJ416135.1 gg_id:366945 sediments sediment station NEC5 Northern Bering Sea clone 140J34
EU491722.1 gg_id:259776 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39
EF174279.1 gg_id:181525 direct activated sludge compost maturation stage clone H49-814
EF125451.1 gg_id:188380 mangrove soil clone MSB-2F4
DQ334616.1 gg_id:175390 Impact metals on sediments heavy metal polluted marine sediment clone HB1-41-8
EU287293.1 gg_id:239219 Pacific arctic surface sediment clone S11-110
FJ902650.1 gg_id:558486 phreatic limestone sinkholes northeastern Mexico biofilm 1m deep hydrothermal ver
GQ259229.1 gg_id:512555 Microbial activities coastal marine sediments and column Svalbard deep water clone
EF061959.1 gg_id:194499 Xiamen China mangrove sediment clone XME27
AY592131.1 gg_id:100439 marine ANAMMOX sediment clone AY592131
EF612422.1 gg_id:241321 historic semiarid lead-zinc mine tailings site soil clone OS-C47
DQ395002.1 gg_id:155659 harbor sediment clone VHS-B4-54
EU491622.1 gg_id:276755 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39
FJ628326.1 gg_id:587067 transition and zone within near-shore basin: brackish water anoxic fjord Nitinat Lake
GU369930.1 gg_id:522232 and mats vents Arc white microbial film on pebble aphotic zone shal hydrothermal v
EU925888.1 gg_id:327055 sediments sediment station DBS1 northern Bering Sea clone 099G35
FJ202726.1 gg_id:304768 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k
FJ545563.1 gg_id:553394 Diveristy Seawater and Sediment Northern North Yel Sea sediment clone S2-30
FJ479452.1 gg_id:564382 species richness estimates obtained nearly and simulated pyrosequencing-generated
EF208680.1 gg_id:201369 Vertical and horizontal structure microbial sandy carbonate sediment clone CI5cm.BC
EU290675.1 gg_id:243727 microbial structure biogeochemical contrasting shelf sediments Namibian upwelling
GQ261760.1 gg_id:550306 shifts taxa and response localized organic loading deep sea sediment whale falls clo
AJ567539.1 gg_id:88336 deep-sea sediment clone MBMPE13
EU491447.1 gg_id:277437 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X4 clone

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EU491127.1	276781	4782.0	4044.9	8099.9	5602.3	4169.2	3297.8
DQ351813.1	146081	13.0	20.5	18.9	36.0	57.7	19.9
FJ202756.1	338034	240.9	891.3	1532.3	530.4	714.9	452.0
AJ567537.1	90195	3268.7	4482.9	4181.5	2815.8	3438.9	4162.3
DQ270631.1	142048	1868.7	1323.0	1511.4	959.5	2180.0	2191.2
EF125454.1	175214	496.9	809.2	1414.6	253.6	255.1	2324.3
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EU491671.1	269207	890.1	1021.1	823.1	127.9	746.8	647.4
EU373852.1	265200	6955.5	6955.2	6364.0	5700.2	5193.7	5159.8
EU617762.1	339270	6726.1	6968.1	6519.9	6511.1	8598.9	8416.0
AB015576.1	7632	5454.3	8328.2	7763.5	6069.6	13665.6	12864.9
EU617760.1	353103	9793.9	10475.1	6770.2	7345.6	12508.0	11558.1
FM242213.1	305299	5021.2	6262.6	5373.2	5808.4	4593.7	7187.3
FJ203584.1	324521	4267.0	6138.1	8381.8	5135.1	8441.3	6727.0
DQ351767.1	145747	4105.4	2494.8	2380.7	4610.2	3223.2	2988.1
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EF174279.1	181525	3957.3	5988.7	7357.3	2775.0	4441.7	6806.3
EF125451.1	188380	3108.2	2970.3	4442.9	3545.0	4946.9	4456.8
DQ334616.1	175390	10480.6	8210.4	7454.1	6800.7	9120.7	8098.3
EU287293.1	239219	4146.6	5598.1	4942.8	4363.0	6940.0	7716.6
FJ902650.1	558486	4033.5	4570.6	6976.2	4002.5	5603.4	4046.8
GQ259229.1	512555	5862.0	5586.8	4978.5	6898.8	8668.0	7189.2
EF061959.1	194499	1354.7	2185.2	1872.3	1159.3	3585.4	1825.9
AY592131.1	100439	11926.2	12841.3	8261.1	10278.6	10655.3	9403.3
EF612422.1	241321	800.3	1034.5	375.5	181.0	392.8	923.1
DQ395002.1	155659	9581.1	12407.1	7461.9	9096.8	13746.7	11815.3
EU491622.1	276755	3674.4	3359.6	3085.5	1875.9	2051.7	1795.6
FJ628326.1	587067	2855.1	3781.6	7017.5	3534.3	7933.3	7199.8
GU369930.1	522232	1672.3	2371.9	5461.2	5883.4	4575.4	6217.4
EU925888.1	327055	1784.0	1499.5	1945.1	1007.0	4022.5	3488.5
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EF208680.1	201369	1714.0	2050.2	2252.0	1015.7	1846.3	2304.2
EU290675.1	243727	9681.0	9220.8	6327.7	7588.9	7486.8	6796.7
GQ261760.1	550306	4139.5	4152.3	4955.6	6890.6	9515.0	6492.3
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EU652512.1 gg_id:279257 Seasonal variation microbial Yel Sea sediment clone D8s-65
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GQ259320.1 gg_id:557119 Microbial activities coastal marine sediments and water column Svalbard surface se
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EU652513.1 gg_id:277629 Seasonal variation microbial Yel Sea sediment clone C8S-5
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GQ337138.1 gg_id:561386 Hydrography shapes biogeography deep Arctic Ocean water depth 1000m clone CB:
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EU287183.1 gg_id:239964 Pacific arctic surface sediment clone P13-90
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AF129550.1 gg_id:7594 Achromatium sp. JD8

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GQ263482.1	584461	3142.6	3457.3	4398.6	4978.0	5000.7	4655.3
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GQ259320.1	557119	593.1	912.7	2364.9	522.9	1247.9	2074.1
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EU488031.1	572374	572.1	1026.0	883.9	422.9	1392.6	798.4
GQ337138.1	561386	2379.1	3499.4	4258.0	3136.0	2249.4	3271.0
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EU491461.1	259137	1061.7	792.1	1050.2	1830.3	1992.2	2817.0
EU287183.1	239964	81.8	133.5	856.9	192.3	508.8	104.3
GQ246393.1	593413	434.7	368.8	539.9	287.6	405.7	145.1
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AY344377.1 gg_id:91521 Lake Kauhako 4 m clone K2-4-12
AY265348.1 gg_id:82929 Dermacentor variabilis symbiont
U91786.1 gg_id:10204 Candidatus Arsenophonus triatominarum
AY264674.1 gg_id:89402 Arsenophonus nasoniae str. ATCC 49151
DQ158206.1 gg_id:140266 Averyella dalhousiensis str. 9501-97 1
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DQ158204.1 gg_id:140650 Averyella dalhousiensis str. 2362-79 4
FJ360760.1 gg_id:325971 Enterobacter aerogenes str. PSB28
DQ481464.1 gg_id:157163 Averyella dalhousiensis str. VTan-2
DQ068917.1 gg_id:139129 microbiota antlions (Myrmeleon mobilis) whole animal laboratory starved antlion O
EU438866.1 gg_id:297157 Enterobacter amnigenus 2
EU741245.1 gg_id:335722 Enterobacter sp. str. KB3
AB291632.1 gg_id:241040 Insecticidal predatory antlion species (Neuroptera: Myrmeleontidae) larvae Myrmel
EU879089.1 gg_id:305870 Pantoea agglomerans str. HDDMN03
AM184285.1 gg_id:161053 Enterobacter ludwigii str. WAB1946
AY676891.1 gg_id:136211 Baumannia cicadellinicola B6
AY676878.1 gg_id:135960 Baumannia cicadellinicola B14
AY676887.1 gg_id:136270 Baumannia cicadellinicola B34
AF465797.1 gg_id:79588 Baumannia cicadellinicola
AY676896.1 gg_id:136019 Baumannia cicadellinicola B47
AY676895.1 gg_id:137136 Baumannia cicadellinicola F02
AF465795.1 gg_id:79106 Baumannia cicadellinicola
AY676877.1 gg_id:135411 Baumannia cicadellinicola B13
U80203.1 gg_id:10307 Brenneria nigrifluens str. ATCC 13028
AJ233416.1 gg_id:10200 Brenneria quercina str. DSM 4561
FJ611885.1 gg_id:588495 Brenneria rubrifaciens str. LMG 2709
AJ233418.1 gg_id:51229 Brenneria rubrifaciens str. DSM 4483
U80207.1 gg_id:10197 Brenneria rubrifaciens str. ATCC 29291
AM237373.1 gg_id:156214 Sodalis glossinidius OS-75
Z96097.1 gg_id:10201 Brenneria salicis str. LMG 2698
AB033772.1 gg_id:52753 Buchnera sp
AB033773.1 gg_id:20966 Buchnera sp
AJ296755.1 gg_id:50183 Buchnera aphidicola (Maculolachnus submacula) (Maculolachnus
FJ655495.1 gg_id:579584 Buchnera aphidicola (Stomaphis aphananthae)
M63251.1 gg_id:9645 Buchnera aphidicola
M63252.1 gg_id:9648 Buchnera aphidicola
FJ655509.1 gg_id:587576 Buchnera aphidicola (Lachnus tropicalis)

AF129552.1	7611	6640.7	7146.3	10408.9	7892.5	11024.7	9571.5
AF129551.1	7610	11440.5	12718.4	13229.0	8575.5	14193.0	10985.2
AF129554.1	7602	6543.3	6277.2	7000.7	6823.6	10546.6	9609.5
DQ066949.1	133344	2156.8	1541.9	152.8	186.9	265.2	920.6
AY344377.1	91521	836.7	1077.1	1425.4	1116.3	2325.6	3085.2
AY265348.1	82929	3569.3	4032.5	7868.5	4609.8	6876.2	7141.1
U91786.1	10204	18.6	20.5	23.6	51.1	64.1	16.7
AY264674.1	89402	475.7	464.3	2755.4	520.9	263.3	1405.9
DQ158206.1	140266	104.8	435.9	2279.9	231.0	253.1	495.2
DQ158205.1	139645	101.0	374.2	2049.4	236.8	111.5	401.4
DQ158204.1	140650	819.3	1011.2	5256.4	1540.1	1758.3	2274.0
FJ360760.1	325971	357.1	595.3	2511.5	553.8	1799.6	1317.8
DQ481464.1	157163	4499.1	3906.2	4324.7	3739.4	2602.3	2492.9
DQ068917.1	139129	2671.6	3374.4	5356.5	4105.3	5245.1	5861.1
EU438866.1	297157	65.2	468.1	996.7	189.4	87.1	315.6
EU741245.1	335722	51.3	201.5	441.9	99.2	77.5	136.9
AB291632.1	241040	859.9	1051.7	4716.0	1784.5	1542.6	2160.2
EU879089.1	305870	38.5	148.4	131.7	84.5	77.5	69.3
AM184285.1	161053	634.1	806.3	2997.7	652.0	516.9	973.8
AY676891.1	136211	3823.6	2695.6	2134.0	2315.5	2139.9	2220.0
AY676878.1	135960	233.1	532.4	250.6	1131.0	79.1	553.3
AY676887.1	136270	326.4	380.9	632.8	561.1	708.9	874.3
AF465797.1	79588	266.6	272.2	561.8	217.7	325.0	239.3
AY676896.1	136019	292.8	128.5	88.1	129.8	61.8	77.2
AY676895.1	137136	275.9	126.1	94.7	117.3	44.2	49.4
AF465795.1	79106	23.6	14.1	12.5	39.9	51.3	20.4
AY676877.1	135411	3283.6	2916.0	2646.1	4046.1	3474.2	3531.5
U80203.1	10307	2545.8	2791.9	3146.1	2940.0	5662.6	7967.2
AJ233416.1	10200	3074.8	3481.9	5553.0	4150.6	2456.0	1969.5
FJ611885.1	588495	125.6	306.5	1397.3	284.3	48.5	253.3
AJ233418.1	51229	4005.4	3317.3	2106.3	4273.5	5316.2	4405.9
U80207.1	10197	5956.8	7372.0	6185.7	5553.4	6385.2	5839.1
AM237373.1	156214	507.5	879.2	1793.1	551.0	106.6	445.6
Z96097.1	10201	1259.4	734.6	2250.0	935.3	765.9	1137.0
AB033772.1	52753	11289.4	9195.0	5849.4	8536.0	12564.6	7237.7
AB033773.1	20966	4486.6	3562.1	3012.7	3563.6	4064.7	3642.2
AJ296755.1	50183	1379.9	1209.7	2016.9	1868.7	1176.0	894.7
FJ655495.1	579584	9441.6	8843.9	8381.3	11153.1	9571.7	7244.7
M63251.1	9645	6535.2	6963.3	3982.9	7297.0	10233.3	6420.3
M63252.1	9648	3063.7	1755.2	842.8	2051.0	3873.8	2026.0
FJ655509.1	587576	6983.9	6156.6	4555.6	7456.6	5775.5	7078.3

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EU334768.1 gg_id:341117 Buchnera aphidicola (Cinara juniperi) str. BCju-1
AJ296752.1 gg_id:41602 Buchnera aphidicola (Baizongia pistaciae)
EU334777.1 gg_id:308536 Buchnera aphidicola (Cinara cedri) str. BCce2-1
AJ296753.1 gg_id:36645 Buchnera aphidicola (Stomaphis quercus)
AJ296747.1 gg_id:23181 Buchnera aphidicola (Pterocomma populeum)
M63254.1 gg_id:9650 Buchnera aphidicola
AJ296758.1 gg_id:23853 Buchnera aphidicola (Panaphis juglandis)
M63250.1 gg_id:9642 Buchnera aphidicola
M63253.1 gg_id:9647 Buchnera aphidicola
Z19056.1 gg_id:9651 Buchnera aphidicola
AJ296750.1 gg_id:53693 Buchnera aphidicola (Pemphigus populi)
AB064508.1 gg_id:40406 Buchnera aphidicola (Yamatocallis tokyoensis) #317 (Yamatocallis
DQ418492.1 gg_id:171684 Buchnera aphidicola (Eriosoma lanigerum) str. Zhaotong
EU334773.1 gg_id:308102 Buchnera aphidicola (Cinara tujafilina) str. BCtu-1
M63255.1 gg_id:9653 Buchnera aphidicola
AJ296754.1 gg_id:24924 Buchnera aphidicola (Tuberolachnus salignus) (Tuberolachnus
FJ655507.1 gg_id:577120 Buchnera aphidicola (Lachnus roboris)
Y11972.1 gg_id:202061 Buchnera aphidicola
L81121.1 gg_id:111650 Buchnera aphidicola
AE016826.1 gg_id:146724 Buchnera aphidicola str. Bp (Baizongia pistaciae)
FJ655512.1 gg_id:510297 Buchnera aphidicola (Nippolachnus piri)
Y11973.1 gg_id:9652 Buchnera aphidicola
AY518294.1 gg_id:105511 Buchnera aphidicola (Aphis fabae fabae)
FJ655500.1 gg_id:560641 Buchnera aphidicola (Stomaphis takahashii)
DQ223869.1 gg_id:165272 Buttiauxella agrestis str. RT1
DQ223870.1 gg_id:172544 Buttiauxella noackiae str. RT7
DQ440549.1 gg_id:153634 Buttiauxella agrestis str. HS-39
AF227860.1 gg_id:73465 Pantoea sp. str. 57916
DQ223871.1 gg_id:167300 Buttiauxella agrestis str. P1
AJ293684.1 gg_id:69815 Buttiauxella agrestis str. S3/3-203
AJ233402.1 gg_id:10052 Buttiauxella ferragutiae str. DSM 9390
FJ716025.1 gg_id:513551 Diet- gut microbiota Lumbricus rubellus fingerprinting technique and cloning intestina
AJ233406.1 gg_id:10056 Buttiauxella warmboldiae str. DSM 9404
NR_025328.1 gg_id:575201 Buttiauxella brennerae str. S1/6-571; DSM 9396
AJ293687.1 gg_id:69978 Buttiauxella noackiae str. BR 626
AJ233403.1 gg_id:10053 Buttiauxella gaviniae str. DSM 9393
AJ233400.1 gg_id:10050 Buttiauxella agrestis str. DSM 4586
X92552.1 gg_id:9961 "Candidatus camponotii"
AY334368.1 gg_id:106321 Camponotus sansabeanus symbiont
AJ245598.1 gg_id:20928 USA clone 14/7
AJ245592.1 gg_id:17213 Peru clone 5-5

EU334768.1	341117	2872.5	1896.2	3042.6	3779.0	2815.2	4958.6
AJ296752.1	41602	2012.6	1226.6	1221.0	1412.1	269.4	503.4
EU334777.1	308536	1844.0	796.6	1652.2	1846.7	736.1	777.1
AJ296753.1	36645	6231.5	4733.4	3644.8	5811.6	3198.3	3000.1
AJ296747.1	23181	1785.2	1650.3	673.2	2026.9	2106.0	2314.2
M63254.1	9650	6798.7	6781.4	2051.8	4930.6	7251.8	7359.8
AJ296758.1	23853	1820.5	1328.9	1242.7	1437.2	1103.3	987.3
M63250.1	9642	111.9	123.0	70.5	106.6	279.9	81.4
M63253.1	9647	308.2	316.3	186.4	254.3	208.2	201.8
Z19056.1	9651	40.7	71.0	77.1	80.3	94.2	60.4
AJ296750.1	53693	4889.3	4185.6	1318.5	2118.9	4816.4	3584.9
AB064508.1	40406	2539.6	1937.5	1608.5	2440.9	711.4	1387.7
DQ418492.1	171684	419.2	453.5	509.7	541.3	903.5	662.8
EU334773.1	308102	11468.5	12091.7	7043.2	8412.0	11663.2	11703.4
M63255.1	9653	51.1	90.3	151.2	62.6	72.8	114.2
AJ296754.1	24924	4955.3	4952.3	3416.2	5932.5	6483.0	4359.2
FJ655507.1	577120	1893.9	2346.1	3245.7	2332.7	3116.6	3478.0
Y11972.1	202061	2460.0	933.7	538.8	3392.9	1005.7	1054.2
L81121.1	111650	4896.9	4482.0	3290.2	5742.1	6583.5	8468.8
AE016826.1	146724	5637.8	10548.9	6284.9	5628.0	6874.3	7099.7
FJ655512.1	510297	6070.9	5651.4	3608.5	5356.5	4814.7	3883.3
Y11973.1	9652	1806.3	751.5	2029.3	971.1	794.1	463.6
AY518294.1	105511	1905.7	2958.5	1640.0	1960.5	1906.8	1256.2
FJ655500.1	560641	6894.9	6690.4	5749.7	10313.7	10759.6	8654.2
DQ223869.1	165272	1458.0	1251.9	1948.4	3207.8	792.1	2576.1
DQ223870.1	172544	3625.5	1946.3	3446.9	4985.6	6690.3	4855.1
DQ440549.1	153634	1060.0	1474.2	2473.8	1448.3	2746.2	2670.1
AF227860.1	73465	467.4	566.8	2680.1	931.0	1585.1	1551.1
DQ223871.1	167300	532.1	510.3	1208.0	1335.6	907.1	842.0
AJ293684.1	69815	979.6	1343.4	5693.1	1740.3	3081.2	3226.2
AJ233402.1	10052	1878.6	1663.4	3847.5	1145.5	2612.3	2807.0
FJ716025.1	513551	132.0	209.0	961.5	373.3	69.7	244.7
AJ233406.1	10056	172.2	435.9	2447.5	373.9	325.1	488.5
NR_025328.1	575201	302.5	468.4	2124.5	574.1	1446.4	1519.0
AJ293687.1	69978	1218.4	1995.3	3805.1	2725.7	5162.2	6019.3
AJ233403.1	10053	270.3	426.5	1685.5	605.4	2545.1	681.2
AJ233400.1	10050	345.0	721.0	2580.7	743.9	1279.8	1438.4
X92552.1	9961	1639.0	1227.6	685.3	1241.8	2152.5	2247.0
AY334368.1	106321	2889.9	1187.6	2244.0	2591.7	2139.8	2356.6
AJ245598.1	20928	3078.7	1685.8	1833.4	3198.0	3013.4	2439.7
AJ245592.1	17213	8757.3	7742.8	7894.8	7576.6	10175.2	9379.5

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k__Bacteria	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria

o__Enterobacteriales	f__Enterobacteriaceae
o__Enterobacteriales	f__Enterobacteriaceae
o__Enterobacteriales	f__Enterobacteriaceae
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o__Enterobacteriales	f__Enterobacteriaceae

g__Candidatus Blochmannia
g__Candidatus Hamiltonella
g__Candidatus Ishikawaella
g__Candidatus Phlomobacter
g__Candidatus Regiella
g__Candidatus Regiella
g__Candidatus Regiella
g__Candidatus Regiella
g__Candidatus Regiella
g__Candidatus Regiella
g__Cedecea
g__Citrobacter
g__Citrobacter
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s__unclassified	7029
s__Candidatus Hamiltonella defensa	7160
s__Candidatus Ishikawaella capsulata	7539
s__Candidatus Phlomobacter fragariae	6601
s__Candidatus Regiella insecticola	6752
s__Candidatus Regiella insecticola	6874
s__Candidatus Regiella insecticola	7188
s__Candidatus Regiella insecticola	7367
s__Candidatus Regiella insecticola	7424
s__Candidatus Regiella insecticola	7479
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s__unclassified	5112
s__unclassified	5124
s__unclassified	5279
s__unclassified	5295
s__unclassified	5298
s__unclassified	5380
s__unclassified	5386
s__unclassified	5413

AJ245596.1 gg_id:48707 Saint Kitts and Nevis clone 12/1
NC_012751.1 gg_id:431766 Candidatus Hamiltonella defensa 5AT (Acyrthosiphon pisum) str. T5A
AB067723.1 gg_id:28528 Megacopta punctatissima symbiont
U91515.1 gg_id:10203 Candidatus Phlomobacter fragariae str. france fragariae
AY136143.1 gg_id:86615 Brachycaudus cardui symbiont
AY136152.1 gg_id:105167 Macrosiphum rosae symbiont
AF293619.1 gg_id:25922 Macrosiphoniella ludovicianae symbiont
FJ357496.1 gg_id:359629 symbionts clones English grain Sitobion avenae F. (Insecta: Homoptera) and host plan
AF293627.1 gg_id:50997 Uroleucon solidaginis symbiont
DQ228285.1 gg_id:150888 Acyrthosiphon pisum symbiont
AF493976.1 gg_id:82917 Cedecea davisae str. DSM 4568
DQ481466.1 gg_id:203232 Citrobacter freundii str. VTan-4
DQ481470.1 gg_id:201655 Citrobacter freundii str. VTan-9
EU468094.1 gg_id:299301 cheetah feces clone CE2_g02_2
GQ154806.1 gg_id:534457 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
GQ155543.1 gg_id:588290 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
DQ816142.1 gg_id:168998 mouse cecum clone aaa88f07
GQ155506.1 gg_id:511336 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
EU467996.1 gg_id:301223 cheetah feces clone CE2_g10
EU468053.1 gg_id:297805 cheetah feces clone CE2_a06_2
GQ155565.1 gg_id:556376 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
EU540206.1 gg_id:283179 profile human microbiota antecubital fossa (inner elbow) skin clone nbt247b06
FJ658620.1 gg_id:509207 Metalworking Fluids and Aerosols Metallurgy Plant metalworking aerosol clone Sumn
AY163805.1 gg_id:101294 Citrobacter freundii str. A1
AM184249.1 gg_id:160975 Citrobacter freundii str. WAB1908
DQ294286.1 gg_id:143708 Citrobacter freundii str. 8
AY259630.1 gg_id:83212 Citrobacter freundii str. WA1
GQ154984.1 gg_id:532730 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
DQ817309.1 gg_id:173691 mouse cecum clone aaa72h09
DQ816132.1 gg_id:167280 mouse cecum clone aaa88d04
GQ155666.1 gg_id:589249 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
AB548827.1 gg_id:530232 Citrobacter freundii str. JCM 24062
GQ154694.1 gg_id:510488 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
FJ581026.1 gg_id:570627 Citrobacter freundii str. IITRL1
DQ192060.1 gg_id:166668 Citrobacter sp. I91-10
EU528229.1 gg_id:280706 Seasonal Dynamics Mudflat Mouth Major Kentucky Lake Reservoir Tributary sedime
DQ816596.1 gg_id:167950 mouse cecum clone aab20b03
DQ816998.1 gg_id:169360 mouse cecum clone aaa94d12
DQ294285.1 gg_id:141265 Citrobacter freundii str. 7
EU365679.1 gg_id:258785 Citrobacter freundii str. M-8
FJ975807.1 gg_id:547342 Human gut microbiome adopts alternative state bowel transplantation ileum effluent

AJ245596.1	48707	901.3	727.5	1434.1	1334.5	2321.6	1836.6
NC_012751.1	431766	179.8	144.9	371.4	240.2	90.6	129.2
AB067723.1	28528	244.2	235.6	349.1	357.1	135.3	112.7
U91515.1	10203	981.2	1222.3	774.0	1252.1	1273.2	1593.1
AY136143.1	86615	619.9	323.8	1430.1	1031.1	397.2	353.6
AY136152.1	105167	1713.0	1432.0	2047.7	769.3	3405.5	1424.8
AF293619.1	25922	706.4	680.4	1857.5	586.8	305.4	368.3
FJ357496.1	359629	4072.5	3698.5	5089.2	3609.3	3624.1	3369.5
AF293627.1	50997	1991.1	895.6	1427.9	3221.1	262.6	899.7
DQ228285.1	150888	748.4	617.1	1292.0	988.6	977.9	311.4
AF493976.1	82917	37.3	259.3	1145.0	132.6	58.5	109.0
DQ481466.1	203232	1068.4	1532.7	1870.7	580.2	1023.2	1767.2
DQ481470.1	201655	56.2	196.8	684.4	111.4	54.9	188.7
EU468094.1	299301	2996.2	2812.7	4600.5	4068.1	4609.6	3556.8
GQ154806.1	534457	3909.7	3452.4	7060.0	5081.9	5696.0	3894.8
GQ155543.1	588290	425.9	953.6	1884.8	452.0	1452.5	923.9
DQ816142.1	168998	179.1	539.3	1422.3	277.4	157.2	195.0
GQ155506.1	511336	890.7	1356.9	2500.9	509.2	1140.3	1858.2
EU467996.1	301223	1798.2	1745.7	2087.5	3770.9	2114.1	1724.5
EU468053.1	297805	167.1	490.3	1401.6	270.2	75.7	374.5
GQ155565.1	556376	334.0	847.6	2919.7	412.5	690.6	1060.9
EU540206.1	283179	529.0	729.3	3078.8	353.1	319.3	428.5
FJ658620.1	509207	305.9	800.6	1321.1	869.2	384.9	655.4
AY163805.1	101294	5718.4	4332.2	2225.0	6110.9	7355.6	5465.6
AM184249.1	160975	149.3	700.8	1727.6	454.0	289.3	558.8
DQ294286.1	143708	1681.4	1232.0	1194.3	1387.0	1667.1	1403.4
AY259630.1	83212	7787.0	6483.2	7242.8	5436.5	9249.6	7361.0
GQ154984.1	532730	582.9	1306.7	3295.2	528.9	885.9	1377.0
DQ817309.1	173691	13.8	16.8	12.4	43.1	61.5	25.1
DQ816132.1	167280	916.9	825.4	538.8	824.9	1682.0	765.0
GQ155666.1	589249	15637.5	15494.1	12503.7	13055.3	13824.3	10858.2
AB548827.1	530232	191.5	477.5	2307.6	614.0	805.0	631.1
GQ154694.1	510488	261.1	635.0	2514.8	583.3	1205.6	1107.9
FJ581026.1	570627	971.4	1400.9	4886.5	2043.0	3114.3	2090.7
DQ192060.1	166668	124.2	548.6	1030.4	329.5	168.2	451.2
EU528229.1	280706	1832.9	2464.0	3800.3	2439.2	2554.3	2426.4
DQ816596.1	167950	339.3	370.2	408.0	1263.0	824.2	459.5
DQ816998.1	169360	719.4	1342.6	2017.5	1150.2	2930.4	627.7
DQ294285.1	141265	26.1	103.9	408.4	211.7	61.0	69.9
EU365679.1	258785	1301.0	2572.5	3555.4	1927.8	6583.1	6419.1
FJ975807.1	547342	645.7	1093.3	3043.4	489.8	2567.6	1350.6

k__Bacteria	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria
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s__Cronobacter dublinensis	4172
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s__unclassified	5567
s__unclassified	5733

EU545403.1 gg_id:534741 Citrobacter freundii str. XW722
EF593056.1 gg_id:251387 Identification cultivable and non-cultivable Nisargruna biogas plant predigester slurry
DQ517285.1 gg_id:161301 Citrobacter freundii str. BRN1
GU374110.1 gg_id:530539 soil East Calcutta wetland clone SRC_NBB9
GQ155532.1 gg_id:579108 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
DQ223880.1 gg_id:168759 Citrobacter sp. str. P11
GQ155589.1 gg_id:552805 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
GQ154756.1 gg_id:510480 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
EU468065.1 gg_id:295328 cheetah feces clone CE2_b11_3
EF371903.1 gg_id:213847 Citrobacter freundii str. TF13
DQ192058.1 gg_id:170521 Citrobacter sp. I91-5
FJ658534.1 gg_id:511169 Metalworking Fluids and Aerosols Metallurgy Plant metalworking aerosol clone Sumn
DQ816058.1 gg_id:169128 mouse cecum clone aaa86g12
GQ155569.1 gg_id:510363 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
GQ155471.1 gg_id:509639 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
GQ154907.1 gg_id:567301 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
AB548831.1 gg_id:522347 Citrobacter freundii str. JCM 24066
GQ154858.1 gg_id:564251 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
DQ816447.1 gg_id:169742 mouse cecum clone aab18b07
GQ155467.1 gg_id:544556 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
AF025373.1 gg_id:9852 Citrobacter werkmanii str. CDC 0876-58
EF059839.1 gg_id:226460 Cronobacter dublinensis str. E465
EF059874.1 gg_id:223014 Cronobacter dublinensis str. E791
EF059879.1 gg_id:224695 Cronobacter dublinensis str. E799; NCTC9846
EF059878.1 gg_id:224208 Cronobacter dublinensis str. E798
EF059887.1 gg_id:219603 Cronobacter muytjensii str. E888
FJ906909.1 gg_id:552376 Cronobacter muytjensii str. Jor112
EF059875.1 gg_id:224339 Cronobacter muytjensii str. E793
EF059849.1 gg_id:224182 Cronobacter muytjensii str. E616
GU227684.1 gg_id:587272 Cronobacter sakazakii str. KYU35
GU227677.1 gg_id:534869 Cronobacter sakazakii str. KYU8
GU122211.1 gg_id:579605 Cronobacter muytjensii str. 05CHPL61
EF059861.1 gg_id:222245 Cronobacter turicensis str. E680
GU122184.1 gg_id:573255 Cronobacter sakazakii str. CDC 20-83; 05CHPL02
EU458321.1 gg_id:297419 spotted hyena feces clone HY1_d03
GU227685.1 gg_id:593345 Cronobacter sakazakii str. KYU37
FJ906905.1 gg_id:584098 Cronobacter muytjensii str. Jor77
GU122215.1 gg_id:557422 Cronobacter sakazakii str. 05CHPL65
FN543093.2 gg_id:569973 Cronobacter turicensis z3032
EF059892.1 gg_id:217736 Cronobacter subsp. dublinensis str. DES187
FN539031.1 gg_id:559715 Cronobacter sp. str. 040407/32

EU545403.1	534741	164.4	736.7	1879.2	362.5	111.2	730.3
EF593056.1	251387	8093.2	7892.9	6053.5	7180.7	9223.9	7082.2
DQ517285.1	161301	222.8	824.6	2523.2	300.6	455.6	1288.5
GU374110.1	530539	94.7	325.0	409.4	245.3	129.2	217.6
GQ155532.1	579108	431.4	1302.1	4339.0	461.2	512.3	1048.8
DQ223880.1	168759	254.3	506.7	529.4	296.3	1041.0	508.8
GQ155589.1	552805	1855.4	2056.2	3880.4	1181.9	2445.2	2690.2
GQ154756.1	510480	633.2	818.5	2253.8	628.1	487.6	1236.4
EU468065.1	295328	7432.4	7748.3	2513.9	4201.5	4220.3	2274.9
EF371903.1	213847	9978.0	13207.0	7725.7	8714.4	9330.1	8196.2
DQ192058.1	170521	1756.2	1782.4	2494.4	944.8	774.1	2138.2
FJ658534.1	511169	4669.6	4488.1	4185.4	4861.5	3954.6	4097.2
DQ816058.1	169128	258.8	807.1	5389.1	585.5	654.8	562.8
GQ155569.1	510363	645.1	1106.7	2905.7	497.2	2394.0	1343.9
GQ155471.1	509639	4311.1	5732.8	5751.8	4450.4	9049.0	6379.0
GQ154907.1	567301	1603.9	1384.5	9236.3	2554.5	2612.7	2925.6
AB548831.1	522347	125.1	514.0	1721.5	345.0	141.4	341.2
GQ154858.1	564251	1280.9	2687.5	5687.0	959.6	3964.3	2817.4
DQ816447.1	169742	155.3	2365.1	1162.8	1358.9	139.3	182.0
GQ155467.1	544556	8077.7	7790.0	5991.5	8054.9	13232.2	9030.3
AF025373.1	9852	144.6	656.0	1038.3	172.0	100.4	494.8
EF059839.1	226460	874.5	799.9	2021.1	1832.4	496.9	732.2
EF059874.1	223014	395.3	688.6	2451.8	826.3	222.3	623.2
EF059879.1	224695	719.8	745.5	1854.1	953.1	513.2	612.4
EF059878.1	224208	475.6	559.0	1692.9	1268.8	753.9	1032.5
EF059887.1	219603	126.4	334.1	1284.6	210.6	103.0	740.5
FJ906909.1	552376	122.1	360.6	1302.6	232.8	112.4	762.9
EF059875.1	224339	355.6	636.4	2150.1	726.2	156.8	1151.9
EF059849.1	224182	3355.4	2697.5	6019.3	5517.2	1046.2	3600.9
GU227684.1	587272	133.5	185.4	674.5	224.7	88.9	208.6
GU227677.1	534869	694.0	1001.6	2201.5	1310.9	302.7	888.2
GU122211.1	579605	2241.6	2397.2	6640.0	4285.5	1033.1	3972.1
EF059861.1	222245	562.3	701.6	2637.2	1038.0	131.8	640.3
GU122184.1	573255	4904.4	6875.9	3151.9	3976.7	3126.6	2357.3
EU458321.1	297419	4692.8	5008.7	3126.1	6051.5	4822.0	6531.1
GU227685.1	593345	205.2	323.1	1322.8	319.9	127.3	402.6
FJ906905.1	584098	1337.7	1387.0	3967.4	2267.7	573.4	2217.1
GU122215.1	557422	1438.0	606.7	1774.9	2331.3	632.4	880.1
FN543093.2	569973	180.8	401.8	1593.6	266.7	70.4	221.1
EF059892.1	217736	200.1	332.6	1369.7	309.1	121.1	393.9
FN539031.1	559715	260.5	510.1	2919.1	358.7	102.9	239.8

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s__Enterobacter cowanii	4196
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EU348325.1 gg_id:353216 symbiont
EU072500.1 gg_id:246330 pentatomid symbionts host gut clone Mh1
CP001836.1 gg_id:520563 Dickeya dadantii str. Ech586
EF530560.1 gg_id:226472 Erwinia chrysanthemi str. ICMP 4649
EU526397.1 gg_id:263449 Erwinia chrysanthemi
AF520709.2 gg_id:61200 Erwinia chrysanthemi str. CFBP 1270
AF520712.1 gg_id:61196 Dickeya dieffenbachiae str. CFBP 2051
EU821584.1 gg_id:366934 Erwinia chrysanthemi str. A5307
AF520711.2 gg_id:61197 Dickeya zeae str. CFBP 2052
AF373199.1 gg_id:66727 Erwinia chrysanthemi str. 571
AB453281.1 gg_id:328862 Edwardsiella ictaluri str. PH-0744
GU176612.1 gg_id:588536 Edwardsiella ictaluri str. HSA-1
FJ405295.1 gg_id:358862 Edwardsiella tarda str. K6
FJ405305.1 gg_id:358984 Edwardsiella tarda str. K16
EU121410.1 gg_id:242592 Edwardsiella tarda str. EH-202
FJ405306.1 gg_id:369144 Edwardsiella tarda str. K17
FJ405294.1 gg_id:364464 Edwardsiella tarda str. K5
FJ405307.1 gg_id:367467 Edwardsiella tarda str. K18
FJ493544.1 gg_id:538059 Edwardsiella tarda str. H1
FJ405304.1 gg_id:358672 Edwardsiella tarda str. K15
GU367394.1 gg_id:518647 Edwardsiella tarda str. Et4
EU259315.1 gg_id:249457 Edwardsiella tarda str. LTB-4
FJ405296.1 gg_id:361185 Edwardsiella tarda str. K7
FJ405299.1 gg_id:366911 Edwardsiella tarda str. K10
GQ181217.1 gg_id:556713 Edwardsiella tarda str. EIB107
EU259316.1 gg_id:252748 Edwardsiella tarda str. WY37
FJ405293.1 gg_id:366652 Edwardsiella tarda str. K4
EU259317.1 gg_id:244611 Edwardsiella tarda str. WY28
FJ405300.1 gg_id:370021 Edwardsiella tarda str. K11
GQ337957.1 gg_id:540452 Edwardsiella tarda str. TsLt
AF015259.1 gg_id:9737 Edwardsiella tarda str. CDC 4411-68
NR_024768.1 gg_id:537841 Edwardsiella hoshinae str. JCM1679
FJ405298.1 gg_id:360292 Edwardsiella tarda str. K9
EF371905.1 gg_id:215399 Edwardsiella tarda str. TF17
EU231639.1 gg_id:256624 Edwardsiella ictaluri str. TCCC11053
FJ405308.1 gg_id:364288 Edwardsiella tarda str. K19
FJ405302.1 gg_id:359327 Edwardsiella tarda str. K13
EF467289.1 gg_id:227142 Edwardsiella tarda str. CD
EU181369.1 gg_id:248470 Rahnella sp. str. LR113
DQ645479.1 gg_id:159919 Escherichia coli str. F4-2
GQ264499.1 gg_id:586406 Structure Simulated Level Waste Site simulated level waste site clone WW3_48

EU348325.1	353216	7540.6	7471.3	8254.9	8477.9	8858.1	7867.0
EU072500.1	246330	1527.1	1377.0	1947.9	2577.2	4617.6	4065.3
CP001836.1	520563	2131.4	2151.8	3036.4	2790.0	1452.2	2943.0
EF530560.1	226472	1533.6	1510.3	2582.2	1492.9	1749.8	2533.0
EU526397.1	263449	218.2	280.2	1918.4	293.8	97.1	332.4
AF520709.2	61200	3854.3	4398.9	4656.9	4596.1	4897.2	5164.0
AF520712.1	61196	1947.0	2094.8	2548.6	3085.4	3804.1	2504.9
EU821584.1	366934	345.8	721.0	1682.1	649.7	1251.4	1464.8
AF520711.2	61197	2256.5	1512.3	3470.1	1694.0	768.2	908.5
AF373199.1	66727	639.4	867.3	2180.7	394.2	937.6	576.7
AB453281.1	328862	597.4	880.8	982.0	415.1	993.0	1049.7
GU176612.1	588536	15343.0	13351.3	9764.9	13685.0	15210.4	14665.9
FJ405295.1	358862	774.4	948.4	5318.3	1042.8	2208.2	2000.5
FJ405305.1	358984	114.2	304.5	1210.3	286.9	164.3	437.9
EU121410.1	242592	1220.7	699.5	2164.6	1934.0	3089.9	2225.3
FJ405306.1	369144	1223.8	755.3	2682.0	1922.7	3083.4	2274.7
FJ405294.1	364464	1836.3	2155.1	849.8	2065.9	2405.0	1616.4
FJ405307.1	367467	10791.6	10637.2	3466.5	6473.4	10541.4	8155.3
FJ493544.1	538059	3363.0	3058.0	1983.7	2775.3	3933.9	2464.3
FJ405304.1	358672	1220.8	734.9	2548.9	1963.7	3078.5	2277.1
GU367394.1	518647	7502.0	3984.7	7196.4	6011.3	8991.9	8181.9
EU259315.1	249457	1145.4	702.1	2388.0	1860.2	2893.1	1968.9
FJ405296.1	361185	764.1	832.9	469.4	2057.6	1819.3	1457.8
FJ405299.1	366911	274.8	613.3	2730.0	441.3	1161.7	668.0
GQ181217.1	556713	203.5	401.0	1857.5	491.3	1118.8	735.5
EU259316.1	252748	1244.8	1773.8	1053.8	2147.1	3081.6	2635.4
FJ405293.1	366652	1236.0	1115.0	5654.9	1038.7	2532.4	2694.4
EU259317.1	244611	56.6	304.2	1023.5	156.7	88.2	444.3
FJ405300.1	370021	1225.8	701.2	1994.8	1914.4	3093.1	2222.5
GQ337957.1	540452	1453.6	1220.8	557.5	352.0	1484.3	1447.9
AF015259.1	9737	1086.8	1044.4	4021.7	2081.1	2458.9	1820.4
NR_024768.1	537841	1239.5	728.1	1736.3	1818.8	2918.2	1946.9
FJ405298.1	360292	2052.5	1403.3	5816.9	3603.4	4406.6	4401.1
EF371905.1	215399	737.7	854.4	999.6	1250.4	805.3	954.8
EU231639.1	256624	252.5	487.6	520.8	251.5	244.0	771.8
FJ405308.1	364288	1756.8	2043.9	2606.2	4476.1	3524.9	4473.0
FJ405302.1	359327	3968.9	2636.3	5993.9	4654.9	6320.3	6354.2
EF467289.1	227142	1200.3	920.4	3745.9	1860.7	2929.0	1979.7
EU181369.1	248470	1687.1	1708.7	5146.5	3208.2	2410.5	3335.8
DQ645479.1	159919	443.5	484.0	1218.4	304.8	747.1	589.7
GQ264499.1	586406	219.1	619.2	838.1	135.8	180.6	575.0

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s__Enterobacter cowanii	4813
s__Enterobacter cowanii	4883
s__Enterobacter cowanii	5930
s__Enterobacter hormaechei	4249
s__Enterobacter hormaechei	4543
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s__Enterobacter hormaechei	6182
s__Enterobacter pulveris	5698
s__unclassified	4790
s__unclassified	5180
s__Candidatus Erwinia dacicola	4442
s__Erwinia rhapontici	4276
s__Erwinia rhapontici	4823
s__Erwinia rhapontici	5192
s__Erwinia rhapontici	5664
s__Erwinia rhapontici	6116

DQ919062.1 gg_id:244516 Enterobacter cowanii str. 6L
EF025326.1 gg_id:176468 Enterobacter cloacae str. SREPS1
EU855207.1 gg_id:355066 Enterobacter sp. str. CTSP29
DQ855282.1 gg_id:216257 Enterobacter sp. str. FMB-1
GQ260085.1 gg_id:561327 Enterobacter cloacae str. ICIRC107
EU047701.1 gg_id:251565 Enterobacter aerogenes str. HC050612-1
EU047702.1 gg_id:256852 Enterobacter cloacae str. HC050612-4
EU047556.1 gg_id:249130 Enterobacter hormaechei str. TMPSB-T10
GU071202.1 gg_id:587429 Enterobacter sp. str. DIT 14
GQ260087.1 gg_id:564431 Enterobacter cloacae str. ICIRC10
AJ508302.1 gg_id:80575 Enterobacter hormaechei str. CIP 103441
AY335554.1 gg_id:129942 Enterobacter aerogenes str. CBNU-20-1
DQ202394.1 gg_id:140607 Enterobacter cloacae str. B5
GQ260081.1 gg_id:587124 Enterobacter cloacae str. ICIRC91
EF210100.1 gg_id:203409 Enterobacter hormaechei str. Z2-7
FJ868805.1 gg_id:541119 Enterobacter sp. str. BSRA1
EF446901.1 gg_id:214586 Enterobacter cloacae str. GW4
AF130914.1 gg_id:10081 Pantoea endophytica str. A42
GQ179978.1 gg_id:575168 Enterobacter hormaechei str. FS11
AY995561.1 gg_id:115488 Enterobacter hormaechei
AJ854063.3 gg_id:108298 Enterobacter nickellidurans str. NiVas 114
GQ260075.1 gg_id:512914 Enterobacter hormaechei str. ICIRC82
FJ976545.1 gg_id:556584 Enterobacter sp. str. LCR36
EU073021.1 gg_id:254448 Enterobacter cloacae HQ040619-1
CU915026.1 gg_id:448667 and dynamics adapted microbiota during degradation Tunisian zarzatine enriched se
DQ837566.1 gg_id:172044 Enterobacter sp. XIV
AB244457.1 gg_id:257506 Enterobacter cloacae str. An20-1
FJ976587.1 gg_id:545162 Enterobacter aerogenes str. LCR78
FJ999766.1 gg_id:385869 Enterobacter hormaechei str. SP
EF179825.1 gg_id:258793 sequences adult Anopheles darlingi (Diptera: Culicidae) mosquitoes clone 4.2
Y17665.1 gg_id:10077 Enterobacter cloacae Nr. 3
EF059890.1 gg_id:218876 Enterobacter hormaechei str. E904
DQ273684.1 gg_id:144399 Evaluation two chromogenic media glucosidase and commercial oligonucleotide pro
AY217654.1 gg_id:84190 Escherichia senegalensis str. F1p
EU302833.1 gg_id:240810 Salmonella sp. str. DAP8
GQ478377.1 gg_id:551552 olive endosymbiont 'Candidatus Erwinia dacicola' switches intracellular extracellular
GQ131582.1 gg_id:460735 Erwinia rhapontici str. 1OP1
Z96087.1 gg_id:9805 Erwinia rhapontici str. LMG 2688
GQ131583.1 gg_id:451112 Erwinia rhapontici str. 1OP6
GQ131584.1 gg_id:410468 Erwinia rhapontici str. 3OP1
U80206.1 gg_id:9811 Erwinia rhapontici str. ATCC 29283

DQ919062.1	244516	7523.1	6330.5	3985.4	5095.0	5801.0	6137.4
EF025326.1	176468	3208.8	2190.5	2221.4	3980.0	5056.9	3429.1
EU855207.1	355066	1729.6	1290.4	2213.7	1782.7	953.4	3087.8
DQ855282.1	216257	1144.0	1559.2	2397.1	710.5	2331.5	1980.5
GQ260085.1	561327	11711.9	9999.9	7519.1	14598.2	14781.7	13632.0
EU047701.1	251565	54.3	545.3	1504.1	144.0	69.0	259.3
EU047702.1	256852	933.5	1186.8	1165.0	712.6	2762.0	1939.0
EU047556.1	249130	132.4	493.5	921.2	235.3	153.2	209.4
GU071202.1	587429	850.8	808.6	1936.8	380.0	1127.5	524.7
GQ260087.1	564431	6038.3	5075.0	3054.2	5775.5	8668.9	8885.0
AJ508302.1	80575	960.4	611.7	1740.4	523.5	458.0	606.6
AY335554.1	129942	1063.5	1594.1	3887.6	2006.9	1803.1	990.8
DQ202394.1	140607	932.9	1124.8	1908.1	1863.5	1985.2	614.5
GQ260081.1	587124	19301.5	18628.2	14259.8	13321.3	15650.2	13650.9
EF210100.1	203409	871.0	1181.1	1950.8	1470.5	1658.2	1753.8
FJ868805.1	541119	152.9	480.8	780.0	418.9	336.9	349.2
EF446901.1	214586	571.2	1085.6	2602.9	1008.6	1621.0	1151.1
AF130914.1	10081	1309.1	1726.1	2663.2	1553.2	3629.8	1688.2
GQ179978.1	575168	526.5	898.7	1252.0	241.8	786.6	557.2
AY995561.1	115488	88.0	453.9	561.6	109.8	98.2	157.4
AJ854063.3	108298	52.4	296.5	859.3	181.4	86.6	248.9
GQ260075.1	512914	46.0	188.8	116.1	84.7	83.6	56.8
FJ976545.1	556584	105.9	444.0	658.6	176.5	127.6	188.4
EU073021.1	254448	9104.6	9086.7	9178.8	7378.7	7607.0	7398.4
CU915026.1	448667	357.5	690.3	1760.2	735.7	205.9	617.4
DQ837566.1	172044	143.9	451.0	993.8	352.6	153.0	242.9
AB244457.1	257506	63.3	257.8	629.4	93.6	96.9	141.8
FJ976587.1	545162	142.8	777.6	1547.5	445.5	154.2	209.0
FJ999766.1	385869	110.4	633.5	1286.9	201.6	106.2	167.5
EF179825.1	258793	2801.3	2694.7	4149.2	3148.0	4883.2	2929.0
Y17665.1	10077	52.6	258.5	1028.1	335.9	106.6	112.2
EF059890.1	218876	117.7	540.8	1512.9	227.9	141.3	188.7
DQ273684.1	144399	457.7	531.9	696.8	664.2	630.3	599.8
AY217654.1	84190	86.0	360.8	795.5	112.7	99.0	179.4
EU302833.1	240810	2056.4	1206.9	1710.6	3050.3	2180.9	1017.4
GQ478377.1	551552	66.3	307.1	402.9	190.5	176.8	291.9
GQ131582.1	460735	5280.2	5991.9	5140.8	7517.3	10597.1	6366.2
Z96087.1	9805	188.6	408.6	1012.3	311.8	294.7	592.6
GQ131583.1	451112	68.8	225.9	1119.2	248.8	580.8	373.0
GQ131584.1	410468	74.3	302.4	1234.0	247.0	588.9	385.8
U80206.1	9811	177.6	838.4	2799.7	1131.1	606.9	734.5

k__Bacteria	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria
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s__Erwinia soli	6224
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s__Erwinia toletana	5774
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s__Escherichia hermannii	4287
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s__Pantoea dispersa	4369
s__unclassified	4169
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s__unclassified	5704

EF540891.1 gg_id:219853 Erwinia soli str. Ew02
AM292080.1 gg_id:179624 Erwinia tasmaniensis str. Et2/99
AM055715.2 gg_id:149797 Erwinia pyrifoliae str. Ejp557
FJ594367.1 gg_id:569261 Erwinia amylovora str. EA312
FJ594360.1 gg_id:566379 Erwinia pyrifoliae str. WT19
AF130965.1 gg_id:9820 Erwinia toletana str. A89
AF130964.1 gg_id:9814 Erwinia toletana str. A82
GQ884173.1 gg_id:582459 Escherichia hermannii str. SH-2
EF059889.1 gg_id:226692 Escherichia hermannii str. E895
EF059869.1 gg_id:223949 Escherichia hermannii str. E757
EU931561.1 gg_id:337373 Pantoea agglomerans str. ZFJ-6
AB297966.1 gg_id:209376 Erwinia sp. str. AC81a (=SUPP41)
GQ024698.1 gg_id:484972 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GU339282.1 gg_id:563485 Pantoea ananatis str. EH55
DQ273680.1 gg_id:141117 Evaluation two chromogenic media glucosidase and commercial oligonucleotide pro
U80201.1 gg_id:9861 Pectobacterium cypripedii str. ATCC 29267
EU289448.1 gg_id:253617 metagenomic approach biosynthesis ansamycin endophytes or symbionts enriched s
EU681952.1 gg_id:281980 Erwinia persicina str. WD1608
FM163487.1 gg_id:289103 Achromobacter xylosoxidans str. RE1
AM055711.1 gg_id:149811 Erwinia billingiae str. Eb661
GQ024758.1 gg_id:484912 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
AF024607.1 gg_id:9823 Pantoea agglomerans str. TAC.I.94.1
GQ043420.1 gg_id:423241 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw96
GQ024848.1 gg_id:484822 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
AF141893.1 gg_id:71250 Erwinia amylovora str. BC202(=Ea491)
GQ024907.1 gg_id:484762 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
EU072495.1 gg_id:239362 pentatomid symbionts host gut clone Ah1
EU362176.1 gg_id:351023 Erwinia sp. str. C3(2008)
FJ595863.1 gg_id:543943 Erwinia pyrifoliae str. WT36
AY373829.2 gg_id:101634 Salmonella subterranea str. FRC1
GU124495.1 gg_id:582297 endosymbiotic (Stal) (rice brown planthopper) Enterobacteriales endosymbiont Nila
GQ024853.1 gg_id:484817 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ024769.1 gg_id:484901 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
AJ233417.1 gg_id:9810 Erwinia rhapontici str. DSM 4484
EF469631.1 gg_id:221786 Dioxyna bidentis ex Bidens tripartita symbiont
AB480771.1 gg_id:539151 Erwinia tasmaniensis str. Acj 205
GQ024837.1 gg_id:484833 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
AM294946.1 gg_id:174382 Erwinia persicina str. LPPA 408
EU336938.2 gg_id:537651 Flavobacterium sp. str. AG13
AF289542.1 gg_id:20321 Erwinia amylovora EA G-5
AF024613.1 gg_id:9827 Pantoea agglomerans str. TAC.XII.93.2

EF540891.1	219853	350.1	486.4	921.8	399.6	1706.4	579.2
AM292080.1	179624	58.4	201.0	1782.6	222.2	116.2	147.1
AM055715.2	149797	134.3	246.5	1173.5	140.8	99.2	193.0
FJ594367.1	569261	193.1	434.0	1694.7	309.3	163.8	344.6
FJ594360.1	566379	793.3	976.8	3008.3	845.1	740.8	1628.2
AF130965.1	9820	333.4	366.2	1335.7	211.4	662.1	55.4
AF130964.1	9814	641.6	724.1	1876.8	655.0	1661.1	970.1
GQ884173.1	582459	82.4	311.9	1209.0	148.1	84.8	612.8
EF059889.1	226692	71.4	370.3	869.2	142.4	84.5	125.7
EF059869.1	223949	293.7	756.2	1249.1	282.6	641.0	1026.4
EU931561.1	337373	1851.3	1909.2	7896.2	5682.5	7029.2	3135.2
AB297966.1	209376	2927.0	2688.7	2881.1	2779.0	2881.6	3744.2
GQ024698.1	484972	11049.8	11072.4	7281.6	10962.4	9418.2	8200.4
GU339282.1	563485	267.2	518.8	2411.8	656.5	1079.2	1249.8
DQ273680.1	141117	1591.4	1139.9	3967.9	2725.7	1274.4	2705.6
U80201.1	9861	179.3	628.0	1197.5	408.1	268.0	349.9
EU289448.1	253617	1674.9	2060.4	1377.9	1226.0	3067.7	2146.8
EU681952.1	281980	103.9	271.1	804.3	227.6	121.1	160.7
FM163487.1	289103	56.5	238.7	228.3	119.9	94.5	150.2
AM055711.1	149811	243.3	516.7	2153.7	573.5	114.3	234.7
GQ024758.1	484912	1255.9	943.1	1262.1	2761.0	4603.8	1348.3
AF024607.1	9823	4832.0	3613.9	3733.6	4772.0	1939.7	2772.7
GQ043420.1	423241	432.4	666.4	3454.3	524.4	1424.0	1211.1
GQ024848.1	484822	4291.5	3482.0	2791.6	6977.3	3412.9	5306.1
AF141893.1	71250	1147.0	973.4	4413.9	1234.3	803.5	1717.5
GQ024907.1	484762	4813.8	5649.3	2166.8	3635.6	4952.4	2526.6
EU072495.1	239362	4952.5	4954.4	7032.6	6354.7	7194.8	3921.5
EU362176.1	351023	92.0	504.8	1834.3	214.9	145.5	187.6
FJ595863.1	543943	3312.2	3380.1	1661.2	559.9	4112.0	3045.1
AY373829.2	101634	1205.7	1210.8	4389.5	1198.3	835.7	2064.1
GU124495.1	582297	696.3	1127.8	2834.1	825.6	1647.2	1084.9
GQ024853.1	484817	9542.6	1068.0	5756.1	8502.9	8600.0	6706.7
GQ024769.1	484901	12458.8	16104.6	10482.8	11190.6	11249.8	10191.4
AJ233417.1	9810	709.5	914.4	1882.0	2603.9	198.2	1202.2
EF469631.1	221786	207.7	352.4	1204.9	397.6	358.6	476.3
AB480771.1	539151	40.6	173.3	2562.8	526.0	1141.1	503.4
GQ024837.1	484833	4029.9	2718.7	6350.3	5212.3	6136.9	6036.1
AM294946.1	174382	251.5	709.0	2393.5	322.9	1173.4	619.6
EU336938.2	537651	205.5	428.6	1537.4	323.5	803.9	429.0
AF289542.1	20321	9808.6	10509.6	8028.3	10328.0	9933.6	8343.7
AF024613.1	9827	1769.3	1967.7	1265.3	1887.6	969.4	1314.3

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AY702662.1 gg_id:169365 Margalefia venezuelensis str. MS12
DQ532292.1 gg_id:171458 Geographical Variation Microbial Burden and Spacecraft Assembly Kennedy Space C
AB480775.1 gg_id:575074 Erwinia tasmaniensis str. Acj 211
FJ595871.1 gg_id:573072 Erwinia amylovora str. LMG2068
GQ097550.1 gg_id:395052 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw
EU926632.1 gg_id:350789 Escherichia albertii str. 1297-05-19
NC_010498.1 gg_id:263846 Escherichia coli str. SECEC SMS-3-5
AE014073.1 gg_id:146636 Shigella flexneri 2a str. 2457T
DQ411026.1 gg_id:151002 Escherichia coli str. FR-2
CP000038.1 gg_id:138890 Shigella sonnei str. Ss046
CU928163.2 gg_id:544923 Escherichia coli str. UMN026
AP010953.1 gg_id:568499 Escherichia coli O26:H11 str. 11368
CP000800.1 gg_id:257376 Escherichia coli str. E24377A
NC_010498.1 gg_id:263845 Escherichia coli str. SECEC SMS-3-5
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AAJV02000007.1 gg_id:340407 Escherichia coli str. E22
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FM180568.1 gg_id:369791 Escherichia coli 0127:H6 str. E2348/69
CP000948.1 gg_id:270792 Escherichia coli substr. DH10B str. K-12
CU928158.2 gg_id:554727 Escherichia fergusonii 35469 str. ATCC 35469T
AAKB02000001.1 gg_id:281891 Escherichia coli str. 53638
CU928163.2 gg_id:544920 Escherichia coli str. UMN026
CU928161.2 gg_id:563144 Escherichia coli str. S88
EU009185.1 gg_id:238337 Shigella dysenteriae str. FBD014
AF233451.1 gg_id:17857 Escherichia coli
EF620924.1 gg_id:255332 Escherichia coli str. SYW003
CU928161.2 gg_id:563145 Escherichia coli str. S88
CU928164.2 gg_id:536217 Escherichia coli str. IAI39
EU470924.1 gg_id:291766 red panda feces clone RP_2aaa03c06
EU470476.1 gg_id:301376 red panda feces clone RP_1aaa02h07
FJ950549.1 gg_id:428533 Escherichia coli str. c247
EU472923.1 gg_id:288465 red panda feces clone RPSD_1aaa04h11
GQ025583.1 gg_id:437123 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
EU472692.1 gg_id:303108 red panda feces clone RPSD_1aaa01c04
GQ008742.1 gg_id:500918 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
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EU472680.1 gg_id:288712 red panda feces clone RPSD_1aaa01d01
EU472729.1 gg_id:290328 red panda feces clone RPSD_1aaa02g10

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AB480775.1	575074	741.5	740.2	3334.6	1301.7	6178.3	3772.4
FJ595871.1	573072	528.8	657.9	2860.9	1047.3	1100.6	1801.5
GQ097550.1	395052	798.1	975.3	834.1	1548.8	696.5	1084.1
EU926632.1	350789	74.6	320.9	810.8	217.6	104.6	403.3
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AE014073.1	146636	53.2	279.5	1783.3	150.5	72.2	351.6
DQ411026.1	151002	80.8	135.8	350.6	143.4	88.7	146.8
CP000038.1	138890	668.3	778.9	2806.2	1024.6	564.4	977.0
CU928163.2	544923	771.8	1245.0	3889.0	1570.6	1451.8	1396.5
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NC_010498.1	263843	346.5	511.5	656.3	488.1	202.5	366.7
AAJV02000011.1	314537	845.5	1162.7	3504.9	1225.5	907.3	1121.0
AAJV02000007.1	340407	801.1	983.4	2694.2	871.0	808.3	981.1
CP000819.1	520568	588.5	568.5	2700.9	781.2	508.7	860.3
CP000800.1	257373	59.8	157.7	227.8	127.5	146.9	149.6
FM180568.1	369791	679.6	724.9	3007.2	1022.6	539.2	1067.1
CP000948.1	270792	1992.6	1475.1	3016.1	3256.3	1888.1	2533.4
CU928158.2	554727	200.5	385.5	798.6	315.2	151.7	217.0
AAKB02000001.1	281891	1690.4	1740.2	5132.7	2025.6	1439.0	2604.3
CU928163.2	544920	1231.5	1339.4	4163.2	1545.9	1420.3	1535.0
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EU009185.1	238337	75.9	152.2	546.6	202.5	106.8	174.5
AF233451.1	17857	1269.6	1216.1	2423.6	2020.2	1501.2	1564.5
EF620924.1	255332	1320.5	1090.4	4539.3	1704.1	944.4	1765.5
CU928161.2	563145	975.2	968.9	3797.8	1505.6	1162.0	1559.1
CU928164.2	536217	1521.8	1657.2	4272.8	1939.4	1207.2	2255.2
EU470924.1	291766	383.8	538.0	1193.4	1309.2	2225.1	1247.7
EU470476.1	301376	153.8	475.4	1433.7	361.2	221.4	958.4
FJ950549.1	428533	1284.9	873.4	2340.7	2330.8	884.6	2264.1
EU472923.1	288465	229.3	543.8	2481.9	593.7	474.5	1061.1
GQ025583.1	437123	193.4	591.2	1934.3	770.2	415.6	627.6
EU472692.1	303108	424.3	711.0	2167.3	950.7	842.0	1078.1
GQ008742.1	500918	217.5	483.0	2030.2	712.4	397.3	691.0
EU471177.1	302439	455.7	638.6	1862.7	1466.2	719.3	1469.3
EU472680.1	288712	269.3	586.0	542.3	318.1	579.0	451.0
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EU464663.1 gg_id:287701 African elephant feces clone AFEL_aai32g02
EU472690.1 gg_id:290223 red panda feces clone RPSD_1aaa02d03
EU471064.1 gg_id:295395 red panda feces clone RP_3aaa04f12
EU472703.1 gg_id:298606 red panda feces clone RPSD_1aaa02d11
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EU472746.1 gg_id:301855 red panda feces clone RPSD_1aaa01e12
EU472863.1 gg_id:302968 red panda feces clone RPSD_1aaa01f04
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EU470870.1 gg_id:289907 red panda feces clone RP_2aaa03c09
EU471112.1 gg_id:290411 red panda feces clone RP_3aaa03e02
EU470511.1 gg_id:297780 red panda feces clone RP_1aaa01c08
DQ456289.1 gg_id:157055 pre-adolescent turkey cecum clone CFT211E11
EU472919.1 gg_id:299707 red panda feces clone RPSD_1aaa04f02
EU470601.1 gg_id:287806 red panda feces clone RP_1aaa02c12
EU466013.1 gg_id:299794 African elephant feces clone AFEL3_aao15g12
EU464642.1 gg_id:300980 African elephant feces clone AFEL_aai32d07
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EU471312.1 gg_id:292771 red panda feces clone RP_3aaa03f11
AM184252.1 gg_id:160249 Escherichia coli str. WAB1911
EU470944.1 gg_id:301988 red panda feces clone RP_2aaa04d11
EU470756.1 gg_id:294273 red panda feces clone RP_2aaa02e05
GQ047713.1 gg_id:390942 Topographical and Temporal Human Skin Microbiome skin palm clone nbw138d02c1
EU472878.1 gg_id:294985 red panda feces clone RPSD_1aaa03c02
EU778391.1 gg_id:314335 Red Panda feces clone RPSD_1aaa02b11
EU472908.1 gg_id:294073 red panda feces clone RPSD_1aaa03d09
EU472772.1 gg_id:300828 red panda feces clone RPSD_1aaa04a05
EU009180.1 gg_id:242457 Shigella boydii str. FBD009
EU471213.1 gg_id:295208 red panda feces clone RP_3aaa04f02
EU470490.1 gg_id:295383 red panda feces clone RP_1aaa02e01
EU470986.1 gg_id:301184 red panda feces clone RP_2aaa04d09
X96965.1 gg_id:9662 Shigella boydii
GQ025582.1 gg_id:466050 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
FJ949576.1 gg_id:444646 Escherichia coli str. G4
EU472929.1 gg_id:297711 red panda feces clone RPSD_1aaa03f07
EU472728.1 gg_id:289118 red panda feces clone RPSD_1aaa03e05
EU462402.1 gg_id:287659 Sumatran orangutan feces clone orang1_aai53h05
GQ493756.1 gg_id:537192 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
EU470610.1 gg_id:300547 red panda feces clone RP_1aaa04e06
FJ673277.1 gg_id:516144 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee

EU768736.1	334493	143.5	340.3	1654.4	569.7	280.2	536.6
EU464663.1	287701	277.8	386.4	828.4	867.3	504.6	763.5
EU472690.1	290223	462.0	459.3	815.9	306.7	4725.0	1860.2
EU471064.1	295395	2872.3	2477.1	5879.4	3224.0	3787.7	4748.6
EU472703.1	298606	172.9	473.9	1332.6	478.4	329.2	560.0
AY319393.1	90202	4218.7	4764.1	3637.8	5383.3	7996.4	8182.3
EU472746.1	301855	1101.4	1105.4	2616.3	1273.7	1189.8	1255.2
EU472863.1	302968	365.7	538.1	1890.9	704.5	419.1	615.4
GQ047684.1	444206	4829.3	4543.2	4303.9	5217.5	9299.9	6770.7
EU465326.1	302392	4566.5	5672.4	4279.9	7226.8	5244.7	4108.1
EU470870.1	289907	8727.6	6862.7	3901.5	9403.9	12326.2	11123.6
EU471112.1	290411	637.3	915.7	3310.1	1118.3	958.3	1531.8
EU470511.1	297780	10823.6	8957.1	10279.8	14666.4	9658.0	8498.2
DQ456289.1	157055	12460.4	11133.9	7404.2	14540.1	16494.6	11843.9
EU472919.1	299707	361.9	638.0	2766.5	731.5	407.3	697.2
EU470601.1	287806	1465.5	1571.1	1614.3	582.9	396.9	1476.4
EU466013.1	299794	676.8	954.3	2918.5	1340.1	710.3	1764.8
EU464642.1	300980	1555.1	2795.0	675.0	1765.2	1095.1	2577.0
EU471166.1	289744	210.6	484.9	889.1	727.9	393.6	555.2
EU471312.1	292771	2018.5	2340.0	2981.5	1609.1	2782.9	2673.5
AM184252.1	160249	2082.4	1440.1	2916.6	2711.4	1831.1	2324.7
EU470944.1	301988	2812.5	3166.2	2797.1	7139.1	3308.6	3965.5
EU470756.1	294273	8781.8	7795.0	5065.8	12006.6	9602.5	11640.9
GQ047713.1	390942	4273.4	2949.3	2129.8	4825.2	3858.5	4542.2
EU472878.1	294985	181.0	495.2	1681.1	633.1	282.5	692.1
EU778391.1	314335	1638.6	1486.5	1312.4	2052.0	2602.6	2825.0
EU472908.1	294073	2169.4	2696.6	1813.3	2247.2	1752.4	2311.9
EU472772.1	300828	379.7	723.9	3064.6	729.1	467.6	1211.4
EU009180.1	242457	1312.2	1794.4	3009.6	1480.4	1243.6	2079.6
EU471213.1	295208	439.8	579.6	1594.9	516.5	442.1	636.8
EU470490.1	295383	427.4	729.3	2895.2	979.5	714.4	1359.5
EU470986.1	301184	3625.4	3429.2	3928.4	3824.1	3779.7	3225.8
X96965.1	9662	550.0	812.6	2382.0	1159.2	1007.8	1033.2
GQ025582.1	466050	101.2	335.2	1292.9	281.4	158.1	358.4
FJ949576.1	444646	2377.7	1803.5	4294.0	3707.3	1728.9	3396.4
EU472929.1	297711	392.9	651.2	2545.7	739.4	587.7	1121.2
EU472728.1	289118	11279.5	12149.2	7373.1	11881.7	12005.7	12760.9
EU462402.1	287659	346.5	589.9	2118.6	719.5	424.3	658.4
GQ493756.1	537192	1612.9	1828.9	2137.3	4940.9	3502.9	5920.6
EU470610.1	300547	635.3	846.2	1935.4	667.7	697.7	760.9
FJ673277.1	516144	829.3	733.6	2422.2	1740.8	765.9	1736.4

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EU458135.1 gg_id:294276 North American black bear feces clone BB2_c08
EU470636.1 gg_id:300616 red panda feces clone RP_1aaa01d05
GQ031087.1 gg_id:414691 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
EU471061.1 gg_id:296334 red panda feces clone RP_3aaa01c11
EU472176.1 gg_id:297981 francois langur feces clone FL_2aaa04b02
GQ069091.1 gg_id:449962 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
EU472840.1 gg_id:298307 red panda feces clone RPSD_1aaa02b06
EU470804.1 gg_id:298326 red panda feces clone RP_2aaa03f10
EU472779.1 gg_id:294637 red panda feces clone RPSD_1aaa01b05
EU472793.1 gg_id:288476 red panda feces clone RPSD_1aaa03g10
EU470706.1 gg_id:293949 red panda feces clone RP_1aaa04g08
EU472879.1 gg_id:303261 red panda feces clone RPSD_1aaa01b03
EU470669.1 gg_id:289152 red panda feces clone RP_1aaa03e06
EU472824.1 gg_id:292653 red panda feces clone RPSD_1aaa02c07
EU472655.1 gg_id:290927 red panda feces clone RPSD_1aaa01f11
CP000036.1 gg_id:144321 Shigella boydii str. Sb227
EU471278.1 gg_id:292133 red panda feces clone RP_3aaa01c09
GQ047978.1 gg_id:419099 Topographical and Temporal Human Skin Microbiome skin palm clone nbw139g11c1
EU776531.1 gg_id:329008 Lion feces clone LI3_aah76c06
EU468090.1 gg_id:288116 cheetah feces clone CE2_f03_3
EU472825.1 gg_id:291515 red panda feces clone RPSD_1aaa01c06
GQ021879.1 gg_id:487789 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
EU472913.1 gg_id:288396 red panda feces clone RPSD_1aaa04e12
EU472700.1 gg_id:288620 red panda feces clone RPSD_1aaa03d10
EU471279.1 gg_id:292445 red panda feces clone RP_3aaa02f07
EU471202.1 gg_id:298795 red panda feces clone RP_3aaa03c11
EU472777.1 gg_id:302310 red panda feces clone RPSD_1aaa01c05
FJ678202.1 gg_id:518667 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU470927.1 gg_id:288122 red panda feces clone RP_2aaa04b12
GQ047075.1 gg_id:391950 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
EU470902.1 gg_id:291899 red panda feces clone RP_2aaa04g09
EU771755.1 gg_id:335863 African elephant feces clone AFEL_aai32a02
EU472815.1 gg_id:292496 red panda feces clone RPSD_1aaa04a06
EU470628.1 gg_id:295268 red panda feces clone RP_1aaa03c11
EU472092.1 gg_id:291590 francois langur feces clone FL_1aaa02e10
EU467743.1 gg_id:289022 North American black bear feces clone BB1_b07
GQ047710.1 gg_id:418353 Topographical and Temporal Human Skin Microbiome skin palm clone nbw138c06c1
DQ819115.1 gg_id:167150 mouse cecal microbiota-colonized zebrafish digestive tract clone aab26a07
EU472848.1 gg_id:303254 red panda feces clone RPSD_1aaa02g11
EU472786.1 gg_id:297825 red panda feces clone RPSD_1aaa02b09

EU471172.1	290556	3211.6	2906.0	820.2	5542.7	5129.7	4879.4
EU458135.1	294276	2823.3	2880.6	2815.1	2751.2	4902.5	4593.1
EU470636.1	300616	224.7	596.7	3050.1	607.4	377.4	1074.6
GQ031087.1	414691	8829.9	8951.5	4651.8	9108.4	8356.3	3311.5
EU471061.1	296334	635.2	1009.3	2455.3	1072.3	1078.7	1138.5
EU472176.1	297981	88.5	320.9	2594.9	214.8	94.5	454.6
GQ069091.1	449962	271.0	556.5	1447.2	967.8	472.4	766.5
EU472840.1	298307	608.5	968.2	2130.6	707.1	1001.6	1236.9
EU470804.1	298326	7039.9	6988.6	4209.7	6027.0	7079.3	8559.9
EU472779.1	294637	6442.0	4972.7	3787.7	5607.1	6094.8	6646.3
EU472793.1	288476	467.9	868.8	634.7	941.3	640.7	695.2
EU470706.1	293949	1404.4	1428.1	1874.8	859.8	1435.4	1367.5
EU472879.1	303261	1267.9	1163.4	3194.4	2270.6	1064.5	1901.3
EU470669.1	289152	12984.0	13532.9	15875.8	13956.6	17336.2	15233.8
EU472824.1	292653	264.2	491.3	289.1	729.8	1664.7	2077.4
EU472655.1	290927	3729.7	4635.9	1327.5	2360.4	1766.0	1689.6
CP000036.1	144321	317.1	717.5	1583.5	265.3	312.8	385.6
EU471278.1	292133	841.6	808.5	2480.9	1737.4	778.1	1588.2
GQ047978.1	419099	8310.2	10173.6	7333.2	5824.9	7888.3	6849.5
EU776531.1	329008	1531.3	1875.5	876.4	2603.2	1990.0	1893.8
EU468090.1	288116	7007.5	4019.9	5321.2	7660.5	5238.4	5823.7
EU472825.1	291515	6316.3	5891.2	3594.8	7000.9	8892.8	5103.2
GQ021879.1	487789	1069.0	1307.7	2112.8	988.9	2506.0	3486.8
EU472913.1	288396	4775.4	5231.5	1612.4	6771.3	9848.7	8082.4
EU472700.1	288620	2271.3	2381.0	2699.6	2694.5	1602.8	2121.0
EU471279.1	292445	418.0	698.4	2427.9	952.5	697.0	1302.1
EU471202.1	298795	3426.9	4200.0	3558.7	4860.0	5196.6	5250.6
EU472777.1	302310	2438.5	3136.7	1721.9	2695.0	2282.3	2151.7
FJ678202.1	518667	85.4	375.4	418.3	149.8	139.1	183.2
EU470927.1	288122	1293.2	1801.0	2845.3	2161.6	3451.9	2575.4
GQ047075.1	391950	2520.3	3446.8	4068.3	2082.0	3364.9	3639.6
EU470902.1	291899	630.5	896.7	1966.2	1120.3	961.9	1386.0
EU771755.1	335863	5906.0	5389.3	3293.3	5804.3	5821.9	8244.3
EU472815.1	292496	376.1	669.4	1178.7	1509.9	598.3	1614.8
EU470628.1	295268	289.7	610.0	1184.6	346.8	366.4	321.2
EU472092.1	291590	152.0	398.7	2699.8	571.0	197.2	626.1
EU467743.1	289022	10133.7	10368.2	7720.7	7658.8	9176.5	12209.3
GQ047710.1	418353	353.8	649.8	1603.4	334.7	1699.8	1117.8
DQ819115.1	167150	3942.2	4411.6	3983.8	4886.3	7430.0	6528.4
EU472848.1	303254	461.1	879.6	884.8	913.8	629.7	738.0
EU472786.1	297825	1075.1	1407.3	2770.7	1736.9	966.0	1959.0

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k__Bacteria	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria

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CP001063.1 gg_id:277854 Shigella boydii str. BS512; CDC 3083-94
EU470556.1 gg_id:293201 red panda feces clone RP_1aaa03b07
EF560788.1 gg_id:233865 Escherichia coli str. BEE3
EU471295.1 gg_id:298340 red panda feces clone RP_3aaa03g05
EU470739.1 gg_id:289190 red panda feces clone RP_2aaa02e12
EU468348.1 gg_id:293649 lion feces clone LI2_aae47f10
GQ031673.1 gg_id:403434 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
EU471240.1 gg_id:289442 red panda feces clone RP_3aaa03h04
EU470710.1 gg_id:290311 red panda feces clone RP_1aaa04a05
EU470675.1 gg_id:301701 red panda feces clone RP_1aaa02e06
NC_011740.1 gg_id:471437 Escherichia fergusonii str. ATCC 35469
EU471997.1 gg_id:292359 francois langur feces clone FL_1aaa02b11
EU472874.1 gg_id:298984 red panda feces clone RPSD_1aaa03c12
EU472807.1 gg_id:293337 red panda feces clone RPSD_1aaa03c08
EU471134.1 gg_id:290740 red panda feces clone RP_3aaa04h08
EU472693.1 gg_id:293094 red panda feces clone RPSD_1aaa04d06
EF620921.1 gg_id:238636 Escherichia coli str. SYW001
EU471242.1 gg_id:293815 red panda feces clone RP_3aaa04h04
EU471056.1 gg_id:302667 red panda feces clone RP_3aaa04h09
GQ007327.1 gg_id:502336 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
AF527826.1 gg_id:71573 Escherichia coli str. RREC II
EU472637.1 gg_id:296080 red panda feces clone RPSD_1aaa03f03
EU470517.1 gg_id:297922 red panda feces clone RP_1aaa02g03
EU458385.1 gg_id:291249 spotted hyena feces clone HY1_a06_1
EU472805.1 gg_id:295661 red panda feces clone RPSD_1aaa01d08
EU472917.1 gg_id:288548 red panda feces clone RPSD_1aaa03c05
GQ047930.1 gg_id:391527 Topographical and Temporal Human Skin Microbiome skin palm clone nbw139b10c
EU472662.1 gg_id:294561 red panda feces clone RPSD_1aaa04b05
EU778485.1 gg_id:305760 Red Panda feces clone RP_1aaa01h12
EU470629.1 gg_id:290610 red panda feces clone RP_1aaa01b03
NC_009800.1 gg_id:245367 Escherichia coli str. HS
FJ950548.1 gg_id:401252 Escherichia coli str. c249
EU470620.1 gg_id:300756 red panda feces clone RP_1aaa02h01
EU472834.1 gg_id:288233 red panda feces clone RPSD_1aaa02g06
EU471158.1 gg_id:289812 red panda feces clone RP_3aaa02c10
GU065251.1 gg_id:535199 Escherichia coli str. BDS3
X80733.1 gg_id:9684 Escherichia
EU472760.1 gg_id:298347 red panda feces clone RPSD_1aaa03e07
GQ008489.1 gg_id:501176 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
EU471035.1 gg_id:291503 red panda feces clone RP_3aaa04d07
EU471245.1 gg_id:288664 red panda feces clone RP_3aaa03f02

CP001063.1	277854	329.8	654.2	1469.2	391.0	342.5	442.4
EU470556.1	293201	1010.5	1108.0	2927.2	1748.2	1690.2	1871.3
EF560788.1	233865	601.3	1030.3	2951.9	739.4	977.3	1057.0
EU471295.1	298340	12508.7	12624.2	10043.4	13384.6	10625.9	9867.7
EU470739.1	289190	197.8	561.8	2148.6	646.7	360.9	862.5
EU468348.1	293649	363.1	540.8	1986.5	688.4	416.0	638.1
GQ031673.1	403434	385.4	799.2	3439.8	807.4	653.0	779.7
EU471240.1	289442	4705.1	5037.4	1814.6	4991.1	7086.2	7197.3
EU470710.1	290311	10373.4	11273.7	11762.8	9962.6	11972.4	10378.0
EU470675.1	301701	895.4	1688.2	3585.9	2695.9	3217.6	3906.0
NC_011740.1	471437	73.3	224.7	481.5	145.0	92.5	200.4
EU471997.1	292359	421.3	708.1	2913.4	983.5	728.3	1355.9
EU472874.1	298984	7297.1	7729.2	8351.1	9510.3	10404.0	9137.7
EU472807.1	293337	418.3	685.0	2556.9	945.1	734.2	1308.3
EU471134.1	290740	2530.3	1936.3	1428.3	1885.9	3765.7	3398.4
EU472693.1	293094	6812.0	6827.8	4866.5	5236.5	5890.2	5870.3
EF620921.1	238636	211.6	451.6	1348.7	1068.6	218.3	968.5
EU471242.1	293815	171.9	323.7	639.5	1016.9	228.0	567.4
EU471056.1	302667	8034.2	8065.8	3256.3	11042.4	10657.6	9640.2
GQ007327.1	502336	5005.5	4476.9	6379.2	4300.9	6540.1	4900.2
AF527826.1	71573	75.5	169.2	150.8	79.2	131.5	63.3
EU472637.1	296080	184.1	486.2	1659.2	695.4	287.0	700.6
EU470517.1	297922	1859.6	1754.8	2554.0	3017.4	1869.5	2810.8
EU458385.1	291249	1079.4	1449.3	1975.7	1698.6	980.2	1892.5
EU472805.1	295661	1594.4	1975.7	3524.1	2438.2	3219.4	3325.8
EU472917.1	288548	5131.1	5017.3	2729.4	4527.5	4087.3	3749.0
GQ047930.1	391527	6534.1	5060.4	3043.7	7167.6	5053.5	5992.5
EU472662.1	294561	1013.5	904.0	1327.9	2086.4	3251.9	2860.5
EU778485.1	305760	1309.2	1064.4	3716.8	2765.8	1308.2	1839.9
EU470629.1	290610	13974.9	13899.8	4827.3	8972.6	12183.7	9917.7
NC_009800.1	245367	710.6	686.7	785.3	480.6	621.3	334.9
FJ950548.1	401252	5350.1	4895.5	2340.1	5014.0	7236.2	5541.6
EU470620.1	300756	1195.0	1460.9	1314.7	2679.7	1777.8	2591.1
EU472834.1	288233	4731.8	4337.4	2950.0	4255.2	3026.9	3527.8
EU471158.1	289812	2353.1	2524.0	1197.9	1827.6	3098.8	3339.0
GU065251.1	535199	3997.1	4419.9	4192.2	2447.0	7682.9	5310.9
X80733.1	9684	755.5	1417.0	1756.2	480.1	3709.2	2486.1
EU472760.1	298347	6587.4	6260.4	4817.4	7178.7	6130.5	6436.6
GQ008489.1	501176	47.4	218.6	640.9	145.5	61.3	144.9
EU471035.1	291503	101.7	319.1	588.0	262.0	366.1	439.8
EU471245.1	288664	601.8	657.7	1511.0	748.2	514.2	810.8

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s__Klebsiella oxytoca	4127
s__Klebsiella oxytoca	4145

DQ819318.1 gg_id:169182 mouse cecal microbiota-colonized zebrafish digestive tract clone aab28d05
EU471044.1 gg_id:297206 red panda feces clone RP_3aaa04h10
NZ_AAKA01000007.1 gg_id:138896 Shigella boydii str. BS512
GQ047653.1 gg_id:418972 Topographical and Temporal Human Skin Microbiome skin palm clone nbw137d03c1
AF527827.1 gg_id:62512 Escherichia coli str. RREC I
EU472717.1 gg_id:301245 red panda feces clone RPSD_1aaa04f12
GQ156189.1 gg_id:535325 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
EU470543.1 gg_id:293816 red panda feces clone RP_1aaa01a09
EU470705.1 gg_id:298055 red panda feces clone RP_1aaa03b10
AM184231.1 gg_id:161699 Shigella boydii str. WAB1890
EU470774.1 gg_id:289364 red panda feces clone RP_2aaa04f07
EU471270.1 gg_id:289897 red panda feces clone RP_3aaa04b12
GQ047626.1 gg_id:430240 Topographical and Temporal Human Skin Microbiome skin palm clone nbw137a04c1
EU470550.1 gg_id:288891 red panda feces clone RP_1aaa01b09
EU470714.1 gg_id:296886 red panda feces clone RP_1aaa02h04
EU472197.1 gg_id:290652 francois langur feces clone FL_2aaa02g07
DQ818739.1 gg_id:173654 mouse cecal microbiota-colonized zebrafish digestive tract clone aab37d01
GQ031721.1 gg_id:428655 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ047960.1 gg_id:432277 Topographical and Temporal Human Skin Microbiome skin palm clone nbw139f02c1
NC_011415.1 gg_id:322518 Escherichia coli str. SE11
NC_011740.1 gg_id:471438 Escherichia fergusonii str. ATCC 35469
EU472904.1 gg_id:300530 red panda feces clone RPSD_1aaa02e02
GQ047656.1 gg_id:430442 Topographical and Temporal Human Skin Microbiome skin palm clone nbw137d07c1
AE014073.1 gg_id:146716 Shigella flexneri 2a str. 2457T
EU471257.1 gg_id:298991 red panda feces clone RP_3aaa02h04
AP009240.1 gg_id:332176 Escherichia coli str. SE11
NC_009801.1 gg_id:241154 Escherichia coli str. E24377A
AF357563.1 gg_id:73454 mpn-isolate group 15
GQ025520.1 gg_id:413814 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
EU472812.1 gg_id:301009 red panda feces clone RPSD_1aaa03f05
EU472915.1 gg_id:291673 red panda feces clone RPSD_1aaa02f08
GQ069064.1 gg_id:438768 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw1
EU470553.1 gg_id:302025 red panda feces clone RP_1aaa04b03
EU708318.1 gg_id:348648 Ewingella americana str. CH6
EU678359.1 gg_id:284672 Ewingella americana str. CH5
U29438.1 gg_id:10324 Ewingella americana str. NCPPB 3905
AY581130.1 gg_id:101409 Ewingella americana B791
EU196321.1 gg_id:246905 Aranicola sp. NP34
AF010251.1 gg_id:10139 Klebsiella granulomatis str. KH 22 d peripheral blood monocytes
AY369139.1 gg_id:94946 Klebsiella pneumoniae
GQ098970.1 gg_id:467551 Topographical and Temporal Human Skin Microbiome skin palm clone nbw504e12c1

DQ819318.1	169182	1806.1	1783.1	1603.4	2114.1	4865.1	4444.2
EU471044.1	297206	3770.1	3696.9	3458.2	4688.7	5607.9	5021.8
NZ_AAKA01000007.1	138896	165.9	510.7	971.9	217.3	154.3	264.3
GQ047653.1	418972	9106.9	9885.5	6801.6	8267.4	7323.8	6672.5
AF527827.1	62512	8072.4	7700.6	5879.2	8195.8	8005.9	7194.3
EU472717.1	301245	195.4	473.4	2968.4	584.1	336.9	1145.6
GQ156189.1	535325	5270.8	4073.9	6059.6	6212.1	7504.9	4451.3
EU470543.1	293816	5767.5	7481.2	4730.0	5326.8	9716.1	8760.6
EU470705.1	298055	2897.1	3127.5	4340.8	2976.7	4055.6	3641.1
AM184231.1	161699	564.1	766.9	3343.0	1281.5	935.9	1317.6
EU470774.1	289364	867.4	716.0	1424.3	2210.3	801.2	1946.4
EU471270.1	289897	6617.9	4244.0	4528.3	9119.1	6509.9	6823.3
GQ047626.1	430240	345.0	601.2	856.4	509.2	397.2	498.2
EU470550.1	288891	433.8	651.3	1178.6	885.0	624.3	644.3
EU470714.1	296886	204.5	374.0	2606.9	844.4	202.5	847.2
EU472197.1	290652	1011.2	1735.3	963.1	1080.3	5312.9	2551.0
DQ818739.1	173654	28.8	138.4	114.7	52.5	72.1	90.0
GQ031721.1	428655	79.4	318.5	632.9	269.5	154.3	196.9
GQ047960.1	432277	3430.5	3775.9	4709.9	2573.0	5114.2	4598.1
NC_011415.1	322518	206.3	562.6	2899.0	734.3	407.2	775.5
NC_011740.1	471438	746.8	781.2	1564.8	595.1	517.7	635.5
EU472904.1	300530	4842.7	3478.9	2733.2	6059.2	4855.1	5143.7
GQ047656.1	430442	2109.7	2068.6	2430.9	3630.9	4016.1	5025.0
AE014073.1	146716	50.6	305.2	1609.9	164.7	85.4	399.9
EU471257.1	298991	11466.4	11659.4	5454.5	10150.0	11261.5	12051.7
AP009240.1	332176	1073.6	931.7	2718.4	1941.8	937.2	1555.6
NC_009801.1	241154	390.0	747.4	1583.7	805.3	896.8	1982.1
AF357563.1	73454	362.9	887.4	2831.5	389.6	602.2	517.6
GQ025520.1	413814	1657.7	2677.9	1723.8	1880.9	4461.2	3356.2
EU472812.1	301009	1129.0	1355.4	3022.1	1601.8	1761.4	1778.9
EU472915.1	291673	9011.3	8440.0	6776.7	7006.2	6243.7	5985.1
GQ069064.1	438768	18179.4	17861.7	19415.9	17227.2	18922.1	17929.1
EU470553.1	302025	206.4	540.8	1475.4	774.0	510.0	628.7
EU708318.1	348648	812.0	916.6	4233.9	1593.7	361.0	777.4
EU678359.1	284672	2726.0	2850.6	5093.4	5419.5	1268.0	3034.7
U29438.1	10324	2609.7	3331.5	6480.0	5991.8	652.0	2432.7
AY581130.1	101409	3123.8	3218.7	3680.6	5644.4	4623.7	5882.4
EU196321.1	246905	398.6	487.3	1660.3	1374.3	113.4	408.3
AF010251.1	10139	541.6	1132.8	5282.4	1068.9	3377.0	1672.1
AY369139.1	94946	798.4	1253.7	2495.7	909.3	2008.9	826.7
GQ098970.1	467551	42.2	203.9	194.7	89.9	62.7	56.6

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AB368777.1 gg_id:284985 Klebsiella pneumoniae
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GQ214541.1 gg_id:554914 Klebsiella pneumoniae str. HDMB-X
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AF394537.1 gg_id:64272 Klebsiella pneumoniae str. 342
CP001891.1 gg_id:527918 Klebsiella variicola str. -22
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CP001891.1 gg_id:527914 Klebsiella variicola str. -22
EF608176.1 gg_id:552087 Klebsiella pneumoniae str. HT24
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DQ185604.1 gg_id:140302 Klebsiella pneumoniae str. Ac01
GQ156091.1 gg_id:550532 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
DQ379507.1 gg_id:153149 Klebsiella pneumoniae str. TSL-4
GQ156048.1 gg_id:578617 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
GU594298.1 gg_id:514480 Klebsiella pneumoniae str. B16

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EF633996.1	244493	45.6	256.5	416.5	88.3	71.9	58.1
AF390083.1	20393	7279.6	7329.5	4900.8	5931.0	7485.7	6346.6
AJ871859.1	113127	1557.7	1820.0	4401.6	1258.1	2707.8	1719.3
AB353046.1	257803	138.5	500.0	2593.4	209.1	120.3	247.8
FJ816026.1	577013	634.7	1037.8	2262.3	643.9	1164.3	495.1
EF633998.1	255739	608.1	1024.0	2751.3	511.8	648.6	987.5
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GQ075941.1	461429	7595.3	10389.3	8618.4	8090.9	9247.8	7761.8
GU119910.1	539869	784.0	1356.2	3369.5	959.2	2315.5	1022.9
GQ098941.1	392581	661.7	1083.8	2770.1	706.2	1113.0	520.1
AF543296.1	58286	45.1	335.0	863.3	93.4	65.0	72.3
AF543283.1	58294	61.2	295.4	1004.1	139.5	77.5	269.4
AJ871861.1	113052	1546.3	1676.5	4116.7	1243.0	2907.0	1704.8
AB004754.1	10108	1046.7	1459.6	3331.5	1969.2	1846.5	824.6
AF319525.3	71572	2814.6	4170.6	9749.8	3328.2	6287.1	4650.6
EU554427.1	272485	437.5	1062.1	3160.0	395.9	186.6	422.7
AJ871862.1	113718	577.7	889.4	1332.3	497.7	1019.5	445.0
AJ871860.1	113819	844.6	1205.3	3261.3	1004.8	1515.7	1109.3
CP000964.1	355056	177.8	429.8	2392.6	621.6	346.4	514.4
EU048272.1	254999	1439.6	1685.8	2963.6	1241.0	2393.2	1291.3
GQ166862.1	585007	66.2	307.2	1306.7	365.9	163.6	253.6
NC_011283.1	339581	218.7	513.9	1960.8	537.8	283.5	376.0
EU078620.1	240372	1588.7	2190.0	4709.6	3422.2	2203.9	2997.9
NC_011283.1	339576	160.7	429.9	1357.8	331.2	503.3	394.0
AB368777.1	284985	217.9	595.1	3059.2	500.8	374.3	592.6
EU240959.1	273616	507.5	965.1	4542.2	1700.6	2833.2	1955.4
FJ593858.1	514856	239.6	708.6	3999.2	678.4	418.8	612.0
GQ214541.1	554914	528.9	1241.3	2728.4	805.1	1233.1	1427.4
EU723828.1	306451	5869.4	4525.0	4153.3	6069.4	2939.9	4841.9
AF394537.1	64272	3470.1	3779.6	6211.9	3941.5	6628.3	6279.2
CP001891.1	527918	193.2	472.2	2078.4	556.5	271.4	441.2
FJ593855.1	516172	70.7	368.9	1268.8	250.3	135.0	276.0
CP001891.1	527914	56.4	160.0	723.2	191.0	89.3	193.6
EF608176.1	552087	10273.2	11917.5	9691.3	11140.4	10435.9	8978.9
GQ155813.1	559700	2821.9	2844.2	5950.8	2974.8	5274.6	5454.4
DQ185604.1	140302	13559.7	12802.3	6632.1	13729.0	17199.9	14605.1
GQ156091.1	550532	381.3	797.0	1384.0	444.3	1799.9	720.5
DQ379507.1	153149	791.0	1053.9	1367.3	2148.3	1796.5	1595.2
GQ156048.1	578617	260.0	659.8	3685.4	813.9	1112.7	1158.1
GU594298.1	514480	575.8	826.6	1445.2	360.0	1498.5	745.2

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EU086097.1 gg_id:241026 Klebsiella pneumoniae str. HR9
EU419756.1 gg_id:258442 Klebsiella pneumoniae str. L17
GQ154831.1 gg_id:582392 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
GQ154786.1 gg_id:554543 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
EU360116.1 gg_id:578618 Klebsiella pneumoniae str. PB24
AF228920.1 gg_id:72626 Klebsiella pneumoniae str. NLEP98-0472
GU594297.1 gg_id:525542 Klebsiella pneumoniae str. A38
GQ497246.1 gg_id:568000 Klebsiella sp. str. A4-1
GQ154902.1 gg_id:587608 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
EU661374.1 gg_id:277703 Klebsiella pneumoniae str. K8
GQ155332.1 gg_id:557261 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
Y11488.1 gg_id:136340 Klebsiella pneumoniae str. AB2844
EU771689.1 gg_id:307981 African elephant feces clone AFEL2_aao29h01
GQ154976.1 gg_id:565044 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
GQ156442.1 gg_id:591675 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
AY292865.1 gg_id:89119 Klebsiella pneumoniae 521
AM184253.1 gg_id:161438 Klebsiella pneumoniae str. WAB1912
EU881978.1 gg_id:350702 Klebsiella pneumoniae str. HDDMN06
GQ154733.1 gg_id:588616 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
NC_012731.1 gg_id:375667 Klebsiella pneumoniae str. NTUH-K2044
EU776082.1 gg_id:319632 Spotted hyena feces clone HY1_f06_2
GQ154886.1 gg_id:584377 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
AY905691.1 gg_id:112401 Klebsiella pneumoniae str. CICC10072
GQ155971.1 gg_id:593698 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
GU374001.1 gg_id:527950 dental caries clone SRC_DSA16
EU435386.1 gg_id:265566 Klebsiella variicola str. V2
GQ155807.1 gg_id:512044 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
GQ155715.1 gg_id:567857 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
EF031070.1 gg_id:215320 Klebsiella sp. CA17
Y11487.1 gg_id:136339 Klebsiella pneumoniae str. ATCC 13883
GQ155784.1 gg_id:534117 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
DQ835530.1 gg_id:243623 Klebsiella oxytoca str. 20
FJ975814.1 gg_id:593892 Human gut microbiome adopts alternative state bowel transplantation ileum effluent
AF511429.1 gg_id:73274 Klebsiella pneumoniae CCCO2
GQ155370.1 gg_id:544564 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
GQ154739.1 gg_id:568190 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
NC_012731.1 gg_id:375666 Klebsiella pneumoniae str. NTUH-K2044
GQ155329.1 gg_id:570828 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
GQ154908.1 gg_id:510655 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
DQ379506.1 gg_id:151643 Klebsiella pneumoniae str. TSL-2
AY114159.1 gg_id:63980 Klebsiella pneumoniae str. 402-2

EU086097.1	241026	234.1	528.2	1392.4	427.9	1825.4	829.6
EU419756.1	258442	131.0	535.9	1405.7	331.7	617.4	469.4
GQ154831.1	582392	957.2	1204.5	4801.3	1592.2	1537.4	2436.5
GQ154786.1	554543	5161.9	4796.0	8989.2	8138.6	7498.9	7344.3
EU360116.1	578618	175.0	617.3	1983.0	199.0	181.3	145.1
AF228920.1	72626	1796.8	1874.7	3776.5	2141.8	3606.5	3414.7
GU594297.1	525542	989.3	983.1	3290.2	1198.3	2615.8	1943.9
GQ497246.1	568000	522.3	1361.2	5088.9	1091.1	2515.6	1809.3
GQ154902.1	587608	1327.5	1540.2	5266.2	2178.1	2217.9	3050.2
EU661374.1	277703	275.0	721.3	2327.3	326.2	308.4	331.0
GQ155332.1	557261	6873.1	5034.0	3657.7	6915.7	6816.6	6202.0
Y11488.1	136340	1988.0	2694.0	3535.6	2204.0	3553.3	3338.6
EU771689.1	307981	158.8	304.5	385.3	320.9	134.0	179.9
GQ154976.1	565044	692.5	1207.5	7716.4	1393.0	2326.7	1557.3
GQ156442.1	591675	321.1	1094.1	2886.4	696.1	2535.7	1469.5
AY292865.1	89119	939.7	975.1	3826.8	1127.9	2376.7	2168.3
AM184253.1	161438	1152.1	1150.1	2670.6	1057.0	1783.5	1354.3
EU881978.1	350702	219.0	641.6	2725.7	707.7	602.1	638.8
GQ154733.1	588616	5023.3	5501.8	6569.4	4778.2	10886.1	9229.7
NC_012731.1	375667	264.9	754.0	2264.5	426.8	752.5	545.0
EU776082.1	319632	3112.9	5945.5	5793.5	5016.3	2889.9	4006.7
GQ154886.1	584377	317.9	816.0	2623.1	439.4	1170.9	854.8
AY905691.1	112401	8163.0	7812.4	3772.8	6745.8	7087.3	6814.0
GQ155971.1	593698	149.6	562.6	2953.8	619.5	251.2	358.4
GU374001.1	527950	319.0	844.2	1427.3	330.2	203.0	746.7
EU435386.1	265566	3476.2	3156.2	10697.3	5752.6	6839.7	8015.3
GQ155807.1	512044	1060.5	1261.3	4804.0	1203.5	2406.1	1881.0
GQ155715.1	567857	4021.9	3336.8	5607.4	4388.7	7621.6	5634.6
EF031070.1	215320	53.7	87.6	46.5	120.9	179.7	201.8
Y11487.1	136339	3134.1	2718.7	5004.6	4425.0	5725.3	3056.0
GQ155784.1	534117	1219.6	1884.1	4985.0	2538.8	8182.9	7508.1
DQ835530.1	243623	319.5	822.3	2652.2	679.6	810.5	677.2
FJ975814.1	593892	9603.5	11174.2	6273.9	7512.6	9681.5	7616.9
AF511429.1	73274	200.4	566.3	2265.1	337.9	243.2	471.5
GQ155370.1	544564	3845.2	4075.6	9830.3	3038.1	8277.7	8999.0
GQ154739.1	568190	4065.1	2733.5	7443.0	6317.0	3168.9	3035.3
NC_012731.1	375666	446.9	850.3	2632.8	550.4	1457.0	895.6
GQ155329.1	570828	4576.6	4203.4	5350.3	4885.4	7497.3	4957.8
GQ154908.1	510655	1209.9	1342.8	5182.0	2426.8	3386.6	2967.1
DQ379506.1	151643	1040.8	1031.0	3259.8	1177.0	2678.2	1942.0
AY114159.1	63980	411.4	839.0	1683.5	546.4	1298.4	1097.1

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EU036754.1 gg_id:327015 Klebsiella sp. str. SA07
GQ154799.1 gg_id:540518 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
NC_012731.1 gg_id:375670 Klebsiella pneumoniae str. NTUH-K2044
GU227150.1 gg_id:584676 Klebsiella oxytoca str. A9-2
GU193983.1 gg_id:584760 Klebsiella pneumoniae str. IITRBL3
AB072699.1 gg_id:76366 Klebsiella pneumoniae F-5-2
GQ154948.1 gg_id:578178 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
GQ155672.1 gg_id:535765 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
EU352755.1 gg_id:269092 Klebsiella pneumoniae str. NK 2.bp-1
NC_012731.1 gg_id:375669 Klebsiella pneumoniae str. NTUH-K2044
AF390084.1 gg_id:37558 Klebsiella pneumoniae str. DM-5
FJ422735.1 gg_id:367184 Klebsiella pneumoniae str. 2N3
FJ222552.1 gg_id:354585 Klebsiella pneumoniae str. MR-M1
GQ154979.1 gg_id:513309 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
GQ154789.1 gg_id:590681 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
EU661373.1 gg_id:279251 Klebsiella pneumoniae str. K11
AF453251.1 gg_id:44635 Klebsiella pneumoniae str. ASR1
GQ156110.1 gg_id:539997 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
X93214.1 gg_id:10144 Klebsiella pneumoniae str. DSM 30102
GQ154895.1 gg_id:593574 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
EF154517.1 gg_id:189557 Klebsiella sp. str. CW-D
GQ156187.1 gg_id:560253 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
DQ226215.1 gg_id:142418 Klebsiella oxytoca DR.Y14
GQ166865.1 gg_id:583479 Klebsiella pneumoniae str. EB55-THQ
AY598354.1 gg_id:109687 Klebsiella pneumoniae str. MCM B-325
GQ154945.1 gg_id:585107 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
GQ154754.1 gg_id:575147 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
AF130981.1 gg_id:32663 Klebsiella pneumoniae str. ATCC13883
DQ444287.1 gg_id:153811 Klebsiella pneumoniae str. 2
GQ155333.1 gg_id:558921 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
AB004752.1 gg_id:10135 Serratia liquefaciens str. JCM1245
EU333881.1 gg_id:259427 Klebsiella granulomatis str. K22-14
GU339255.1 gg_id:532790 Klebsiella pneumoniae str. EH25
GQ155711.1 gg_id:589879 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
CP001891.1 gg_id:527920 Klebsiella variicola str. -22
FJ975784.1 gg_id:564752 Human gut microbiome adopts alternative state bowel transplantation ileum effluent
Y17668.1 gg_id:10149 Klebsiella pneumoniae str. Klebs313
EU661378.1 gg_id:278276 Klebsiella pneumoniae str. K42
GQ154950.1 gg_id:510291 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
GQ156083.1 gg_id:588769 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
EF551363.1 gg_id:222010 Raoultella planticola str. Rs-2

EU036754.1	327015	1109.1	1220.2	5074.1	1206.9	3233.6	1696.8
GQ154799.1	540518	1014.8	1273.5	4443.3	1520.5	2870.0	2413.8
NC_012731.1	375670	144.5	420.8	1034.0	194.9	258.6	194.5
GU227150.1	584676	9036.9	7500.4	5888.3	6945.3	13310.5	9986.2
GU193983.1	584760	1549.7	2101.9	1716.5	2282.2	2993.6	2570.4
AB072699.1	76366	7584.1	7719.8	7183.2	6775.7	7160.5	5884.0
GQ154948.1	578178	1495.3	1729.8	5094.6	1728.4	3536.8	3054.6
GQ155672.1	535765	5273.4	4723.4	8993.7	5013.1	8328.1	6257.2
EU352755.1	269092	12294.5	14103.6	11103.5	10725.7	14674.7	12325.3
NC_012731.1	375669	998.6	1006.6	2643.5	1082.2	1987.9	1366.0
AF390084.1	37558	275.2	729.0	1716.3	533.5	1952.9	905.2
FJ422735.1	367184	1392.5	1307.6	1345.9	1049.2	1165.2	1192.3
FJ222552.1	354585	65.2	255.9	689.9	95.8	185.7	111.8
GQ154979.1	513309	415.1	912.2	3845.0	1354.9	604.6	645.4
GQ154789.1	590681	679.5	1236.3	6864.3	1392.8	2368.3	1480.7
EU661373.1	279251	1049.8	926.0	3144.7	1124.8	1988.1	1488.4
AF453251.1	44635	11688.9	12440.3	8199.3	10869.4	11615.9	10522.3
GQ156110.1	539997	2469.3	2759.4	5527.5	2595.3	4020.3	4905.8
X93214.1	10144	1043.5	1077.1	2971.8	1193.6	2624.9	2194.4
GQ154895.1	593574	4953.8	3492.6	8486.7	7365.8	4493.8	5079.9
EF154517.1	189557	78.7	135.3	125.1	173.0	769.8	357.9
GQ156187.1	560253	3649.4	3296.5	11645.5	5683.0	7796.5	6293.8
DQ226215.1	142418	10845.7	12618.9	5240.3	7319.3	8805.1	8066.0
GQ166865.1	583479	239.8	474.1	1264.0	506.6	509.4	385.9
AY598354.1	109687	1193.1	1132.3	2721.4	1044.3	1826.2	1396.2
GQ154945.1	585107	979.7	1077.6	6322.5	1826.5	2585.5	2351.7
GQ154754.1	575147	269.9	562.6	2312.2	654.8	1260.5	1011.2
AF130981.1	32663	1039.2	1309.3	1611.2	636.2	7266.6	2495.9
DQ444287.1	153811	204.4	512.8	1002.9	321.2	1278.8	534.3
GQ155333.1	558921	2044.0	2152.7	5341.7	1296.2	3227.7	3138.3
AB004752.1	10135	283.4	706.5	3489.5	1182.9	5537.2	2462.8
EU333881.1	259427	3807.5	3715.6	10000.3	6123.5	6506.9	8536.6
GU339255.1	532790	185.1	509.8	1046.5	254.3	234.5	160.1
GQ155711.1	589879	1066.9	1257.8	4935.4	1331.5	2401.5	1893.5
CP001891.1	527920	2154.6	2426.5	2864.3	2635.1	2683.3	2406.0
FJ975784.1	564752	3470.6	2594.1	4717.2	4176.9	4098.6	2928.3
Y17668.1	10149	412.5	844.6	982.3	295.6	1270.4	962.9
EU661378.1	278276	1912.2	1637.9	3539.0	1998.8	2748.5	2829.5
GQ154950.1	510291	1715.7	1414.8	4434.1	1708.7	1515.3	2278.9
GQ156083.1	588769	41.5	168.1	783.2	230.4	300.1	142.4
EF551363.1	222010	426.1	819.2	2599.0	545.7	1451.3	1136.7

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s__unclassified	6192
s__Leclercia adecarboxylata	4908
s__Leclercia adecarboxylata	5803

EU128493.1 gg_id:238762 Klebsiella pneumoniae str. SWU-27
GQ156192.1 gg_id:575548 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
NC_012731.1 gg_id:375665 Klebsiella pneumoniae str. NTUH-K2044
GQ154748.1 gg_id:556070 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
GQ155398.1 gg_id:579246 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
DQ837568.1 gg_id:168382 Klebsiella sp. III
EU734822.1 gg_id:349243 Pseudomonas aeruginosa str. NBRAJG90
GQ155863.1 gg_id:539970 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
GQ155396.1 gg_id:509168 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
EF091148.1 gg_id:213635 Klebsiella pneumoniae str. 99
EF566882.1 gg_id:273896 Klebsiella pneumoniae
FJ947063.1 gg_id:512541 Klebsiella pneumoniae str. fJ1
GQ155406.1 gg_id:572306 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
AY660026.2 gg_id:123487 Xenorhabdus poinarii
NC_012731.1 gg_id:375668 Klebsiella pneumoniae str. NTUH-K2044
CP001891.1 gg_id:527919 Klebsiella variicola str. -22
GQ154942.1 gg_id:575251 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
GQ155346.1 gg_id:542868 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
FJ975804.1 gg_id:548574 Human gut microbiome adopts alternative state bowel transplantation ileum effluent
EU078621.1 gg_id:251954 Klebsiella pneumoniae str. HR16
FJ593857.1 gg_id:532313 Klebsiella sp. str. AL060224_03
EU360793.1 gg_id:262483 Klebsiella pneumoniae str. ECU-21
GQ155955.1 gg_id:536479 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
FJ975797.1 gg_id:593596 Human gut microbiome adopts alternative state bowel transplantation ileum effluent
GQ155996.1 gg_id:571066 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
GQ155800.1 gg_id:537085 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
GQ155680.1 gg_id:590210 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
GQ155924.1 gg_id:590080 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
NC_012731.1 gg_id:375671 Klebsiella pneumoniae str. NTUH-K2044
GQ154887.1 gg_id:511908 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
EF127829.1 gg_id:197404 Klebsiella oxytoca str. LF-1
GQ155740.1 gg_id:512312 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
FJ436718.1 gg_id:358763 Klebsiella pneumoniae str. FIUMS1
GQ155340.1 gg_id:511148 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
GQ155822.1 gg_id:513383 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
AJ233420.1 gg_id:27939 Klebsiella pneumoniae str. DSM 30104
DQ223868.1 gg_id:166493 Kluyvera intermedia str. P3
NR_028802.1 gg_id:564215 Kluyvera intermedia str. 256; ATCC 33110
NR_028803.1 gg_id:573005 Kluyvera cryocrescens str. 12993; ATCC 33435
AJ277978.1 gg_id:22764 Leclercia adecarboxylata str. WG 162
AY451327.1 gg_id:99716 Leclercia adecarboxylata str. TERIPS4040

EU128493.1	238762	2253.3	1889.4	3671.2	2096.1	2322.9	1914.5
GQ156192.1	575548	403.4	711.0	1242.9	430.8	1801.7	712.2
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GQ154748.1	556070	2549.4	3056.1	4184.9	2322.2	4478.6	3705.1
GQ155398.1	579246	1130.8	1756.8	2406.3	2336.1	4216.4	3372.8
DQ837568.1	168382	1231.0	1997.3	1468.5	1076.2	5571.2	2697.7
EU734822.1	349243	10900.0	12631.4	5553.2	10608.2	11724.4	11710.7
GQ155863.1	539970	177.9	694.4	3814.8	739.9	591.3	727.3
GQ155396.1	509168	709.1	939.4	2406.2	784.0	4422.0	1682.3
EF091148.1	213635	180.9	633.1	3284.6	695.9	579.2	677.5
EF566882.1	273896	1067.0	1033.9	2541.0	1103.9	1858.6	1349.3
FJ947063.1	512541	329.9	824.9	3150.3	555.2	1202.1	780.4
GQ155406.1	572306	783.6	949.1	2849.7	1998.2	1955.6	3135.0
AY660026.2	123487	3006.0	3837.4	3304.6	2805.6	3662.3	3800.6
NC_012731.1	375668	306.6	709.1	2960.5	575.7	1426.3	1024.0
CP001891.1	527919	699.5	3035.3	2916.0	887.8	786.6	2793.3
GQ154942.1	575251	5675.6	6144.8	5136.4	4297.3	7459.0	4736.1
GQ155346.1	542868	1043.5	1237.2	4371.8	1498.6	2849.3	2384.3
FJ975804.1	548574	11460.5	9783.8	7004.2	11360.3	13694.1	9815.3
EU078621.1	251954	259.0	650.0	1791.6	594.1	1750.7	976.5
FJ593857.1	532313	493.2	1120.6	5052.9	1053.7	986.4	743.4
EU360793.1	262483	338.4	845.6	1169.7	187.4	1496.9	886.9
GQ155955.1	536479	311.0	462.6	1065.4	482.4	418.0	1447.1
FJ975797.1	593596	122.1	507.1	2947.8	778.0	217.1	482.9
GQ155996.1	571066	7915.4	7616.2	6478.9	6158.3	6177.0	5311.5
GQ155800.1	537085	9217.1	9265.7	8228.4	7864.1	9721.2	9079.5
GQ155680.1	590210	3384.8	3299.3	4533.8	3710.9	6759.6	4973.1
GQ155924.1	590080	225.2	728.6	3153.4	772.0	578.2	673.0
NC_012731.1	375671	330.7	639.5	1534.0	496.2	2403.7	773.4
GQ154887.1	511908	2348.6	2122.0	2026.1	1719.5	2832.2	3791.7
EF127829.1	197404	98.0	535.4	1765.6	334.9	103.0	139.5
GQ155740.1	512312	2426.2	2504.2	5678.6	2629.2	5180.3	5280.7
FJ436718.1	358763	1085.3	1009.1	2553.9	1021.2	1774.5	1358.1
GQ155340.1	511148	1868.3	2232.6	5371.4	1900.0	4522.5	3722.6
GQ155822.1	513383	237.5	796.9	1216.4	215.4	172.5	172.7
AJ233420.1	27939	800.3	971.4	2079.8	712.4	598.8	832.7
DQ223868.1	166493	57.6	253.8	2283.5	173.2	92.6	397.8
NR_028802.1	564215	961.1	1376.9	4500.8	2758.8	1731.6	1068.8
NR_028803.1	573005	63.9	124.3	2842.4	204.2	70.2	318.9
AJ277978.1	22764	1176.2	1437.0	3358.2	2432.6	3527.3	2291.4
AY451327.1	99716	112.9	471.1	1398.1	163.5	93.9	384.7

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AM184272.1 gg_id:161078 Pantoea agglomerans str. WAB1933
AJ853891.1 gg_id:108534 Enterobacter ludwigii str. EN-119 = DSMZ 16688
AF157695.1 gg_id:10087 Enterobacter cloacae str. drh3
AY335552.1 gg_id:137221 Pantoea agglomerans str. CBNU-14-1
AJ232240.1 gg_id:10085 isolate: SS-Unknown-1129 clone
FJ592988.1 gg_id:432552 Pantoea agglomerans str. SB-2
EU302838.1 gg_id:247855 Pantoea sp. str. DAP13
AJ276393.1 gg_id:71494 Leclercia adecarboxylata str. LBV 449
DQ011248.1 gg_id:136462 genes Da Qing Oil field microbial indicates presence variety sulfate-reducing fermen
AM184263.1 gg_id:161505 Pantoea agglomerans str. WAB1924
FJ587505.1 gg_id:586247 Pantoea sp. str. C-4-1
FJ593002.1 gg_id:447010 Pantoea agglomerans str. ST-1
GQ337696.1 gg_id:568247 Enterobacter aerogenes str. S18
AF511434.1 gg_id:65397 Enterobacter cloacae CCCO10
FN555402.1 gg_id:509744 Pantoea sp. I-Bh20-21
FM210031.1 gg_id:334606 Enterobacter cancerogenus str. T2P18
EF428996.1 gg_id:208785 Pantoea agglomerans str. GIST-CPs1
AY691545.1 gg_id:103577 Pantoea agglomerans str. ChDC YP3
GQ280809.1 gg_id:567944 Enterobacter sp. str. PE-R
FJ950684.1 gg_id:408750 Enterobacter ludwigii str. d44
EU590682.1 gg_id:258931 Pantoea agglomerans str. BH-18
AM184264.1 gg_id:161559 Pantoea agglomerans str. WAB1925
AB004691.1 gg_id:10075 Pantoea agglomerans str. JCM1236
AY488028.1 gg_id:99221 Enterobacter sp. str. BL-2
EU557027.1 gg_id:266569 Enterobacter ludwigii str. KU201-3
GQ070505.1 gg_id:376025 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw:
EF011164.1 gg_id:192215 Enterobacter hormaechei str. PT4
DQ011253.1 gg_id:132962 stratum sewage clone 6
EU302840.1 gg_id:257817 Pantoea sp. str. DAP15
FM210030.1 gg_id:306906 Enterobacter cancerogenus str. R27c
EF429005.1 gg_id:211593 Pantoea agglomerans str. GIST-Out2
GQ374474.1 gg_id:533493 Pantoea agglomerans str. GS2
AY792266.1 gg_id:123510 Humic Lake clone CrystalBog5A11
AM184254.1 gg_id:160936 Pantoea agglomerans str. WAB1913
AM184266.1 gg_id:161444 Pantoea agglomerans str. WAB1927
EU884395.1 gg_id:368993 Enterobacter cloacae str. XA-2
GQ478022.1 gg_id:570352 Enterobacter cloacae str. ham3
EU164545.1 gg_id:239199 Enterobacter hormaechei 4
AY900169.1 gg_id:142410 Pantoea agglomerans str. PCA0067
AF199029.1 gg_id:27763 Pantoea agglomerans str. SP1
GQ284566.1 gg_id:547400 Enterobacter ludwigii str. AR1.22

AM184272.1	161078	4127.6	4321.8	5011.8	4781.2	6361.3	3538.3
AJ853891.1	108534	1138.8	1316.8	2308.0	1887.7	2908.3	1791.8
AF157695.1	10087	162.6	559.6	1522.8	296.5	513.2	239.1
AY335552.1	137221	1130.6	1891.9	2225.1	1099.5	5448.0	2876.6
AJ232240.1	10085	5161.9	5508.5	5846.6	6068.9	3849.5	5239.9
FJ592988.1	432552	996.8	1114.6	2583.0	831.3	1161.8	977.4
EU302838.1	247855	818.5	1275.4	2068.1	771.9	3921.8	1933.4
AJ276393.1	71494	3094.5	3344.5	6728.6	4232.5	4651.9	4461.2
DQ011248.1	136462	830.8	1045.7	1306.3	1174.8	3402.0	3618.7
AM184263.1	161505	1602.7	1892.1	4361.5	2742.6	2182.1	2036.6
FJ587505.1	586247	162.6	556.1	1882.1	438.2	533.7	266.0
FJ593002.1	447010	1007.3	1268.1	2728.4	1927.7	1755.9	754.7
GQ337696.1	568247	5170.0	7534.5	4826.7	5357.2	8997.1	6326.2
AF511434.1	65397	203.3	662.1	1753.0	487.5	575.7	345.4
FN555402.1	509744	365.2	737.6	1351.7	368.9	1188.5	574.1
FM210031.1	334606	2804.1	2775.6	6207.4	3897.2	3565.2	3811.4
EF428996.1	208785	981.5	1261.3	2061.3	2114.0	2329.2	1481.6
AY691545.1	103577	971.3	1058.4	2206.8	1914.6	1164.6	998.5
GQ280809.1	567944	2821.4	3840.9	2476.9	3727.8	3722.5	3366.4
FJ950684.1	408750	1138.9	1325.8	2414.9	2005.9	2934.6	1751.8
EU590682.1	258931	763.0	1097.0	5477.6	1444.6	1923.2	2072.1
AM184264.1	161559	200.2	541.8	1702.5	458.5	945.9	362.6
AB004691.1	10075	1052.3	1130.6	1975.8	1175.9	2460.0	1567.8
AY488028.1	99221	3472.6	3788.3	5141.2	3942.5	5215.6	4086.3
EU557027.1	266569	794.9	982.5	1026.8	1852.6	2157.9	1571.0
GQ070505.1	376025	1083.1	1320.2	3137.0	2362.3	3517.7	2127.9
EF011164.1	192215	9624.2	9017.6	6355.9	9995.6	17168.9	13490.8
DQ011253.1	132962	1070.6	1422.7	2445.6	1978.2	1826.5	800.6
EU302840.1	257817	225.1	547.2	644.0	255.3	982.1	715.0
FM210030.1	306906	185.7	622.8	1998.2	565.5	584.3	401.9
EF429005.1	211593	1403.8	1463.5	2190.8	1281.8	1294.5	1629.2
GQ374474.1	533493	2788.4	1346.8	3119.3	2720.4	1066.5	1487.3
AY792266.1	123510	132.6	503.3	863.2	168.6	263.3	133.1
AM184254.1	160936	2138.9	1864.0	3454.2	2611.1	2335.4	1911.6
AM184266.1	161444	113.5	706.1	1315.2	229.1	88.3	186.4
EU884395.1	368993	867.9	1238.9	3594.2	2366.6	1731.8	1545.3
GQ478022.1	570352	165.5	527.0	1628.0	545.3	477.9	396.5
EU164545.1	239199	4093.2	2608.6	1252.6	3722.6	6289.4	4907.5
AY900169.1	142410	841.3	1060.5	1833.7	743.8	2601.3	1648.3
AF199029.1	27763	2373.4	3003.7	4255.8	1480.6	4378.0	3037.8
GQ284566.1	547400	781.4	987.9	4124.3	1482.7	1680.7	2700.0

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AY691544.1 gg_id:103441 Pantoea agglomerans str. ChDC YP2
DQ011254.1 gg_id:136479 genes Da Qing Oil field microbial indicates presence variety sulfate-reducing fermen
GQ374471.1 gg_id:570229 Pantoea agglomerans str. XJ1
GQ856082.1 gg_id:556086 Leclercia adecarboxylata str. LMG 2803
EF446899.1 gg_id:205646 Pantoea agglomerans str. AT2
DQ392984.1 gg_id:156431 Pantoea agglomerans str. e
GU166185.1 gg_id:558052 intestinal tract larvae (Musca domestica) direct cloning and sequencing genes whea
DQ358125.1 gg_id:163102 Morganella morganii str. AP28
AB089243.1 gg_id:83678 Morganella morganii str. JCM1672
AY043168.1 gg_id:40697 Morganella morganii
DQ358138.1 gg_id:162198 Morganella psychrotolerans str. U2/6
AB099401.1 gg_id:85614 Proteus vulgaris str. AU34
AY792272.1 gg_id:121180 Humic Lake clone CrystalBog1F6
AY616166.1 gg_id:104851 Pantoea agglomerans str. TJA 98.VII.6
GU338400.1 gg_id:544871 Pantoea ananatis str. E-1-4
DQ068767.1 gg_id:168031 Pantoea sp. str. Co9945
EF688011.1 gg_id:330341 Pantoea deleyii str. LMG 24200
AY530796.1 gg_id:104588 Pantoea ananatis str. PA 4
AY924374.1 gg_id:114198 Pantoea agglomerans str. Sc-1
AY741162.1 gg_id:163464 Pantoea agglomerans str. S33
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AY898642.1 gg_id:112237 Pantoea ananatis str. BD 435
GQ332198.1 gg_id:534397 Pantoea ananatis str. M408
AB033602.1 gg_id:9868 Pantoea agglomerans
GQ383918.1 gg_id:592050 Pantoea ananatis str. 4CBJ1
FJ611846.1 gg_id:509337 Pantoea ananatis str. LMG 2676
GU324264.1 gg_id:591038 Pantoea ananatis str. M471
EF602556.1 gg_id:228308 Pantoea ananatis str. ESS29
FJ611812.1 gg_id:585566 Pantoea ananatis str. ATCC 27995
FJ611861.1 gg_id:589121 Pantoea oleae str. CFBP 6632
DQ129257.1 gg_id:152527 microarray level air two cities Texas urban aerosol clone AKIW987
AF130949.1 gg_id:9937 Pantoea agglomerans str. A87
AF130918.1 gg_id:9921 Pantoea agglomerans str. new*47con
DQ365569.1 gg_id:148250 Pantoea ananatis str. JA04
EU849107.1 gg_id:351329 Pantoea agglomerans str. PSB-UJ2-21
AF130917.1 gg_id:9920 Pantoea agglomerans str. A46
FJ611831.1 gg_id:537318 Pantoea agglomerans str. P9QLB
AY941838.1 gg_id:114491 Pantoea agglomerans str. XW123
EF516970.1 gg_id:218720 grassland soil clone FCPS402
AF130932.1 gg_id:9887 Pantoea agglomerans str. A62
GQ367483.1 gg_id:557905 Pantoea sp. str. A18/07

AY691544.1	103441	1470.6	2397.3	1338.2	1771.0	4001.9	2875.9
DQ011254.1	136479	5970.5	4790.1	2277.6	3907.2	7079.0	6252.4
GQ374471.1	570229	227.7	716.1	1390.9	305.1	545.7	319.9
GQ856082.1	556086	1273.8	1543.2	3631.4	2443.5	3525.0	2339.4
EF446899.1	205646	1418.4	1717.1	4071.5	1841.5	1740.0	2286.6
DQ392984.1	156431	2800.3	2892.6	3669.7	4679.4	5473.8	3273.5
GU166185.1	558052	1984.1	1608.3	2633.9	3494.9	2099.1	3542.8
DQ358125.1	163102	341.3	632.3	1993.6	1034.2	2097.1	1587.9
AB089243.1	83678	4171.6	5578.9	4589.3	6556.7	7969.7	8071.2
AY043168.1	40697	15136.4	14580.6	9824.2	12300.0	16209.2	13687.6
DQ358138.1	162198	228.1	400.6	5264.6	1482.9	384.9	489.0
AB099401.1	85614	30.8	143.4	238.5	127.0	73.3	104.4
AY792272.1	121180	92.6	496.1	2323.8	194.4	109.0	440.6
AY616166.1	104851	4208.6	4469.7	8727.5	4891.5	5953.7	5722.6
GU338400.1	544871	216.3	372.9	1770.1	378.3	1482.7	418.2
DQ068767.1	168031	9718.4	8052.7	7889.5	7933.1	6198.9	7544.9
EF688011.1	330341	491.8	1001.8	2384.2	1244.0	939.7	1628.8
AY530796.1	104588	9995.0	9821.2	8197.0	10287.3	14005.8	10260.5
AY924374.1	114198	1947.3	1428.1	3970.4	1425.1	1230.1	1938.7
AY741162.1	163464	3540.7	3551.7	5872.3	2768.4	7537.7	3733.9
EU072497.1	239619	1546.0	2845.5	1089.8	1412.9	2382.3	2245.5
AY898642.1	112237	14698.2	15150.3	14130.5	12383.6	17062.0	15139.2
GQ332198.1	534397	803.7	1285.6	2611.4	1069.4	2510.9	1223.4
AB033602.1	9868	1487.3	827.8	760.6	1112.7	1565.9	1241.0
GQ383918.1	592050	8099.0	9021.9	6311.2	6653.2	9264.9	7042.6
FJ611846.1	509337	178.7	343.1	1621.9	320.5	186.5	342.7
GU324264.1	591038	158.1	469.2	1264.0	275.0	194.8	339.4
EF602556.1	228308	17276.0	18087.9	13142.6	15190.6	21225.9	17981.8
FJ611812.1	585566	979.9	861.3	2092.6	502.7	557.4	1026.9
FJ611861.1	589121	1129.6	952.1	1773.8	2537.2	636.8	766.9
DQ129257.1	152527	28.4	26.9	62.2	60.8	46.7	55.5
AF130949.1	9937	1219.0	2387.7	3099.2	1352.8	2386.0	4408.1
AF130918.1	9921	1976.7	2498.3	3053.1	1686.8	3136.8	3002.1
DQ365569.1	148250	1503.2	1958.7	1738.6	666.2	5147.5	2147.2
EU849107.1	351329	1081.0	1223.1	1722.0	476.4	1225.5	730.0
AF130917.1	9920	1526.5	1435.6	2492.2	1829.1	1945.3	3027.9
FJ611831.1	537318	672.4	1125.2	4757.4	799.2	850.7	1695.1
AY941838.1	114491	5425.8	6666.9	3818.1	5475.2	8298.8	6848.0
EF516970.1	218720	10.1	12.7	11.8	38.3	55.7	10.2
AF130932.1	9887	4384.5	4693.6	4444.8	3654.9	6132.2	5142.9
GQ367483.1	557905	122.9	239.0	1301.7	182.5	148.9	776.2

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o__Enterobacteriales	f__Enterobacteriaceae
o__Enterobacteriales	f__Enterobacteriaceae
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s__unclassified	4909
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s__unclassified	6129
s__unclassified	6188
s__unclassified	6194
s__unclassified	7630
s__Pectobacterium atrosepticum	4508
s__Pectobacterium atrosepticum	5992
s__Pectobacterium wasabiae	4216
s__Pectobacterium wasabiae	4445
s__Pectobacterium wasabiae	5028

AF130952.2 gg_id:9896 Pantoea agglomerans str. A92
AF130929.1 gg_id:9926 Pantoea agglomerans str. A59
DQ065752.1 gg_id:132248 Pantoea agglomerans str. I10
FJ999930.1 gg_id:560342 Pantoea agglomerans str. EQH1
AF130940.1 gg_id:9931 Pantoea agglomerans str. A72
AF130931.1 gg_id:9927 Pantoea agglomerans str. A61
AF130899.1 gg_id:9913 Pantoea agglomerans str. A21
FN421660.1 gg_id:578714 proteogenomics physiology phyllosphere soybean clone 14_E10
AF130961.1 gg_id:9897 Pantoea agglomerans str. A9
AY092079.1 gg_id:67501 Pantoea agglomerans str. 732
AF130930.1 gg_id:9886 Pantoea agglomerans str. A60
EF050809.1 gg_id:175147 Pantoea agglomerans str. PGHL10
FJ611807.1 gg_id:563259 Pantoea agglomerans str. ACW 55802
AF130943.1 gg_id:9892 Pantoea agglomerans str. A77
FJ592987.1 gg_id:433061 Pantoea agglomerans str. SB-1
AY679762.1 gg_id:102249 USA: Hawaii clone Nv5.2
AJ251466.1 gg_id:73786 Pantoea agglomerans str. NCTC9381T
AM234150.1 gg_id:153891 Pantoea agglomerans str. IZSPGC
U80202.1 gg_id:9906 Pantoea agglomerans str. ATCC 33243
AF130905.1 gg_id:9914 Pantoea agglomerans str. A27
AF130939.1 gg_id:9891 Pantoea agglomerans str. A71
AM293681.1 gg_id:256894 Pantoea agglomerans str. PTA-AF2
FJ611835.1 gg_id:564421 Pantoea agglomerans str. LMG 2595
EU379306.1 gg_id:266034 Pantoea agglomerans str. 6R-J-7b
AF130926.1 gg_id:9924 Pantoea agglomerans str. A56
GQ169378.1 gg_id:537971 Pantoea eucalypti str. IEXa
FJ999950.1 gg_id:561323 Pantoea agglomerans str. EQH21
AF130935.1 gg_id:9890 Pantoea agglomerans str. A67
FM202484.1 gg_id:345858 Pantoea agglomerans str. EV2
AF130933.1 gg_id:9888 Pantoea agglomerans str. A63
EU598802.1 gg_id:267618 Pantoea agglomerans
GQ225111.1 gg_id:584259 Pantoea agglomerans str. NBRISRM
AF130942.1 gg_id:9933 Pantoea agglomerans str. A74
GQ130025.1 gg_id:463204 Genetic inventory 'JPL-SAF' during MSL mission spacecraft assembly clean room floc
AM184091.1 gg_id:155126 Pantoea agglomerans str. 45
FM202485.1 gg_id:322033 Pantoea agglomerans str. EV3
NC_004547.2 gg_id:471486 Pectobacterium atrosepticum str. SCRI1043
NC_004547.2 gg_id:471485 Pectobacterium atrosepticum str. SCRI1043
EF530546.1 gg_id:221979 Pectobacterium wasabiae str. NZEC8974
EF178667.1 gg_id:178973 Pectobacterium wasabiae str. NZEC12
EF178665.1 gg_id:193423 Pectobacterium wasabiae str. NZEC9

AF130952.2	9896	4447.4	5732.9	5713.2	3835.6	5263.5	4907.4
AF130929.1	9926	4142.4	5102.8	3560.8	3632.6	5131.7	5364.1
DQ065752.1	132248	127.2	327.5	2104.2	243.8	730.1	380.6
FJ999930.1	560342	4837.4	4310.1	4350.3	4337.9	5416.2	4832.7
AF130940.1	9931	4358.8	4661.6	3499.4	3568.9	4627.2	6113.7
AF130931.1	9927	11362.0	11013.1	7422.7	9321.4	13231.9	10774.5
AF130899.1	9913	4711.0	5011.9	5113.6	3829.5	4619.8	4306.8
FN421660.1	578714	677.8	797.7	3286.3	1535.0	852.6	780.6
AF130961.1	9897	3402.0	3871.7	2996.7	2486.5	3041.4	2618.3
AY092079.1	67501	1214.9	1575.6	1522.5	596.1	2529.5	1135.8
AF130930.1	9886	4187.3	4281.4	3922.0	2822.3	5114.2	3011.5
EF050809.1	175147	7219.5	3816.1	9808.2	8365.6	1407.5	3142.5
FJ611807.1	563259	112.0	653.5	1158.6	273.1	129.6	1323.6
AF130943.1	9892	457.4	620.4	2355.6	753.3	2027.5	1473.0
FJ592987.1	433061	511.9	738.7	3187.3	635.8	1178.6	1054.4
AY679762.1	102249	33.6	203.0	469.0	105.8	67.1	121.2
AJ251466.1	73786	4474.2	4979.1	4707.6	3077.9	6310.2	3833.5
AM234150.1	153891	3564.1	3847.8	2707.6	3396.7	4854.0	5831.0
U80202.1	9906	5924.9	6806.3	5300.0	5406.8	8798.4	6917.4
AF130905.1	9914	4356.4	5078.7	3520.5	3658.8	4072.7	4263.8
AF130939.1	9891	4017.3	4523.7	4325.8	2881.0	4171.3	3197.7
AM293681.1	256894	4640.7	4901.8	4477.5	3772.0	4607.6	4341.0
FJ611835.1	564421	517.8	763.5	3270.6	634.2	1179.5	991.7
EU379306.1	266034	140.7	258.9	1278.2	186.1	671.0	796.1
AF130926.1	9924	891.6	1223.7	2388.7	1465.3	2334.8	3729.6
GQ169378.1	537971	297.4	694.6	2052.0	568.9	560.2	688.4
FJ999950.1	561323	12640.2	11715.5	6485.9	9251.3	16005.8	15863.3
AF130935.1	9890	4368.5	4618.8	4688.2	3632.2	6132.0	5108.4
FM202484.1	345858	1600.7	1965.6	3865.0	3439.4	841.5	2096.7
AF130933.1	9888	4376.2	4670.7	4207.4	3687.5	6134.0	5068.0
EU598802.1	267618	4419.2	4884.0	4031.5	3418.3	4123.7	3411.7
GQ225111.1	584259	12062.2	12791.9	7080.9	7999.3	12946.6	10189.9
AF130942.1	9933	8317.9	8530.0	8421.6	5973.2	9989.2	9412.5
GQ130025.1	463204	47.5	2208.1	3171.6	2366.4	2648.5	3395.2
AM184091.1	155126	6392.9	5199.8	9340.0	5921.8	6293.4	5532.7
FM202485.1	322033	5825.9	5956.9	5263.3	4976.1	5288.8	3968.7
NC_004547.2	471486	260.7	348.0	1178.6	357.7	1814.2	682.4
NC_004547.2	471485	643.9	836.0	1765.0	3063.4	486.9	1688.6
EF530546.1	221979	4368.1	1753.6	1105.1	3930.1	1496.4	1920.0
EF178667.1	178973	799.6	1123.5	1842.4	1292.3	1373.3	2757.3
EF178665.1	193423	70.9	280.9	463.8	183.4	103.5	431.9

k__Bacteria	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria
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o__Enterobacteriales	f__Enterobacteriaceae
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g__Pectobacterium
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s__Pectobacterium wasabiae	5351
s__Pectobacterium wasabiae	5356
s__Pectobacterium wasabiae	5542
s__Pectobacterium wasabiae	5809
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s__Photorhabdus temperata	6501
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s__unclassified	6270
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s__unclassified	7618
s__Plesiomonas shigelloides	4654
s__Proteus mirabilis	6273
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s__Proteus mirabilis	6738
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s__Proteus mirabilis	7563
s__Proteus mirabilis	7584
s__Proteus vulgaris	6559
s__Proteus vulgaris	6793
s__Proteus vulgaris	7063
s__Proteus vulgaris	7091
s__Proteus vulgaris	7099

FJ652619.1 gg_id:509543 Pectobacterium carotovorum str. cc303
NR_026047.1 gg_id:559459 Pectobacterium wasabiae str. SR91; ATCC 43316
CP001790.1 gg_id:523636 Pectobacterium wasabiae str. WPP163
EF530558.1 gg_id:218029 Pectobacterium wasabiae str. ICMP 9121
EF530556.1 gg_id:225898 Pectobacterium vasculorum str. ICMP 4226
Z96090.1 gg_id:9790 Pectobacterium carotovorum str. LMG 2386
EF178668.1 gg_id:182325 Pectobacterium atrosepticum str. NZEC20
AY278669.1 gg_id:87761 Photorhabdus sp. str. MOL
Z76750.1 gg_id:10266 Photorhabdus temperata str. Mge1
AY296252.1 gg_id:88447 Photorhabdus temperata
AY280573.1 gg_id:91820 Photorhabdus asymbiotica subsp. australis str. MB
Z76752.1 gg_id:10225 Photorhabdus asymbiotica str. ATCC 43949
Z76749.1 gg_id:10224 Photorhabdus luminescens str. Q614
EU930336.1 gg_id:326018 Photorhabdus luminescens str. KR04
EU930345.1 gg_id:323175 Photorhabdus luminescens str. HG29
EU136627.1 gg_id:238203 Photorhabdus sp. 3240
FJ006729.1 gg_id:356553 Photorhabdus luminescens str. SRK8
Z76744.1 gg_id:10222 Photorhabdus luminescens str. Brecon
Z76740.1 gg_id:10217 Photorhabdus luminescens str. Tn-5*2
FJ006727.1 gg_id:307512 Photorhabdus luminescens str. SRK6
AY216500.1 gg_id:85814 Photorhabdus sp. str. Q614
GQ359965.1 gg_id:579651 Plesiomonas shigelloides str. PIM23
AJ301682.1 gg_id:19524 Proteus mirabilis str. CIP103181T (ATCC29906T)
AJ634474.1 gg_id:105166 Proteus penneri str. ENT229
DQ453959.1 gg_id:154694 Proteus vulgaris str. T-6
DQ826507.1 gg_id:164105 Proteus vulgaris
EF194105.1 gg_id:203330 Proteus mirabilis D3
DQ777867.1 gg_id:166692 Proteus mirabilis
EU411047.1 gg_id:277121 Proteus mirabilis str. GK IV
DQ512963.1 gg_id:161130 Proteus sp. str. HS7514
AB079370.1 gg_id:19687 Proteus mirabilis str. U1-2
DQ449631.1 gg_id:156998 Proteus mirabilis str. O
AY820623.1 gg_id:108937 Proteus mirabilis
NZ_ABVP01000020.1 gg_id:470879 Proteus penneri str. ATCC 35198
EF626945.1 gg_id:238632 Proteus mirabilis str. TMPSB2
FJ581028.1 gg_id:560629 Proteus mirabilis str. IITRM5
GQ292550.1 gg_id:541537 Proteus vulgaris str. TEM11
NZ_ABVP01000020.1 gg_id:470878 Proteus penneri str. ATCC 35198
J01874.1 gg_id:37204 Proteus vulgaris
DQ885258.1 gg_id:170701 Proteus penneri str. NCTC 12737
DQ885257.1 gg_id:172390 Proteus vulgaris str. ATCC 29905

FJ652619.1	509543	313.2	502.0	2124.3	969.8	1486.0	1143.2
NR_026047.1	559459	12277.6	11803.0	11573.4	9339.1	10003.5	7486.1
CP001790.1	523636	1929.9	2070.2	3366.3	2971.7	3178.7	4229.4
EF530558.1	218029	678.9	656.6	1798.1	856.1	324.7	774.9
EF530556.1	225898	363.7	678.1	2842.5	742.7	2912.2	794.4
Z96090.1	9790	1788.3	1725.0	1728.2	725.3	670.3	932.6
EF178668.1	182325	264.2	658.6	2380.9	954.4	1937.3	1263.7
AY278669.1	87761	1578.2	1867.2	2265.2	3097.1	2350.1	2929.5
Z76750.1	10266	42.4	123.2	515.9	125.2	65.3	147.6
AY296252.1	88447	7077.8	6422.5	2708.7	7322.7	9522.6	7646.2
AY280573.1	91820	4459.4	5239.2	4761.4	4232.9	8458.4	8878.8
Z76752.1	10225	355.3	259.9	983.2	944.9	878.0	1284.9
Z76749.1	10224	12457.4	12104.4	7359.6	9496.9	12792.6	12546.0
EU930336.1	326018	1863.9	2699.1	2740.6	1412.4	3918.6	2002.3
EU930345.1	323175	570.6	536.3	1082.3	2021.7	451.3	663.6
EU136627.1	238203	2765.4	3705.9	4930.0	3615.6	5583.7	4449.4
FJ006729.1	356553	7960.0	10213.5	8881.5	8760.3	11120.2	9584.4
Z76744.1	10222	1279.6	947.5	973.6	1224.2	1096.0	1041.6
Z76740.1	10217	774.7	661.6	1672.0	1509.6	937.8	1087.8
FJ006727.1	307512	1674.5	1932.4	2657.3	2170.3	3071.9	3414.9
AY216500.1	85814	412.7	354.1	895.9	822.4	1329.8	2024.8
GQ359965.1	579651	47.4	133.5	67.0	78.7	68.1	65.9
AJ301682.1	19524	13431.7	12443.7	7332.0	11643.5	10206.7	8890.7
AJ634474.1	105166	341.2	818.9	1096.7	334.3	2420.0	417.2
DQ453959.1	154694	9112.3	9482.0	8686.2	7080.2	10417.9	9025.9
DQ826507.1	164105	1738.0	1314.1	5345.7	2350.5	2332.3	2377.8
EF194105.1	203330	11522.4	11842.0	6470.5	9854.3	12922.1	8881.9
DQ777867.1	166692	931.7	1110.4	2326.2	1382.7	936.5	817.5
EU411047.1	277121	2861.3	3191.6	1919.7	3076.5	1808.1	780.4
DQ512963.1	161130	306.6	340.0	2850.3	801.7	856.9	672.8
AB079370.1	19687	1439.2	1180.2	2178.9	3236.9	2297.8	1926.5
DQ449631.1	156998	1685.1	1618.6	2694.7	5640.6	2393.1	3726.6
AY820623.1	108937	4247.9	2550.1	3073.8	6085.0	3442.8	3989.5
NZ_ABVP01000020.1	470879	264.5	475.8	2978.0	777.1	1031.0	447.0
EF626945.1	238632	3921.8	3269.1	2536.8	6205.0	6615.1	3800.7
FJ581028.1	560629	932.4	1182.8	2228.8	1503.4	921.2	853.2
GQ292550.1	541537	1435.6	1435.9	4388.3	2820.9	2300.4	2864.7
NZ_ABVP01000020.1	470878	612.5	742.5	4508.3	1691.3	1119.0	1047.0
J01874.1	37204	2819.0	1952.0	6084.8	4660.6	3203.9	5022.1
DQ885258.1	170701	575.3	652.8	3725.5	1460.7	1068.7	934.9
DQ885257.1	172390	1754.6	1443.9	3579.5	3883.1	2954.0	4403.3

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EF528263.1 gg_id:225923 Proteus vulgaris str. CICCHLJ Q33
DQ499636.1 gg_id:170332 Proteus vulgaris
DQ205432.1 gg_id:139753 Proteus vulgaris str. knp3
DQ885259.1 gg_id:170436 Proteus myxofaciens str. NCIMB 13273
AJ301684.1 gg_id:36854 Providencia alcalifaciens str. CIP8290T (ATCC9886T)
DQ885261.1 gg_id:162080 Providencia alcalifaciens str. NCTC 10286
FJ418572.1 gg_id:360427 Providencia alcalifaciens str. Sam130-1A
DQ885265.1 gg_id:168679 Providencia heimbachae str. NCTC 12003
AF008581.1 gg_id:45337 Providencia stuartii str. ATCC 29914T
ABJD02000003.1 gg_id:286806 Providencia stuartii str. ATCC 25827
ABJD02000097.1 gg_id:280258 Providencia stuartii str. ATCC 25827
DQ885263.1 gg_id:162918 Providencia rettgeri str. NCTC 11801
AM040754.1 gg_id:130404 Moellerella wisconsensis str. DSM 5676
AM040492.1 gg_id:128082 Providencia rettgeri str. DSM 4542
EU464842.1 gg_id:294417 Hartmann's mountain zebra feces clone AFZEB_aaj71g06
AY803746.1 gg_id:108983 Providencia stuartii str. PGS13
EF192136.1 gg_id:206430 Providencia vermicola ANU201
DQ824609.1 gg_id:197650 human fecal clone RL185_aaj70d03
AB161460.1 gg_id:155411 Providencia sp. str. WW2
DQ824552.1 gg_id:187905 human fecal clone RL185_aaj69e11
DQ824750.1 gg_id:194664 human fecal clone RL185_aaj72f10
FJ811860.1 gg_id:591962 Rahnella aquatilis str. 3-WCH
FM209488.1 gg_id:309913 Rahnella aquatilis str. TS18
FJ222589.1 gg_id:315615 Rahnella sp. str. N2-2
FJ811859.1 gg_id:587642 Rahnella aquatilis str. 2B-CDF
U88438.1 gg_id:10313 Rahnella sp. 'CDC Bonn7' str. CDC Bonn7
EF685273.1 gg_id:239195 Hepialus gonggaensis sequencing libraries larva guts clone Hg09
U88437.1 gg_id:10312 Rahnella sp. 'CDC 658-79' str. CDC 658-79
FJ811853.1 gg_id:551657 Rahnella aquatilis str. 9-BCH
EF515255.1 gg_id:218905 Electricigen Enrichment MFC upf microbial fuel cell anode clone 22a08
EU294414.1 gg_id:255855 Raoultella ornithinolytica str. cl40 sullage
AB099407.1 gg_id:86680 Raoultella planticola str. 8433
EF057396.1 gg_id:199546 Raoultella ornithinolytica str. D70
EF515335.1 gg_id:223344 Electricigen Enrichment MFC upf microbial fuel cell anode clone 23a10
AB004756.2 gg_id:136418 Raoultella ornithinolytica str. JCM7251
EF515290.1 gg_id:227203 Electricigen Enrichment MFC upf microbial fuel cell anode clone 22d12
AB099400.1 gg_id:84971 Raoultella planticola str. 4131
EF515418.1 gg_id:220845 Electricigen Enrichment MFC upf microbial fuel cell anode clone 24b10
EU545405.1 gg_id:542722 Raoultella planticola str. XW10
FJ823046.1 gg_id:563810 Raoultella ornithinolytica str. gx-110

EU373433.1	268928	1893.0	1620.2	4606.4	2224.5	3159.6	2622.4
EF528263.1	225923	1139.2	933.0	4334.6	3796.1	1160.1	2612.9
DQ499636.1	170332	849.7	1017.2	4877.8	1594.9	2339.6	1361.9
DQ205432.1	139753	1127.9	1023.8	5042.4	2596.1	1330.0	2106.0
DQ885259.1	170436	1335.1	974.7	5935.4	2329.6	1080.1	1939.2
AJ301684.1	36854	6762.3	6035.4	4565.4	7367.1	6641.4	7037.0
DQ885261.1	162080	41.1	120.7	313.0	176.2	1697.2	106.9
FJ418572.1	360427	516.3	161.9	2358.7	1812.9	85.0	722.9
DQ885265.1	168679	335.8	759.4	1429.7	1153.4	114.0	441.0
AF008581.1	45337	17923.3	15432.8	17843.4	13601.7	21402.2	18390.7
ABJD02000003.1	286806	831.9	2306.0	1747.7	1270.4	581.3	1425.1
ABJD02000097.1	280258	31.7	134.2	479.2	137.2	78.1	174.7
DQ885263.1	162918	358.1	384.2	1632.1	756.1	1174.6	2264.1
AM040754.1	130404	36.2	232.7	310.8	115.9	77.9	130.4
AM040492.1	128082	3030.1	2909.4	2657.5	5440.9	4450.3	6511.2
EU464842.1	294417	425.3	516.8	1112.6	560.5	1157.1	752.7
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EF192136.1	206430	2489.3	3175.4	1540.2	1835.6	2347.0	1582.1
DQ824609.1	197650	6509.8	3609.6	3999.1	3607.3	7020.1	5894.6
AB161460.1	155411	897.7	789.0	1573.2	1047.3	632.4	395.1
DQ824552.1	187905	600.5	684.4	1690.7	2300.3	3180.0	1114.8
DQ824750.1	194664	3675.6	3476.5	4437.3	3843.2	5370.3	6255.7
FJ811860.1	591962	6727.5	4698.3	11571.7	8828.3	9505.3	10184.5
FM209488.1	309913	4054.7	4047.2	6079.8	7643.1	2900.7	4775.0
FJ222589.1	315615	1432.9	1117.4	2965.0	2796.9	2512.3	3145.3
FJ811859.1	587642	1163.6	1069.9	3609.3	1603.9	1965.1	1830.2
U88438.1	10313	4910.5	3576.1	5238.0	6829.1	3927.5	5189.5
EF685273.1	239195	11183.3	11454.6	12580.5	14018.4	14073.7	13488.7
U88437.1	10312	2070.7	2020.5	4421.7	4712.4	2331.2	2827.0
FJ811853.1	551657	4400.1	4190.7	10911.3	6964.3	3148.5	3557.9
EF515255.1	218905	204.2	363.7	1351.5	336.2	365.2	299.2
EU294414.1	255855	378.1	763.7	3134.0	640.7	508.6	702.1
AB099407.1	86680	680.4	871.9	3176.7	1073.9	2482.8	806.9
EF057396.1	199546	1872.0	2452.1	6470.5	2922.0	4425.4	3928.0
EF515335.1	223344	6025.6	5853.6	7548.8	7537.0	10986.2	7105.0
AB004756.2	136418	400.0	554.0	3673.5	554.6	163.3	319.4
EF515290.1	227203	881.7	1222.0	3749.7	1458.8	1675.5	1184.5
AB099400.1	84971	878.0	914.9	2976.0	1817.3	3027.1	1097.6
EF515418.1	220845	330.0	433.6	512.1	734.5	203.3	280.4
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FJ823046.1	563810	1852.1	1518.4	3558.3	4841.8	786.1	3565.2

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s__Raoultella ornithinolytica	4938
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EF515374.1 gg_id:223756 Electricigen Enrichment MFC upf microbial fuel cell anode clone 23e09
EF515458.1 gg_id:223163 Electricigen Enrichment MFC upf microbial fuel cell anode clone 24f06
EF515419.1 gg_id:227289 Electricigen Enrichment MFC upf microbial fuel cell anode clone 24b11
U78182.1 gg_id:49258 Raoultella ornithinolytica str. CIP 103 364 T
Y17662.1 gg_id:10128 Raoultella ornithinolytica str. 590681
EF515201.1 gg_id:222043 Electricigen Enrichment MFC upf microbial fuel cell anode clone 21c07
EF515264.1 gg_id:225880 Electricigen Enrichment MFC upf microbial fuel cell anode clone 22b06
EU294412.1 gg_id:257519 Raoultella ornithinolytica str. 38 sullage
EF433545.1 gg_id:211783 Klebsiella sp. str. WW2
AB099403.1 gg_id:86319 Raoultella planticola str. ATCC 43176
EF515440.1 gg_id:217863 Electricigen Enrichment MFC upf microbial fuel cell anode clone 24d09
EF515404.1 gg_id:224329 Electricigen Enrichment MFC upf microbial fuel cell anode clone 24a05
Y17666.1 gg_id:10130 Raoultella ornithinolytica str. FSK9555
AY770415.1 gg_id:134449 insect gut clone
FJ975874.1 gg_id:566870 Human gut microbiome adopts alternative state bowel transplantation ileum effluent
DQ333356.1 gg_id:149677 Raoultella planticola str. 33-4ch
FJ975862.1 gg_id:511415 Human gut microbiome adopts alternative state bowel transplantation ileum effluent
AY946284.1 gg_id:114650 Kluyvera cryocrescens 27
Y17663.1 gg_id:10129 Raoultella planticola str. 7444
GQ154930.1 gg_id:511427 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
EU256396.1 gg_id:243243 Bacillus megaterium str. SZN4
FJ975841.1 gg_id:562152 Human gut microbiome adopts alternative state bowel transplantation ileum effluent
AF129444.1 gg_id:42955 Raoultella planticola str. ATCC 33558T
GQ154871.1 gg_id:583590 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
GQ154720.1 gg_id:509089 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
GQ154727.1 gg_id:533667 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
AF511435.1 gg_id:65398 Serratia fonticola CCCO11b
GQ156035.1 gg_id:545206 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
X93215.1 gg_id:10127 Raoultella planticola str. DSM 3069 T
FJ975867.1 gg_id:569459 Human gut microbiome adopts alternative state bowel transplantation ileum effluent
GU374107.1 gg_id:525406 soil East Calcutta wetland clone SRC_NBB7
Y17659.1 gg_id:10126 Raoultella planticola str. ATCC33531T
GQ155652.1 gg_id:566917 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
FJ405282.1 gg_id:356864 Citrobacter sp. str. F41
GQ154876.1 gg_id:584525 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
GQ154760.1 gg_id:535915 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
EU704230.1 gg_id:296868 human biliary stents clone KLONE12
GQ156448.1 gg_id:593522 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
EU560831.1 gg_id:565501 Assessment genetic Apriona germari (Hope) larvae normalization techniques intestir
DQ223874.1 gg_id:170406 Obesumbacterium proteus str. RT6
EU939439.1 gg_id:329096 Fecal wild pygmy loris feces clone WF16S_295

EF515374.1	223756	396.6	517.8	2152.9	892.2	456.5	528.6
EF515458.1	223163	4665.2	4564.0	5743.5	7517.8	9208.1	8115.2
EF515419.1	227289	89.7	210.6	601.0	146.2	664.9	254.0
U78182.1	49258	430.4	544.0	2522.5	945.1	475.3	511.7
Y17662.1	10128	324.6	409.6	1927.7	633.5	158.8	296.5
EF515201.1	222043	80.7	222.7	235.3	152.2	176.7	120.8
EF515264.1	225880	865.8	1052.7	3368.0	1401.7	1429.3	1059.7
EU294412.1	257519	108.0	247.4	1407.0	225.9	103.9	359.4
EF433545.1	211783	593.3	626.1	2350.3	1236.6	255.7	360.6
AB099403.1	86319	1130.3	1478.6	3294.0	1874.0	5134.1	2074.1
EF515440.1	217863	5636.8	5482.4	5092.6	6566.0	7480.5	5637.4
EF515404.1	224329	5440.0	5020.2	4534.0	6949.4	7572.2	6876.2
Y17666.1	10130	877.3	1345.0	3887.7	1388.8	2161.7	1505.1
AY770415.1	134449	2252.7	1634.3	4881.2	3772.8	2278.2	3327.9
FJ975874.1	566870	1950.5	1424.7	7176.7	2335.3	3873.4	3085.4
DQ333356.1	149677	281.7	582.6	3481.9	476.1	339.5	369.7
FJ975862.1	511415	6509.4	6453.2	4402.9	4542.4	4297.5	4810.7
AY946284.1	114650	1547.8	1430.6	2723.6	1150.3	3485.0	2273.7
Y17663.1	10129	369.2	380.7	2507.4	503.4	149.9	150.8
GQ154930.1	511427	1266.9	1274.4	3571.7	4821.2	2786.8	3917.0
EU256396.1	243243	3732.7	2072.1	4297.0	3566.9	2064.4	1916.4
FJ975841.1	562152	6573.2	5081.0	5841.9	5139.5	7338.1	5783.7
AF129444.1	42955	275.8	466.2	2370.2	431.2	301.4	360.9
GQ154871.1	583590	2656.6	3749.2	3485.8	2288.3	3670.8	3547.3
GQ154720.1	509089	2230.8	2507.3	1935.5	1330.1	2755.0	1780.7
GQ154727.1	533667	4209.6	3355.4	7727.2	4719.7	6267.5	5573.6
AF511435.1	65398	2603.8	3543.1	2447.2	1713.8	2581.7	2223.6
GQ156035.1	545206	620.6	806.7	3055.9	1607.1	1566.5	1232.0
X93215.1	10127	116.2	277.2	1510.0	235.3	89.4	197.9
FJ975867.1	569459	119.2	492.5	1511.2	202.3	244.8	875.6
GU374107.1	525406	1147.5	1511.0	3249.2	836.8	1046.3	1424.3
Y17659.1	10126	924.0	996.6	2607.5	1323.4	1085.8	911.6
GQ155652.1	566917	1199.3	985.6	4203.2	1210.5	826.9	1276.7
FJ405282.1	356864	476.0	818.7	3290.0	510.6	1640.8	1443.9
GQ154876.1	584525	3837.1	3112.7	7963.8	2697.5	3047.7	2774.3
GQ154760.1	535915	180.1	857.0	4097.2	1525.5	1711.2	1538.5
EU704230.1	296868	374.9	696.0	2613.6	533.2	756.3	419.1
GQ156448.1	593522	446.3	1169.8	2261.1	1695.1	1863.2	923.4
EU560831.1	565501	48.1	84.5	272.3	78.5	48.7	101.2
DQ223874.1	170406	4618.4	4011.5	2055.1	3308.5	1552.8	1476.5
EU939439.1	329096	770.4	1212.8	2810.8	482.2	2400.3	6205.7

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AF181574.1 gg_id:73261 Raoultella planticola 7
GQ154719.1 gg_id:542496 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
DQ133596.1 gg_id:138380 Pantoea agglomerans str. B1
FJ823007.1 gg_id:533363 Raoultella ornithinolytica str. gx-49
GQ154944.1 gg_id:578463 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
EF608520.1 gg_id:234549 predatory Poecilus chalcites their response lab rearing and antibiotic treatment diges
EU560759.1 gg_id:538000 Assessment genetic intestinal flora Apriona germari (Hope) larvae -RFLP techniques
DQ113752.1 gg_id:132380 dog duodenum clone D1-50
GQ154965.1 gg_id:550873 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
GQ156483.1 gg_id:540487 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
GQ156476.1 gg_id:579281 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
GQ154749.1 gg_id:536503 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
GQ154730.1 gg_id:575117 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
X93216.1 gg_id:10131 Raoultella planticola str. DR3
GQ156507.1 gg_id:535104 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
AF129443.1 gg_id:25616 Raoultella planticola str. ATCC 33531T
AB364958.1 gg_id:235818 Raoultella ornithinolytica str. R1
GQ154797.1 gg_id:540793 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
AJ508301.1 gg_id:80910 Enterobacter kobei str. CIP 105566
EU870376.1 gg_id:315511 Enterobacter sp. str. SZDA
AF029226.1 gg_id:9779 Salmonella bongori str. JEO 4162
EU014682.1 gg_id:241394 Salmonella bongori str. DSM 13772
EF604050.1 gg_id:231538 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF604013.1 gg_id:233727 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF604026.1 gg_id:233581 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF604059.1 gg_id:233315 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF604025.1 gg_id:232625 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
DQ344533.1 gg_id:147628 Salmonella serovar Typhimurium subsp. enterica
EF604459.1 gg_id:228090 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF604061.1 gg_id:230866 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF604251.1 gg_id:228632 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF604271.1 gg_id:230532 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF604068.1 gg_id:232240 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF604369.1 gg_id:229101 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF604430.1 gg_id:230474 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
DQ344536.1 gg_id:148570 Salmonella paratyphi
EF604057.1 gg_id:229934 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
Z49264.1 gg_id:9760 Salmonella typhimurium str. E10 NCTC 8391
EF604005.1 gg_id:229722 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF604076.1 gg_id:234402 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF604396.1 gg_id:229998 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse

AF181574.1	73261	116.2	232.6	1525.2	369.7	75.9	132.9
GQ154719.1	542496	171.2	407.3	1161.3	524.3	1662.0	692.8
DQ133596.1	138380	1088.0	1049.9	3720.7	654.2	1206.7	1452.1
FJ823007.1	533363	658.0	1136.2	3710.5	1104.8	1028.7	1001.4
GQ154944.1	578463	856.8	1015.8	2595.6	1072.9	1935.4	1969.6
EF608520.1	234549	17.3	23.3	22.4	56.4	71.8	24.8
EU560759.1	538000	946.5	871.6	1820.6	1865.3	1769.1	2149.2
DQ113752.1	132380	189.5	394.1	1231.0	288.7	61.3	133.0
GQ154965.1	550873	2938.3	3405.7	8387.4	4168.4	4387.0	3426.0
GQ156483.1	540487	533.4	1124.2	2519.6	1907.2	1523.5	1326.0
GQ156476.1	579281	88.1	298.9	1558.6	137.3	184.0	303.8
GQ154749.1	536503	1927.2	1344.3	8747.7	2075.2	1941.5	2019.8
GQ154730.1	575117	2964.3	3207.9	2697.8	4583.0	1887.2	2936.5
X93216.1	10131	421.9	993.4	643.7	948.5	3499.6	3549.4
GQ156507.1	535104	189.4	3944.0	2512.6	3742.3	4951.6	4951.7
AF129443.1	25616	912.0	983.1	2429.7	1315.6	1159.3	850.0
AB364958.1	235818	5960.1	6268.9	6288.4	5178.2	7193.9	5649.7
GQ154797.1	540793	3791.6	3826.2	4293.0	2920.1	1839.3	1972.9
AJ508301.1	80910	3113.3	1831.6	5446.9	3799.4	2329.2	2984.2
EU870376.1	315511	410.7	764.3	2235.0	411.2	570.4	1234.9
AF029226.1	9779	109.2	371.8	1192.9	147.2	61.7	255.2
EU014682.1	241394	607.6	1294.5	1983.2	800.8	1647.1	1725.1
EF604050.1	231538	169.9	352.7	675.8	445.6	419.4	621.0
EF604013.1	233727	3701.4	1335.1	879.6	3071.1	463.3	917.5
EF604026.1	233581	7424.0	7354.8	3608.2	3823.1	4085.5	4362.0
EF604059.1	233315	8033.1	8931.3	6533.7	7455.3	11899.6	12542.2
EF604025.1	232625	7520.3	6633.6	5057.5	7523.3	10580.0	11066.1
DQ344533.1	147628	798.9	949.6	2708.2	478.1	295.4	829.4
EF604459.1	228090	7371.8	6126.8	1814.6	7827.7	10377.5	12924.4
EF604061.1	230866	291.7	291.1	274.0	331.9	862.0	957.0
EF604251.1	228632	1841.4	1844.3	1115.7	2257.4	3071.1	3136.6
EF604271.1	230532	1073.3	1258.1	1654.2	901.2	1662.8	1053.8
EF604068.1	232240	350.6	616.4	792.6	442.3	430.8	628.9
EF604369.1	229101	7404.6	5846.0	4305.1	7855.1	4902.5	6324.1
EF604430.1	230474	42.8	53.0	84.7	66.9	49.7	32.7
DQ344536.1	148570	722.0	870.2	682.1	472.2	692.7	774.3
EF604057.1	229934	4102.1	4057.0	3483.3	2824.8	5414.3	5618.0
Z49264.1	9760	177.4	617.6	1173.9	895.2	247.4	353.5
EF604005.1	229722	6107.4	4346.4	2960.2	6337.9	6641.8	8601.6
EF604076.1	234402	226.6	332.7	259.3	266.9	622.0	632.9
EF604396.1	229998	8955.7	5757.3	5691.0	9580.5	5578.9	6431.0

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EF604267.1 gg_id:231474 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF604034.1 gg_id:231667 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF604355.1 gg_id:231430 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF605237.1 gg_id:232727 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF604242.1 gg_id:230860 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF604458.1 gg_id:230835 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF604038.1 gg_id:231547 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF604070.1 gg_id:234703 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF604265.1 gg_id:232599 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EU073022.1 gg_id:253204 Salmonella sp. 'group B' HQ010915-1
EF604087.1 gg_id:235257 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF604376.1 gg_id:227666 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF604048.1 gg_id:233068 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EU118102.1 gg_id:249888 Salmonella enteritidis str. E3
EF604237.1 gg_id:227737 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
DQ683179.1 gg_id:165358 Salmonella paratyphi str. 50973
EF604419.1 gg_id:228264 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
DQ153191.1 gg_id:138268 Salmonella typhimurium str. S1.I
EF604015.1 gg_id:230265 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF604056.1 gg_id:229595 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF605231.1 gg_id:228781 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EU118104.1 gg_id:247090 Salmonella enteritidis str. E4
EF604039.1 gg_id:228911 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
AB273733.1 gg_id:256256 Salmonella enterica subsp. houtenae str. GTC 1734
AF130890.2 gg_id:9770 Pantoea agglomerans str. A11
EF604075.1 gg_id:230988 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF604427.1 gg_id:231487 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
FJ609417.1 gg_id:572114 Salmonella enterica str. PRSC-1
EF604238.1 gg_id:233123 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
AF227869.1 gg_id:40959 Salmonella subsp. enterica serovar Typhimurium str. 65946 subsp.
NC_003197.1 gg_id:128871 Salmonella typhimurium LT2 str. LT2; SGSC 1412; ATCC 700720
FJ377885.1 gg_id:363910 Salmonella typhi str. MR9
EF604017.1 gg_id:235063 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF604089.1 gg_id:227942 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF605240.1 gg_id:230644 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF604062.1 gg_id:230359 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF604030.1 gg_id:232928 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF604003.1 gg_id:233622 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF604016.1 gg_id:227916 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF604423.1 gg_id:234837 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse

EF604073.1	227660	5961.7	4936.9	3105.0	5981.1	8461.6	10049.2
EF604267.1	231474	2736.9	2134.0	2610.5	2008.9	2642.1	4045.4
EF604034.1	231667	173.1	325.8	836.5	485.9	419.0	575.3
EF604355.1	231430	344.8	581.7	689.1	497.5	445.4	628.8
EF605237.1	232727	141.8	274.3	681.8	244.4	372.0	390.5
EF604242.1	230860	746.2	961.3	604.6	285.2	122.9	266.6
EF604458.1	230835	1290.6	1171.3	1221.8	434.6	1268.3	1562.6
EF604038.1	231547	4382.1	3883.0	2153.8	2007.6	3396.5	3214.5
EF604070.1	234703	12450.5	10622.0	8333.8	10209.4	9044.6	10037.9
EF604265.1	232599	9993.0	8417.7	6210.0	9665.2	11285.5	10639.4
EU073022.1	253204	1014.9	1484.9	1115.4	1711.3	3004.7	1829.7
EF604087.1	235257	748.4	1001.5	1289.6	805.1	458.2	825.9
EF604376.1	227666	735.0	980.5	2468.0	579.3	308.9	721.2
EF604048.1	233068	2061.1	1645.2	1907.0	3301.2	2210.1	2562.4
EU118102.1	249888	332.5	654.4	888.0	528.9	440.7	543.8
EF604237.1	227737	17923.6	13840.7	11570.3	14952.7	14608.5	13096.3
DQ683179.1	165358	283.9	641.2	933.5	532.4	149.4	315.9
EF604419.1	228264	2548.0	1505.5	2837.5	1340.3	1277.3	2005.6
DQ153191.1	138268	138.7	442.9	683.3	229.9	121.5	201.0
EF604015.1	230265	1489.4	1528.8	2533.7	1632.9	1306.0	1939.2
EF604056.1	229595	129.4	356.8	1052.9	196.2	96.7	347.5
EF605231.1	228781	8502.4	6834.2	2045.5	9577.8	11987.3	12485.3
EU118104.1	247090	28.0	105.6	330.8	69.0	61.7	64.5
EF604039.1	228911	11834.8	8095.8	7222.0	10131.6	9155.9	9777.1
AB273733.1	256256	1531.7	1883.5	3211.9	1602.8	2275.7	4537.8
AF130890.2	9770	200.3	301.4	879.8	383.3	695.0	246.5
EF604075.1	230988	156.4	300.2	701.2	364.9	414.7	487.3
EF604427.1	231487	7467.5	6257.9	1814.1	5841.8	7137.6	5776.7
FJ609417.1	572114	14958.6	13709.8	12203.8	9357.1	13599.8	10170.2
EF604238.1	233123	1458.3	1542.1	2429.7	1342.9	1265.2	1759.2
AF227869.1	40959	212.3	669.8	519.8	221.3	159.8	172.1
NC_003197.1	128871	101.0	274.0	576.3	192.8	111.7	173.1
FJ377885.1	363910	4530.9	3101.8	6066.8	3360.3	5000.6	4171.5
EF604017.1	235063	672.8	802.3	1410.4	408.3	276.6	476.0
EF604089.1	227942	449.4	667.4	711.0	501.9	434.7	534.0
EF605240.1	230644	554.9	622.6	344.7	610.7	696.4	877.2
EF604062.1	230359	295.0	299.8	775.5	643.4	718.6	615.4
EF604030.1	232928	7546.2	5578.3	5040.0	7682.2	7343.1	7289.2
EF604003.1	233622	10656.4	9894.2	9179.2	11588.1	12758.9	13224.0
EF604016.1	227916	1559.2	1710.0	1119.2	921.5	801.1	1381.6
EF604423.1	234837	605.2	822.2	1408.9	1133.5	1796.6	1431.1

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EF604394.1 gg_id:229717 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF604064.1 gg_id:232978 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
Z47544.1 gg_id:9756 Salmonella typhi str. Ty2 ATCC 19430
EF604385.1 gg_id:233497 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF604103.1 gg_id:232094 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF604429.1 gg_id:229314 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF604416.1 gg_id:231885 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
AB273736.1 gg_id:248512 Salmonella enterica subsp. arizonae str. GTC 1732
AE008820.1 gg_id:34689 Salmonella typhimurium LT2 str. LT2; SGSC 1412; ATCC 700720 LT2
EF604012.1 gg_id:228028 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF605229.1 gg_id:234498 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF605238.1 gg_id:232278 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF604380.1 gg_id:227822 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF604124.1 gg_id:232989 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF604049.1 gg_id:229879 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EU118106.1 gg_id:241765 Salmonella enteritidis str. E6
EF604278.1 gg_id:229337 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF604417.1 gg_id:234591 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF604046.1 gg_id:228201 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF604418.1 gg_id:228980 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF604007.1 gg_id:231467 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF604266.1 gg_id:232902 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF604004.1 gg_id:230964 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF604058.1 gg_id:229270 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF604250.1 gg_id:231095 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF604370.1 gg_id:232705 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF604258.1 gg_id:229218 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF604382.1 gg_id:227996 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF604042.1 gg_id:234592 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF605236.1 gg_id:231367 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF604252.1 gg_id:228883 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
AF008580.1 gg_id:52635 Salmonella enterica arizonae subsp. IIIa str. ATCC 13314T
EU118080.1 gg_id:247476 Salmonella paratyphi str. A5
EU118113.1 gg_id:249809 Salmonella typhi str. T6
EU118101.1 gg_id:251997 Salmonella enteritidis str. E2
EF604366.1 gg_id:233919 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
AB273735.1 gg_id:255286 Salmonella enterica subsp. diarizonae str. GTC 1733
EF604389.1 gg_id:228797 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF604006.1 gg_id:230459 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF604041.1 gg_id:234900 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse

EF604371.1	231981	699.3	819.0	1705.1	681.9	313.1	670.7
EF604394.1	229717	7496.3	6283.5	4936.7	8275.0	14318.8	14330.3
EF604064.1	232978	14659.7	8647.3	11047.9	12687.8	10789.8	14995.7
Z47544.1	9756	200.1	917.9	3217.7	768.7	105.0	700.7
EF604385.1	233497	9946.0	9151.8	5458.5	9739.5	8384.1	7895.6
EF604103.1	232094	893.0	1757.2	1957.9	4658.2	2751.0	2936.9
EF604429.1	229314	725.4	888.2	1361.5	469.9	297.8	585.6
EF604416.1	231885	329.2	330.7	1229.3	793.1	744.0	778.0
AB273736.1	248512	49.1	158.6	794.9	64.8	62.6	166.1
AE008820.1	34689	186.5	356.6	1169.7	456.4	445.9	659.2
EF604012.1	228028	6729.2	4591.4	4178.1	4928.8	7358.3	6098.9
EF605229.1	234498	35.7	113.4	491.8	128.1	51.2	296.1
EF605238.1	232278	7759.7	7291.4	4885.4	7128.9	10451.1	10453.8
EF604380.1	227822	5949.0	5279.9	1785.2	5706.8	8571.0	9152.7
EF604124.1	232989	581.3	705.7	274.0	331.9	1606.5	1699.8
EF604049.1	229879	2118.2	1262.1	2267.4	1692.1	3448.1	1524.5
EU118106.1	241765	53.7	232.3	833.0	117.3	90.8	197.9
EF604278.1	229337	240.1	471.3	829.9	458.6	1094.3	985.3
EF604417.1	234591	4592.1	4542.3	4937.0	3234.8	6914.3	6574.6
EF604046.1	228201	11391.9	7808.7	4105.5	10023.3	8715.7	9402.7
EF604418.1	228980	10448.7	8865.9	6412.2	8952.0	12543.9	13710.6
EF604007.1	231467	97.2	287.1	1780.3	270.6	95.6	448.4
EF604266.1	232902	3218.0	3862.7	2627.9	4464.0	5725.3	5580.6
EF604004.1	230964	170.8	351.3	637.6	438.9	417.3	567.5
EF604058.1	229270	793.6	1248.1	2924.0	634.9	452.7	949.8
EF604250.1	231095	3647.3	3484.2	2207.8	2409.2	4475.7	4765.3
EF604370.1	232705	677.6	806.0	1436.5	458.1	278.8	509.8
EF604258.1	229218	3487.1	3086.5	1510.4	1603.6	3789.5	4484.7
EF604382.1	227996	14351.2	13687.1	7459.9	9385.8	9419.0	13683.2
EF604042.1	234592	1988.0	1356.0	1827.8	3513.5	2727.6	3834.4
EF605236.1	231367	664.0	834.7	1223.5	1138.6	1123.9	1401.5
EF604252.1	228883	789.5	903.3	4886.1	913.9	1037.3	1987.6
AF008580.1	52635	60.5	61.7	44.2	70.5	83.0	37.1
EU118080.1	247476	178.3	243.4	1200.0	436.6	282.4	461.3
EU118113.1	249809	239.4	946.5	1285.0	407.3	208.6	444.8
EU118101.1	251997	151.0	243.9	516.7	211.0	342.0	347.9
EF604366.1	233919	4785.6	4282.3	6417.8	3685.8	6399.0	5218.4
AB273735.1	255286	34.9	235.8	207.5	89.4	61.6	35.2
EF604389.1	228797	812.9	1002.7	3352.8	592.0	290.1	932.9
EF604006.1	230459	5821.2	5064.3	5040.1	5294.7	5427.2	6622.1
EF604041.1	234900	2614.1	2464.5	1960.3	2980.3	4508.4	3659.8

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s__Serratia entomophila	5076
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s__Serratia fonticola	4763
s__Serratia fonticola	4801
s__Serratia fonticola	4999
s__Serratia fonticola	5113
s__Serratia fonticola	5216
s__Serratia fonticola	5585
s__Serratia fonticola	5714
s__Serratia fonticola	5980

EF604259.1 gg_id:233544 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF604264.1 gg_id:230650 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF604071.1 gg_id:234981 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF604053.1 gg_id:232636 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF604065.1 gg_id:233811 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF604269.1 gg_id:228519 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF604055.1 gg_id:228129 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF604029.1 gg_id:232688 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF604368.1 gg_id:229317 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF604047.1 gg_id:228301 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF604229.1 gg_id:230785 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF604290.1 gg_id:228932 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF604350.1 gg_id:230452 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF604231.1 gg_id:228528 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF605222.1 gg_id:228682 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
X80676.1 gg_id:9753 Salmonella sp str. ATCC 9712
EF603996.1 gg_id:230075 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF603990.1 gg_id:229961 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
FN555100.1 gg_id:557204 Salmonella enterica str. 22/M185/01/98
EF603999.1 gg_id:230399 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF603993.1 gg_id:240102 Salmonella enterica serovar typhimurium exploits inflammation compete intestinal m
EF605223.1 gg_id:228777 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF603997.1 gg_id:233210 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF604009.1 gg_id:231236 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF604439.1 gg_id:229380 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF604378.1 gg_id:257266 Salmonella enterica serovar typhimurium exploits inflammation compete intestinal m
EF604233.1 gg_id:229474 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF605227.1 gg_id:230960 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF605226.1 gg_id:230722 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF604352.1 gg_id:233030 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
AF170176.1 gg_id:9773 Salmonella typhimurium LT2 str. SGSC1412
GU370899.1 gg_id:560434 Serratia entomophila str. AB2
AM696814.1 gg_id:222538 sequencing libraries indoor dust clone BF0001A101
AM696771.1 gg_id:221173 sequencing libraries indoor dust clone BF0001A058
AM696796.1 gg_id:219190 sequencing libraries indoor dust clone BF0001A083
AM696772.1 gg_id:217269 sequencing libraries indoor dust clone BF0001A059
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AM696738.1 gg_id:225895 sequencing libraries indoor dust clone BF0001A025
AM696786.1 gg_id:225765 sequencing libraries indoor dust clone BF0001A073
AM696767.1 gg_id:222647 sequencing libraries indoor dust clone BF0001A054

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EF604264.1	230650	161.3	304.5	729.1	418.3	417.1	527.6
EF604071.1	234981	1776.1	928.5	976.6	3627.0	2231.8	1784.5
EF604053.1	232636	4900.6	3882.5	4136.2	4311.1	6595.8	10159.3
EF604065.1	233811	2912.6	2823.8	938.7	1495.0	2551.1	2829.0
EF604269.1	228519	844.2	2373.7	1585.0	299.6	743.0	3357.2
EF604055.1	228129	574.1	900.8	2177.0	746.1	1220.6	1498.1
EF604029.1	232688	4640.2	4445.6	778.5	1226.3	654.1	3380.4
EF604368.1	229317	2055.2	1727.6	2290.1	3407.7	2263.9	2617.0
EF604047.1	228301	9713.5	6011.6	5485.6	8840.1	13969.7	14759.0
EF604229.1	230785	62.3	245.4	672.3	173.4	90.5	206.3
EF604290.1	228932	1251.1	1356.2	998.3	917.3	3617.3	3457.4
EF604350.1	230452	4797.1	4689.4	2368.2	3253.5	4505.3	4220.9
EF604231.1	228528	14678.3	13419.0	10322.7	11543.6	12373.4	10562.3
EF605222.1	228682	733.1	1071.0	1392.7	722.0	1149.9	1186.8
X80676.1	9753	6434.7	5598.1	4899.0	8250.8	2426.8	4812.6
EF603996.1	230075	7023.4	5550.5	3803.3	6383.0	9604.8	7499.4
EF603990.1	229961	980.1	1326.4	1516.4	974.9	1845.6	1616.0
FN555100.1	557204	103.3	384.8	702.5	185.4	193.8	124.7
EF603999.1	230399	763.6	1138.1	1359.6	709.4	1182.5	1253.3
EF603993.1	240102	5761.7	4698.6	2207.8	5315.3	9011.3	6490.9
EF605223.1	228777	560.0	915.2	1380.9	624.9	1155.6	1313.5
EF603997.1	233210	5675.0	5831.8	2273.4	5146.5	6179.4	4423.8
EF604009.1	231236	744.2	926.0	2553.8	467.4	296.6	784.4
EF604439.1	229380	3872.6	3407.9	797.2	4654.9	6836.5	7327.0
EF604378.1	257266	1770.2	1267.1	2208.8	1912.7	1607.2	3196.5
EF604233.1	229474	2559.1	2104.9	2059.7	2159.3	2955.4	2401.8
EF605227.1	230960	2200.1	2185.9	959.6	1482.0	3527.6	3186.9
EF605226.1	230722	10950.3	10363.3	6950.0	8726.0	11319.2	10254.7
EF604352.1	233030	502.9	813.0	1385.0	507.8	439.6	642.7
AF170176.1	9773	119.0	378.1	677.1	222.8	203.2	171.1
GU370899.1	560434	114.1	483.1	2787.1	287.1	476.2	603.8
AM696814.1	222538	901.8	940.5	5959.2	729.6	1397.2	1379.6
AM696771.1	221173	1500.7	1524.9	6235.5	1722.5	1598.8	1173.6
AM696796.1	219190	1579.4	1497.1	6348.9	1669.6	1496.5	1140.3
AM696772.1	217269	5991.3	5255.5	7017.1	7273.0	5872.3	5758.6
AM696727.1	220748	1538.0	1476.6	5845.0	1619.1	896.1	1193.8
AM696722.1	226184	1988.1	1467.7	5616.3	2680.8	1486.4	1334.3
AM696738.1	225895	1574.0	1369.6	5490.1	1573.1	820.3	1063.9
AM696786.1	225765	458.8	885.5	5249.0	636.2	785.4	882.9
AM696767.1	222647	1522.8	1379.7	5176.1	1450.9	845.2	1084.3

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EF491959.1 gg_id:217974 Serratia grimesii str. OS9
FJ527456.1 gg_id:510879 Pectobacterium subsp. carotovorum str. Ecc1-6
DQ399752.1 gg_id:155266 Serratia sp. B-2002
FJ811864.1 gg_id:576728 Serratia liquefaciens str. 2-BCH
DQ399748.1 gg_id:155784 Serratia sp. B-1135
DQ501957.1 gg_id:222053 Serratia marcescens
AF124037.1 gg_id:10034 Serratia marcescens
EU302853.1 gg_id:240155 Serratia marcescens str. DAP28
FM202483.1 gg_id:317955 Serratia marcescens str. EV1
FM163485.2 gg_id:290724 Serratia marcescens str. BC16
EU407551.1 gg_id:269227 Serratia marcescens str. UFLA-25LS
GQ906774.1 gg_id:586809 Serratia marcescens str. MR-4
DQ182325.1 gg_id:140269 Serratia marcescens str. RS-10
GQ900612.1 gg_id:581996 Serratia marcescens str. A51
FJ655527.1 gg_id:585145 symbiont
EU558694.1 gg_id:264527 Serratia marcescens str. ITA-3
AF124040.1 gg_id:10036 Serratia marcescens
EU558695.1 gg_id:269858 Serratia marcescens str. ITA-4
DQ182326.1 gg_id:140317 Serratia marcescens str. RS-1
AY395011.1 gg_id:97959 Serratia marcescens NAB5
FM213393.2 gg_id:314820 Serratia marcescens str. MN51
AF511431.1 gg_id:65407 Serratia marcescens CCCO6
FJ655529.1 gg_id:590124 symbiont
GQ404683.1 gg_id:571200 Serratia ureilytica str. LSA
EF102861.1 gg_id:249491 Serratia marcescens str. P-4-8RR
FJ976596.1 gg_id:509322 Serratia marcescens
DQ472000.1 gg_id:158703 Serratia marcescens str. C-1
FJ612597.1 gg_id:587160 Serratia marcescens str. SK-07
AY223838.1 gg_id:85525 Serratia marcescens str. ost 3
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NC_009832.1 gg_id:242206 Serratia proteamaculans str. 568
NC_009832.1 gg_id:242205 Serratia proteamaculans str. 568
AJ233434.1 gg_id:10173 Serratia proteamaculans str. DSM 4543
AJ288155.1 gg_id:22004 Serratia proteamaculans 182
M27040.1 gg_id:10162 symbiont S of Acyrthosiphon pisum
EU348323.1 gg_id:332506 symbiont
AF293624.1 gg_id:37966 Uroleucon caligatum symbiont
FJ655545.1 gg_id:590146 symbiont
FJ655524.1 gg_id:583608 symbiont
FJ655485.1 gg_id:566162 symbiont

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EF491959.1	217974	1118.5	614.7	2110.0	2030.3	692.8	1447.8
FJ527456.1	510879	1192.1	640.7	2151.9	1931.6	747.3	1436.6
DQ399752.1	155266	1761.9	1125.6	4166.5	3366.5	1260.2	2059.7
FJ811864.1	576728	752.3	560.9	1234.2	2509.8	726.9	1486.4
DQ399748.1	155784	2590.5	1764.2	5511.6	4876.2	2310.1	3177.8
DQ501957.1	222053	1232.6	1074.0	6152.8	535.5	682.3	1888.9
AF124037.1	10034	4246.3	3458.2	2185.9	5013.4	5042.6	5925.4
EU302853.1	240155	5216.9	3314.1	5673.4	6288.9	4077.3	4571.6
FM202483.1	317955	140.0	508.4	3102.4	276.3	398.8	834.4
FM163485.2	290724	3998.1	3400.6	2223.6	3646.2	6225.3	5472.0
EU407551.1	269227	5774.4	4714.7	3893.1	4609.0	6235.9	5733.0
GQ906774.1	586809	7044.8	6281.1	7139.9	7585.1	6092.6	5899.8
DQ182325.1	140269	2880.3	3426.9	1343.6	4671.2	4484.2	3904.3
GQ900612.1	581996	13628.5	14320.8	17449.4	11575.6	13373.4	11921.3
FJ655527.1	585145	11609.8	9773.6	7027.3	6478.5	12553.0	9871.0
EU558694.1	264527	9830.6	9063.4	5794.1	6346.4	5307.0	5127.8
AF124040.1	10036	3223.4	3244.5	1362.3	2327.5	1549.5	1542.5
EU558695.1	269858	7782.0	8285.1	2763.8	4494.0	5577.8	4165.7
DQ182326.1	140317	693.1	660.7	1901.5	793.9	169.1	804.5
AY395011.1	97959	11448.3	9605.4	5810.7	9208.3	6888.9	9780.1
FM213393.2	314820	116.6	503.4	1828.7	284.1	95.7	545.1
AF511431.1	65407	2845.4	417.2	1886.2	3299.4	4797.7	4009.4
FJ655529.1	590124	15278.7	17462.3	14361.0	12240.9	14735.4	12097.3
GQ404683.1	571200	1444.0	1250.9	3129.8	1322.5	723.4	1473.0
EF102861.1	249491	387.3	544.7	2775.8	337.8	307.5	970.3
FJ976596.1	509322	20355.4	22370.1	7019.2	12456.7	10193.8	8465.2
DQ472000.1	158703	3176.2	2063.3	2593.6	4580.6	1978.2	2189.2
FJ612597.1	587160	3006.1	2401.2	4373.9	3930.7	4575.4	3328.4
AY223838.1	85525	6690.8	6755.1	3254.5	4134.1	6575.6	5822.1
NZ_AAUN01000015.1	180897	1239.2	1329.6	3445.2	906.5	441.8	950.2
NC_009832.1	242206	3007.6	2141.6	3134.3	356.0	523.3	609.6
NC_009832.1	242205	515.9	723.8	3233.3	1000.1	126.0	767.4
AJ233434.1	10173	2215.6	1582.2	3171.9	2059.0	396.8	2099.9
AJ288155.1	22004	10364.3	8782.6	2536.7	3219.7	6414.2	5089.8
M27040.1	10162	188.0	329.3	1195.7	382.5	73.5	416.0
EU348323.1	332506	865.4	1519.3	1630.1	1771.9	1939.0	1599.8
AF293624.1	37966	10747.0	11565.0	7062.1	8123.9	10379.8	9064.9
FJ655545.1	590146	1175.8	1090.9	4685.9	2086.2	1107.9	1959.8
FJ655524.1	583608	1978.0	1708.0	3166.8	1743.0	2545.1	1382.3
FJ655485.1	566162	3720.2	4765.0	4333.2	4474.2	4021.3	3931.2

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AY822592.1 gg_id:114933 Aphis craccivora symbiont
AJ233430.1 gg_id:10170 Serratia grimesii str. DSM 30063
AB334771.1 gg_id:247431 Serratia proteamaculans str. MPU8
EU024331.1 gg_id:240135 intestinal microflora Hepialus gonggaensis larvae RFLP larval gut clone Hg03
EU554429.1 gg_id:275241 Pseudomonas fluorescens str. Ag03
FJ527460.1 gg_id:563283 Pectobacterium subsp. carotovorum str. Ecc4-4
AM696803.1 gg_id:220457 sequencing libraries indoor dust clone BF0001A090
AM696807.1 gg_id:218471 sequencing libraries indoor dust clone BF0001A094
AM696726.1 gg_id:220805 sequencing libraries indoor dust clone BF0001A013
FJ469981.1 gg_id:544455 Serratia grimesii str. N10-1
U93263.1 gg_id:10181 Aranicola proteolyticus
AJ279002.1 gg_id:33276 Serratia fonticola str. IB4
DQ321559.1 gg_id:146025 gut- microorganisms larvae and adults southern pine beetle Dendroctonus frontalis
AY253924.1 gg_id:83887 Serratia liquefaciens k 100
FJ811865.1 gg_id:546427 Serratia liquefaciens str. 1-BCH
EU266583.1 gg_id:256972 Serratia plymuthica str. RG 6
FJ527469.1 gg_id:569600 Pectobacterium subsp. carotovorum str. Ecc7-1
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GU292825.1 gg_id:541724 Serratia sp. str. L5
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EU236755.1 gg_id:250856 Serratia plymuthica str. R1
EU031768.1 gg_id:249473 Serratia sp. str. BS18
AM696754.1 gg_id:218671 sequencing libraries indoor dust clone BF0001A041
AB004751.1 gg_id:10186 Serratia rubidaea str. JCM1240
AJ233429.1 gg_id:10169 Serratia fonticola str. DSM 4576
AJ279044.1 gg_id:27304 Serratia quinivorans subsp. quinovora str. CP6
AM696750.1 gg_id:218954 sequencing libraries indoor dust clone BF0001A037
AY236502.1 gg_id:82090 Serratia fonticola UTAD54
EF428991.1 gg_id:213522 Serratia sp. str. GIST-WP3w2
AM696780.1 gg_id:226629 sequencing libraries indoor dust clone BF0001A067
FJ811862.1 gg_id:589835 Serratia proteamaculans str. 3-CDF
AM696788.1 gg_id:222984 sequencing libraries indoor dust clone BF0001A075
DQ991163.1 gg_id:189593 Serratia grimesii
EU075114.1 gg_id:239779 Serratia sp. str. Lac5
AM696779.1 gg_id:224560 sequencing libraries indoor dust clone BF0001A066
FJ790328.1 gg_id:387955 Serratia sp. C1(2009) str. C1
AM157437.1 gg_id:142918 Serratia proteamaculans mother C4

FJ655482.1	576678	10481.9	10796.4	6211.5	11386.0	8653.6	7865.9
AY822592.1	114933	8453.3	6971.1	8128.1	9804.7	7216.9	6112.1
AJ233430.1	10170	252.8	234.8	1917.2	306.2	578.5	534.8
AB334771.1	247431	2574.3	1777.3	5290.7	5051.2	2263.3	3071.8
EU024331.1	240135	4685.1	4005.9	2782.9	6627.4	6273.2	6453.6
EU554429.1	275241	555.2	903.8	4462.3	532.9	156.1	730.9
FJ527460.1	563283	1067.0	630.8	3269.2	1891.3	1349.8	1638.1
AM696803.1	220457	405.9	448.7	2234.8	474.1	540.1	582.4
AM696807.1	218471	4081.0	3277.4	7413.2	4516.2	3241.0	3723.6
AM696726.1	220805	6182.8	6376.3	6734.4	5939.8	5976.5	6577.4
FJ469981.1	544455	1111.3	600.9	2031.0	1973.8	653.9	1181.6
U93263.1	10181	564.0	651.7	3164.9	636.1	905.4	953.6
AJ279002.1	33276	216.6	359.7	1386.6	297.3	289.2	265.7
DQ321559.1	146025	5240.2	5493.9	7538.3	6352.7	10299.0	10718.8
AY253924.1	83887	748.6	715.2	2792.9	1232.5	358.0	1123.6
FJ811865.1	546427	1332.9	889.3	2099.5	3566.8	1377.0	1763.2
EU266583.1	256972	548.6	381.1	1771.5	746.5	1480.6	1182.1
FJ527469.1	569600	1431.8	918.5	2045.4	340.6	113.0	432.4
EU557336.1	261400	7285.7	5503.3	3920.3	8835.7	12168.8	8629.8
DQ103512.1	131626	457.5	594.4	2714.2	597.0	5233.7	675.9
GU292825.1	541724	1030.4	960.0	3486.4	694.7	148.2	607.1
AM696720.1	217962	3686.0	3318.9	7598.1	5010.6	3885.9	5007.6
AY040208.1	64290	211.0	232.9	1511.1	186.8	325.9	511.1
FN556576.1	526416	1676.2	1195.2	4891.8	3529.8	1686.1	2135.9
EU236755.1	250856	4366.5	1744.0	1430.7	4332.2	2482.1	2450.9
EU031768.1	249473	2723.1	2132.3	5598.6	4606.6	2102.3	3071.1
AM696754.1	218671	5171.1	3552.0	8750.8	7755.9	6159.9	8267.6
AB004751.1	10186	1453.3	940.0	2487.6	1211.1	1420.1	939.1
AJ233429.1	10169	2095.4	1652.8	4054.7	5145.1	808.4	2799.3
AJ279044.1	27304	887.5	536.2	1673.5	1292.2	215.6	461.9
AM696750.1	218954	661.1	988.1	4537.9	757.3	513.1	797.5
AY236502.1	82090	3638.2	2444.7	6457.3	2897.7	1867.5	2347.7
EF428991.1	213522	1950.3	2622.0	2941.7	2307.8	4787.8	3562.1
AM696780.1	226629	2695.6	2768.4	3084.7	2628.1	1641.5	4140.1
FJ811862.1	589835	531.0	472.5	1583.3	2759.3	450.5	1055.5
AM696788.1	222984	6814.6	5054.1	7937.7	9341.0	7907.6	10095.4
DQ991163.1	189593	285.9	242.2	1572.0	305.1	540.5	662.8
EU075114.1	239779	2664.8	2015.7	3227.5	281.1	101.1	431.3
AM696779.1	224560	4114.2	3388.7	7137.0	4502.0	3141.4	3938.3
FJ790328.1	387955	89.1	285.4	1475.7	215.9	82.2	318.4
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AJ279054.1 gg_id:30929 Serratia ficaria str. NCTC 12148
DQ833334.1 gg_id:166089 Title: Anaerobic Reductive Dechlorination Vinyl Chloride ly Enriched AuSable River Se
DQ123840.1 gg_id:148321 Serratia liquefaciens str. JF-1116
AJ306725.1 gg_id:27899 Serratia liquefaciens str. CIP 103238T
AY573038.1 gg_id:101976 Yersinia sp. str. ARCTIC-P11
AJ233436.1 gg_id:10189 Serratia rubidaea str. DSM 4480
EU196322.1 gg_id:247118 Hafnia sp. NP33
AF286870.1 gg_id:43863 Serratia odorifera str. DSM 4582
AM696715.1 gg_id:223409 sequencing libraries indoor dust clone BF0001A002
AM992015.1 gg_id:293839 Serratia sp. str. 5.3R
AM696774.1 gg_id:226256 sequencing libraries indoor dust clone BF0001A061
EU250329.1 gg_id:254678 Serratia entomophila str. Mor4.1
EF451956.1 gg_id:206221 Serratia proteamaculans str. 18A1
AY308053.1 gg_id:88177 Serratia sp. str. AZ22R6
FJ527455.1 gg_id:512247 Pectobacterium subsp. carotovorum str. Ecc7-2
AB009954.1 gg_id:10175 unclassified proteobacteria str. L101
AJ288154.1 gg_id:71258 Serratia sp. SK-3-30-2
AM696805.1 gg_id:225126 sequencing libraries indoor dust clone BF0001A092
DQ321632.1 gg_id:149012 spb29A1-1
AF286869.1 gg_id:34707 Serratia fonticola str. LMG 7882
FJ527459.1 gg_id:556535 Pectobacterium subsp. carotovorum str. Ecc1-7
EF428994.1 gg_id:216947 Serratia sp. str. GIST-WP4w1
AY243097.1 gg_id:85224 Serratia liquefaciens str. Hf1
AM696787.1 gg_id:219390 sequencing libraries indoor dust clone BF0001A074
AM992014.1 gg_id:290849 Serratia sp. str. 5.1R
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FJ811861.1 gg_id:557977 Serratia proteamaculans str. 2A-CDF
AM696769.1 gg_id:225884 sequencing libraries indoor dust clone BF0001A056
AY902209.1 gg_id:113392 Serratia proteamaculans str. BR5
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FJ405353.1 gg_id:365131 Escherichia coli str. 4097
NC_004337.1 gg_id:140570 Shigella flexneri 2a str. 301

AM696721.1	220737	1988.2	1460.7	4559.3	2867.4	1313.6	1631.0
AJ279054.1	30929	1541.0	898.1	2697.3	1517.6	1397.4	1392.5
DQ833334.1	166089	2903.8	2192.8	5858.6	4625.3	2100.0	3067.2
DQ123840.1	148321	1506.0	1203.8	2094.9	1441.0	3295.6	2380.0
AJ306725.1	27899	362.4	310.8	2024.8	449.5	613.1	801.2
AY573038.1	101976	262.6	353.2	2494.9	606.9	323.4	778.8
AJ233436.1	10189	55.7	142.0	1530.9	290.3	144.9	239.5
EU196322.1	247118	7019.8	4917.4	9849.4	6832.3	6154.2	7849.1
AF286870.1	43863	699.6	783.3	2991.1	1451.1	1886.4	1756.6
AM696715.1	223409	6480.3	4077.7	5023.8	7143.1	8429.1	7809.1
AM992015.1	293839	212.7	294.0	1297.5	376.0	296.8	717.4
AM696774.1	226256	624.1	1010.4	5049.3	754.2	545.3	838.1
EU250329.1	254678	558.9	806.6	1498.6	348.7	1477.4	1396.4
EF451956.1	206221	1091.2	698.5	287.2	1539.9	1040.3	1060.8
AY308053.1	88177	1760.6	1140.2	4007.1	3320.4	1274.4	2099.6
FJ527455.1	512247	3191.5	2072.2	2763.5	216.1	103.2	421.5
AB009954.1	10175	1069.8	1042.9	1481.0	2385.0	2950.5	3036.9
AJ288154.1	71258	6691.5	7402.4	4468.8	7778.7	12621.4	9690.3
AM696805.1	225126	279.7	650.2	4452.0	470.1	422.7	684.7
DQ321632.1	149012	1718.4	912.3	1797.2	1566.3	2371.8	2137.9
AF286869.1	34707	1922.0	2145.0	4006.6	2649.4	318.1	1032.3
FJ527459.1	556535	1138.4	662.5	2631.8	2591.8	1288.0	1715.5
EF428994.1	216947	7835.6	7958.1	6577.3	5567.0	5596.7	5370.7
AY243097.1	85224	1082.7	678.4	3341.9	2248.9	1147.6	1564.0
AM696787.1	219390	6245.4	4238.4	7325.2	4793.3	7586.9	6367.7
AM992014.1	290849	4053.8	3578.8	4689.4	5567.9	5052.4	4454.7
EU024350.1	253194	551.1	442.3	2233.8	2170.5	277.5	1160.3
FJ811861.1	557977	226.6	245.1	1830.0	163.0	232.6	517.0
AM696769.1	225884	5246.0	4540.2	5427.6	3014.4	5391.9	4999.7
AY902209.1	113392	275.5	292.0	859.1	577.2	186.0	400.1
DQ530081.1	160086	10011.2	8828.1	9902.8	11140.3	14367.9	12767.9
FJ655531.1	586383	368.3	355.2	376.5	399.6	79.5	347.6
FJ655517.1	554574	5392.2	5024.5	4364.8	5985.9	4368.7	5241.3
AY620432.1	99056	45.1	96.0	111.7	99.9	105.9	88.2
EU348314.1	316943	1939.2	1164.4	3831.6	4224.7	1078.1	2194.9
EU348315.1	352486	2065.5	1327.5	2214.8	1952.7	874.3	887.0
FJ655518.1	576533	12867.0	10342.0	5463.2	7805.8	10553.3	10179.1
EU348318.1	355736	8618.9	7573.9	3076.9	4897.6	3983.4	3700.5
NC_007606.1	145027	1688.3	495.3	4799.3	1695.1	744.2	779.9
FJ405353.1	365131	485.6	783.4	2393.4	1541.2	1278.9	1495.5
NC_004337.1	140570	235.7	585.9	3110.7	551.4	734.5	703.4

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s__Shigella flexneri	5024
s__Shigella flexneri	5485
s__Shigella flexneri	5675
s__Shigella flexneri	5784
s__Shigella flexneri	6154
s__unclassified	4296
s__unclassified	4328
s__unclassified	4525
s__unclassified	4571
s__unclassified	4759
s__unclassified	4771
s__unclassified	4810
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s__unclassified	4890
s__unclassified	4900
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s__unclassified	5666
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s__unclassified	5828
s__unclassified	5849
s__unclassified	5870
s__unclassified	5892
s__unclassified	6034
s__unclassified	6058
s__unclassified	6100
s__endosymbiont of Columbicola columbae	6521
s__Sodalis glossinidius	6210
s__unclassified	4396
s__unclassified	4768
s__unclassified	5786
s__unclassified	6144
s__unclassified	6191
s__unclassified	6272

NC_008258.1 gg_id:168839 Shigella flexneri 5 str. 8401
AE014073.1 gg_id:146756 Shigella flexneri 2a str. 2457T
EF643608.1 gg_id:249718 Shigella flexneri str. FBD001shig
NC_008258.1 gg_id:168833 Shigella flexneri 5 str. 8401
NC_004741.1 gg_id:129308 Shigella flexneri 2a str. 2457T
EU467921.1 gg_id:293331 cheetah feces clone CE2_b06
GQ048030.1 gg_id:421118 Topographical and Temporal Human Skin Microbiome skin palm clone nbw140e08c1
GQ141872.1 gg_id:410166 Escherichia coli str. petra-05
EU766807.1 gg_id:342976 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1
EF528266.1 gg_id:222400 Escherichia coli str. CICCHLJ Q41
GQ155203.1 gg_id:543477 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
EU458164.1 gg_id:296929 North American black bear feces clone BB2_g06
GQ007663.1 gg_id:502000 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GU594305.1 gg_id:521179 Escherichia coli str. B50
GQ155258.1 gg_id:588262 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
EU470621.1 gg_id:293683 red panda feces clone RP_1aaa03d04
X96966.1 gg_id:9686 Shigella dysenteriae
GQ155109.1 gg_id:543251 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
GQ155303.1 gg_id:577035 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
GQ155087.1 gg_id:586921 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
GQ155248.1 gg_id:548241 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
AY098487.1 gg_id:66579 Escherichia coli AK108
DQ819201.1 gg_id:162903 mouse cecal microbiota-colonized zebrafish digestive tract clone aab27a07
GQ155047.1 gg_id:513655 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
GQ155132.1 gg_id:551754 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
EU472747.1 gg_id:293399 red panda feces clone RPSD_1aaa03h08
EU778502.1 gg_id:304899 Red Panda feces clone RPSD_1aaa03a11
GQ155304.1 gg_id:563327 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
GQ047990.1 gg_id:441018 Topographical and Temporal Human Skin Microbiome skin palm clone nbw140a03c1
GQ155143.1 gg_id:593967 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
AM184304.1 gg_id:159905 Shigella flexneri str. WAB1966
GQ155305.1 gg_id:578663 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
GQ155234.1 gg_id:590391 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
AB303383.1 gg_id:246629 slender pigeon louse Columbicola columbae symbiont
AY861702.1 gg_id:112007 Sodalis glossinidius str. GA-SG
AF005235.1 gg_id:9987 primary endosymbiont Sitophilus oryzae str. SFr of
AF548137.1 gg_id:96697 symbiont
AM774412.1 gg_id:237905 Biostraticola tofi str. BF36
AF548139.1 gg_id:95263 symbiont
AF548142.1 gg_id:95903 symbiont
DQ133565.1 gg_id:148901 Preliminary survey insects (Hemiptera: Coccoidea) scale insect clone

NC_008258.1	168839	414.1	527.4	1632.0	1065.7	933.4	884.4
AE014073.1	146756	218.0	462.3	2549.8	434.2	764.5	569.9
EF643608.1	249718	267.4	462.6	2021.8	646.3	814.5	577.9
NC_008258.1	168833	167.3	360.8	2210.4	324.1	333.7	607.9
NC_004741.1	129308	170.1	381.4	2277.1	362.8	344.5	548.8
EU467921.1	293331	1513.7	1473.9	4373.1	2484.1	1348.9	2124.8
GQ048030.1	421118	4505.8	4952.6	5405.8	3614.9	4727.9	4976.3
GQ141872.1	410166	1010.2	1019.6	4033.8	1775.8	1183.7	1752.8
EU766807.1	342976	972.9	1075.4	4074.6	1509.7	1161.9	1605.8
EF528266.1	222400	569.1	704.4	2318.7	711.0	556.0	854.2
GQ155203.1	543477	431.4	1128.4	2579.2	213.4	1994.9	983.9
EU458164.1	296929	3631.3	4364.6	6629.1	4240.2	4452.3	7588.2
GQ007663.1	502000	640.2	732.2	3049.2	1048.6	552.8	1075.2
GU594305.1	521179	1227.7	1354.6	4159.0	1533.5	1438.2	1543.1
GQ155258.1	588262	7066.4	7213.2	12045.2	6602.2	9364.0	8372.2
EU470621.1	293683	7672.1	8809.1	6195.5	8917.8	7408.7	5242.4
X96966.1	9686	9785.6	5503.5	14697.1	9686.7	5166.1	5400.4
GQ155109.1	543251	1289.3	1477.5	3378.3	1524.1	1661.2	1494.5
GQ155303.1	577035	8100.1	8091.1	4629.5	4744.7	5665.0	5158.4
GQ155087.1	586921	12134.1	10406.9	9902.9	11248.9	14863.2	10133.4
GQ155248.1	548241	10303.3	10823.1	14037.5	8477.7	13721.3	11615.2
AY098487.1	66579	896.0	1943.7	1004.3	459.0	4912.3	2296.5
DQ819201.1	162903	7723.9	5258.9	4424.0	9658.0	4668.9	5818.1
GQ155047.1	513655	4101.0	6382.5	5431.5	3695.1	9802.7	5700.8
GQ155132.1	551754	1052.1	1391.7	5542.6	1146.6	1298.8	1661.4
EU472747.1	293399	619.9	735.4	1789.5	622.8	700.9	681.0
EU778502.1	304899	935.0	965.9	3046.2	1543.5	1237.1	1473.6
GQ155304.1	563327	1302.0	1264.6	3215.2	1563.9	1444.2	1432.6
GQ047990.1	441018	4715.6	4204.8	4759.8	4678.9	4153.6	5082.3
GQ155143.1	593967	801.3	1179.3	5093.8	787.1	854.9	1110.1
AM184304.1	159905	560.0	773.8	4323.8	750.2	530.9	999.9
GQ155305.1	578663	13846.1	11835.0	4503.3	4028.0	9362.6	7170.4
GQ155234.1	590391	1327.2	1376.3	4586.3	1563.0	1436.6	1605.1
AB303383.1	246629	3838.6	3341.5	7099.3	6469.7	6649.1	8006.6
AY861702.1	112007	689.9	771.5	1137.9	579.1	2012.6	1822.9
AF005235.1	9987	1606.5	1039.8	1008.9	2087.4	1134.9	1200.4
AF548137.1	96697	126.8	155.9	1090.8	220.4	70.1	103.6
AM774412.1	237905	285.0	368.2	1032.1	227.6	114.4	310.9
AF548139.1	95263	3333.4	2916.3	2697.8	4672.1	4728.1	4131.1
AF548142.1	95903	2684.7	1676.1	4284.5	3579.8	1676.3	3002.5
DQ133565.1	148901	5912.9	5865.8	6405.3	5145.1	10112.7	6684.8

k__Bacteria	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria
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g__Tatumella
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g__Thorsiella
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s__Pantoea citrea	6071
s__Tatumella morbirosei	4867
s__Tatumella ptyseos	5764
s__unclassified	4475
s__unclassified	4788
s__unclassified	5098
s__unclassified	5528
s__unclassified	6567
s__Citrobacter farmeri	4447
s__Citrobacter farmeri	5210
s__Citrobacter farmeri	5555
s__Citrobacter farmeri	5584
s__Citrobacter farmeri	5780
s__Citrobacter farmeri	5790
s__Citrobacter farmeri	5875
s__Citrobacter farmeri	5990
s__Citrobacter rodentium	4772
s__Enterobacter radicincitans	6229
s__Kluyvera ascorbata	4413
s__Kluyvera ascorbata	4743
s__Kluyvera ascorbata	4872
s__unclassified	4283
s__unclassified	4565
s__unclassified	4628
s__unclassified	4898
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s__unclassified	5224
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s__Cimex lectularius endosymbiont	4577
s__unclassified	4116
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s__unclassified	4131
s__unclassified	4155
s__unclassified	4159

EF688008.1 gg_id:341714 Pantoea citrea str. LMG 22049
FJ617235.1 gg_id:570566 Tatumella morbirosei str. LMG 23359
AJ233437.1 gg_id:10066 Tatumella ptyseos str. DSM 5000
EU877956.1 gg_id:565203 Tatumella ptyseos str. UAPS07005
EU215774.1 gg_id:257750 Tatumella saanichensis str. 06-3099
FJ611886.1 gg_id:552042 Pantoea punctata str. LMG 22097
EF688007.1 gg_id:330933 Pantoea terrea str. LMG 22051
AY837748.1 gg_id:142906 Thorsellia anophelis str. CCUG 49520 H2.1
GU185859.1 gg_id:535185 Citrobacter amalonaticus str. SA01
AB088049.1 gg_id:77675 Citrobacter sp. str. VA53
AB504755.1 gg_id:386435 Citrobacter farmeri
EU030438.1 gg_id:350440 Citrobacter farmeri
FN433041.1 gg_id:573221 Citrobacter farmeri CCM30B
DQ187379.1 gg_id:140670 Citrobacter amalonaticus
AY379978.1 gg_id:98643 Salmonella sp. str. AHL 6
FN433046.1 gg_id:561185 Citrobacter farmeri CCM35B
NR_028686.1 gg_id:586695 Citrobacter sedlakii str. I-75; CDC 4696-86
EU931550.1 gg_id:335500 Klebsiella oxytoca str. ZFJ-11
AF176567.1 gg_id:71543 Kluyvera ascorbata str. CDC 2064/78
AM933758.1 gg_id:332628 Kluyvera ascorbata 4105
AJ627203.1 gg_id:106098 Kluyvera ascorbata 276
AF025370.1 gg_id:9766 Citrobacter amalonaticus str. CDC 9020-77
GQ205104.1 gg_id:558666 Enterobacter sp. str. RF-100
DQ923474.1 gg_id:235571 Enterobacter sp. str. g1
FJ593851.1 gg_id:527723 Enterobacter sp. str. MTP_050512_17
AY683044.1 gg_id:137822 Enterobacter sp. str. CBMB30
EU753977.1 gg_id:315576 Enterobacter sp. str. FR7
NR_024861.1 gg_id:559750 Citrobacter farmeri str. CDC 2991-81; CIP 104553
EF025329.1 gg_id:178177 Enterobacter cloacae subsp. dissolvens str. SREPS 3
AB475140.1 gg_id:518801 Cimex lectularius endosymbiont str. SYDL
GQ492450.1 gg_id:590760 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
AAJU02000050.1 gg_id:311814 Escherichia coli str. F11
EU773756.1 gg_id:323418 Cheetah feces clone CE2_h04_1
AB244469.1 gg_id:253351 Enterobacter cloacae str. NC1111
AM980865.1 gg_id:369200 Escherichia coli str. ATCC 35218
EU460669.1 gg_id:289561 polar bear feces clone PB2_aai24b09
AB244459.1 gg_id:248864 Citrobacter freundii str. C3-1
FJ811872.1 gg_id:586506 Enterobacter aerogenes str. 11-WCH
GQ047957.1 gg_id:440793 Topographical and Temporal Human Skin Microbiome skin palm clone nbw139e11c1
AY253921.1 gg_id:85035 Rahnella aquatilis m 46
GQ155272.1 gg_id:575075 Human gut microbiome adopts alternative state bowel transplantation ileum intesti

EF688008.1	341714	1246.1	1380.1	5287.3	1624.2	1108.9	1651.8
FJ617235.1	570566	88.0	166.7	1076.2	96.5	74.8	69.1
AJ233437.1	10066	1850.2	963.5	890.9	2051.2	409.4	667.1
EU877956.1	565203	441.4	701.1	855.1	971.4	424.1	793.1
EU215774.1	257750	35.7	115.1	1444.2	116.1	81.4	146.7
FJ611886.1	552042	1098.5	1054.9	1101.2	445.8	1090.4	713.9
EF688007.1	330933	436.5	704.8	2258.5	347.7	182.4	664.3
AY837748.1	142906	25.6	54.4	92.3	65.5	58.7	23.3
GU185859.1	535185	73.5	307.6	1589.2	113.0	65.6	326.4
AB088049.1	77675	371.8	830.9	908.8	1364.0	1293.0	754.6
AB504755.1	386435	102.6	256.4	240.6	145.3	96.8	199.0
EU030438.1	350440	47.9	208.5	1021.2	132.5	61.7	139.0
FN433041.1	573221	14962.3	13267.6	8550.3	8911.9	10753.6	10919.6
DQ187379.1	140670	104.5	327.2	1166.7	276.0	125.0	287.2
AY379978.1	98643	186.8	351.9	1000.9	190.8	137.6	379.5
FN433046.1	561185	229.7	585.9	2085.5	178.4	170.5	168.5
NR_028686.1	586695	43.6	174.2	253.9	79.8	117.7	106.4
EU931550.1	335500	1784.6	2338.6	4433.4	2313.1	3479.7	3165.6
AF176567.1	71543	103.5	224.9	921.9	431.6	262.7	277.1
AM933758.1	332628	86.4	439.8	608.5	401.5	141.2	319.6
AJ627203.1	106098	268.5	594.0	2971.2	381.7	175.6	435.6
AF025370.1	9766	139.9	408.2	1862.1	165.4	146.7	543.8
GQ205104.1	558666	213.1	785.1	1958.2	456.0	1100.8	1097.3
DQ923474.1	235571	179.9	558.3	2375.9	680.4	737.7	359.5
FJ593851.1	527723	6197.2	5497.4	5893.1	6102.9	10269.4	4736.2
AY683044.1	137822	2398.7	2578.9	5545.7	3180.7	3805.8	3027.7
EU753977.1	315576	2644.0	2707.6	2803.0	3784.7	5213.3	4605.2
NR_024861.1	559750	145.6	306.0	1387.6	160.9	91.3	290.2
EF025329.1	178177	257.0	312.0	744.9	398.1	732.4	294.2
AB475140.1	518801	1578.2	1377.5	2127.5	1351.5	2279.8	3181.7
GQ492450.1	590760	462.4	609.4	2426.1	787.5	496.4	796.1
AAJU02000050.1	311814	631.8	1064.2	3541.0	1135.8	1150.3	1099.4
EU773756.1	323418	13819.8	12487.3	11033.5	9955.0	13376.3	12281.2
AB244469.1	253351	1334.3	1741.8	4392.0	1644.5	1836.1	2082.3
AM980865.1	369200	483.2	976.4	721.3	923.7	3059.7	3537.8
EU460669.1	289561	575.3	1125.3	3042.1	875.2	884.8	776.5
AB244459.1	248864	502.7	996.6	1484.5	471.5	1275.2	797.0
FJ811872.1	586506	2481.2	2737.3	2099.1	3104.5	3288.3	2973.7
GQ047957.1	440793	10504.7	9580.9	8819.7	9956.5	9765.5	7502.4
AY253921.1	85035	6534.3	4075.3	8752.9	6184.7	8047.8	6616.1
GQ155272.1	575075	12222.9	11292.7	8226.2	10291.2	13902.5	13731.2

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AF373174.1 gg_id:72751 Erwinia chrysanthemi str. GSPB 413
GQ167172.1 gg_id:592775 Effects Hydraulic Retention Time on Anaerobic Hydrogenation Performance Microbi
EU472695.1 gg_id:288236 red panda feces clone RPSD_1aaa02d08
GQ047715.1 gg_id:441491 Topographical and Temporal Human Skin Microbiome skin palm clone nbw138d06c1
GQ155218.1 gg_id:561972 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
EU723822.1 gg_id:345487 Shigella sonnei str. HDDMG06
AB479110.1 gg_id:561984 Escherichia hermannii str. YS-11
GQ155226.1 gg_id:513466 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
GQ155033.1 gg_id:572044 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
EU472730.1 gg_id:290622 red panda feces clone RPSD_1aaa01a11
EU470818.1 gg_id:288035 red panda feces clone RP_2aaa01b05
ABHR01000009.1 gg_id:292182 Escherichia coli O157:H7 str. EC4401
EU472797.1 gg_id:295950 red panda feces clone RPSD_1aaa03d01
DQ441386.1 gg_id:184632 human intestinal biopsy clone CD135
EF179843.1 gg_id:271664 sequences adult Anopheles darlingi (Diptera: Culicidae) mosquitoes clone 1.1
GQ047641.1 gg_id:385282 Topographical and Temporal Human Skin Microbiome skin palm clone nbw137b10c1
GQ491694.1 gg_id:593660 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
AY689045.1 gg_id:105300 Enterobacter sp. str. 6B_5
EF189919.1 gg_id:365055 Pantoea stewartii 40G RT2A
EU466029.1 gg_id:295053 African elephant feces clone AFEL3_aao16b08
FN433049.1 gg_id:547245 Citrobacter braakii CCM33B
EU460308.1 gg_id:299829 polar bear feces clone PB1_aai26c12
GQ155101.1 gg_id:565925 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
GQ047977.1 gg_id:445372 Topographical and Temporal Human Skin Microbiome skin palm clone nbw139g10c1
EU472889.1 gg_id:293518 red panda feces clone RPSD_1aaa03f04
EU471175.1 gg_id:293468 red panda feces clone RP_3aaa01g02
AY792270.1 gg_id:122049 Humic Lake clone CrystalBog1E3
FJ364672.1 gg_id:370240 feces adult twins and mothers; TS19 clone TS19_a01f10
EU460405.1 gg_id:294051 polar bear feces clone PB1_aai28b07
DQ818978.1 gg_id:168683 mouse cecal microbiota-colonized zebrafish digestive tract clone aab40d10
DQ133536.1 gg_id:138463 Citrobacter freundii str. GM1
EU470874.1 gg_id:300686 red panda feces clone RP_2aaa01h11
AJ223409.1 gg_id:9789 Pectobacterium cacticida
EF608524.1 gg_id:228556 predatory Poecilus chalcites their response lab rearing and antibiotic treatment diges
AY227805.1 gg_id:100736 Pantoea dispersa UQ68J
GQ155135.1 gg_id:578405 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
EF551364.1 gg_id:223793 Enterobacter cloacae str. Rs-35
GQ156545.1 gg_id:510870 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
GQ025567.1 gg_id:419206 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ031700.1 gg_id:436114 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
EF643377.1 gg_id:236811 Mangroveibacter plantisponsor str. MSSRF40

AF373174.1	72751	38.9	113.5	1283.3	143.0	76.7	158.6
GQ167172.1	592775	1031.0	848.6	2321.3	1554.8	2100.2	1480.7
EU472695.1	288236	10630.4	11615.8	4696.6	8950.1	10256.6	9159.1
GQ047715.1	441491	226.8	365.0	1076.7	986.3	1054.4	1098.2
GQ155218.1	561972	1079.8	1520.3	4645.5	1549.2	2333.1	1673.9
EU723822.1	345487	1489.0	1081.0	2317.2	1780.6	965.0	1621.3
AB479110.1	561984	618.9	1379.7	6115.4	834.3	1724.1	1225.6
GQ155226.1	513466	1283.6	1435.5	2412.3	1525.2	1551.5	1434.9
GQ155033.1	572044	1021.0	1160.8	2890.5	790.8	814.8	1279.8
EU472730.1	290622	2118.1	2116.6	5544.9	2828.0	2038.4	3108.9
EU470818.1	288035	1320.8	1409.6	4854.7	2142.8	1561.0	2105.6
ABHR01000009.1	292182	2068.7	1019.3	2385.2	3492.2	823.9	2094.7
EU472797.1	295950	1491.6	1458.6	3885.5	2408.2	1362.2	2050.3
DQ441386.1	184632	1463.4	1454.2	4893.7	2005.6	1311.4	1961.0
EF179843.1	271664	1727.6	1435.6	1097.3	1350.2	583.7	906.5
GQ047641.1	385282	1904.1	1416.4	1281.1	3317.7	2433.8	3260.4
GQ491694.1	593660	4043.2	4226.6	3908.7	4434.2	3583.7	3698.8
AY689045.1	105300	122.9	686.1	2400.7	290.2	145.0	286.7
EF189919.1	365055	1886.8	1456.4	4003.2	611.3	1226.0	734.8
EU466029.1	295053	871.2	1677.4	2887.6	1048.7	2237.0	2020.1
FN433049.1	547245	62.7	363.4	1443.1	148.5	43.3	266.1
EU460308.1	299829	7981.9	7806.7	3921.4	7464.8	5722.6	5657.3
GQ155101.1	565925	880.6	1150.3	3575.2	962.0	1047.8	1634.0
GQ047977.1	445372	674.6	1188.9	1234.4	651.1	1922.0	1702.1
EU472889.1	293518	1855.7	2288.2	2944.6	1853.1	5859.6	4305.6
EU471175.1	293468	452.8	618.3	771.7	254.5	533.3	445.5
AY792270.1	122049	11920.5	12708.7	13965.6	12939.4	17466.2	16768.1
FJ364672.1	370240	830.9	1450.8	3698.1	1573.2	1501.3	1640.1
EU460405.1	294051	1176.5	1152.5	3122.9	1933.1	1219.6	1599.1
DQ818978.1	168683	4280.2	3916.0	5963.1	6236.7	6579.1	6783.7
DQ133536.1	138463	470.6	845.9	1763.0	494.1	499.8	541.8
EU470874.1	300686	8444.8	7052.3	4337.9	11151.1	9627.0	8478.7
AJ223409.1	9789	187.5	580.6	822.0	588.6	930.1	1705.0
EF608524.1	228556	276.5	455.5	580.6	141.3	259.7	1067.2
AY227805.1	100736	251.4	395.5	1750.5	158.0	188.4	471.2
GQ155135.1	578405	4987.7	4122.2	5725.0	4838.6	6915.6	7423.7
EF551364.1	223793	883.2	958.2	1833.0	1043.4	2401.7	1020.6
GQ156545.1	510870	241.4	675.5	1992.3	499.2	1618.3	1557.2
GQ025567.1	419206	1859.2	2755.0	6550.1	2759.2	3615.3	3125.4
GQ031700.1	436114	9275.6	10665.6	7785.7	9234.6	13740.3	13448.8
EF643377.1	236811	73.6	366.0	486.9	254.7	104.1	247.3

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EU472645.1 gg_id:299105 red panda feces clone RPSD_1aaa01f02
EU472888.1 gg_id:287425 red panda feces clone RPSD_1aaa01a08
GQ280089.1 gg_id:564812 Enterobacter sp. str. JS-19
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EU472787.1 gg_id:292501 red panda feces clone RPSD_1aaa04h10
AF273037.1 gg_id:25611 Samsonia erythrinae
EU459221.1 gg_id:292667 hedgehog feces clone HH_aai34c03
DQ418491.1 gg_id:167165 Pectobacterium sp. str. Zhaotong
EU766876.1 gg_id:338288 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1
GQ155237.1 gg_id:576536 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
EU471097.1 gg_id:288710 red panda feces clone RP_3aaa04h05
GQ492914.1 gg_id:574632 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
GQ032083.1 gg_id:402097 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
EU471321.1 gg_id:301319 red panda feces clone RP_3aaa04c11
GQ047644.1 gg_id:442743 Topographical and Temporal Human Skin Microbiome skin palm clone nbw137c01c1
GQ102003.1 gg_id:443904 Topographical and Temporal Human Skin Microbiome skin palm clone nbw502d01c1
EU468008.1 gg_id:294204 cheetah feces clone CE2_b02_1
EU762556.1 gg_id:321515 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A
GQ493642.1 gg_id:551110 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
GQ155290.1 gg_id:561147 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
GQ155055.1 gg_id:509758 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
GQ492249.1 gg_id:536894 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
EU470678.1 gg_id:290999 red panda feces clone RP_1aaa02d02
EF515346.1 gg_id:226413 Electricigen Enrichment MFC upf microbial fuel cell anode clone 23b11
EU472809.1 gg_id:299738 red panda feces clone RPSD_1aaa02d05
EU596536.1 gg_id:273327 Pantoea agglomerans str. SZ009
EU289465.1 gg_id:240399 metagenomic approach biosynthesis ansamycin endophytes or symbionts enriched s
AB548574.1 gg_id:531505 Escherichia coli str. JCM 24001
EU466771.1 gg_id:289838 African elephant feces clone AFEL2_aao29c08
EU472860.1 gg_id:295962 red panda feces clone RPSD_1aaa02g08
GQ155181.1 gg_id:512375 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
GQ114745.1 gg_id:385051 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
EU472794.1 gg_id:294989 red panda feces clone RPSD_1aaa03a08
FJ683754.1 gg_id:530543 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ248277.1 gg_id:142545 carbon tetrachloride contaminated soil clone TA2
EU772604.1 gg_id:322410 North American Black Bear feces clone BB1_h09
GU166291.1 gg_id:588020 Pantoea sp. str. Y1
E05133.1 gg_id:28107 Escherichia coli

GQ031723.1	442225	13698.6	13349.9	11972.0	11994.3	11344.9	10882.3
EF515479.1	221689	2566.1	3086.9	3299.4	2809.7	8881.1	4432.8
GQ099252.1	408166	2410.6	2589.3	5317.6	6283.3	3438.5	3570.7
EU472645.1	299105	3535.0	3700.0	4521.2	3973.0	3204.0	3872.2
EU472888.1	287425	2701.6	3421.3	1399.0	170.9	3786.1	4111.8
GQ280089.1	564812	217.1	562.7	930.3	295.4	107.2	149.9
EU470635.1	289750	1250.4	1121.9	3279.1	2210.0	1096.2	1945.5
EU472787.1	292501	2017.4	971.4	2081.8	2948.9	799.9	1833.3
AF273037.1	25611	3109.8	3447.0	7301.2	2871.3	4098.0	4400.0
EU459221.1	292667	1276.3	749.9	2399.2	1115.3	2378.4	1550.9
DQ418491.1	167165	343.9	757.5	1574.2	602.4	777.5	595.9
EU766876.1	338288	5383.5	5295.2	8214.1	6842.3	7177.3	8125.9
GQ155237.1	576536	12089.2	9593.6	8095.2	9366.4	9681.3	8980.1
EU471097.1	288710	6722.4	7743.8	2756.0	6192.2	5758.4	4797.6
GQ492914.1	574632	6338.8	6436.4	6819.7	6653.6	5610.3	5149.2
GQ032083.1	402097	3886.4	3160.0	6144.2	6159.4	4333.3	4145.7
EU471321.1	301319	2540.1	2256.1	2204.7	4282.2	3120.5	4685.9
GQ047644.1	442743	7797.0	6223.3	3537.8	10078.7	7228.4	6640.6
GQ102003.1	443904	2393.5	1456.7	5187.7	4268.8	2385.1	1355.8
EU468008.1	294204	360.7	817.0	1926.8	504.1	213.2	513.5
EU762556.1	321515	2282.8	1921.7	3593.7	2836.7	2246.3	2411.7
GQ493642.1	551110	2983.5	3827.9	9040.0	3597.8	6473.4	6140.6
GQ155290.1	561147	4118.3	5238.0	9501.5	5245.4	8549.5	9727.0
GQ155055.1	509758	1417.8	1577.1	3552.8	1551.4	1594.0	1505.6
GQ492249.1	536894	1552.4	1932.2	2928.6	3088.2	2971.4	2404.8
EU470678.1	290999	668.2	975.3	971.0	2257.2	2126.5	2991.4
EF515346.1	226413	140.5	201.9	848.5	267.1	204.7	372.1
EU472809.1	299738	7834.1	6033.7	4634.6	9480.4	6610.7	5909.6
EU596536.1	273327	185.0	379.2	2504.8	437.0	1289.1	374.1
EU289465.1	240399	868.6	1179.6	1688.1	1103.9	2502.6	1321.7
AB548574.1	531505	581.8	724.7	3016.2	1397.2	970.7	1357.8
EU466771.1	289838	1757.9	1549.2	4557.1	2797.8	1578.6	2674.6
EU472860.1	295962	3156.8	2862.3	2290.9	3978.6	1962.0	3150.1
GQ155181.1	512375	4826.1	5169.3	10313.1	4440.7	8561.7	6613.0
GQ114745.1	385051	6148.5	5156.3	9223.6	6053.5	7053.3	6872.4
EU472794.1	294989	4706.4	4879.0	9164.6	6941.7	5508.8	7904.4
FJ683754.1	530543	4054.4	4168.8	10934.9	6036.0	4888.1	5303.4
DQ248277.1	142545	39.7	52.8	35.4	73.8	61.0	50.3
EU772604.1	322410	942.0	960.3	3278.0	1393.1	1180.3	1352.6
GU166291.1	588020	260.8	444.8	1684.8	512.0	142.6	381.3
E05133.1	28107	1687.2	1258.4	3865.1	2938.7	1567.6	2482.9

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X80679.1 gg_id:9700 Shigella flexneri
GQ025616.1 gg_id:409079 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
AB548828.1 gg_id:514244 Citrobacter freundii str. JCM 24063
GQ304782.1 gg_id:585624 Shigella flexneri str. A6
NC_008253.1 gg_id:162759 Escherichia coli str. 536
GQ101929.1 gg_id:465791 Topographical and Temporal Human Skin Microbiome skin palm clone nbw501a07c1
AJ010486.1 gg_id:9947 Enterobacter pyrinus str. KCTC2520
DQ785510.1 gg_id:171754 Pectobacterium carotovorum str. ZJR1
EU472892.1 gg_id:289762 red panda feces clone RPSD_1aaa01f07
GQ031973.1 gg_id:484652 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw:
AM419020.1 gg_id:196793 Rahnella sp. str. NJ-8
EU470589.1 gg_id:290393 red panda feces clone RP_1aaa03e10
EU530394.1 gg_id:261413 mucosa adherent and invasive microbes adenoma colorectal cancer profile non-ader
AB004744.1 gg_id:10064 Enterobacter asburiae str. JCM6051
EU887834.1 gg_id:349857 and RFLP slurry Nisargruna biogas plant aerobic predigester clone 11A
GU594302.1 gg_id:519860 Escherichia coli str. A23
GQ155206.1 gg_id:569366 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
EF515196.1 gg_id:226252 Electricigen Enrichment MFC upf microbial fuel cell anode clone 21b10
EF560793.1 gg_id:238066 Escherichia coli str. BEG21
DQ818882.1 gg_id:166890 mouse cecal microbiota-colonized zebrafish digestive tract clone aab39b10
GQ155211.1 gg_id:546826 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
EU470583.1 gg_id:302277 red panda feces clone RP_1aaa04a10
FJ906906.1 gg_id:571278 Cronobacter muytjensii str. Jor93
DQ068925.1 gg_id:139022 microbiota antlions (Myrmeleon mobilis) whole animal laboratory starved antlion O
AM184307.1 gg_id:160426 Pantoea agglomerans str. WAB1969
GQ009455.1 gg_id:500210 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw77
GQ102029.1 gg_id:442720 Topographical and Temporal Human Skin Microbiome skin palm clone nbw502f06c1
GQ155009.1 gg_id:566225 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
AP010960.1 gg_id:546416 Escherichia coli O111:H- str. 11128
X80729.1 gg_id:9692 Escherichia coli str. PK3
GQ155095.1 gg_id:510292 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
GU223214.1 gg_id:581700 Enterobacter cloacae str. SK_C-2
U92195.1 gg_id:9714 Salmonella enterica subsp. houtenae serovar Houten str. Sh1 subsp.
GQ102010.1 gg_id:386695 Topographical and Temporal Human Skin Microbiome skin palm clone nbw502d08c
GQ491972.1 gg_id:550764 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
GQ031668.1 gg_id:440795 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
FJ009375.1 gg_id:338379 Enterobacter cancerogenus str. H3
AJ605115.1 gg_id:112171 Escherichia coli str. BL21
AB548825.1 gg_id:514639 Citrobacter freundii str. JCM 24060
DQ392983.1 gg_id:156485 Pantoea agglomerans str. d
GQ154854.1 gg_id:511626 Human gut microbiome adopts alternative state bowel transplantation ileum intesti

X80679.1	9700	103.1	529.2	1978.3	476.4	366.5	338.2
GQ025616.1	409079	14430.0	15149.3	6197.1	8002.9	10952.3	10117.0
AB548828.1	514244	274.7	941.0	3424.8	496.9	218.6	758.5
GQ304782.1	585624	2515.1	1939.1	3514.6	3467.1	1851.8	2240.6
NC_008253.1	162759	1707.7	2149.0	3641.7	2517.1	2609.6	2575.3
GQ101929.1	465791	1877.4	2176.3	4429.4	3550.0	2132.1	1999.0
AJ010486.1	9947	5472.9	5114.3	2867.7	3129.0	2096.3	2374.0
DQ785510.1	171754	2699.8	3394.6	6473.5	3807.2	2147.0	2269.7
EU472892.1	289762	96.3	247.8	656.4	287.1	260.7	330.1
GQ031973.1	484652	1623.9	1835.2	987.4	1196.0	579.5	2001.2
AM419020.1	196793	236.0	376.6	716.8	440.4	1595.5	293.5
EU470589.1	290393	12804.3	11626.2	8985.2	12688.3	11543.2	9945.2
EU530394.1	261413	17470.1	18005.7	11664.7	12144.3	16165.8	13231.4
AB004744.1	10064	232.4	789.1	1946.6	374.4	887.7	828.7
EU887834.1	349857	4333.0	2923.1	4413.6	2915.2	6205.6	4467.0
GU594302.1	519860	827.7	1171.9	3717.2	1544.7	1379.8	1677.4
GQ155206.1	569366	1242.0	1423.9	5627.8	1571.1	1513.9	1660.7
EF515196.1	226252	493.7	616.9	2308.8	325.6	140.2	510.4
EF560793.1	238066	962.8	993.8	3086.4	1385.0	1120.7	1314.8
DQ818882.1	166890	18222.2	16766.2	13628.7	17532.1	19463.6	19024.4
GQ155211.1	546826	8796.0	8031.8	6014.1	7449.5	10280.2	10605.3
EU470583.1	302277	984.8	875.2	2010.7	1519.2	1162.6	1398.6
FJ906906.1	571278	1782.9	1718.2	1391.9	2642.0	1943.1	2490.0
DQ068925.1	139022	3042.3	3693.2	2309.0	3965.8	4595.6	5516.9
AM184307.1	160426	381.4	846.4	1566.6	427.9	827.3	194.7
GQ009455.1	500210	6899.3	4607.2	6567.5	2677.6	738.8	2818.3
GQ102029.1	442720	5174.0	4065.3	5637.6	8892.3	3561.1	3931.5
GQ155009.1	566225	1885.0	2154.9	6635.5	3176.7	3009.2	4542.2
AP010960.1	546416	751.5	1207.3	3365.6	1512.1	1445.0	1312.6
X80729.1	9692	643.2	751.5	1979.2	1045.8	579.3	1424.9
GQ155095.1	510292	565.5	1030.8	2879.5	693.7	409.2	1062.9
GU223214.1	581700	13982.2	15337.3	6948.0	11500.9	13536.1	13492.0
U92195.1	9714	558.8	789.2	816.0	756.9	793.4	2196.3
GQ102010.1	386695	1193.3	1600.7	4049.0	2053.5	2411.8	1780.7
GQ491972.1	550764	818.2	1124.0	4601.7	858.2	792.6	1117.4
GQ031668.1	440795	1772.7	3428.9	3661.0	840.4	985.4	1790.0
FJ009375.1	338379	947.1	1259.5	3281.8	848.7	2823.4	1632.9
AJ605115.1	112171	13912.5	12576.1	14628.7	11768.9	11141.2	9851.2
AB548825.1	514639	180.0	1015.4	2375.5	440.6	334.6	654.4
DQ392983.1	156485	118.8	524.3	1113.9	220.7	130.0	181.6
GQ154854.1	511626	580.8	958.0	3250.9	1242.1	1559.4	1335.9

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Z96085.1 gg_id:9839 Erwinia psidii str. LMG 7034
GQ031716.1 gg_id:435217 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
EU464991.1 gg_id:302227 African elephant feces clone AFYEL_aaj66d03
CP001790.1 gg_id:523633 Pectobacterium wasabiae str. WPP163
GQ025498.1 gg_id:405896 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ155325.1 gg_id:582831 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
FJ611867.1 gg_id:538150 Enterobacter cancerogenus str. LMG 2693
EF418614.1 gg_id:216720 Escherichia coli str. WR
GQ156571.1 gg_id:566976 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
EU466945.1 gg_id:296544 African elephant feces clone AFEL2_aao31f11
GQ155259.1 gg_id:553265 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
CP000247.1 gg_id:169669 Escherichia coli str. 536
EU464454.1 gg_id:293609 African elephant feces clone AFEL_aai29d08
GU171376.1 gg_id:580156 Rahnella aquatilis str. 5YN04-01
AM157447.1 gg_id:141508 Escherichia coli mother V4
FJ906795.1 gg_id:568033 Erwinia chrysanthemi str. Lichuan2
FJ997269.1 gg_id:430317 Escherichia coli str. DSPV 247T
GQ155006.1 gg_id:568846 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
GQ155014.1 gg_id:538134 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
EU472748.1 gg_id:290732 red panda feces clone RPSD_1aaa04e08
EU780667.1 gg_id:307587 Pantoea sp. str. CWB304
GQ031664.1 gg_id:465153 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ155195.1 gg_id:582588 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
EF446900.1 gg_id:210269 Enterobacter cloacae str. AW3
GQ101953.1 gg_id:441943 Topographical and Temporal Human Skin Microbiome skin palm clone nbw501f08c1
EF560774.1 gg_id:233520 Escherichia coli str. 228
AM184220.1 gg_id:159834 Enterobacter cloacae str. WAB1878
EU937744.1 gg_id:329159 Enterobacter sakazakii str. JG 09 Iti 7
DQ444288.1 gg_id:154803 Klebsiella oxytoca str. 17
GQ047998.1 gg_id:430834 Topographical and Temporal Human Skin Microbiome skin palm clone nbw140a11c1
GQ156028.1 gg_id:566205 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
EF102835.1 gg_id:257820 Pectobacterium carotovorum str. G-1-7
EU470480.1 gg_id:291647 red panda feces clone RP_1aaa02b02
DQ068852.1 gg_id:139468 microbiota antlions (Myrmeleon mobilis) GI tract freshly caught antlion OTU9 clone
EU470518.1 gg_id:288607 red panda feces clone RP_1aaa01b06
CU915024.1 gg_id:449170 and dynamics adapted microbiota during degradation Tunisian zarzatine enriched se
CP001637.1 gg_id:524975 Escherichia coli str. DH1
EU472906.1 gg_id:298938 red panda feces clone RPSD_1aaa02d07
GQ155318.1 gg_id:509391 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
AY690711.1 gg_id:101221 Erwinia sp. str. MK01
GQ048037.1 gg_id:462729 Topographical and Temporal Human Skin Microbiome skin palm clone nbw140f06c1

Z96085.1	9839	1396.7	1722.9	4051.1	1959.8	2458.8	2653.9
GQ031716.1	435217	1599.4	1597.7	5536.5	2198.6	1837.1	2496.2
EU464991.1	302227	6994.3	10128.4	3322.6	6614.6	7780.3	7314.0
CP001790.1	523633	903.9	1013.2	1945.3	2932.2	162.3	1113.8
GQ025498.1	405896	12732.4	14137.9	7073.2	8339.2	8281.7	6784.3
GQ155325.1	582831	623.8	1096.9	4525.0	742.7	1036.7	1238.2
FJ611867.1	538150	62.1	545.7	1458.6	137.7	68.8	208.1
EF418614.1	216720	760.0	893.8	2598.5	718.3	780.2	1091.0
GQ156571.1	566976	1068.5	1404.5	3281.6	892.5	863.8	2024.2
EU466945.1	296544	8492.9	8049.1	3220.6	9435.7	12952.4	12421.5
GQ155259.1	553265	846.9	1186.2	2914.9	713.8	640.4	1839.7
CP000247.1	169669	205.7	735.2	1758.0	317.8	293.4	1378.1
EU464454.1	293609	1616.4	1871.1	5242.8	2037.7	1472.1	2612.9
GU171376.1	580156	1570.2	1866.8	4810.6	2296.8	323.6	966.2
AM157447.1	141508	4856.0	4268.3	4010.7	5828.0	3810.8	3228.2
FJ906795.1	568033	1874.2	2236.6	2862.6	2349.0	4212.3	4582.8
FJ997269.1	430317	766.2	998.3	848.5	1848.5	913.5	1522.6
GQ155006.1	568846	5265.4	4799.5	7507.3	5991.0	11393.5	5808.8
GQ155014.1	538134	3643.2	3202.8	4623.4	3723.8	5802.3	5714.5
EU472748.1	290732	10888.1	11712.0	5010.3	7006.1	10990.6	8736.2
EU780667.1	307587	919.5	742.7	2971.1	1116.2	859.4	933.7
GQ031664.1	465153	1252.9	1550.7	4217.7	2023.3	1485.7	1835.0
GQ155195.1	582588	6184.4	5657.1	7018.1	8007.2	10044.3	6634.8
EF446900.1	210269	45.7	86.6	118.9	492.6	1873.6	608.0
GQ101953.1	441943	4142.1	3500.5	3837.0	7690.7	6224.5	5809.6
EF560774.1	233520	773.6	971.4	2660.1	713.2	789.7	868.4
AM184220.1	159834	127.6	594.8	1256.3	205.4	135.1	227.0
EU937744.1	329159	1080.5	1024.0	1317.5	2234.7	2340.3	1652.8
DQ444288.1	154803	265.0	424.2	846.0	231.1	242.1	313.0
GQ047998.1	430834	3719.8	4018.7	4676.1	5377.6	4621.8	6277.8
GQ156028.1	566205	6862.5	6129.7	5250.8	4864.6	10026.6	6688.4
EF102835.1	257820	796.7	930.7	1840.5	683.3	2958.8	1908.1
EU470480.1	291647	4103.9	2113.7	4644.4	6546.5	7060.3	6813.7
DQ068852.1	139468	145.5	397.8	1583.5	259.8	190.9	359.7
EU470518.1	288607	241.1	487.3	794.2	145.9	260.1	946.0
CU915024.1	449170	49.7	424.0	375.4	134.9	83.7	105.2
CP001637.1	524975	25.8	328.9	383.7	105.6	64.3	204.9
EU472906.1	298938	1462.7	1472.2	4319.2	2003.6	1311.2	1929.0
GQ155318.1	509391	3945.9	5307.0	5282.8	5582.1	7724.9	7230.9
AY690711.1	101221	1586.7	2231.3	2718.7	2038.7	3007.5	3514.1
GQ048037.1	462729	10128.0	10326.4	9384.5	8199.4	11537.0	9019.3

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FJ370038.1 gg_id:359179 feces adult twins and mothers; TS55 clone TS55_a03g03
FJ976607.1 gg_id:540908 Enterobacter sp. str. LCR98
CU928161.2 gg_id:563140 Escherichia coli str. S88
AY834756.1 gg_id:110694 Rhodopseudomonas palustris str. 2c
GQ099129.1 gg_id:380807 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
DQ223872.1 gg_id:164430 Buttiauxella sp. str. P5
NZ_AAJU01000010.1 gg_id:139105 Escherichia coli str. F11
EU471308.1 gg_id:294785 red panda feces clone RP_3aaa03b08
GQ155251.1 gg_id:594208 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
GQ155172.1 gg_id:544931 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
EU472722.1 gg_id:295041 red panda feces clone RPSD_1aaa03b06
GQ416532.1 gg_id:565456 Temporal succession biological degreasing systems clone F7jun.10
EU216734.1 gg_id:329496 Pantoea sp. str. LMG 5345
Z96077.1 gg_id:10042 Enterobacter nimipressuralis str. LMG 10245-T
GQ025526.1 gg_id:446114 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ095671.1 gg_id:410941 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw4
AF130892.2 gg_id:10079 Pantoea endophytica str. A13
GQ155872.1 gg_id:581530 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
AY253920.1 gg_id:86492 Rahnella aquatilis k 62
GQ025170.1 gg_id:405718 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1
AJ583836.1 gg_id:95192 Pantoea agglomerans str. Pa4842
GQ102051.1 gg_id:394557 Topographical and Temporal Human Skin Microbiome skin palm clone nbw502h07c
GQ155846.1 gg_id:510610 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
FJ969376.1 gg_id:394960 Pectobacterium carotovorum str. KKH3
CP000948.1 gg_id:270797 Escherichia coli substr. DH10B str. K-12
EU468003.1 gg_id:290774 cheetah feces clone CE2_a06_1
AE005174.2 gg_id:128878 Escherichia coli O157:H7 str. EDL933
GQ155038.1 gg_id:554226 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
GQ492044.1 gg_id:572998 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
EU472657.1 gg_id:297746 red panda feces clone RPSD_1aaa04c10
DQ278909.1 gg_id:144626 Enterobacter sp. str. Eg8
EF560790.1 gg_id:228008 Escherichia coli str. BEE13
EU430750.1 gg_id:260369 Enterobacter sp. str. ZJUPD6
NZ_ACGN01000123.1 gg_id:470367 Escherichia coli str. 83972
DQ068760.1 gg_id:172586 Salmonella sp. str. Co9936
AF395913.1 gg_id:38659 Enterobacter aerogenes
GQ492576.1 gg_id:535166 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
GQ101935.1 gg_id:375951 Topographical and Temporal Human Skin Microbiome skin palm clone nbw501b03c
GQ047665.1 gg_id:449134 Topographical and Temporal Human Skin Microbiome skin palm clone nbw137e10c
EU471071.1 gg_id:297139 red panda feces clone RP_3aaa03f12
AB286558.1 gg_id:217008 Reducing production and domination comamonadaceae reducing oxygen supply was

FJ370038.1	359179	597.7	619.2	2721.7	786.9	516.7	876.8
FJ976607.1	540908	551.5	1251.3	2409.8	332.3	4912.6	1584.1
CU928161.2	563140	78.7	244.3	961.8	309.5	107.6	256.2
AY834756.1	110694	477.9	884.5	1360.3	1018.6	2514.6	3015.6
GQ099129.1	380807	15708.4	12264.0	7319.9	14330.8	20188.1	13408.5
DQ223872.1	164430	1569.6	837.1	977.8	2202.0	1861.1	712.5
NZ_AAJU01000010.1	139105	471.5	620.7	658.8	1113.4	592.7	834.8
EU471308.1	294785	1078.5	1106.9	1599.4	2009.5	4878.5	2595.1
GQ155251.1	594208	3994.1	4046.9	3544.1	2528.4	4420.2	3795.8
GQ155172.1	544931	4048.1	3810.4	4123.5	4394.8	5177.9	6601.8
EU472722.1	295041	8843.6	7170.8	6498.6	10409.7	7619.9	9837.6
GQ416532.1	565456	627.6	1472.4	2342.0	562.8	906.3	821.1
EU216734.1	329496	49.1	150.2	821.9	105.5	91.5	58.2
Z96077.1	10042	111.3	358.7	1136.0	260.0	209.2	406.4
GQ025526.1	446114	10529.0	10859.7	7851.9	8567.8	9853.6	9427.1
GQ095671.1	410941	4250.4	3697.2	6168.4	5452.1	6003.0	5821.4
AF130892.2	10079	13478.1	13327.0	10572.4	11625.3	11176.8	9915.2
GQ155872.1	581530	681.4	1120.8	3964.1	1152.9	1166.6	1169.5
AY253920.1	86492	2693.8	1489.4	1405.8	5113.8	2253.9	2268.5
GQ025170.1	405718	2595.3	2242.2	1720.8	3327.4	3683.8	3823.8
AJ583836.1	95192	197.2	688.2	1324.0	436.2	292.9	568.1
GQ102051.1	394557	2852.2	2364.5	4954.4	2487.6	4427.2	2662.1
GQ155846.1	510610	82.6	388.9	567.3	163.9	146.2	832.6
FJ969376.1	394960	92.2	213.4	1192.0	167.6	106.5	237.0
CP000948.1	270797	416.0	836.0	575.1	858.6	547.8	684.7
EU468003.1	290774	11810.2	12118.4	5384.5	7459.4	7133.5	8372.0
AE005174.2	128878	2393.4	1357.8	779.9	2945.6	3970.5	2034.1
GQ155038.1	554226	13883.2	13513.3	9179.1	10994.8	17549.5	14244.1
GQ492044.1	572998	6052.6	5973.3	5363.5	5774.4	6132.5	5450.7
EU472657.1	297746	1238.1	1172.3	3897.5	2205.9	1040.0	1944.5
DQ278909.1	144626	928.5	1276.8	5976.5	1731.1	2087.9	2943.7
EF560790.1	228008	779.9	871.6	2154.2	640.4	524.0	723.1
EU430750.1	260369	2709.3	2821.8	2697.1	2155.2	3555.5	2982.4
NZ_ACGN01000123.1	470367	423.2	771.4	3118.1	1107.2	908.7	1072.5
DQ068760.1	172586	658.8	1591.4	3942.0	793.5	2291.5	3116.1
AF395913.1	38659	106.8	522.4	993.5	187.2	176.3	315.5
GQ492576.1	535166	9295.2	9918.7	13367.2	11529.7	13831.4	12279.1
GQ101935.1	375951	1085.1	1420.8	2915.5	3028.2	3240.0	1827.4
GQ047665.1	449134	8774.6	7971.7	4124.3	11339.9	6421.6	6188.0
EU471071.1	297139	5526.3	4994.0	4898.8	8840.5	8073.2	9219.5
AB286558.1	217008	58.7	321.1	1591.2	226.1	107.1	288.4

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GQ155099.1 gg_id:540372 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
GQ099217.1 gg_id:375279 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ114706.1 gg_id:453826 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
EU472653.1 gg_id:297848 red panda feces clone RPSD_1aaa01e06
AM184226.1 gg_id:160051 Enterobacter sp. str. WAB1884
AF520708.1 gg_id:61203 Dickeya dianthicola str. CFBP 1200
EF489443.1 gg_id:219392 Pantoea agglomerans str. GIST-NKst1
EF153300.1 gg_id:186788 identification gut fourth-instar red imported fire ant (Solenopsis Buren) larvae GI trac
EF560782.1 gg_id:233200 Escherichia coli str. BE33
U90758.1 gg_id:10315 Rahnella genosp. 3 str. DSM 30078
AJ233409.1 gg_id:10306 Brenneria alni str. DSM 11811
EU761873.1 gg_id:346129 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1
GQ155273.1 gg_id:591917 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
EU464932.1 gg_id:290119 African elephant feces clone AFYEL_aaj65d02
GQ025120.1 gg_id:438223 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1:
GQ025542.1 gg_id:460697 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
EU430755.1 gg_id:259306 Enterobacter sp. str. ZJUPD1
EU430752.1 gg_id:267416 Enterobacter sp. str. ZJUPD4
EU430753.1 gg_id:270355 Enterobacter sp. str. ZJUPD3
DQ223881.1 gg_id:168597 Citrobacter gillenii str. P9
NC_004431.1 gg_id:128802 Escherichia coli str. CFT073
EU471669.1 gg_id:297637 Asiatic elephant feces clone AE1_aaa03f11
DQ112330.1 gg_id:136199 Pantoea agglomerans str. RS-18
EU470656.1 gg_id:287789 red panda feces clone RP_1aaa03g09
DQ068872.1 gg_id:139038 microbiota antlions (Myrmeleon mobilis) whole animal freshly caught antlion OTU1(
GQ048022.1 gg_id:442026 Topographical and Temporal Human Skin Microbiome skin palm clone nbw140d07c:
AM062693.1 gg_id:249744 Enterobacter amnigenus p412
EU471187.1 gg_id:291079 red panda feces clone RP_3aaa04e11
GU185862.1 gg_id:587224 Enterobacter ludwigii str. HSBN1
GQ155216.1 gg_id:583212 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
AM491468.1 gg_id:213014 Aranicola sp. str. Nj-67
GQ101988.1 gg_id:430225 Topographical and Temporal Human Skin Microbiome skin palm clone nbw502b08c:
GQ155035.1 gg_id:587112 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
EU471045.1 gg_id:293597 red panda feces clone RP_3aaa02e12
EU458408.1 gg_id:295685 spotted hyena feces clone HY1_f04
GU374094.1 gg_id:526760 soil East Calcutta wetland clone SRC_NBB2
GQ047705.1 gg_id:399615 Topographical and Temporal Human Skin Microbiome skin palm clone nbw138b11c:
DQ298156.1 gg_id:142765 Escherichia sp. SWM_Isolation_4
EU472916.1 gg_id:287896 red panda feces clone RPSD_1aaa04b06
U88545.1 gg_id:9669 Salmonella typhi str. St111
EU472820.1 gg_id:294893 red panda feces clone RPSD_1aaa03c03

GQ155099.1	540372	1041.5	1235.8	2996.0	1126.6	1336.4	1437.9
GQ099217.1	375279	9813.0	12349.3	9931.1	11420.5	13901.3	13151.8
GQ114706.1	453826	5183.6	3647.1	5669.7	4591.6	4164.0	5510.1
EU472653.1	297848	1915.1	2128.8	4903.1	2244.3	1803.3	2979.6
AM184226.1	160051	58.4	391.7	1685.4	202.9	78.5	297.0
AF520708.1	61203	4504.5	5215.4	8614.3	5927.1	7196.0	6683.8
EF489443.1	219392	647.3	1088.0	2598.7	1290.5	1656.0	1005.5
EF153300.1	186788	414.0	1012.5	878.4	431.0	3681.1	1131.9
EF560782.1	233200	5719.5	4779.3	6784.7	9171.7	7073.4	8214.2
U90758.1	10315	1290.8	1713.0	4474.3	1543.7	1252.3	1598.1
AJ233409.1	10306	1465.2	2207.9	2136.8	2087.5	4492.3	3724.1
EU761873.1	346129	973.6	945.6	3676.5	1485.9	1154.3	1466.0
GQ155273.1	591917	12112.2	13569.3	4593.9	4056.3	8314.0	8865.0
EU464932.1	290119	6392.0	6995.6	2199.9	7227.9	3144.6	2941.7
GQ025120.1	438223	7052.2	5287.6	3991.2	7784.6	6685.8	5658.5
GQ025542.1	460697	828.9	1425.7	3344.7	1608.1	1634.5	1395.3
EU430755.1	259306	3327.6	3403.6	4057.9	4350.0	6559.4	6622.3
EU430752.1	267416	3341.3	3596.6	1874.5	3235.4	6359.9	4958.2
EU430753.1	270355	1096.2	1821.6	4528.1	910.5	5681.2	3387.2
DQ223881.1	168597	5141.3	5228.6	1756.6	6568.8	10692.6	8802.8
NC_004431.1	128802	1313.0	1775.8	4201.5	1833.8	1931.8	2223.7
EU471669.1	297637	6302.0	5071.3	5006.1	7006.6	7189.2	9090.6
DQ112330.1	136199	379.3	1056.2	1607.6	458.1	2283.2	846.1
EU470656.1	287789	5651.9	4377.6	8053.0	4835.8	6035.3	5887.0
DQ068872.1	139038	2329.9	2538.6	7868.0	3647.3	4253.4	6018.4
GQ048022.1	442026	9822.0	8603.8	7029.6	9421.6	7954.9	7989.8
AM062693.1	249744	1083.2	981.3	3693.2	644.3	1291.7	1547.0
EU471187.1	291079	561.3	721.6	2201.0	718.9	535.6	866.6
GU185862.1	587224	466.3	754.5	1542.7	1306.7	2507.2	2785.7
GQ155216.1	583212	1899.8	1611.9	2205.0	1658.2	1316.3	1765.8
AM491468.1	213014	4115.2	3382.4	4201.4	2908.8	2798.7	3313.3
GQ101988.1	430225	6076.0	3630.4	10479.9	8848.6	1731.1	3570.5
GQ155035.1	587112	1324.6	1269.7	3660.4	1557.2	1444.0	1528.3
EU471045.1	293597	5995.0	6453.4	7799.3	9582.9	10895.8	10282.4
EU458408.1	295685	1431.5	1519.7	2012.7	3526.5	3067.2	2499.4
GU374094.1	526760	2205.8	3231.4	3837.5	1570.9	1989.3	2202.2
GQ047705.1	399615	442.4	839.2	563.9	852.7	544.6	681.9
DQ298156.1	142765	8094.4	6856.3	6064.0	9965.2	11156.7	9068.8
EU472916.1	287896	1457.2	1375.3	4570.9	2003.9	1313.2	2141.0
U88545.1	9669	100.5	522.6	494.1	129.1	209.0	154.4
EU472820.1	294893	152.8	468.6	2102.3	240.6	168.7	597.2

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FJ975840.1 gg_id:590619 Human gut microbiome adopts alternative state bowel transplantation ileum effluent
EU472736.1 gg_id:294375 red panda feces clone RPSD_1aaa01e05
EU855221.1 gg_id:347116 Enterobacter aerogenes str. CTSP48
GQ070404.1 gg_id:392752 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw:
FJ267520.2 gg_id:343017 Escherichia blattae str. DSM 4481
FJ683659.1 gg_id:523290 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
X80680.1 gg_id:9721 Shigella dysenteriae
GU272220.1 gg_id:592196 Escherichia coli str. wz_1977
DQ223879.1 gg_id:168024 Enterobacter amnigenus str. P4
EU472796.1 gg_id:292881 red panda feces clone RPSD_1aaa04e04
EU464977.1 gg_id:302241 African elephant feces clone AFYEL_aaj66b03
GQ101931.1 gg_id:441169 Topographical and Temporal Human Skin Microbiome skin palm clone nbw501a10c1
EU471959.1 gg_id:298277 francois langur feces clone FL_1aaa03d06
CU915010.1 gg_id:456734 and dynamics adapted microbiota during degradation Tunisian zarzatine enriched se
EU554444.1 gg_id:273128 Enterobacter asburiae str. Ag18
GQ099291.1 gg_id:395047 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
EF446895.1 gg_id:210966 Acinetobacter radioresistens str. Philippines-11
ABHO01000021.1 gg_id:285987 Escherichia coli O157:H7 str. EC4196
GQ155878.1 gg_id:549556 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
GQ155057.1 gg_id:568864 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
FJ975887.1 gg_id:534463 Human gut microbiome adopts alternative state bowel transplantation ileum effluent
FJ593037.1 gg_id:572846 Pectobacterium wasabiae str. JU-1
GQ155094.1 gg_id:593339 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
CU928162.2 gg_id:547290 Escherichia coli str. ED1a
EF620926.1 gg_id:254200 Escherichia coli str. WD02
EF620923.1 gg_id:254591 Escherichia coli str. SYW004
GQ047692.1 gg_id:449355 Topographical and Temporal Human Skin Microbiome skin palm clone nbw138a03c1
FJ906925.1 gg_id:562225 Cronobacter sakazakii str. Jor204
NR_024706.1 gg_id:562424 Pseudomonas flectens str. ATCC 12775
FJ581031.1 gg_id:568374 Cronobacter sakazakii str. IITRM16
GQ165811.1 gg_id:548859 Enterobacter aerogenes str. IEY
FJ949577.1 gg_id:373419 Escherichia coli str. H1
EU778499.1 gg_id:325455 Red Panda feces clone RPSD_1aaa03f09
GQ099209.1 gg_id:452629 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
EU472713.1 gg_id:289582 red panda feces clone RPSD_1aaa03f02
EU537173.1 gg_id:285808 profile human microbiota antecubital fossa (inner elbow) skin clone nbt67h04
EU470953.1 gg_id:293383 red panda feces clone RP_2aaa01e06
EF604173.1 gg_id:233448 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF102834.1 gg_id:242926 Pantoea agglomerans str. G-4-13-2
GU374071.1 gg_id:516475 soil East Calcutta wetland clone SRC_NBB14
EF515452.1 gg_id:224577 Electricigen Enrichment MFC upf microbial fuel cell anode clone 24e12

FJ975840.1	590619	287.5	701.6	1850.2	621.2	698.6	326.7
EU472736.1	294375	5278.9	4418.6	7626.5	7909.6	5847.9	8223.4
EU855221.1	347116	121.4	620.3	1685.0	249.9	169.4	301.3
GQ070404.1	392752	64.1	130.5	494.1	191.5	84.3	117.2
FJ267520.2	343017	1757.1	1201.9	1864.8	2014.9	938.2	1759.3
FJ683659.1	523290	52.1	625.5	2197.1	310.5	62.6	460.8
X80680.1	9721	2195.0	2409.7	4774.8	4269.1	4134.5	5643.7
GU272220.1	592196	2405.1	1204.1	3451.1	4524.5	1268.1	2924.0
DQ223879.1	168024	8777.5	6964.5	2606.0	5303.2	3211.0	2573.7
EU472796.1	292881	1128.6	1328.1	3278.2	1934.1	1296.3	1899.5
EU464977.1	302241	145.6	419.2	2588.6	539.1	76.3	415.5
GQ101931.1	441169	728.9	1563.3	4095.6	2907.8	1774.7	2400.9
EU471959.1	298277	12249.4	11226.7	6998.6	10121.0	12017.4	13256.1
CU915010.1	456734	97.4	605.8	1456.8	299.1	74.2	403.7
EU554444.1	273128	1721.3	4671.0	2600.9	3451.2	7533.7	4807.0
GQ099291.1	395047	9855.9	11078.8	9277.7	10792.3	5892.4	6675.0
EF446895.1	210966	812.7	950.3	955.6	1917.8	811.1	748.8
ABHO01000021.1	285987	2707.6	2552.2	2891.2	4188.9	4219.9	3835.4
GQ155878.1	549556	58.1	417.7	1522.4	337.7	76.8	193.9
GQ155057.1	568864	1292.0	1307.4	3129.7	1546.4	1445.9	1415.5
FJ975887.1	534463	2157.1	2647.6	2002.0	1154.6	2218.8	891.4
FJ593037.1	572846	319.6	355.7	599.8	511.2	711.0	1179.4
GQ155094.1	593339	7935.5	8059.6	9091.5	6889.3	8877.4	6804.8
CU928162.2	547290	1711.3	2103.9	4521.8	2555.2	2604.6	2651.4
EF620926.1	254200	12730.3	13788.2	4279.0	9095.3	11030.7	10428.4
EF620923.1	254591	1089.0	1239.7	1522.3	1851.2	1123.4	1397.6
GQ047692.1	449355	6167.9	5125.5	5637.0	9105.1	8978.8	8072.9
FJ906925.1	562225	420.3	485.1	1632.4	457.8	549.5	714.5
NR_024706.1	562424	3567.4	1497.7	2990.2	3832.3	2280.9	2852.9
FJ581031.1	568374	11750.1	12625.2	7946.7	9213.5	10748.1	9445.9
GQ165811.1	548859	120.9	563.5	2854.2	234.7	108.3	368.9
FJ949577.1	373419	3372.2	2518.9	5297.1	4084.1	2752.4	4054.7
EU778499.1	325455	14220.3	15411.8	9597.3	13141.0	14199.5	14009.0
GQ099209.1	452629	4773.9	4140.6	7390.3	7847.8	5330.8	4248.6
EU472713.1	289582	4779.2	4350.9	2742.0	4461.3	3079.4	4206.1
EU537173.1	285808	242.2	531.9	1466.6	899.5	413.5	774.0
EU470953.1	293383	2714.0	2578.2	2058.4	4229.2	4499.7	4727.6
EF604173.1	233448	1246.0	1589.4	1249.8	1254.8	2353.9	1900.1
EF102834.1	242926	137.2	572.5	4120.1	217.0	156.8	433.2
GU374071.1	516475	8684.0	8833.1	7811.6	6717.4	5834.6	5351.5
EF515452.1	224577	190.6	457.6	3767.4	451.7	507.5	378.9

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AY792274.1 gg_id:119416 Humic Lake clone CrystalBog5H4
AY501386.1 gg_id:99525 Pantoea sp. str. PPE7
GQ155204.1 gg_id:509434 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
GQ155021.1 gg_id:544405 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
AM184290.1 gg_id:160595 Pantoea agglomerans str. WAB1951
AF015258.1 gg_id:10180 Aquamonas haywardensis str. CDC 2404-94 EG121
EU471256.1 gg_id:291269 red panda feces clone RP_3aaa02b01
AM157425.1 gg_id:141026 Escherichia coli mother C3
EU078564.1 gg_id:236821 Enterobacter sp. str. R11-2
AJ871857.1 gg_id:113218 Klebsiella oxytoca str. SB136=ATCC 49131
AF130958.2 gg_id:10082 Pantoea endophytica str. A6
GQ155121.1 gg_id:575470 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
EU471089.1 gg_id:292812 red panda feces clone RP_3aaa04g10
EU472826.1 gg_id:300494 red panda feces clone RPSD_1aaa02e07
AY831405.1 gg_id:112441 Escherichia coli str. AB1157
GQ099170.1 gg_id:396992 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
CP000819.1 gg_id:520569 Escherichia coli B str. REL606
EU555536.1 gg_id:266023 Escherichia coli str. CNM 477-02
EU239468.1 gg_id:255707 Enterobacter asburiae str. XJUHX-5
FN433037.1 gg_id:543947 Escherichia fergusonii CCM27B
EU778487.1 gg_id:305294 Red Panda feces clone RPSD_1aaa03c07
AF373173.1 gg_id:66748 Erwinia chrysanthemi str. 340
EU471241.1 gg_id:297916 red panda feces clone RP_3aaa01a04
AM933759.1 gg_id:330563 Kluyvera ascorbata 1919
FJ811870.1 gg_id:578058 Pantoea sp. str. 1-CDF
AJ971890.1 gg_id:136113 Erwinia sp. Ob 05
EU470487.1 gg_id:302808 red panda feces clone RP_1aaa04c12
EF560781.1 gg_id:230035 Escherichia coli str. BE30
AM184235.1 gg_id:160492 Enterobacter ludwigii str. WAB1894
EU535068.1 gg_id:283165 profile human skin microbiota ear punch biopsy female C57BL/6J mouse clone nbt18
GQ479959.1 gg_id:561718 Enterobacter aerogenes str. MZQ-HZ01
DQ086778.1 gg_id:136046 Enterobacter cloacae str. I5
AE005674.2 gg_id:128438 Shigella flexneri 2a str. 301
FJ405334.1 gg_id:366426 Escherichia coli str. 4061
EU470595.1 gg_id:289857 red panda feces clone RP_1aaa04h08
AJ233414.1 gg_id:9838 Erwinia mallotivora str. DSM 4565
GQ048031.1 gg_id:436643 Topographical and Temporal Human Skin Microbiome skin palm clone nbw140e09c1
AJ308467.1 gg_id:34327 Enterobacter sp. 22
AJ309974.1 gg_id:45848 enterobacterium str. dtb112
AY825036.1 gg_id:109467 Enterobacter aerogenes str. NTG-01
GQ493841.1 gg_id:580139 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice

AY792274.1	119416	1648.0	1501.2	2410.3	681.4	412.5	1350.3
AY501386.1	99525	875.2	769.0	2847.6	1548.2	621.2	673.2
GQ155204.1	509434	4087.8	3950.2	4384.5	4417.2	5203.2	7187.6
GQ155021.1	544405	11023.7	12099.8	7855.5	8507.9	9618.0	7432.2
AM184290.1	160595	4849.3	5419.9	749.5	4162.4	4127.9	4411.2
AF015258.1	10180	18.8	28.0	26.7	51.4	55.0	17.5
EU471256.1	291269	8587.6	8744.4	5909.4	10397.3	7183.2	5618.9
AM157425.1	141026	976.4	978.3	3718.4	1495.4	1174.8	1476.1
EU078564.1	236821	188.2	714.8	1019.7	493.7	868.2	1253.0
AJ871857.1	113218	1135.0	1253.5	1979.0	785.0	585.9	1343.4
AF130958.2	10082	926.4	951.0	1205.4	1182.3	484.9	468.5
GQ155121.1	575470	11896.7	9828.5	6170.9	10214.7	13292.2	10511.3
EU471089.1	292812	2993.8	3029.1	1979.6	4216.2	7324.0	6401.4
EU472826.1	300494	795.0	1099.1	4115.9	787.4	805.0	1036.3
AY831405.1	112441	4284.8	3319.3	2812.8	4914.1	4125.5	4770.3
GQ099170.1	396992	4540.5	2541.5	3248.2	6170.3	4563.7	3076.7
CP000819.1	520569	807.4	994.0	2979.2	1118.8	699.2	1147.5
EU555536.1	266023	529.0	891.7	699.7	716.1	469.9	540.7
EU239468.1	255707	288.6	774.7	1280.8	392.0	133.2	289.4
FN433037.1	543947	783.3	1090.6	3827.0	787.5	855.1	923.2
EU778487.1	305294	1835.9	1519.4	3884.3	3166.1	1662.8	2913.8
AF373173.1	66748	539.3	687.9	1187.8	548.0	1436.7	1862.1
EU471241.1	297916	2523.7	2380.7	4530.4	4195.1	2810.4	4352.5
AM933759.1	330563	4091.6	1712.2	995.1	4287.4	915.1	922.2
FJ811870.1	578058	1058.3	1087.0	1373.4	1557.5	2086.1	874.8
AJ971890.1	136113	481.8	602.8	1474.9	776.2	1195.1	2059.9
EU470487.1	302808	1227.7	1078.0	2937.8	2183.6	975.6	1876.8
EF560781.1	230035	1581.0	2652.4	3361.8	1982.7	1323.7	3034.0
AM184235.1	160492	829.4	1334.1	2784.9	797.6	2798.6	1620.0
EU535068.1	283165	246.8	954.4	911.7	1012.5	629.9	731.2
GQ479959.1	561718	7105.4	6122.5	7796.0	7333.4	8274.9	6242.5
DQ086778.1	136046	101.4	444.8	1347.3	310.5	98.9	243.9
AE005674.2	128438	982.8	1026.9	3698.7	1491.7	1161.8	1480.9
FJ405334.1	366426	14407.2	14719.4	15775.1	14369.4	17806.9	15280.7
EU470595.1	289857	124.9	597.5	1302.3	416.8	174.9	385.5
AJ233414.1	9838	2049.0	2018.4	5336.0	1551.5	2435.7	2795.9
GQ048031.1	436643	8219.4	9170.3	4309.2	4654.5	4164.1	4250.6
AJ308467.1	34327	486.3	657.8	2397.6	305.2	124.1	548.0
AJ309974.1	45848	30.5	154.1	141.3	99.7	60.2	78.2
AY825036.1	109467	467.5	624.5	2715.5	987.8	282.2	421.1
GQ493841.1	580139	1547.6	1844.0	2140.9	3081.1	2973.6	2342.6

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EU464476.1 gg_id:301303 African elephant feces clone AFEL_aai29g04
GQ047964.1 gg_id:468430 Topographical and Temporal Human Skin Microbiome skin palm clone nbw139f07c1
GQ155178.1 gg_id:539032 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
GQ156080.1 gg_id:588129 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
EU472802.1 gg_id:290812 red panda feces clone RPSD_1aaa04f09
AB273732.1 gg_id:243322 Shigella sonnei str. GTC 781
FJ906921.1 gg_id:542455 Cronobacter sakazakii str. Jor176
EU472837.1 gg_id:295363 red panda feces clone RPSD_1aaa02h08
GQ155060.1 gg_id:509438 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
GQ031670.1 gg_id:381600 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
AB273742.1 gg_id:245432 Cedecea lapagei str. GTC 346
FJ405361.1 gg_id:358229 Rahnella aquatilis str. SPb
EU471082.1 gg_id:295799 red panda feces clone RP_3aaa04g04
FJ366024.1 gg_id:361492 feces adult twins and mothers; TS25 clone TS25_a01g12
EU472850.1 gg_id:301348 red panda feces clone RPSD_1aaa03d12
FJ975869.1 gg_id:513372 Human gut microbiome adopts alternative state bowel transplantation ileum effluent
ABHO01000013.1 gg_id:286158 Escherichia coli O157:H7 str. EC4196
DQ347522.1 gg_id:147724 Paracoccus sp. B-1012
DQ124676.1 gg_id:136582 Enterobacter aerogenes str. S2-1
U90314.1 gg_id:9706 Salmonella subsp. enterica serovar Blockley str. Sb1 subsp.
X80725.1 gg_id:9741 Escherichia coli str. ATCC 11775T
FM180568.1 gg_id:369788 Escherichia coli 0127:H6 str. E2348/69
DQ068864.1 gg_id:139117 microbiota antlions (Myrmeleon mobilis) whole animal freshly caught antlion OTU1(
GQ493963.1 gg_id:583626 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
EU834264.1 gg_id:332053 Raoultella ornithinolytica str. DS44
EF178670.1 gg_id:180411 Erwinia chrysanthemi str. NZEC135
EU857633.1 gg_id:366089 Shigella flexneri
AM933754.1 gg_id:340632 Kluyvera cryocrescens 169
EU472757.1 gg_id:301762 red panda feces clone RPSD_1aaa02d04
EF560786.1 gg_id:231669 Escherichia coli str. BE45
GQ025603.1 gg_id:416339 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
FJ811871.1 gg_id:552136 Enterobacter aerogenes str. 7-WCH
EU773798.1 gg_id:346813 Cheetah feces clone CE2_e03
GQ047918.1 gg_id:402513 Topographical and Temporal Human Skin Microbiome skin palm clone nbw139a08c1
EU778388.1 gg_id:354647 Red Panda feces clone RP_1aaa02f05
EU471154.1 gg_id:297213 red panda feces clone RP_3aaa03f09
AF024608.1 gg_id:9727 Pantoea agglomerans str. TAC.III.94.1
GQ155244.1 gg_id:571288 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
GQ025550.1 gg_id:382453 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GU186121.1 gg_id:584341 Pantoea agglomerans str. IHB B 1383
EU460458.1 gg_id:293981 polar bear feces clone PB2_aai21b06

EU464476.1	301303	1614.7	1794.6	4444.7	2020.1	1490.0	2542.0
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GQ156080.1	588129	678.9	1014.2	3038.2	1147.1	1174.0	1092.8
EU472802.1	290812	2168.7	2667.8	4071.1	1911.1	5331.8	4281.2
AB273732.1	243322	1152.8	1284.5	1694.6	1603.8	1042.9	1362.3
FJ906921.1	542455	6029.6	7142.9	8855.3	6506.5	7732.3	6506.5
EU472837.1	295363	11781.8	13699.1	13869.3	12120.6	13160.7	13076.9
GQ155060.1	509438	6290.8	6538.3	11510.7	5968.9	9673.4	8559.4
GQ031670.1	381600	971.9	1820.1	5650.8	1755.8	4514.4	2502.0
AB273742.1	245432	3063.8	3191.7	5003.4	3640.1	3243.4	4858.8
FJ405361.1	358229	1860.0	2060.3	4679.1	4315.1	1516.6	2084.7
EU471082.1	295799	12068.6	13613.7	9654.3	13375.7	10506.3	10534.9
FJ366024.1	361492	6634.3	5794.4	5102.0	8752.9	6115.5	5684.9
EU472850.1	301348	7126.8	9030.6	6793.3	9244.5	12023.7	9831.3
FJ975869.1	513372	1579.9	1569.3	4305.6	1942.6	3057.0	2718.9
ABHO01000013.1	286158	2047.8	1062.4	2122.8	2949.8	814.7	1963.8
DQ347522.1	147724	1229.5	1251.2	3246.9	1527.1	1438.2	1464.3
DQ124676.1	136582	91.7	248.1	1540.1	415.0	120.2	586.9
U90314.1	9706	7604.9	7619.1	5582.1	7225.8	9573.3	8999.8
X80725.1	9741	954.9	998.7	2807.8	1510.1	1162.0	1431.4
FM180568.1	369788	1274.7	950.1	3326.2	1028.5	783.9	1263.2
DQ068864.1	139117	246.3	369.7	1236.5	539.8	391.7	671.4
GQ493963.1	583626	2560.5	2666.7	7057.8	3269.3	3851.0	5521.0
EU834264.1	332053	73.1	450.1	1309.0	186.0	109.0	336.9
EF178670.1	180411	989.9	1735.4	1361.8	434.0	7048.4	2930.8
EU857633.1	366089	986.3	914.4	1647.5	1461.4	1183.0	1839.6
AM933754.1	340632	884.2	1215.2	5485.4	939.9	2288.2	1757.1
EU472757.1	301762	16654.2	16675.8	9694.4	14166.7	14567.5	18498.6
EF560786.1	231669	600.6	1129.4	3516.5	1229.5	1058.2	1176.1
GQ025603.1	416339	210.8	531.3	1730.1	563.3	475.5	647.9
FJ811871.1	552136	11461.6	10339.6	8601.4	13265.9	17889.9	14324.0
EU773798.1	346813	1956.0	2690.3	2796.6	1609.4	1107.0	1638.7
GQ047918.1	402513	1574.0	1142.6	2716.0	2401.3	1188.5	1939.6
EU778388.1	354647	1675.4	1240.5	3576.2	2938.8	1661.9	2383.9
EU471154.1	297213	555.6	1442.7	782.4	393.4	3137.9	2506.8
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GQ155244.1	571288	16176.8	15340.4	14414.5	13515.9	15695.9	12786.4
GQ025550.1	382453	3084.9	4494.2	4123.4	4684.8	4826.1	5796.0
GU186121.1	584341	7441.2	7225.6	6883.0	8641.6	10064.9	9704.3
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GQ154883.1 gg_id:547125 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
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GQ101940.1 gg_id:429707 Topographical and Temporal Human Skin Microbiome skin palm clone nbw501b10c1
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GQ416891.1 gg_id:572750 Temporal succession biological degreasing systems clone F1jun.25
FJ192752.1 gg_id:308904 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior
EF515391.1 gg_id:220037 Electricigen Enrichment MFC upf microbial fuel cell anode clone 23g08
GQ492620.1 gg_id:561719 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
GQ155307.1 gg_id:553345 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
GQ493735.1 gg_id:590258 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
AM184247.1 gg_id:161342 Enterobacter aerogenes str. WAB1906
FJ405332.1 gg_id:367948 Escherichia coli str. 4059
EF560785.1 gg_id:232471 Escherichia coli str. BE42
GQ155160.1 gg_id:585374 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
GQ114876.1 gg_id:466445 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
AB273737.1 gg_id:236285 Trabulsiella guamensis str. GTC 1379
EU240950.1 gg_id:272583 Enterobacter hormaechei str. YO-B
GQ085256.1 gg_id:409792 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw273b02c
AB548824.1 gg_id:529730 Citrobacter freundii str. JCM 24059
GQ031696.1 gg_id:454885 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ155185.1 gg_id:582498 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
AJ233421.1 gg_id:9796 Leminorella grimontii str. DSM 5078
FJ364615.1 gg_id:362183 feces adult twins and mothers; TS19 clone TS19_a01a10
EU471104.1 gg_id:297764 red panda feces clone RP_3aaa03f01
FJ611877.1 gg_id:582578 Enterobacter sp. str. ATCC 27981
FJ404760.1 gg_id:368274 Mangroveibacter sp. str. WG-1
NZ_ABHL02000001.1 gg_id:316857 Escherichia coli O157:H7 str. EC4045
NC_002655.2 gg_id:150516 Escherichia coli O157:H7 str. EDL933
GQ155256.1 gg_id:545159 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
FJ608656.1 gg_id:566084 Klebsiella pneumoniae str. EP4
EU468018.1 gg_id:301955 cheetah feces clone CE2_c10_2
FJ178002.1 gg_id:333293 Escherichia coli str. AC 521
EU430751.1 gg_id:272055 Enterobacter sp. str. ZJUPD5
GQ492150.1 gg_id:537226 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice

GQ048476.1	467365	2082.4	1534.2	2925.1	2720.1	1833.6	2489.3
GQ024535.1	485135	569.4	689.8	3205.8	676.5	464.4	858.2
Z96089.1	9989	136.4	282.2	1581.8	207.8	88.8	398.7
GQ154883.1	547125	1100.6	1279.2	4772.5	2693.0	2420.3	2409.1
GQ025585.1	403646	384.7	662.5	2289.8	1049.7	470.8	1285.8
EU684953.1	295125	603.5	874.3	3741.9	1655.2	2282.1	2412.4
AB244472.1	248467	73.8	425.9	2114.2	147.0	113.5	472.9
GU594308.1	531073	11015.8	12339.3	9231.6	9467.5	15535.3	13656.2
EU470599.1	303181	11272.9	12560.6	9894.0	12138.8	9483.0	7934.0
GQ101940.1	429707	5082.8	3975.3	3999.6	6034.8	12424.8	7471.0
FJ906923.1	548205	6236.7	6208.3	6919.1	4403.3	3372.7	3204.1
GQ416891.1	572750	5108.3	5582.4	3625.7	2690.1	2221.5	2484.8
FJ192752.1	308904	24.2	141.8	133.1	44.9	51.8	46.3
EF515391.1	220037	57.3	179.7	397.1	184.5	146.5	141.9
GQ492620.1	561719	4194.0	4746.7	4879.2	6167.6	7648.3	7811.3
GQ155307.1	553345	2191.4	1969.4	6518.4	3615.6	2231.0	2954.2
GQ493735.1	590258	603.0	897.8	4041.7	977.9	563.4	1151.3
AM184247.1	161342	313.0	905.8	2200.5	444.4	928.5	949.9
FJ405332.1	367948	3347.6	3013.3	9236.6	5179.9	4981.6	4897.8
EF560785.1	232471	620.1	1242.4	681.8	359.4	3930.5	3673.3
GQ155160.1	585374	8299.3	8280.0	10487.2	7615.8	8334.4	7949.9
GQ114876.1	466445	563.9	996.0	1819.1	1407.4	3667.5	5596.0
AB273737.1	236285	194.7	766.4	3365.7	1411.2	1400.4	1404.0
EU240950.1	272583	779.3	914.8	2062.4	488.4	556.4	1736.9
GQ085256.1	409792	1545.7	2483.7	2669.9	2627.0	1608.2	2585.9
AB548824.1	529730	238.2	1002.1	2447.2	786.5	962.7	1004.5
GQ031696.1	454885	383.5	472.9	597.0	910.5	1508.1	3508.0
GQ155185.1	582498	1042.2	1219.0	3570.5	1128.6	1337.2	1472.1
AJ233421.1	9796	662.6	1254.5	4674.9	1963.1	1857.1	2410.9
FJ364615.1	362183	382.2	933.9	3353.1	1051.8	750.7	1090.7
EU471104.1	297764	2529.7	2373.6	4872.3	4207.8	2905.7	4146.6
FJ611877.1	582578	267.4	754.8	3823.4	498.3	1503.7	858.9
FJ404760.1	368274	136.1	214.9	686.1	341.4	803.4	392.0
NZ_ABHL02000001.1	316857	2031.3	2311.6	2798.7	2939.3	3793.0	3056.5
NC_002655.2	150516	1339.4	754.0	1510.5	1818.0	328.2	768.5
GQ155256.1	545159	1013.1	1152.2	4051.7	1375.6	1208.5	1393.9
FJ608656.1	566084	11838.5	10980.6	4139.3	9555.2	13914.0	9940.0
EU468018.1	301955	1191.0	1237.0	4644.2	1790.5	985.8	1826.5
FJ178002.1	333293	11383.7	7635.1	5246.5	10110.2	9832.1	7247.8
EU430751.1	272055	1048.1	1859.9	3349.6	746.3	5025.5	3199.5
GQ492150.1	537226	1737.0	1676.5	3827.1	2317.3	1412.1	2802.2

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EU460263.1 gg_id:295242 polar bear feces clone PB1_aai25f03
EU275356.1 gg_id:256517 Enterobacter amnigenus str. CONC4
GQ493157.1 gg_id:592185 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
NC_007946.1 gg_id:156719 Escherichia coli str. UTI89
GQ069665.1 gg_id:467129 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
EU460420.1 gg_id:292398 polar bear feces clone PB1_aai28d07
U88546.1 gg_id:9709 Salmonella paratyphi
EF059884.1 gg_id:226386 Enterobacter pyrinus str. E872
U90318.1 gg_id:9667 Salmonella enteritidis str. SE22
EF604220.1 gg_id:231694 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous
FJ975783.1 gg_id:580915 Human gut microbiome adopts alternative state bowel transplantation ileum effluent
EU472654.1 gg_id:299365 red panda feces clone RPSD_1aaa01b07
FJ997270.1 gg_id:422465 Escherichia coli str. DSPV 284T
GQ045414.1 gg_id:378815 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ155041.1 gg_id:590526 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
GQ048012.1 gg_id:433171 Topographical and Temporal Human Skin Microbiome skin palm clone nbw140c06c1
GQ154774.1 gg_id:512283 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
GQ085555.1 gg_id:400155 Topographical and Temporal Human Skin Microbiome skin palm clone nbw277e02c1
FJ745300.1 gg_id:529154 Enterobacter sp. str. DHM-1T
GQ101981.1 gg_id:447089 Topographical and Temporal Human Skin Microbiome skin palm clone nbw502a11c1
EU471150.1 gg_id:289419 red panda feces clone RP_3aaa01h02
EU472682.1 gg_id:302297 red panda feces clone RPSD_1aaa01b01
EF604226.1 gg_id:231697 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous
FM180568.1 gg_id:369789 Escherichia coli 0127:H6 str. E2348/69
CP001790.1 gg_id:523634 Pectobacterium wasabiae str. WPP163
NC_002655.2 gg_id:150515 Escherichia coli O157:H7 str. EDL933
FJ976591.1 gg_id:586643 Enterobacter cloacae str. LCR82
EU471123.1 gg_id:297308 red panda feces clone RP_3aaa04c06
EU470963.1 gg_id:291712 red panda feces clone RP_2aaa01f10
GQ047956.1 gg_id:386610 Topographical and Temporal Human Skin Microbiome skin palm clone nbw139e10c1
GQ155268.1 gg_id:536948 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
EU472798.1 gg_id:287407 red panda feces clone RPSD_1aaa04f01
GQ069125.1 gg_id:405545 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
NC_008563.1 gg_id:176526 Escherichia coli str. APEC O1
FJ463821.1 gg_id:363666 Escherichia coli str. 4107
GQ416550.1 gg_id:543441 Temporal succession biological degreasing systems clone F7jun.28
GQ047909.1 gg_id:463156 Topographical and Temporal Human Skin Microbiome skin palm clone nbw138h09c
EU472766.1 gg_id:302258 red panda feces clone RPSD_1aaa01d04
EU470754.1 gg_id:298335 red panda feces clone RP_2aaa03f01
GQ016868.1 gg_id:492799 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw826d1
GQ048034.1 gg_id:414459 Topographical and Temporal Human Skin Microbiome skin palm clone nbw140f03c1

EU460263.1	295242	758.4	1231.4	3405.2	1500.9	1342.0	1357.4
EU275356.1	256517	506.4	641.0	2467.5	319.3	141.4	579.1
GQ493157.1	592185	1984.6	2150.9	3430.0	3769.8	2835.4	3768.6
NC_007946.1	156719	693.5	598.2	3366.6	1040.4	503.4	1094.7
GQ069665.1	467129	961.6	1297.1	820.0	969.9	1421.8	1364.9
EU460420.1	292398	1104.7	1364.4	4195.0	1000.9	993.0	1413.3
U88546.1	9709	35.9	161.1	247.6	81.1	76.9	112.3
EF059884.1	226386	733.3	1069.5	1689.0	466.4	666.0	741.3
U90318.1	9667	6346.2	6185.8	5187.0	6441.7	9859.5	9473.8
EF604220.1	231694	160.2	422.5	765.4	380.0	326.0	562.1
FJ975783.1	580915	8541.5	9384.5	4588.8	4618.9	4766.4	3084.5
EU472654.1	299365	2311.2	2762.2	1623.3	2307.6	1744.4	2216.3
FJ997270.1	422465	4381.7	1879.1	1880.5	5589.6	3304.8	4008.4
GQ045414.1	378815	3419.3	3025.3	4778.8	3516.4	4853.0	5793.8
GQ155041.1	590526	8299.5	6586.1	9000.0	8070.1	8119.0	8371.2
GQ048012.1	433171	2958.6	2282.1	4497.5	3876.0	3148.2	3588.8
GQ154774.1	512283	943.7	1277.5	4860.2	1600.2	1469.1	2528.6
GQ085555.1	400155	815.6	570.1	1368.1	408.5	1712.0	1862.9
FJ745300.1	529154	1009.3	1309.9	3572.7	895.4	2856.3	1647.3
GQ101981.1	447089	862.0	1193.6	2673.3	2067.0	5300.9	4058.6
EU471150.1	289419	1667.7	1640.5	1218.6	1996.2	2620.7	2969.1
EU472682.1	302297	1714.3	1610.6	5042.6	2068.5	1358.5	2697.9
EF604226.1	231697	5269.5	6436.1	7918.4	6469.1	7737.0	7165.6
FM180568.1	369789	701.6	1061.0	1150.2	1082.5	753.6	895.6
CP001790.1	523634	609.9	885.9	1237.9	1135.1	1670.6	2615.0
NC_002655.2	150515	1760.2	1467.8	4786.3	2843.9	1675.9	2671.3
FJ976591.1	586643	899.5	1645.3	2609.8	1152.5	6866.6	4373.9
EU471123.1	297308	8408.7	11011.2	7058.8	8837.1	9568.1	6967.1
EU470963.1	291712	2184.2	1994.0	4342.6	3819.0	2541.4	4072.9
GQ047956.1	386610	3343.6	2410.8	3968.2	7132.6	2868.3	4775.8
GQ155268.1	536948	14262.6	16495.1	18195.7	13144.2	13010.5	13009.6
EU472798.1	287407	980.9	1491.7	2925.6	1798.2	2339.7	1755.5
GQ069125.1	405545	8165.3	9234.5	6691.3	8298.4	11792.9	9928.9
NC_008563.1	176526	2661.7	1868.9	4323.7	3791.9	3267.0	2611.1
FJ463821.1	363666	4814.8	4279.0	1070.1	6386.3	8368.9	9743.8
GQ416550.1	543441	1392.8	1431.1	5812.0	1459.3	2420.5	1932.0
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EU472766.1	302258	1606.0	1925.7	3889.9	2669.6	3266.0	3896.8
EU470754.1	298335	6460.3	6635.1	2830.4	8213.2	11529.6	10790.6
GQ016868.1	492799	186.8	535.2	1592.9	718.1	401.7	674.5
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EU470945.1 gg_id:294418 red panda feces clone RP_2aaa03f03
GQ025521.1 gg_id:442426 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
EU460321.1 gg_id:296919 polar bear feces clone PB1_aai26e07
AY941834.1 gg_id:114469 Pantoea agglomerans str. XW112
AB269763.1 gg_id:167919 Escherichia coli str. AE1-2
GQ155076.1 gg_id:587663 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
EU471300.1 gg_id:297539 red panda feces clone RP_3aaa02b11
GQ099117.1 gg_id:373130 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
DQ836638.1 gg_id:165472 gut- microorganisms pupa and adults pine engraver gut Ips pini larva clone ips8e3
GQ095896.1 gg_id:412687 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw4
NZ_AAJU02000034.1 gg_id:351276 Escherichia coli str. F11
AB428447.1 gg_id:331682 Ewingella americana str. GLD
FJ605379.1 gg_id:449339 Enterobacter cloacae str. AceL-1
AJ884896.1 gg_id:191235 Rahnella sp. N1EH1
GQ155165.1 gg_id:589437 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
Z14096.1 gg_id:9994 Parasite BEV of E.variegatus
GQ493261.1 gg_id:592641 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
GQ155053.1 gg_id:511492 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
EU470684.1 gg_id:292570 red panda feces clone RP_1aaa03a02
DQ356903.1 gg_id:153848 Pantoea agglomerans str. P29
GQ025092.1 gg_id:386644 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1:
EU470757.1 gg_id:292134 red panda feces clone RP_2aaa02d12
DQ347838.1 gg_id:145311 Enterobacter cloacae Ecl_IIT-BT08
EF059824.1 gg_id:222822 Enterobacter sakazakii str. E283
GU594312.1 gg_id:531208 Escherichia coli str. E36
FJ368408.1 gg_id:361452 feces adult twins and mothers; TS3 clone TS3_a04a06
GQ155271.1 gg_id:586018 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
EU816587.1 gg_id:305982 Enterobacter sp. str. MB-2-2-4
EF604008.1 gg_id:228026 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
GQ047651.1 gg_id:462723 Topographical and Temporal Human Skin Microbiome skin palm clone nbw137c11c1
EU472845.1 gg_id:300896 red panda feces clone RPSD_1aaa03f06
EU472732.1 gg_id:293451 red panda feces clone RPSD_1aaa02f03
EU420928.1 gg_id:274149 Citrobacter freundii str. SA-A5-98
GQ155187.1 gg_id:592787 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
FM180568.1 gg_id:369793 Escherichia coli 0127:H6 str. E2348/69
FJ823386.1 gg_id:592076 Escherichia coli str. TCP-1
FJ975788.1 gg_id:589157 Human gut microbiome adopts alternative state bowel transplantation ileum effluent
EU471298.1 gg_id:293377 red panda feces clone RP_3aaa01g05
EU560861.1 gg_id:547859 Assessment genetic Apriona germari (Hope) larvae normalization techniques intestir
EF515421.1 gg_id:217233 Electricigen Enrichment MFC upf microbial fuel cell anode clone 24c02
NZ_ABHT01000152.1 gg_id:260777 Escherichia coli O157:H7 str. EC4501

EU470945.1	294418	1441.6	1611.4	3292.1	1829.2	2007.2	2547.3
GQ025521.1	442426	2802.9	3040.0	4381.3	4111.5	3801.2	3674.8
EU460321.1	296919	11016.4	12344.0	8657.3	12375.9	9178.3	8015.2
AY941834.1	114469	129.8	617.7	2650.9	218.2	97.8	278.0
AB269763.1	167919	300.6	301.2	1459.7	615.3	253.0	509.2
GQ155076.1	587663	426.5	725.1	2146.0	1172.3	479.8	1803.2
EU471300.1	297539	596.2	632.6	2592.7	793.8	493.4	870.1
GQ099117.1	373130	7420.0	7114.3	4020.2	9641.4	10070.4	7302.5
DQ836638.1	165472	290.4	927.5	905.5	902.2	300.3	141.1
GQ095896.1	412687	1859.0	1464.0	3026.8	3252.1	1894.2	2530.2
NZ_AAJU02000034.1	351276	709.5	1272.2	1711.2	1613.7	988.5	1994.2
AB428447.1	331682	3810.3	3205.9	5485.0	5071.1	2026.7	2855.6
FJ605379.1	449339	2767.4	2069.7	5059.4	4696.1	3498.4	5061.4
AJ884896.1	191235	702.1	876.3	1199.7	536.6	491.6	916.1
GQ155165.1	589437	1402.6	1549.8	6060.3	1388.5	1665.3	1913.0
Z14096.1	9994	1318.4	894.5	1912.8	2884.1	2036.3	441.3
GQ493261.1	592641	602.1	911.2	3912.7	984.8	536.2	1144.2
GQ155053.1	511492	16996.1	13007.5	6520.7	10850.6	13233.5	12844.3
EU470684.1	292570	4802.5	4938.0	1813.9	3444.3	4664.3	2863.0
DQ356903.1	153848	1193.5	1605.2	4885.4	1675.4	4788.1	3454.6
GQ025092.1	386644	738.5	958.7	1947.7	1070.3	684.5	2150.1
EU470757.1	292134	6077.5	7186.4	2421.4	9117.5	10124.6	8615.8
DQ347838.1	145311	1677.0	2169.9	2637.4	3983.2	3115.5	2465.0
EF059824.1	222822	692.2	790.2	2659.7	902.7	507.0	757.7
GU594312.1	531208	394.1	795.9	2728.1	715.1	617.0	736.9
FJ368408.1	361452	6229.2	5554.4	3670.9	4564.7	4024.9	2713.5
GQ155271.1	586018	11974.9	11540.8	5493.2	9925.1	13929.4	14362.7
EU816587.1	305982	7386.5	7092.0	4361.8	8733.1	8969.9	7905.6
EF604008.1	228026	1136.8	1629.7	1449.6	1079.0	1678.2	1160.6
GQ047651.1	462723	9936.2	9793.2	10495.4	12666.7	14814.3	12626.2
EU472845.1	300896	2264.0	2527.9	6001.9	3377.6	3487.1	3682.1
EU472732.1	293451	3176.3	2755.0	2430.6	3991.7	1984.5	3661.1
EU420928.1	274149	335.5	996.8	2339.7	357.4	677.6	1184.0
GQ155187.1	592787	1303.7	1380.9	3525.6	1567.8	1436.6	1477.4
FM180568.1	369793	96.6	251.8	1809.3	341.7	100.1	408.2
FJ823386.1	592076	355.4	1294.2	2464.3	1074.5	789.4	1835.5
FJ975788.1	589157	216.3	784.8	2556.4	258.0	1014.2	2107.0
EU471298.1	293377	1525.4	1416.7	4386.1	2466.0	1282.8	2192.3
EU560861.1	547859	321.9	381.9	929.6	178.4	457.8	338.8
EF515421.1	217233	4913.4	4995.5	8994.4	3633.6	6464.2	4862.5
NZ_ABHT01000152.1	260777	1277.3	914.0	1509.3	1441.1	542.6	654.3

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FJ369784.1 gg_id:366939 feces adult twins and mothers; TS51 clone TS51_a04g06
GQ048041.1 gg_id:388811 Topographical and Temporal Human Skin Microbiome skin palm clone nbw140f10c1
GQ155197.1 gg_id:585037 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
EU472785.1 gg_id:299402 red panda feces clone RPSD_1aaa01c08
Z83204.1 gg_id:9679 Escherichia coli
FJ364841.1 gg_id:365623 feces adult twins and mothers; TS19 clone TS19_a03g09
AF373200.1 gg_id:66725 Erwinia chrysanthemi str. 572
EU130557.1 gg_id:244222 Escherichia coli str. LR09
Z96093.1 gg_id:9800 Erwinia chrysanthemi str. LMG 2804
EU472665.1 gg_id:299098 red panda feces clone RPSD_1aaa04f11
EU470631.1 gg_id:287354 red panda feces clone RP_1aaa02h10
GQ023992.1 gg_id:485677 Topographical and Temporal Human Skin Microbiome skin palm clone nbw124h03c1
GQ259886.1 gg_id:582624 Shigella sonnei str. 136
EU554428.1 gg_id:273485 Enterobacter cloacae str. Ag02
GQ155046.1 gg_id:538073 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
EU535123.1 gg_id:280193 profile human microbiota antecubital fossa (inner elbow) skin clone nbt171c02
EU464506.1 gg_id:297762 African elephant feces clone AFEL_aai30c11
GQ048005.1 gg_id:385167 Topographical and Temporal Human Skin Microbiome skin palm clone nbw140b08c1
AB273744.1 gg_id:236091 Erwinia aphidicola str. GTC 1688
GQ154843.1 gg_id:553840 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
EU470615.1 gg_id:291008 red panda feces clone RP_1aaa04d04
GQ025492.1 gg_id:441988 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ026798.1 gg_id:457125 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
EU778387.1 gg_id:356210 Red Panda feces clone RPSD_1aaa04a08
EU470573.1 gg_id:301959 red panda feces clone RP_1aaa03e03
GQ154857.1 gg_id:580141 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
GQ047689.1 gg_id:449074 Topographical and Temporal Human Skin Microbiome skin palm clone nbw137h10c1
CU928161.2 gg_id:563141 Escherichia coli str. S88
EF059842.1 gg_id:224891 Enterobacter asburiae str. E531
EU467838.1 gg_id:297319 North American black bear feces clone BB1_b07_2
GQ492166.1 gg_id:590121 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
GQ492874.1 gg_id:535252 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
FJ405333.1 gg_id:369236 Escherichia coli str. 4060
AY373830.1 gg_id:105259 Trabulsiella guamensis
AB198445.1 gg_id:135844 termite gut wall fraction clone RsW01-004
GQ025599.1 gg_id:389061 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ114854.1 gg_id:415761 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
U90316.1 gg_id:9661 Salmonella typhimurium str. Stm1
DQ068855.1 gg_id:138975 microbiota antlions (Myrmeleon mobilis) GI tract freshly caught antlion OTU6 clone
EU470655.1 gg_id:297290 red panda feces clone RP_1aaa04h06
GQ031692.1 gg_id:383643 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n

FJ369784.1	366939	4186.6	3690.8	2234.7	3882.9	2775.9	1726.3
GQ048041.1	388811	17823.4	17304.6	12547.7	17024.8	17488.8	16296.9
GQ155197.1	585037	1034.8	1132.6	5041.7	1371.1	1208.5	1513.6
EU472785.1	299402	4681.1	4984.8	6220.2	6044.2	4281.2	6059.8
Z83204.1	9679	1116.4	1170.0	1793.3	2037.0	1154.9	1686.7
FJ364841.1	365623	1459.2	1717.1	2506.4	2180.8	2800.2	2515.8
AF373200.1	66725	4854.1	5997.7	4750.3	8150.7	10308.6	9131.4
EU130557.1	244222	428.8	614.8	1891.6	1301.7	904.3	1048.5
Z96093.1	9800	1752.4	1516.8	5007.8	3491.3	2209.9	3469.9
EU472665.1	299098	5831.6	5304.6	9300.8	9954.1	7596.2	7738.0
EU470631.1	287354	1164.0	933.0	2298.8	972.5	854.1	1362.0
GQ023992.1	485677	241.3	371.3	1212.6	1216.6	569.1	1692.8
GQ259886.1	582624	4257.6	3905.8	5922.7	5998.5	10285.1	5951.3
EU554428.1	273485	168.0	265.9	405.0	182.0	97.8	119.5
GQ155046.1	538073	1294.0	1520.0	3493.3	1547.9	1666.8	1512.8
EU535123.1	280193	234.4	438.6	1202.4	854.7	407.6	716.2
EU464506.1	297762	2361.9	2251.9	3300.0	4082.5	1897.6	2077.7
GQ048005.1	385167	2283.5	3149.6	4010.8	4457.3	4147.0	2892.6
AB273744.1	236091	231.3	669.4	1963.1	390.0	189.4	286.4
GQ154843.1	553840	419.5	911.7	3028.2	400.1	514.1	934.2
EU470615.1	291008	7021.1	8316.7	2734.2	9471.1	12177.2	9473.3
GQ025492.1	441988	635.5	1152.6	2910.8	1405.8	1321.1	1256.1
GQ026798.1	457125	4400.3	2097.4	2236.2	5071.1	2165.9	2631.1
EU778387.1	356210	7888.3	8744.1	5898.8	10358.4	10677.4	9539.7
EU470573.1	301959	1526.6	1330.9	3437.6	2470.4	1406.4	2087.9
GQ154857.1	580141	273.4	1131.3	8734.6	693.2	446.7	992.0
GQ047689.1	449074	1587.8	1247.7	3750.6	2940.0	1679.6	2447.1
CU928161.2	563141	1612.1	1241.6	3086.9	1476.1	867.2	1595.4
EF059842.1	224891	182.4	817.9	2429.3	335.9	183.9	528.4
EU467838.1	297319	4968.4	5353.2	4931.7	4563.7	7605.0	8535.2
GQ492166.1	590121	5187.6	6132.4	4322.3	5847.7	4731.0	3740.5
GQ492874.1	535252	7244.6	7003.1	5910.1	6601.8	9360.2	9045.2
FJ405333.1	369236	572.4	629.9	852.9	1268.4	2054.5	1751.6
AY373830.1	105259	4456.6	5436.6	5521.1	4274.8	7760.6	6658.5
AB198445.1	135844	278.4	703.7	5198.1	386.9	279.6	917.3
GQ025599.1	389061	582.3	1149.4	3079.1	864.0	781.8	780.1
GQ114854.1	415761	11006.5	9462.8	4132.4	5957.9	4954.3	5266.8
U90316.1	9661	360.5	663.6	2216.2	996.7	743.7	608.9
DQ068855.1	138975	261.5	577.8	2029.2	275.7	216.8	362.1
EU470655.1	297290	4389.7	3712.3	6131.3	5911.5	4683.9	5496.2
GQ031692.1	383643	215.7	429.6	2326.6	542.8	406.1	702.9

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DQ086780.1 gg_id:128319 Serratia grimesii str. I21
EF191171.1 gg_id:189337 Escherichia coli dcm
EF515376.1 gg_id:225183 Electricigen Enrichment MFC upf microbial fuel cell anode clone 23e11
GQ155116.1 gg_id:511824 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
GQ155122.1 gg_id:569621 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
EF428236.2 gg_id:218527 Enterobacter hormaechei str. HDYM-06
GQ155942.1 gg_id:574837 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
DQ818881.1 gg_id:164892 mouse cecal microbiota-colonized zebrafish digestive tract clone aab39b09
EF515182.1 gg_id:226172 Electricigen Enrichment MFC upf microbial fuel cell anode clone 21a07
GQ047658.1 gg_id:400299 Topographical and Temporal Human Skin Microbiome skin palm clone nbw137d10c1
GQ155319.1 gg_id:511367 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
GQ493947.1 gg_id:532961 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
AP010953.1 gg_id:568503 Escherichia coli O26:H11 str. 11368
GQ102038.1 gg_id:456984 Topographical and Temporal Human Skin Microbiome skin palm clone nbw502g05c1
CU928161.2 gg_id:563143 Escherichia coli str. S88
GQ069819.1 gg_id:465176 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw1
FJ975865.1 gg_id:554433 Human gut microbiome adopts alternative state bowel transplantation ileum effluent
FJ368169.1 gg_id:362886 feces adult twins and mothers; TS3 clone TS3_a01a10
EU472720.1 gg_id:289568 red panda feces clone RPSD_1aaa03g08
GQ155176.1 gg_id:512507 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
AM933757.1 gg_id:353249 Kluyvera cryocrescens 4701
CU928162.2 gg_id:547289 Escherichia coli str. ED1a
NZ_ABHK01000009.1 gg_id:260250 Escherichia coli O157:H7 str. EC4206
EU472859.1 gg_id:302247 red panda feces clone RPSD_1aaa03f11
GQ155100.1 gg_id:539752 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
GQ047953.1 gg_id:434609 Topographical and Temporal Human Skin Microbiome skin palm clone nbw139e07c1
EU472801.1 gg_id:295032 red panda feces clone RPSD_1aaa04g01
AF373203.1 gg_id:66723 Erwinia chrysanthemi str. GSPB 1406
EU723875.1 gg_id:349834 Shigella sp. str. 121405
GQ033388.1 gg_id:388657 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw1
AY360397.1 gg_id:93777 Erwinia chrysanthemi str. S3-1
EU275357.1 gg_id:250107 Pantoea agglomerans str. CONC7
EU560857.1 gg_id:562063 Assessment genetic Apriona germari (Hope) larvae normalization techniques intestir
EU471032.1 gg_id:295686 red panda feces clone RP_2aaa01c11
AB288903.1 gg_id:201514 termite gut homogenate clone BOf5-16
GU594301.1 gg_id:516250 Escherichia coli str. A5
EF515211.1 gg_id:217868 Electricigen Enrichment MFC upf microbial fuel cell anode clone 21d06
GQ155921.1 gg_id:548341 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
EU009178.1 gg_id:250393 Shigella boydii str. FBD007
GQ491471.1 gg_id:588423 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
EF608546.1 gg_id:230213 predatory Poecilus chalcites their response lab rearing and antibiotic treatment diges

DQ086780.1	128319	43.7	418.5	2840.0	183.8	97.1	344.0
EF191171.1	189337	2934.1	1189.7	2371.4	2776.0	829.3	1548.9
EF515376.1	225183	713.7	613.3	1278.8	219.9	108.3	865.6
GQ155116.1	511824	5528.0	5761.0	13151.9	6254.7	7165.5	8071.9
GQ155122.1	569621	1724.9	2217.3	6313.3	2998.0	3625.9	5132.6
EF428236.2	218527	1902.3	1916.4	4312.5	2098.8	3244.0	4439.3
GQ155942.1	574837	2592.1	2651.4	3016.5	1329.8	3186.9	2558.6
DQ818881.1	164892	1312.2	831.7	3104.4	1967.1	967.8	1556.7
EF515182.1	226172	10209.1	9923.5	6148.3	3109.4	7669.7	5893.4
GQ047658.1	400299	4201.3	4317.6	6785.9	5062.4	6911.2	5454.1
GQ155319.1	511367	1614.9	2180.8	6083.6	1918.9	2588.5	2929.1
GQ493947.1	532961	5777.0	6188.0	5314.3	9842.8	7925.7	6666.7
AP010953.1	568503	3466.8	4987.2	7073.6	8963.5	6557.4	4816.3
GQ102038.1	456984	2595.0	2622.2	5690.6	4235.6	3301.2	3455.0
CU928161.2	563143	652.0	651.9	3476.8	1067.1	512.0	1116.2
GQ069819.1	465176	10818.5	13112.6	9277.0	8380.5	12395.6	9519.0
FJ975865.1	554433	2605.3	3636.2	9296.7	3323.1	5610.2	4756.4
FJ368169.1	362886	500.0	761.6	827.6	949.7	714.1	818.0
EU472720.1	289568	318.7	589.6	1088.8	706.4	637.5	958.7
GQ155176.1	512507	612.3	981.1	3681.4	696.1	1033.6	1133.7
AM933757.1	353249	829.3	759.4	1170.2	2054.0	1667.9	1019.5
CU928162.2	547289	303.8	314.7	1436.1	599.9	256.8	522.3
NZ_ABHK01000009.1	260250	3105.5	1770.7	1466.5	6453.3	2024.1	3337.0
EU472859.1	302247	1345.7	1188.8	3368.6	3501.0	1344.7	2638.2
GQ155100.1	539752	866.1	1001.0	4149.3	759.6	721.2	1011.0
GQ047953.1	434609	9791.1	10028.1	12942.6	11297.7	13247.2	12544.6
EU472801.1	295032	140.5	339.1	575.3	225.9	232.9	350.2
AF373203.1	66723	57.2	287.0	1508.7	388.0	948.2	353.0
EU723875.1	349834	640.4	840.0	1870.5	688.5	567.2	1776.4
GQ033388.1	388657	1391.9	1862.2	822.7	1157.0	514.5	1768.6
AY360397.1	93777	635.8	583.9	1643.0	493.8	619.8	418.7
EU275357.1	250107	52.9	282.2	619.0	115.3	68.6	87.7
EU560857.1	562063	3153.3	3124.6	3286.8	4286.1	7703.4	4827.9
EU471032.1	295686	794.6	937.7	2713.5	875.0	823.1	973.3
AB288903.1	201514	1157.4	1480.0	2013.7	405.3	1286.4	1589.3
GU594301.1	516250	997.6	926.3	3355.6	1544.2	1180.8	1480.3
EF515211.1	217868	577.2	953.3	1463.7	517.2	4991.8	1653.4
GQ155921.1	548341	533.0	922.3	2309.8	426.8	525.5	844.2
EU009178.1	250393	200.9	588.0	2971.7	704.0	415.5	731.7
GQ491471.1	588423	3679.9	3083.7	6236.7	5121.3	5170.4	4279.5
EF608546.1	230213	646.9	794.2	1024.2	2489.3	253.8	763.2

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AB368994.1 gg_id:569024 and microbial oils produced Asia petroleum crude oil (Arabian Extra light) clone PT-A
CP001637.1 gg_id:524976 Escherichia coli str. DH1
AM184214.1 gg_id:161150 Pantoea agglomerans str. WAB1872
EU472148.1 gg_id:288731 francois langur feces clone FL_2aaa02a09
EF515321.1 gg_id:219651 Electricigen Enrichment MFC upf microbial fuel cell anode clone 22h03
EF011116.1 gg_id:199506 Enterobacter cancerogenus str. EBD
EF471230.1 gg_id:226404 Enterobacter sp. str. BBTR105
CP001790.1 gg_id:523631 Pectobacterium wasabiae str. WPP163
AM157436.1 gg_id:141413 Escherichia coli mother C4
CP000247.1 gg_id:169667 Escherichia coli str. 536
EU470717.1 gg_id:302020 red panda feces clone RP_1aaa02h08
FJ368186.1 gg_id:366961 feces adult twins and mothers; TS3 clone TS3_a01c05
EU778424.1 gg_id:326151 Red Panda feces clone RPSD_1aaa01b11
AY804014.1 gg_id:112448 Escherichia coli str. T10
EU471322.1 gg_id:303145 red panda feces clone RP_3aaa04b03
GQ029738.1 gg_id:413180 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw926f08
EU554433.1 gg_id:273281 Shigella boydii str. Ag07
EU472761.1 gg_id:301142 red panda feces clone RPSD_1aaa02f12
L10328.1 gg_id:9702 Escherichia coli
EF560776.1 gg_id:232981 Escherichia coli str. BE14
EF676101.1 gg_id:257345 Klebsiella oxytoca str. XJU-1
GQ102000.1 gg_id:409168 Topographical and Temporal Human Skin Microbiome skin palm clone nbw502c09c1
AJ854062.1 gg_id:108296 Serratia ureolytica str. NiVa 51
GQ099091.1 gg_id:389986 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ031106.1 gg_id:395646 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
FJ368221.1 gg_id:369163 feces adult twins and mothers; TS3 clone TS3_a01f08
CP000247.1 gg_id:169665 Escherichia coli str. 536
EU470534.1 gg_id:296475 red panda feces clone RP_1aaa04e05
EU471185.1 gg_id:290380 red panda feces clone RP_3aaa03b07
GQ927306.1 gg_id:540402 Enterobacter sp. str. M6
EU761952.1 gg_id:316329 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1
FJ364654.1 gg_id:368156 feces adult twins and mothers; TS19 clone TS19_a01e03
GU186117.1 gg_id:593155 Enterobacter cloacae str. IHB B 1374
GU594309.1 gg_id:521580 Escherichia coli str. AB6
U88435.1 gg_id:10311 Rahnella sp. 'CDC 21234' str. CDC 21234
EU470575.1 gg_id:302778 red panda feces clone RP_1aaa03a07
EU999992.2 gg_id:343920 Enterobacter ludwigii str. T4384
EU240200.1 gg_id:236031 interfering detection phytoplasma universal phytoplasmic primers Mexico
EU460602.1 gg_id:298145 polar bear feces clone PB2_aai23c03
EU472738.1 gg_id:302314 red panda feces clone RPSD_1aaa03d08
NZ_AAJU02000035.1 gg_id:318422 Escherichia coli str. F11

AB368994.1	569024	5182.7	4962.2	6005.8	8668.9	8277.9	12251.5
CP001637.1	524976	221.8	464.7	630.4	877.0	406.0	612.5
AM184214.1	161150	90.5	238.2	447.5	144.9	169.6	145.6
EU472148.1	288731	9197.4	8734.2	12167.2	9047.5	8976.5	8236.9
EF515321.1	219651	97.1	285.7	1060.6	276.9	101.0	287.6
EF011116.1	199506	1041.3	1611.9	7116.6	1843.5	1799.7	2855.1
EF471230.1	226404	63.0	86.4	68.6	71.4	118.0	46.0
CP001790.1	523631	1115.3	1337.3	3262.3	1413.9	686.4	1438.8
AM157436.1	141413	27.5	148.0	338.4	106.7	45.5	77.6
CP000247.1	169667	8879.3	8913.8	3014.3	2717.0	5631.6	4439.1
EU470717.1	302020	1753.3	1496.3	3522.4	2827.5	1689.3	2529.1
FJ368186.1	366961	4568.9	4517.3	7246.2	6212.0	7036.6	8605.2
EU778424.1	326151	1188.8	1477.9	1714.8	2243.5	3109.3	2071.3
AY804014.1	112448	190.6	306.4	1097.9	852.8	296.5	1004.7
EU471322.1	303145	699.9	1095.8	2253.1	1443.0	4403.4	5164.6
GQ029738.1	413180	896.0	1041.7	2601.6	1625.3	780.9	1401.7
EU554433.1	273281	1416.5	1776.5	5189.8	1788.1	3314.7	2822.7
EU472761.1	301142	1207.8	1130.0	3277.9	2131.6	969.8	1872.6
L10328.1	9702	862.5	991.3	636.2	1630.3	3817.1	1961.4
EF560776.1	232981	1096.6	752.5	2218.0	952.8	796.7	1211.7
EF676101.1	257345	804.3	1097.8	2700.7	480.8	1709.8	1767.1
GQ102000.1	409168	10386.5	8199.4	7822.8	10699.5	13419.0	10254.6
AJ854062.1	108296	90.2	412.1	1068.1	213.2	79.9	190.0
GQ099091.1	389986	1370.1	1453.7	3914.2	2583.2	1883.3	1430.3
GQ031106.1	395646	2723.9	3236.4	1903.9	3426.3	3836.8	1231.6
FJ368221.1	369163	185.7	291.0	871.3	1078.1	178.4	654.2
CP000247.1	169665	1982.1	1430.7	2650.8	3219.6	1907.9	2479.6
EU470534.1	296475	135.4	542.3	1696.3	238.7	165.1	385.3
EU471185.1	290380	2994.1	1649.7	3946.4	2669.9	4752.4	4014.5
GQ927306.1	540402	11059.2	11495.0	4675.8	10737.1	12905.8	10866.6
EU761952.1	316329	1592.1	1111.2	2992.0	2157.8	1644.0	2029.4
FJ364654.1	368156	944.2	1086.7	1903.8	1827.9	1630.5	2361.3
GU186117.1	593155	10214.0	9646.2	7045.4	10589.1	16907.3	12779.1
GU594309.1	521580	1649.2	1430.8	3368.6	3134.3	1581.9	2153.4
U88435.1	10311	2453.9	2115.2	5909.4	5369.6	3733.6	4430.5
EU470575.1	302778	11788.3	12156.6	18060.7	12796.6	17062.1	14159.7
EU999992.2	343920	1343.8	1528.2	2848.7	2247.3	2011.1	1289.9
EU240200.1	236031	398.8	426.9	2335.5	1809.8	3092.3	700.3
EU460602.1	298145	1519.9	1689.9	3548.6	2078.7	1076.8	1729.8
EU472738.1	302314	7216.7	6830.0	3553.4	8187.2	4633.0	4536.3
NZ_AAJU02000035.1	318422	527.9	946.5	994.5	1211.2	696.2	1414.3

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AJ233424.1 gg_id:10115 Pragia fontium str. DSM 5563
GQ101959.1 gg_id:464725 Topographical and Temporal Human Skin Microbiome skin palm clone nbw501g08c1
GQ099081.1 gg_id:403628 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ155052.1 gg_id:574054 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
AF511430.1 gg_id:65406 Escherichia coli CCCO4
AY344368.2 gg_id:91670 Lake Kauhako 30 m clone K2-30-35
GQ098908.1 gg_id:406048 Topographical and Temporal Human Skin Microbiome skin palm clone nbw503g03c1
FJ976582.1 gg_id:592530 Enterobacter cancerogenus str. LCR73
CP000247.1 gg_id:169666 Escherichia coli str. 536
EF102825.1 gg_id:257388 Enterobacter sp. str. G-226-1
GQ154770.1 gg_id:589091 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
GQ025541.1 gg_id:431917 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
EF219421.2 gg_id:441069 Enterobacter cloacae str. ATCC 43560
U92197.1 gg_id:9711 Salmonella subsp. enterica serovar Agona str. Sa1 subsp.
GQ154820.1 gg_id:535230 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
GQ031713.1 gg_id:452836 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
NZ_ABHM02000001.1 gg_id:317271 Escherichia coli O157:H7 str. EC4042
GQ155096.1 gg_id:594320 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
FJ859683.1 gg_id:573410 Enterobacter ludwigii str. BIHB 336
GQ155198.1 gg_id:586724 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
CP000468.1 gg_id:175186 Escherichia coli str. APEC O1
NC_008563.1 gg_id:176527 Escherichia coli str. APEC O1
GQ155253.1 gg_id:582117 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
FJ976590.1 gg_id:581741 Enterobacter sp. str. LCR81
FJ811874.1 gg_id:593519 Enterobacter aerogenes str. 5-WCH
ABHS01000007.1 gg_id:302893 Escherichia coli O157:H7 str. EC4486
X80726.1 gg_id:9698 Shigella sonnei
FJ364922.1 gg_id:363434 feces adult twins and mothers; TS19 clone TS19_a04g07
FM180568.1 gg_id:369792 Escherichia coli 0127:H6 str. E2348/69
AAMJ02000006.1 gg_id:342676 Shigella dysenteriae str. 1012
EU778390.1 gg_id:333367 Red Panda feces clone RPSD_1aaa01b09
EU554431.1 gg_id:273912 Shigella flexneri str. Ag05
AF400480.1 gg_id:18267 Secondary endosymbiont Bemisia tabaci clone TANZ3-2 of
DQ837613.1 gg_id:164437 structures honeybee intestines and their response insecticidal proteins gut clone HB
DQ026512.1 gg_id:134671 Xenorhabdus sp. str. PDBC SCX7
GU480985.1 gg_id:521599 Xenorhabdus hominickii
AB030020.1 gg_id:32418 Antonina crawii (Insecta Homoptera Pseudooccidae) symbiont
AF286129.1 gg_id:21132 eubacterium Aleurodicus dugesii
AF476107.1 gg_id:63935 Planococcus citri symbiont
AY676889.1 gg_id:136328 Baumannia cicadellinicola B37
AF400474.1 gg_id:50143 Secondary endosymbiont Bemisia tabaci clone IND34

AJ233424.1	10115	327.5	647.6	2311.2	586.1	1235.7	2105.8
GQ101959.1	464725	10430.2	10648.0	8882.6	10174.2	10795.6	8893.3
GQ099081.1	403628	10173.8	10247.0	10816.6	8923.7	10024.5	7576.0
GQ155052.1	574054	1282.3	1453.5	3338.7	1535.4	1772.2	1443.6
AF511430.1	65406	1057.7	985.1	2749.6	1760.4	1174.6	1572.6
AY344368.2	91670	29.3	360.2	210.5	47.8	68.4	234.7
GQ098908.1	406048	802.7	1623.4	2889.6	2650.8	654.4	1460.9
FJ976582.1	592530	1277.8	1558.1	1946.8	1920.7	6401.0	5844.7
CP000247.1	169666	632.2	1090.8	3550.6	1122.9	1160.8	1105.5
EF102825.1	257388	487.7	788.6	3744.4	850.0	956.0	1379.2
GQ154770.1	589091	1944.8	2949.5	6650.8	2414.8	5307.2	5116.0
GQ025541.1	431917	285.4	458.4	2400.2	757.0	293.3	1109.8
EF219421.2	441069	259.3	668.5	1739.3	368.4	924.9	748.0
U92197.1	9711	6489.1	5660.5	4898.1	7456.2	10142.2	8499.1
GQ154820.1	535230	3705.6	3533.6	4158.0	2314.8	5418.6	3878.2
GQ031713.1	452836	7943.0	9002.5	9997.6	9352.2	12098.9	10665.5
NZ_ABHM02000001.1	317271	2722.2	2566.5	3407.2	4264.4	4207.5	3906.0
GQ155096.1	594320	228.7	572.8	1569.0	464.0	437.8	994.3
FJ859683.1	573410	78.4	241.0	464.3	118.8	166.2	133.9
GQ155198.1	586724	868.4	1180.7	3142.2	745.2	841.4	878.0
CP000468.1	175186	228.5	449.8	2462.8	668.9	286.1	631.5
NC_008563.1	176527	161.8	585.1	3409.6	329.3	381.8	542.2
GQ155253.1	582117	869.1	1066.3	2665.6	929.7	868.7	1528.0
FJ976590.1	581741	229.4	637.3	673.6	656.3	1378.2	2320.1
FJ811874.1	593519	11958.1	11641.5	8482.2	13084.4	19967.9	14186.5
ABHS01000007.1	302893	2046.0	987.2	1211.6	2931.0	831.5	1881.5
X80726.1	9698	647.2	798.4	2061.0	1047.2	573.3	1438.3
FJ364922.1	363434	339.6	843.6	3535.2	447.7	515.7	569.6
FM180568.1	369792	1090.0	815.9	3534.9	1006.7	787.9	1076.8
AAMJ02000006.1	342676	2339.1	2503.2	6153.7	4283.1	4637.9	5881.6
EU778390.1	333367	7296.0	7320.4	3246.6	9550.5	8651.6	6944.3
EU554431.1	273912	675.8	582.8	3143.4	1176.4	869.0	1681.5
AF400480.1	18267	14075.4	14855.6	9843.5	10994.2	15110.8	13254.6
DQ837613.1	164437	7386.0	6712.5	8088.5	6737.1	8245.2	9463.6
DQ026512.1	134671	1074.2	945.1	2705.8	1116.2	2465.8	1630.0
GU480985.1	521599	2868.3	2866.5	4612.0	5976.6	1586.6	3745.1
AB030020.1	32418	155.5	134.1	496.9	403.6	377.3	355.9
AF286129.1	21132	24.7	38.7	61.1	48.3	77.6	41.0
AF476107.1	63935	30.0	34.9	28.5	41.3	64.7	34.5
AY676889.1	136328	654.0	1040.4	1939.4	1588.9	3861.0	3628.8
AF400474.1	50143	191.2	146.1	498.7	455.8	67.1	135.3

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FJ655540.1 gg_id:567856 symbiont
EU348311.1 gg_id:338822 symbiont
DQ837612.1 gg_id:170811 structures honeybee intestines and their response insecticidal proteins gut clone HB
AY660027.2 gg_id:119010 Xenorhabdus bovienii str. PDBC SCX6
AB064513.1 gg_id:49541 Buchnera aphidicola (Yamatocallis tokyoensis) #207 (Yamatocallis
DQ068832.1 gg_id:139463 microbiota antlions (Myrmeleon mobilis) GI tract freshly caught antlion OTU7 clone
AF476104.1 gg_id:63945 Dysmicoccus neobrevipes symbiont
GU374099.1 gg_id:531978 soil East Calcutta wetland clone SRC_NBB4
AY676885.1 gg_id:136092 Baumannia cicadellinicola B30
FJ655533.1 gg_id:592467 symbiont
DQ133564.1 gg_id:146333 Preliminary survey insects (Hemiptera: Coccoidea) scale insect clone
AB013087.1 gg_id:9649 symbiont
FJ655532.1 gg_id:542044 symbiont
EU348312.1 gg_id:348059 symbiont
GQ154740.1 gg_id:534965 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
AF286125.1 gg_id:52069 symbiont
AB083058.1 gg_id:60304 Placobdelloides siamensis symbiont
AF263559.1 gg_id:54656 Cacopsylla myrthi symbiont
AF077608.1 gg_id:9978 symbiont
AF286128.1 gg_id:27576 symbiont
AF400478.1 gg_id:52003 Secondary endosymbiont Bemisia tabaci clone TANZ15 of
AY167945.1 gg_id:76905 Isolation and identification hyper-ammonia producing swine storage pits manure
AY676882.1 gg_id:136397 Baumannia cicadellinicola B23
AF476110.1 gg_id:63934 Vryburgia amaryllidis symbiont
AY999971.1 gg_id:200690 Placobdelloides jaegerskioeldi symbiont
AF476101.1 gg_id:63942 Antonina pretiosa symbiont
AF286127.1 gg_id:20298 symbiont
NC_004344.2 gg_id:141977 Wigglesworthia glossinidia endosymbiont Glossina brevipalpis
EF153305.1 gg_id:192342 identification gut red imported fire ant (Solenopsis Buren) GI tract Solenopsis invicta
AB083059.1 gg_id:55799 Parabdella sp. symbiont
DQ211709.1 gg_id:164016 Xenorhabdus sp. str. FRM16
D78008.1 gg_id:10301 Xenorhabdus japonica str. SK-1T (=IAM14265T)
GU480979.1 gg_id:529286 Xenorhabdus griffiniae str. T87
GQ923884.1 gg_id:589696 Xenorhabdus sp. str. KB-3
DQ205450.1 gg_id:173648 Xenorhabdus sp. str. USNJ01
GU480982.1 gg_id:526425 Xenorhabdus sp. str. R00I-293
GQ373385.2 gg_id:526191 Xenorhabdus sp. str. SGas1
AY286478.1 gg_id:87839 Xenorhabdus nematophila
FN667741.1 gg_id:524496 Xenorhabdus bovienii str. SS-2004
AB243427.1 gg_id:160641 Xenorhabdus sp. str. MY8 IkWj136
GU480989.1 gg_id:517099 Xenorhabdus szentirmaii

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DQ837612.1	170811	1076.0	1795.8	726.2	772.5	231.2	126.3
AY660027.2	119010	3083.3	2223.5	5236.1	3881.9	4049.9	4497.4
AB064513.1	49541	126.8	109.0	75.2	172.7	87.4	150.2
DQ068832.1	139463	272.5	138.6	156.2	186.6	66.4	165.6
AF476104.1	63945	1221.7	1164.0	2393.5	963.6	1663.5	923.2
GU374099.1	531978	1473.8	1411.6	1069.4	843.1	1714.2	1288.4
AY676885.1	136092	287.4	300.7	165.2	98.7	69.4	64.2
FJ655533.1	592467	7060.6	6227.7	6897.4	6576.6	5984.9	4825.8
DQ133564.1	146333	20797.9	20879.5	16394.2	15284.1	22455.5	17984.2
AB013087.1	9649	1265.5	623.0	225.8	2708.3	763.4	1478.7
FJ655532.1	542044	1459.6	1874.8	2506.2	3686.0	3794.4	3996.7
EU348312.1	348059	5603.1	5388.8	3979.8	5611.7	6920.9	8053.5
GQ154740.1	534965	771.7	697.7	1041.9	2445.4	1331.8	1552.7
AF286125.1	52069	244.1	435.8	256.2	587.2	642.4	450.6
AB083058.1	60304	1504.3	1368.1	246.3	1144.2	1714.3	1271.9
AF263559.1	54656	5718.0	5657.1	3084.7	5357.8	5211.2	3768.9
AF077608.1	9978	122.6	124.3	1217.9	439.7	196.5	283.5
AF286128.1	27576	37.7	131.1	317.0	76.7	78.4	40.4
AF400478.1	52003	2426.4	1446.1	3912.5	3276.8	2461.9	2876.2
AY167945.1	76905	1860.6	775.8	994.0	2831.7	547.1	1100.9
AY676882.1	136397	2467.7	3664.1	3062.2	3043.7	3149.8	2411.0
AF476110.1	63934	115.3	275.2	1010.6	233.7	155.7	444.4
AY999971.1	200690	4844.5	3561.7	2219.2	3761.0	3446.3	2749.3
AF476101.1	63942	4642.5	2964.1	2675.1	5000.1	6315.2	5075.5
AF286127.1	20298	24.0	29.3	60.0	46.1	67.3	25.3
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EF153305.1	192342	1953.9	3829.4	2098.8	2124.8	1867.9	2558.7
AB083059.1	55799	2637.7	2799.8	899.3	1982.8	5951.9	4468.0
DQ211709.1	164016	516.0	1613.7	1542.7	925.8	1474.0	1397.0
D78008.1	10301	242.9	636.5	5338.6	1464.0	405.1	870.7
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DQ205450.1	173648	2039.4	1117.1	2700.1	1342.7	234.7	1145.3
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GQ373385.2	526191	352.6	291.7	1795.0	380.3	1209.0	677.2
AY286478.1	87839	380.4	858.2	2355.8	1312.0	2043.3	1673.7
FN667741.1	524496	1170.4	2149.5	1800.1	954.4	902.1	1109.4
AB243427.1	160641	288.7	815.0	1659.2	2065.7	1446.7	1470.8
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AY278675.1 gg_id:86906 Xenorhabdus beddingii str. DSM4764
D78006.1 gg_id:10299 Xenorhabdus beddingii str. DSM4764
AY317154.1 gg_id:89531 Xenorhabdus bovienii str. CB54
GU480981.1 gg_id:527534 Xenorhabdus bovienii str. Monsanto
GU480988.1 gg_id:515326 Xenorhabdus bovienii str. Li6
DQ208305.1 gg_id:167325 Xenorhabdus bovienii str. TB20
DQ205453.1 gg_id:163330 Xenorhabdus bovienii str. USNY95
D78007.1 gg_id:10244 Xenorhabdus bovienii str. ATCC35271T
FJ860885.1 gg_id:545382 Xenorhabdus bovienii str. USAR01
X82252.1 gg_id:10246 Xenorhabdus bovienii str. DSM 4766
DQ329379.1 gg_id:146743 Xenorhabdus budapestensis str. CB43
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GU480992.1 gg_id:520060 Xenorhabdus innexi
EU190977.1 gg_id:266440 Xenorhabdus kozodoii str. FR48
FJ860884.1 gg_id:591393 Xenorhabdus nematophila str. K97
AY278674.1 gg_id:87960 Xenorhabdus nematophila str. DSM3370
EU513180.1 gg_id:264777 Xenorhabdus poinarii str. SRK 1
DQ211703.1 gg_id:169069 Xenorhabdus poinarii str. AZ26
EU250472.1 gg_id:246846 Xenorhabdus poinarii str. Iran2
GU480993.1 gg_id:527414 Xenorhabdus stockiae str. T9
DQ646382.1 gg_id:161501 Yersinia kristensenii str. 03
AAYR01000001.1 gg_id:261186 Yersinia pestis biovar Antiqua str. UG05-0454
AF365943.1 gg_id:30561 Yersinia pseudotuberculosis str. 204
EU434476.1 gg_id:274633 Yersinia kristensenii str. b281
AJ232236.1 gg_id:10381 Yersinia pestis SS-Yp-114
FJ641890.1 gg_id:559301 Yersinia intermedia str. 5375
EF179132.1 gg_id:264397 Yersinia ruckeri str. CCUG 14190
NC_006155.1 gg_id:128947 Yersinia pseudotuberculosis IP 32953 str. IP32953
AJ627595.1 gg_id:107083 Yersinia kristensenii str. Y156
FJ641877.1 gg_id:543977 Yersinia intermedia str. Nr13/84
CP000720.1 gg_id:257703 Yersinia pseudotuberculosis str. IP 31758
AJ232239.1 gg_id:10384 Yersinia pestis SS-Yp-117
X75274.1 gg_id:10388 Yersinia pestis
FJ641882.1 gg_id:573766 Yersinia intermedia str. H9-36/83
DQ646383.1 gg_id:161584 Yersinia aldovae str. 04
EF515428.1 gg_id:224468 Electricigen Enrichment MFC upf microbial fuel cell anode clone 24c09
EF179120.1 gg_id:258690 Yersinia massiliensis str. CCUG 53444
NZ_AAYR01000015.1 gg_id:263525 Yersinia pestis biovar Antiqua str. UG05-0454
X75276.1 gg_id:10393 Yersinia rohdei
X75273.1 gg_id:10365 Yersinia frederiksenii

FN667741.1	524492	1453.4	2004.6	4066.8	2069.2	2286.9	2806.9
AY278675.1	86906	1026.7	1483.8	2595.1	1388.1	1229.3	1894.8
D78006.1	10299	350.5	357.7	2814.5	1426.3	1920.0	1156.7
AY317154.1	89531	1411.6	2058.4	2756.0	2313.7	1337.0	2077.3
GU480981.1	527534	1620.4	1923.9	4164.4	2334.9	2323.2	2863.5
GU480988.1	515326	9440.0	12135.8	7550.8	10494.1	17718.4	15187.6
DQ208305.1	167325	1484.9	2105.0	2920.0	2581.8	1351.4	2162.2
DQ205453.1	163330	4726.3	4160.3	8184.6	8337.8	5080.1	6298.3
D78007.1	10244	4554.4	5659.2	10011.9	8014.7	9193.0	9857.7
FJ860885.1	545382	1520.1	1930.3	4251.0	2338.2	2323.1	2901.5
X82252.1	10246	2793.9	3251.0	6627.7	4041.6	4851.7	5299.3
DQ329379.1	146743	1290.4	1040.4	5598.8	1613.9	3622.5	2203.7
GU480990.1	529536	661.8	789.7	6241.1	1166.4	1401.3	1709.2
GU480992.1	520060	3798.0	3373.2	6878.3	5853.1	5535.0	6038.1
EU190977.1	266440	533.5	900.6	2942.6	2040.0	2250.4	2294.7
FJ860884.1	591393	3889.3	5119.0	5831.6	4194.8	4371.0	5059.2
AY278674.1	87960	165.3	237.4	1813.4	276.3	73.0	279.7
EU513180.1	264777	9449.5	8019.0	8251.8	10935.3	8315.3	7882.1
DQ211703.1	169069	1506.3	2219.9	3736.9	1971.1	2307.8	1857.6
EU250472.1	246846	208.4	619.7	2041.8	389.2	438.8	167.4
GU480993.1	527414	1665.4	2011.3	3578.3	1975.6	1452.3	1547.9
DQ646382.1	161501	2776.3	3230.4	5765.3	2950.3	4035.9	5551.4
AAYR01000001.1	261186	3414.7	2481.5	772.7	4268.8	4926.5	4460.1
AF365943.1	30561	637.5	528.3	1586.4	806.6	161.8	251.9
EU434476.1	274633	32.5	189.4	1035.1	68.0	56.7	141.5
AJ232236.1	10381	2302.2	2258.7	3041.8	1221.4	702.2	861.4
FJ641890.1	559301	555.5	896.2	3703.0	991.8	777.3	848.9
EF179132.1	264397	148.6	261.1	1087.2	270.0	157.2	234.8
NC_006155.1	128947	5296.3	4645.0	3938.5	5750.9	8145.9	6419.1
AJ627595.1	107083	6019.2	7466.0	6546.3	5577.3	7319.1	7664.5
FJ641877.1	543977	35.1	182.0	896.7	144.6	99.3	143.1
CP000720.1	257703	355.0	512.5	2238.3	804.5	506.4	759.5
AJ232239.1	10384	234.5	481.6	2785.3	273.8	862.5	807.0
X75274.1	10388	682.7	948.3	3447.5	1595.1	547.1	1027.7
FJ641882.1	573766	722.9	1310.3	4970.5	1256.4	965.4	1253.6
DQ646383.1	161584	13960.5	13259.1	11288.3	12160.7	14200.8	12382.1
EF515428.1	224468	9280.0	9140.8	7170.7	10523.1	5611.9	5363.7
EF179120.1	258690	137.0	335.7	1415.9	454.9	793.6	469.9
NZ_AAYR01000015.1	263525	212.2	455.6	2903.7	229.0	836.4	744.2
X75276.1	10393	924.9	1708.1	2395.3	1465.3	1836.7	1488.0
X75273.1	10365	6048.0	7251.3	6863.8	6784.7	9973.7	6298.0

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s__unclassified	3219
s__Coxiella burnetii	2573
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AAYV01000006.1 gg_id:264324 Yersinia pestis biovar Antiqua str. E1979001
EF179125.1 gg_id:275713 Yersinia aldovae str. CCUG 18770
NZ_ABAT01000008.1 gg_id:260769 Yersinia pestis biovar Orientalis str. F1991016
AJ232237.1 gg_id:10382 Yersinia pestis SS-Yp-115
AJ627597.1 gg_id:107378 Yersinia aleksici str. Y159
NR_027543.1 gg_id:535819 Yersinia bercovieri str. CNY 7506; ATCC 43970
U63135.1 gg_id:10347 Yersinia enterocolitica German
AF282308.1 gg_id:41539 Yersinia enterocolitica str. 8081
Z49830.1 gg_id:10349 Yersinia enterocolitica str. ER-31406-92 serotype O:5
GU596500.1 gg_id:527323 Yersinia enterocolitica str. GP2
EF179130.1 gg_id:272269 Yersinia enterocolitica str. CCUG 8239A
X68674.1 gg_id:10341 Yersinia enterocolitica serotype 0:3; strain 11472 Princess Alexandra Hospital Brisbane A
EU523225.1 gg_id:269635 Yersinia enterocolitica str. KM1
DQ486901.1 gg_id:158291 Yersinia frederiksenii 49
AF366384.1 gg_id:34461 Yersinia rohdei str. ATCC 43380
EF179123.1 gg_id:265704 Yersinia intermedia str. CCUG 11292
DQ917929.1 gg_id:163194 Yersinia intermedia str. H-27
NR_027546.1 gg_id:557655 Yersinia mollaretii str. CNY 7263; ATCC 43969
NZ_ACCA01000078.1 gg_id:382211 Yersinia kristensenii str. ATCC 33638
FM955884.1 gg_id:546539 Yersinia kristensenii str. Asd MY-1
EU401667.1 gg_id:263404 Yersinia ruckeri
X75275.1 gg_id:10363 Yersinia ruckeri
FJ873802.1 gg_id:534783 Yersinia ruckeri str. LY0903
AY359283.1 gg_id:102805 Aquicella siphonis str. SGT-108
EF688351.1 gg_id:245537 soil clone F4-96
FJ542924.1 gg_id:526380 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone B
EU801111.1 gg_id:320125 It's all ranking aquatic Delaware Bay NJ clone 2C229435
FM877663.1 gg_id:362619 Microbial several mining wastes Bulgaria vicinity uranium mine Sliven clone Sliv-27
EF019154.1 gg_id:212714 aspen rhizosphere clone Amb_16S_1801
FJ382597.1 gg_id:542155 Potentially pathogenic and air stem cell transplant summer hospital shower water BM
AY734242.1 gg_id:135830 dynamics aquifers indicates presence stable autochthonous microbial endokarst spri
AJ252651.1 gg_id:36918 agricultural soil clone SC-I-71
NR_025763.1 gg_id:552844 Aquicella lusitana str. SGT-39; CIP 107650
GQ054582.1 gg_id:454783 Topographical and Temporal Human Skin Microbiome skin back clone nbw1092b02c
FJ793155.1 gg_id:529786 Archaea and Hot Spring Thailand Tao Dam hot spring clone TDB06
FJ542873.1 gg_id:529296 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone A
DQ083104.1 gg_id:132329 Fnctnl and rspnss mcrbl cntr-old fld sl cln X174
EF540406.1 gg_id:227017 oil-shale semi-coke solid waste clone 4_15MK
NC_011527.1 gg_id:356835 Coxiella burnetii str. CbuG_Q212
EU881324.1 gg_id:314162 (maize-sweet cropping field) Karst region maize-sweet potato cropland soil clone KM
EU143669.1 gg_id:251151 Coxiella-like infection Psittacine birds liver clone 1358

AAYV01000006.1	264324	2281.5	2556.7	2747.8	3172.1	4640.2	4203.6
EF179125.1	275713	1412.5	1252.2	3295.6	715.8	463.5	1176.0
NZ_ABAT01000008.1	260769	222.6	381.0	1800.2	247.3	807.3	712.6
AJ232237.1	10382	259.3	498.8	2989.1	289.0	803.4	746.8
AJ627597.1	107378	1269.8	1116.4	3731.6	3667.3	2539.9	4442.8
NR_027543.1	535819	544.8	1131.2	1570.6	1118.3	2666.0	3468.1
U63135.1	10347	841.7	859.2	2180.2	1437.9	1159.8	1225.7
AF282308.1	41539	108.4	211.9	1403.4	342.8	112.6	510.0
Z49830.1	10349	2207.2	3135.5	6949.9	4386.5	2087.7	3449.7
GU596500.1	527323	195.1	273.1	1694.9	477.0	408.4	619.7
EF179130.1	272269	715.4	715.7	1965.7	1015.9	1376.0	1023.9
X68674.1	10341	1522.1	1790.2	3232.8	644.3	2417.9	2104.8
EU523225.1	269635	1595.3	2184.4	5993.1	3771.9	1847.7	2661.0
DQ486901.1	158291	2435.6	2320.8	2410.4	2864.2	2112.7	2770.6
AF366384.1	34461	765.4	571.5	2541.5	301.5	93.6	365.3
EF179123.1	265704	263.1	583.6	2483.4	279.3	690.7	897.4
DQ917929.1	163194	454.6	626.0	2783.2	841.9	217.8	527.3
NR_027546.1	557655	1155.5	2122.6	6184.4	2096.3	5539.5	6293.0
NZ_ACCA01000078.1	382211	26.6	37.5	326.7	44.4	51.9	43.1
FM955884.1	546539	32.2	163.6	1027.7	48.9	58.6	131.2
EU401667.1	263404	407.0	609.6	2053.3	1051.2	227.9	389.2
X75275.1	10363	1380.9	1454.5	2598.3	1730.6	1146.0	984.2
FJ873802.1	534783	295.2	482.8	2604.6	507.2	111.5	307.2
AY359283.1	102805	232.7	421.5	985.7	809.3	1207.0	314.4
EF688351.1	245537	6691.4	7681.6	8851.1	7719.8	13190.5	10013.0
FJ542924.1	526380	2300.6	3341.5	5869.9	3034.0	5506.0	2105.7
EU801111.1	320125	765.7	945.0	5601.7	1088.3	6457.2	877.9
FM877663.1	362619	5921.5	6940.3	13170.8	8674.0	11740.4	5425.0
EF019154.1	212714	3901.7	3961.0	10717.3	5771.9	7647.7	4319.0
FJ382597.1	542155	8305.6	8081.6	9789.3	9954.7	12139.1	10879.8
AY734242.1	135830	370.5	552.2	1270.3	800.3	735.7	528.0
AJ252651.1	36918	7526.0	6488.4	4023.0	3502.3	5356.4	3533.2
NR_025763.1	552844	59.5	132.1	750.0	232.1	419.8	247.1
GQ054582.1	454783	2061.0	2173.9	4793.8	2431.8	5386.7	3012.7
FJ793155.1	529786	5506.8	5806.9	9950.1	9539.9	11103.5	6824.6
FJ542873.1	529296	6065.9	4942.1	8007.9	7150.7	9656.0	5710.5
DQ083104.1	132329	71.8	264.7	1360.2	379.8	211.3	354.5
EF540406.1	227017	28.8	123.3	2614.1	435.5	168.5	117.7
NC_011527.1	356835	275.6	474.4	2793.0	508.3	1031.5	594.7
EU881324.1	314162	5333.3	5728.5	4171.0	4771.3	4379.2	4048.5
EU143669.1	251151	8913.6	8157.2	10303.1	8565.3	11562.2	10045.7

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EU143670.1 gg_id:254854 Coxiella-like infection Psittacine birds liver clone 1357
AB001519.1 gg_id:8016 Haemaphysalis longicornis symbiont
NZ_AAQJ02000001.1 gg_id:237975 Rickettsiella grylli
FJ542982.1 gg_id:524171 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone B
FJ542909.1 gg_id:527108 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone A
AY447040.1 gg_id:107683 hepatopancreatic symbiont clone 7
AF286124.1 gg_id:73506 eubacterium Cecidotrioza sozanica
AF327558.1 gg_id:50747 Folsomia candida symbiont
U97547.1 gg_id:8028 Rickettsiella grylli
FJ437936.1 gg_id:574974 Benthic okenone production Fayetteville New York Green Lake surface sediments 16.
EU134738.1 gg_id:235968 tallgrass prarie soil clone FFCH12405
DQ396123.1 gg_id:154082 deep-sea octacoral clone ctg_NISA227
AF526927.2 gg_id:55626 Mars Odyssey Orbiter and encapsulation facility clone T5-3
GQ346963.1 gg_id:547615 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
EU491737.1 gg_id:265658 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39
GQ402591.1 gg_id:587585 Accessing microbial biodiversity and metabolic potential tropical -based approach p
DQ450792.1 gg_id:160953 Microbial Alpine Tundra Wet Meadow Soil: Chloroflexi Cold Water-Saturated saturat
EU134722.1 gg_id:251564 tallgrass prarie soil clone FFCH7120
AY326588.1 gg_id:136759 Amazon soil clone 776-1
GQ339152.1 gg_id:515598 Comprehensive Investigation on Iron Cycling Freshwater Seep ing Microscopy Cultiv
EU802753.1 gg_id:319778 It's all ranking aquatic Northeast Colon Panama clone 4C230126
EU050790.1 gg_id:256320 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_07_86
EU276556.1 gg_id:359663 -DGGE and Approaches Analyze Effect Agricultural Practices on Soil agricultural soil c
EF515889.1 gg_id:218114 grassland soil clone FCPS672
EU134752.1 gg_id:255441 tallgrass prarie soil clone FFCH15063
DQ083100.1 gg_id:137191 Functional and responses microbial century-old field soil clone X14
EU881328.1 gg_id:353731 (maize-sweet cropping field) Karst region maize-sweet potato cropland soil clone KM
EU735697.1 gg_id:340556 archaeal structures oil contaminated and soils China pristine soil Jidong Oilfield clone
EF580986.1 gg_id:279663 Survey Microbial Freshwater Calcareous Mats freshwater calcareous mat clone CM6
AF255638.1 gg_id:32355 EBPR sludge clone Ebpr13
FJ638597.1 gg_id:511763 Temperature dependent succession sulfate reducing muddy southwestern Taiwan hc
AM746627.1 gg_id:244768 Proteinimicrobium ihbtica str. HMPB3
AB058914.1 gg_id:49724 Legionella sp. OY6
EU134756.1 gg_id:240701 tallgrass prarie soil clone FFCH15686
AB179493.1 gg_id:99390 sedimentary rock clone MIZ02
AJ536872.1 gg_id:78512 uranium mining waste pile soil sample clone JG30a-KF-94 proteobacterium
EU134735.1 gg_id:257122 tallgrass prarie soil clone FFCH11666
FJ542953.1 gg_id:514449 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone B
EU937889.1 gg_id:334207 Biogeochemistry Iron Oxidation Circumneutral Freshwater Habitat riparian iron oxidi
EU328043.1 gg_id:278735 dynamics during bioremediation crude oil contaminated moderate saline soil clone B
EU134784.1 gg_id:239870 tallgrass prarie soil clone FFCH2111

EU143670.1	254854	9304.3	8377.9	7196.8	8267.7	13230.8	8481.2
AB001519.1	8016	444.6	1441.6	2526.3	1324.1	4274.8	2570.7
NZ_AAQJ02000001.1	237975	4371.6	5714.3	8022.5	6253.2	10878.3	6327.6
FJ542982.1	524171	13570.7	14836.7	14150.3	12650.7	18055.3	13801.1
FJ542909.1	527108	7900.8	8721.9	10200.5	8704.9	9593.2	8348.2
AY447040.1	107683	8495.7	9048.5	12614.7	9884.6	11773.0	8634.3
AF286124.1	73506	7446.3	6719.3	7074.4	6133.7	8842.5	5914.7
AF327558.1	50747	5230.8	6446.2	9911.3	8747.6	11036.5	7297.1
U97547.1	8028	8112.8	9134.7	10728.3	8889.0	10821.7	6907.9
FJ437936.1	574974	824.2	1979.4	4355.1	1564.6	4425.4	2805.3
EU134738.1	235968	5176.6	7085.8	10704.1	5549.6	12575.4	6587.5
DQ396123.1	154082	105.0	284.8	736.6	170.7	835.9	705.1
AF526927.2	55626	70.3	121.1	503.6	191.5	879.9	175.2
GQ346963.1	547615	8645.0	7221.7	7164.2	8042.9	9428.0	7077.0
EU491737.1	265658	8919.4	9597.7	13433.4	8739.6	12712.1	10702.2
GQ402591.1	587585	3606.7	3747.7	5837.0	4037.1	4678.4	4143.4
DQ450792.1	160953	4639.4	5449.3	6556.6	6575.7	8156.4	6509.7
EU134722.1	251564	2475.6	2057.2	3975.6	2205.3	4951.3	1107.2
AY326588.1	136759	419.7	784.8	691.7	704.9	3094.9	1688.1
GQ339152.1	515598	2133.5	2554.6	5918.7	3391.1	4248.1	2951.7
EU802753.1	319778	73.7	134.2	786.9	205.0	113.7	72.6
EU050790.1	256320	6036.1	6876.0	6741.9	6676.7	8370.3	5696.4
EU276556.1	359663	10239.7	11172.5	9690.0	11124.0	9136.1	9435.0
EF515889.1	218114	1298.0	566.6	1153.7	951.3	1186.3	404.1
EU134752.1	255441	537.4	1225.5	1222.0	2219.1	1762.9	1727.5
DQ083100.1	137191	49.9	81.0	1072.6	143.9	125.6	62.3
EU881328.1	353731	8304.1	6369.2	8923.7	7851.6	8239.0	10585.0
EU735697.1	340556	10479.8	9267.1	7530.3	8694.2	11477.0	9395.6
EF580986.1	279663	5384.3	4597.2	7025.1	6283.9	8664.7	3738.7
AF255638.1	32355	3290.1	3053.0	2432.6	1878.2	4652.9	2828.5
FJ638597.1	511763	2141.9	2360.2	2477.2	1732.2	3110.3	1877.4
AM746627.1	244768	1177.1	1115.1	5082.3	1120.5	363.8	560.5
AB058914.1	49724	30.1	47.1	66.5	59.4	70.4	39.2
EU134756.1	240701	5524.2	5535.5	5633.0	4699.9	5802.6	3667.7
AB179493.1	99390	7094.4	5503.5	5641.2	4120.6	4653.1	4112.4
AJ536872.1	78512	2285.2	2842.9	2406.4	4892.7	5652.2	2541.2
EU134735.1	257122	1311.5	2087.7	6140.7	1980.1	6680.9	3513.3
FJ542953.1	514449	4389.6	4464.7	3604.9	3874.7	4434.0	3004.0
EU937889.1	334207	9052.0	7193.4	8270.0	8230.5	10739.2	10018.6
EU328043.1	278735	3579.6	5103.7	6718.0	3497.9	8109.3	4034.0
EU134784.1	239870	8747.3	8156.8	4699.7	9336.2	7178.5	7078.1

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s__Legionella brunensis	3163

GU362970.1 gg_id:575883 and archaeal biogeochemical cycling genes within Qiongdongnan basin Sea: pilot stu
DQ396109.1 gg_id:156557 deep-sea octacoral clone ctg_NISA135
EU803079.1 gg_id:326446 It's all ranking aquatic Northeast Colon Panama clone 4C230497
AJ252619.1 gg_id:36221 agricultural soil clone SC-I-16
FJ444660.1 gg_id:578973 Cotton Rhizosphere cotton rhizosphere clone 2h-38
FJ444646.1 gg_id:587687 Cotton Rhizosphere cotton rhizosphere clone 2h-15
DQ431905.1 gg_id:207732 microorganisms catalyzing nitrogen removal and organic matter metabolism perme
GQ349429.1 gg_id:569326 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
EF515899.1 gg_id:225991 grassland soil clone FCPT587
EU735661.1 gg_id:325840 archaeal structures oil contaminated and soils China pristine soil Jidong Oilfield clone
CU466806.1 gg_id:317285 Evry wastewater treatment plant anoxic basin clone
AB294332.1 gg_id:215917 Microbial structure deep coal seem groundwater stream clone SWB21
EU202847.1 gg_id:347934 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo
FJ545549.1 gg_id:511371 Diveristy Seawater and Sediment Northern North Yel Sea sediment clone S2-5
GU305791.1 gg_id:534111 Research on changes structure during algae outbreak oligotrophic lakes (YangHe res
FJ205343.1 gg_id:535383 Prokaryotic deep-sea hydrothermal region East Lau Spreading Centre deep marine se
GQ350354.1 gg_id:587874 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
EU925916.1 gg_id:303457 sediments sediment station DBS1 northern Bering Sea clone 152H67
AB015255.1 gg_id:8026 deepest cold-seep area Japan Trench clone JTB256 proteobacterium
EF574681.1 gg_id:229650 site S25 near Coco's Island marine clone S25_1025
EU644214.1 gg_id:282458 and Samoylov Island Lena active layer -centred polygon near surface horizon; Rim_T
AF235121.1 gg_id:74504 North Sea clone KTc0924
EU134760.1 gg_id:238980 tallgrass prarie soil clone FFCH7560
EU249954.1 gg_id:246142 Polyphasic description Pocillopora seawater adjacent Pacillopora meandrina coral co
EF575249.1 gg_id:232669 site S25 near Coco's Island marine clone S25_1593
EU134712.1 gg_id:245968 tallgrass prarie soil clone FFCH5316
FJ468390.1 gg_id:555059 Bioaugmentation Pseudomonas sp. strain MHP41 promotes attenuation and changes
FJ236047.1 gg_id:334364 three Parisian treatment plants approaches drinking water clone Orly7
FJ437972.1 gg_id:539237 Benthic okenone production Fayetteville New York Green Lake surface sediments 16.
EF575079.1 gg_id:237689 site S25 near Coco's Island marine clone S25_1423
FJ205338.1 gg_id:555799 Prokaryotic deep-sea hydrothermal region East Lau Spreading Centre deep marine se
AF255642.1 gg_id:22253 EBPR sludge clone Ebpr12
EU386125.1 gg_id:272458 Biogeographical and microbes sediments on subseafloor sediment South China Sea c
EU134733.1 gg_id:237253 tallgrass prarie soil clone FFCH11328
EU134753.1 gg_id:248221 tallgrass prarie soil clone FFCH15155
EF019986.1 gg_id:216743 aspen rhizosphere clone Elev_16S_1373
EU805209.1 gg_id:326155 It's all ranking aquatic 250 miles Panama City clone 6C233205
EU834797.1 gg_id:541438 Microbiology Aerobic Phosphorus Removal Process aerobic phosphorus-removing se
FJ712415.1 gg_id:523629 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) K
EU193049.1 gg_id:357896 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo
Z32636.1 gg_id:8006 Legionella brunensis

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DQ396109.1	156557	30.0	43.5	104.5	78.3	56.3	33.2
EU803079.1	326446	367.0	636.3	4100.9	1219.5	651.3	1340.6
AJ252619.1	36221	7343.9	8359.1	9367.5	7513.1	11604.5	12526.9
FJ444660.1	578973	5831.9	6112.2	9120.3	4665.1	4744.5	3802.9
FJ444646.1	587687	3271.4	3430.1	4205.9	3724.1	4123.4	2040.4
DQ431905.1	207732	41.8	182.4	1219.0	212.0	1619.0	239.0
GQ349429.1	569326	8007.2	6262.0	7995.8	7405.8	8384.4	7668.3
EF515899.1	225991	1339.5	1090.9	3035.2	2533.5	3362.1	961.6
EU735661.1	325840	8103.4	6821.5	5229.2	7087.4	8464.6	7656.2
CU466806.1	317285	4730.2	6268.0	6725.9	5682.2	9483.6	5708.9
AB294332.1	215917	19.0	46.5	112.2	62.6	109.4	39.0
EU202847.1	347934	3360.1	3475.5	6151.6	2476.2	6020.5	4428.3
FJ545549.1	511371	3059.8	4412.6	4546.7	4110.4	5003.1	6392.6
GU305791.1	534111	3286.1	2920.8	4827.9	8572.5	4921.4	5853.6
FJ205343.1	535383	6488.9	5532.6	7583.1	6916.2	9063.3	6112.5
GQ350354.1	587874	6378.1	6616.3	8417.4	6674.9	9175.1	7363.9
EU925916.1	303457	5122.4	4697.9	7583.2	5721.5	6042.4	4982.9
AB015255.1	8026	23.7	49.8	106.5	50.9	137.9	71.6
EF574681.1	229650	912.2	1515.5	3337.4	1196.2	2153.1	1702.8
EU644214.1	282458	6522.4	6569.5	6363.4	5788.0	5828.9	10338.2
AF235121.1	74504	49.2	119.4	114.0	124.4	80.7	80.6
EU134760.1	238980	6944.1	8731.3	15834.1	9520.7	11920.5	11143.7
EU249954.1	246142	9228.3	8502.1	6686.8	9475.4	12339.0	8347.8
EF575249.1	232669	392.8	452.5	1740.5	294.6	1935.1	1129.7
EU134712.1	245968	5034.6	5253.7	7579.1	9946.7	5896.7	5658.1
FJ468390.1	555059	748.9	790.1	5006.2	947.0	1063.1	608.3
FJ236047.1	334364	11126.7	11894.6	10175.1	9399.4	10172.9	9935.0
FJ437972.1	539237	5238.8	6048.5	8623.8	5110.3	11679.3	7413.2
EF575079.1	237689	2325.3	2704.7	4396.0	2527.1	3968.6	2835.2
FJ205338.1	555799	4207.8	4793.0	6061.8	3485.5	6476.2	5456.7
AF255642.1	22253	75.6	169.9	425.6	174.3	404.0	183.3
EU386125.1	272458	2508.7	2770.6	4758.2	2345.0	3943.9	3614.7
EU134733.1	237253	464.2	1104.1	6464.6	608.4	3035.0	683.5
EU134753.1	248221	3392.6	3865.3	6087.4	2298.3	7084.8	7077.7
EF019986.1	216743	625.7	1401.4	5440.1	2479.0	4690.6	1081.1
EU805209.1	326155	6910.0	6646.0	9781.8	7880.5	12090.6	9258.6
EU834797.1	541438	8273.2	7184.3	5997.4	6409.1	8725.9	7737.0
FJ712415.1	523629	9328.5	9252.9	13056.8	12002.2	13498.5	11973.6
EU193049.1	357896	2786.9	3985.4	5737.3	2444.6	4811.2	2902.8
Z32636.1	8006	322.1	671.7	1057.2	896.5	7786.1	760.1

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AF129524.1 gg_id:51847 Legionella pneumophila str. E5C1; ATCC700713
X97361.1 gg_id:7908 Legionella sp str. LLAP8
NC_006368.1 gg_id:129226 Legionella pneumophila str. Paris
AB233212.1 gg_id:140544 Legionella landfill str. OA1-4
FJ542889.1 gg_id:522337 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone A
FJ612289.1 gg_id:592165 and Biogeochemistry Dongping Lake Ecosystems lake water clone DP7.5.15
NR_026522.1 gg_id:565488 Legionella tucsonensis str. 087-AZ-H; ATCC 49180
EU250236.1 gg_id:246283 acid mine drainage clone GXDC-22
FJ230896.1 gg_id:315994 under Level Antibiotic Selection Pressures river water clone F20
EU134790.1 gg_id:244967 tallgrass prarie soil clone FFCH3904
GQ002634.1 gg_id:507027 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbu
GQ264139.1 gg_id:564434 Structure Simulated Level Waste Site simulated level waste site clone WC3_79
DQ814490.1 gg_id:168390 zebrafish digestive tract clone aaa29e09
Z49722.1 gg_id:7972 Legionella fairfieldensis
DQ413099.1 gg_id:154202 Microbial -dependent and Approaches Anaerobic/Aerobic SBR Reactor EBPR sludge
Z49724.1 gg_id:7994 "Legionella donaldsonii"
DQ337039.1 gg_id:145455 subsurface water clone EV818EB5CPSAJJ36
AY792279.1 gg_id:123281 Humic Lake clone CrystalBog1D4
FJ744881.1 gg_id:549676 Transporter genes expressed coastal response dissolved organic carbon surface wate
AY662002.1 gg_id:137028 uranium-contaminated groundwater clone 300G-C11
DQ667196.1 gg_id:171418 Legionella taurinensis str. ATCC 700508
X97363.1 gg_id:7946 Legionella sp str. LLAP10
FM877662.1 gg_id:359700 Microbial several mining wastes Bulgaria vicinity uranium mine Sliven clone Sliv-17
DQ327699.1 gg_id:166988 Biological filtration limits carbon availability affects downstream biofilm formation a
FJ542894.1 gg_id:518474 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone A
X97356.1 gg_id:7948 Legionella sp str. LLAP2
AF467296.1 gg_id:64661 Xanthomonas sp. clone 88_5_2
AY598719.2 gg_id:99452 Amoeba proteus symbiotic
AY957913.1 gg_id:114944 drinking water biofilm clone B3NR56D11
GU062706.1 gg_id:590087 Legionella sp. str. NML 93L054
Z49720.1 gg_id:7915 Legionella cherrii
Z49733.1 gg_id:7976 Legionella quinlivanii
AY050582.1 gg_id:21751 MCB-contaminated groundwater-treating reactor clone GOUTA10
Z49739.1 gg_id:7955 Legionella worsliensis
EU937840.1 gg_id:331322 Biogeochemistry Iron Oxidation Circumneutral Freshwater Habitat riparian iron oxidi
FJ543058.1 gg_id:528709 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone B
EU800944.1 gg_id:306074 It's all ranking aquatic Delaware Bay NJ clone 2C229203
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AJ969023.1 gg_id:120376 Legionella anisa UCSC 25
FJ479065.1 gg_id:590656 species richness estimates obtained nearly and simulated pyrosequencing-generated

NR_024969.1	575576	2461.3	2438.3	6846.2	3357.9	14224.5	3025.9
AF129524.1	51847	3187.6	2812.0	2372.2	5670.3	3861.7	3257.8
X97361.1	7908	3116.8	3715.3	6621.9	5026.5	7899.2	3278.3
NC_006368.1	129226	6489.1	7081.4	7653.1	5658.9	10539.2	1959.1
AB233212.1	140544	291.8	796.0	6346.8	856.5	7788.8	574.2
FJ542889.1	522337	4096.2	5287.6	5894.8	6056.3	11232.7	7741.9
FJ612289.1	592165	9508.6	8574.2	4863.5	5517.8	5887.8	5836.7
NR_026522.1	565488	8771.2	8588.3	5059.7	9850.0	15533.9	14072.3
EU250236.1	246283	650.4	648.3	2386.1	492.8	3587.1	800.0
FJ230896.1	315994	2029.5	1697.9	7111.6	1956.3	6555.2	1122.0
EU134790.1	244967	3896.0	5846.8	7276.1	5073.3	13342.1	10055.3
GQ002634.1	507027	3495.7	3415.8	10004.3	9002.8	6222.1	5238.8
GQ264139.1	564434	11968.8	11131.5	11090.9	5958.1	19003.4	10116.9
DQ814490.1	168390	927.0	606.3	4799.3	810.2	15102.9	1109.0
Z49722.1	7972	112.3	287.4	1140.7	201.7	813.9	93.1
DQ413099.1	154202	426.4	1002.2	2978.7	1805.5	7353.8	2033.6
Z49724.1	7994	168.3	361.2	1691.2	201.0	5872.3	99.0
DQ337039.1	145455	89.1	309.5	803.2	147.9	7652.5	229.3
AY792279.1	123281	58.5	97.6	440.4	231.9	144.0	78.5
FJ744881.1	549676	2640.4	2683.8	6703.9	4801.3	13370.8	8062.2
AY662002.1	137028	690.5	1109.0	4220.7	316.3	4585.8	1474.6
DQ667196.1	171418	1129.0	1650.1	3379.4	1927.5	5254.6	4139.1
X97363.1	7946	6881.2	7732.7	3131.4	4701.7	9115.4	5623.4
FM877662.1	359700	6754.7	7093.9	14049.6	7553.9	21643.4	9574.2
DQ327699.1	166988	165.1	261.4	475.6	99.9	435.9	48.4
FJ542894.1	518474	3023.5	2720.9	3482.0	3135.6	6247.7	2231.5
X97356.1	7948	3639.0	3700.4	7470.8	4959.8	18737.8	6806.1
AF467296.1	64661	40.8	107.0	428.5	100.1	249.7	146.4
AY598719.2	99452	79.9	148.4	2241.4	331.8	1438.8	68.6
AY957913.1	114944	326.1	411.0	4700.4	741.9	9311.6	4048.9
GU062706.1	590087	313.0	729.6	3116.8	414.9	3457.1	1824.8
Z49720.1	7915	12.7	23.0	19.0	57.7	1108.6	46.5
Z49733.1	7976	4860.8	4975.5	3678.4	4672.9	6181.6	4931.6
AY050582.1	21751	3758.9	2791.8	7189.0	5983.3	7386.4	4582.3
Z49739.1	7955	962.1	1531.3	6183.2	1008.4	17440.8	909.6
EU937840.1	331322	5761.7	5834.3	10155.0	5900.1	8652.0	9834.7
FJ543058.1	528709	2301.1	2132.0	3190.4	927.0	7433.5	1153.8
EU800944.1	306074	9250.8	8454.4	6310.4	5152.8	10300.3	6580.3
Z49719.1	7922	865.4	1187.1	2422.6	4118.5	1713.6	3644.7
AJ969023.1	120376	5009.5	5722.7	4669.3	8359.7	9185.2	7213.1
FJ479065.1	590656	2546.0	3358.7	5133.9	3666.1	11088.1	4568.7

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EF516979.1 gg_id:226108 grassland soil clone FCPP464
GQ347573.1 gg_id:555343 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
DQ327700.1 gg_id:163406 Biological filtration limits carbon availability affects downstream biofilm formation a
EU835422.1 gg_id:318862 structure and quorum sensing reverse osmosis RO membrane biofilm clone 1B17
Z49741.1 gg_id:7937 Legionella lytica str. LLAP-3 legionella like amoebal pathogen
Z32640.1 gg_id:7984 Legionella israelensis
EU236319.1 gg_id:298170 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg1bF3
GQ054315.1 gg_id:463932 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw1108
EU134769.1 gg_id:243485 tallgrass prarie soil clone FFCH9178
Z49729.1 gg_id:7954 Legionella moravica
Z49728.3 gg_id:7971 Legionella londiniensis
AB255083.1 gg_id:173398 corroded concrete clone IC-85
Z49736.1 gg_id:7956 Legionella shakespearei
Z49725.1 gg_id:7929 Legionella gratiana
Z49735.1 gg_id:7931 Legionella santicrucis
DQ413067.1 gg_id:153948 Microbial -dependent and Approaches Anaerobic/Aerobic SBR Reactor EBPR sludge
EU800974.1 gg_id:311942 It's all ranking aquatic Delaware Bay NJ clone 2C229243
FJ382013.1 gg_id:543450 Potentially pathogenic and air stem cell transplant winter hospital shower water BMT
Z49727.1 gg_id:7973 Legionella lansingensis
Z49734.1 gg_id:7927 Legionella sainthelensi
AM747393.1 gg_id:236913 Legionella dresdeniensis str. W03-356
EU835407.1 gg_id:318176 structure and quorum sensing reverse osmosis RO membrane biofilm clone 1T17
EU835445.1 gg_id:340760 structure and quorum sensing reverse osmosis RO membrane biofilm clone 2B20
Z49717.1 gg_id:7974 Legionella birminghamiensis
Z32641.1 gg_id:7991 Tatlockia maceachernii
AF227162.1 gg_id:52462 Tatlockia micdadei str. ATCC33218
Z32642.1 gg_id:7981 Legionella oakridgenesis
AJ919271.1 gg_id:114678 Legionella nautarum
GQ388900.1 gg_id:551369 quality deterioration drinking system during serious red water outbreak clone Z61
FJ236838.1 gg_id:328884 Legionella sp. str. CDC-3041-AUS-E
EU134750.1 gg_id:238279 tallgrass prarie soil clone FFCH14647
Z49730.3 gg_id:7982 Legionella nautarum
NR_025196.1 gg_id:556395 Legionella busanensis str. K9951; KCTC 12084
AF122884.2 gg_id:8008 Legionella beliardensis str. Montbeliard A1
GQ009403.1 gg_id:500261 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw77
EF612978.1 gg_id:233794 acid mine drainage clone YSK16S-15
EF036512.1 gg_id:191570 Legionella jordanis NML 060502
EF471571.1 gg_id:270320 Fast Screening and Estuarine Operon Libraries whole surface water Chesapeake Bay
EF520577.1 gg_id:229517 structure lakes: what controls ? acid-impacted lake clone ADK-RXe02-02
DQ458002.1 gg_id:158776 acid mine drainage clone DX32
EU491749.1 gg_id:263538 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39

EF516979.1	226108	4273.5	3382.5	1445.8	2440.8	1933.7	1303.8
GQ347573.1	555343	1817.8	1825.2	2861.6	2623.3	7839.4	2776.2
DQ327700.1	163406	184.6	335.8	1184.4	313.7	6211.9	143.7
EU835422.1	318862	8220.9	6416.3	7690.6	8545.5	8224.0	7070.6
Z49741.1	7937	2979.0	2996.0	3862.4	2981.0	15398.5	4655.5
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EU236319.1	298170	2113.9	2493.3	3625.5	3325.6	5811.7	2365.8
GQ054315.1	463932	3129.8	2983.8	4656.6	2758.1	6784.7	1848.4
EU134769.1	243485	831.7	512.2	4183.5	1388.0	5829.2	1330.7
Z49729.1	7954	5155.1	5809.3	6823.8	6981.6	13820.1	6265.0
Z49728.3	7971	1236.2	1449.0	3139.8	876.8	6230.4	1788.0
AB255083.1	173398	593.3	1268.8	4344.7	3953.5	9127.8	3698.8
Z49736.1	7956	11535.9	11944.1	10817.7	12170.3	20261.9	12411.3
Z49725.1	7929	5299.5	5713.8	7741.5	6714.7	7418.1	5490.5
Z49735.1	7931	1320.3	1941.6	1473.3	1468.3	4477.8	1814.4
DQ413067.1	153948	2406.2	2192.2	4148.4	6526.1	8101.0	3408.6
EU800974.1	311942	4581.7	5015.8	12348.4	6430.2	10967.5	3993.4
FJ382013.1	543450	4201.1	5068.5	6493.6	7349.7	17464.4	16049.9
Z49727.1	7973	49.5	62.4	177.0	96.0	1034.4	170.6
Z49734.1	7927	1097.2	450.1	4671.1	1236.0	11013.0	3078.6
AM747393.1	236913	2507.1	2354.4	4768.4	3216.8	8078.3	2948.7
EU835407.1	318176	2186.5	2218.8	6613.9	4051.1	10262.7	3040.1
EU835445.1	340760	10243.2	8682.9	5697.8	9956.8	15446.0	8500.9
Z49717.1	7974	449.4	1040.1	1995.5	768.2	6595.7	2001.4
Z32641.1	7991	2825.3	2590.2	2104.1	1918.6	3321.0	1719.1
AF227162.1	52462	50.2	109.8	352.7	107.8	873.3	75.7
Z32642.1	7981	111.3	273.0	543.7	454.0	2028.0	297.5
AJ919271.1	114678	8685.3	10725.5	7029.9	8548.7	9998.2	6975.2
GQ388900.1	551369	4388.6	5386.9	4062.4	4247.5	7941.1	7198.7
FJ236838.1	328884	437.9	982.6	5239.6	719.9	4596.9	3469.0
EU134750.1	238279	8389.9	8923.7	6149.1	5308.5	10830.1	8073.8
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AF122884.2	8008	1194.7	1622.7	5124.3	1428.8	9928.7	1967.1
GQ009403.1	500261	2392.3	2055.9	1726.4	562.7	3901.4	2510.0
EF612978.1	233794	1678.7	2347.7	6476.1	3620.9	6924.4	3049.3
EF036512.1	191570	1127.0	1013.7	1832.6	1001.2	4625.7	3761.8
EF471571.1	270320	1882.0	2003.7	4674.3	3118.0	7108.7	2279.2
EF520577.1	229517	917.5	2076.4	7429.5	1019.7	10141.3	3594.4
DQ458002.1	158776	57.8	152.2	221.8	103.7	161.8	53.4
EU491749.1	263538	891.4	1056.1	2012.7	830.3	1028.3	1931.2

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EU491259.1 gg_id:276006 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak
EU386109.1 gg_id:264331 Biogeographical and microbes sediments on subseafloor sediment South China Sea c
GQ850579.1 gg_id:559606 bottom water northern Bering Sea clone d131
AY050590.1 gg_id:52016 MCB-contaminated groundwater-treating reactor clone GOUTB2
GQ261748.1 gg_id:550690 shifts taxa and response localized organic loading deep sea sediment whale falls clo
EU491526.1 gg_id:268607 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR4C
EU491716.1 gg_id:267408 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39
GQ472814.1 gg_id:574241 Biodiversity planktonic Northern surface water northern Bering Sea clone b45
EU735642.1 gg_id:312981 archaeal structures and pristine soils China oil contaminated soil Jidong Oilfield clone
EF520571.1 gg_id:230249 structure lakes: what controls ? acid-impacted lake clone ADK-HDe02-30
EF516119.1 gg_id:221947 grassland soil clone FCPU740
GU118075.1 gg_id:554366 Threatened Corals Provide Microbial Habitats clone Apal_M08
EU236332.1 gg_id:297516 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg5a2A5
FJ744812.1 gg_id:546723 Transporter genes expressed coastal response dissolved organic carbon surface wate
EU236289.1 gg_id:292187 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone HgCo16
Z49726.1 gg_id:8012 Legionella jamestownensis
Z49723.1 gg_id:7977 Legionella geestiana
Z49716.1 gg_id:7978 Legionella adelaidensis
AY536226.1 gg_id:101534 host gut clone LAgut--P14
DQ295893.1 gg_id:145412 Cohn's Crenothrix filamentous oxidizer unusual methane monooxygenase physical e
GQ390223.1 gg_id:548160 oxic-anoxic interface meromictic crater lake Lac Pavin clone eub62A8
AB504955.1 gg_id:565012 structure microorganisms reddish-brown iron-rich snow clone oze05B47
DQ837251.1 gg_id:247086 Archaeal and pristine National Park Spain Donana coastal aquifer clone 49S1_2B_45
FJ502272.1 gg_id:509929 Co-occurrence denitrification and nitrogen fixation meromictic lake (Switzerland) Lak
AF152597.1 gg_id:8098 Methylobacter psychrophilus str. Z-0021
AJ583183.1 gg_id:94840 radioactive site ground water clone S15B-MN136
AB240527.1 gg_id:141423 microbial structure rhizosphere biofilm Sapporo root-base (80 160 mm) Phragmites S
DQ984190.1 gg_id:205851 Clonothrix fusca str. AW-b
AF351235.1 gg_id:48494 coal tar waste-contaminated groundwater clone 8-4 proteobacterium
DQ367735.1 gg_id:150338 Fluorescence Situ Hybridization-F Cytometry-Cell Sorting-Based Method Enrichment
AB240465.1 gg_id:141872 microbial structure rhizosphere biofilm Sapporo root-tip (0 40 mm) Phragmites Sosei
EF125436.1 gg_id:175001 mangrove soil clone MSB-2D7
AB240522.1 gg_id:140993 microbial structure rhizosphere biofilm Sapporo root-base (80 160 mm) Phragmites S
DQ066944.1 gg_id:135917 Lake Washington sediment clone pLW-18
DQ066943.1 gg_id:131019 Lake Washington sediment clone pLW-17
M95657.1 gg_id:8104 Methylobacter luteus str. 11914
AF304195.1 gg_id:40043 Methylobacter luteus str. NCIMB 11914
AF304197.1 gg_id:37065 Methylobacter marinus str. A45
DQ270621.1 gg_id:142869 hydrothermal carbonate chimney clone LC1133B-99
AJ704662.1 gg_id:109268 marine sediment clone HMMVBeg-7
DQ521819.1 gg_id:160617 Anaerobic Methane Oxidizing ANME-1b Archaea Hypersaline Sediments Gulf Mexic

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EU386109.1	264331	2031.8	2608.1	2516.3	2684.2	2856.5	3591.7
GQ850579.1	559606	2704.7	2626.5	6302.7	3205.1	6533.2	5060.5
AY050590.1	52016	9901.4	10517.5	6702.3	8409.1	14322.5	15676.9
GQ261748.1	550690	2313.8	3237.7	5383.3	1832.3	4856.2	5321.4
EU491526.1	268607	43.4	45.7	176.3	193.4	678.2	1618.7
EU491716.1	267408	1680.0	1739.6	994.1	1326.6	2488.8	3490.6
GQ472814.1	574241	1868.4	2059.7	3744.6	1070.7	4120.3	3430.7
EU735642.1	312981	9112.0	9321.0	7560.4	7492.6	12644.7	8020.3
EF520571.1	230249	157.5	447.1	245.2	299.7	802.8	447.1
EF516119.1	221947	43.2	119.4	808.3	135.2	1044.5	63.1
GU118075.1	554366	3481.3	3632.7	5544.4	4018.3	10747.9	5168.2
EU236332.1	297516	2919.8	3419.2	4246.5	5397.1	8332.6	4917.0
FJ744812.1	546723	5046.4	3892.8	6139.8	3858.0	6953.0	6557.9
EU236289.1	292187	5623.3	6100.7	8321.2	5029.0	15440.2	7763.3
Z49726.1	8012	355.5	283.3	840.3	273.2	2534.5	606.2
Z49723.1	7977	50.7	74.4	558.1	97.3	554.7	56.9
Z49716.1	7978	269.7	600.6	2133.2	900.2	1522.8	262.8
AY536226.1	101534	1493.2	2185.1	5365.6	1089.2	8182.5	3245.8
DQ295893.1	145412	642.1	590.9	1231.7	870.8	282.5	464.5
GQ390223.1	548160	2129.1	1593.9	3570.6	1549.0	989.7	1518.0
AB504955.1	565012	4801.5	2886.5	3828.3	6089.3	6910.0	6111.8
DQ837251.1	247086	4474.1	2009.5	2988.2	4393.6	3428.2	3311.3
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AF152597.1	8098	3754.4	885.3	2108.5	2404.3	1077.9	404.0
AJ583183.1	94840	1963.3	1210.5	2851.9	1321.3	227.6	312.2
AB240527.1	141423	4906.6	4536.5	6151.0	3752.5	7560.9	2820.4
DQ984190.1	205851	3222.8	1664.6	3009.6	2805.8	622.8	973.0
AF351235.1	48494	3239.2	2064.7	6306.1	2522.7	8118.4	3341.7
DQ367735.1	150338	5836.3	4470.9	6947.7	6309.7	9391.8	5660.5
AB240465.1	141872	298.8	256.8	168.1	207.6	65.4	26.0
EF125436.1	175001	896.5	789.9	1057.8	996.7	1646.7	125.1
AB240522.1	140993	2594.9	1052.4	3560.0	2695.1	642.1	444.9
DQ066944.1	135917	3927.3	3760.8	4413.5	3264.4	4400.3	2764.2
DQ066943.1	131019	829.3	469.7	783.4	2149.2	820.1	660.5
M95657.1	8104	2495.1	2121.4	3194.2	3442.2	3362.5	2619.4
AF304195.1	40043	4595.6	1662.2	3064.6	3264.5	500.4	1049.3
AF304197.1	37065	2610.0	1752.0	1816.1	2462.5	1676.3	888.0
DQ270621.1	142869	3739.4	4059.7	3232.5	4103.5	7516.4	4004.3
AJ704662.1	109268	4538.4	3892.4	2635.2	5174.9	4575.9	4950.7
DQ521819.1	160617	1187.4	933.3	1052.0	1578.8	2743.4	1328.7

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EU491680.1 gg_id:269280 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39
AB294957.1 gg_id:224998 -dependent & analyses hydrothermal system off Taketomi Island Japan microbial ma
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AB476280.1 gg_id:549573 Compositional and functional transition epibiotic microbial hydrothermal vent galath
FJ264669.1 gg_id:339219 Manganese and Iron Dependent Anaerobic Oxidation Methane methane seep sedime
FJ717256.1 gg_id:555227 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United Kingc
DQ070797.1 gg_id:145621 Prokaryotic Structures Seafloor Basalts Varying Age and Juan de Fuca Ridge basalt gl
DQ270620.1 gg_id:144477 hydrothermal carbonate chimney clone LC1133B-86
GU302420.1 gg_id:555130 Spatial structure and activity sedimentary microbial underlying Beggiatoa spp. mat h
AB042414.1 gg_id:24022 Maorithyas hadalis gill thioautotrophic symbiont II gill
DQ513099.1 gg_id:161529 Microbial life fluids ridge flank crustal fluid clone FS274-37B-03
AB245479.1 gg_id:146843 Sulfurivirga caldicularium str. MM1
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AJ617834.1 gg_id:110041 oxic-anoxic interphase flooded paddy soil clone D14307
U89297.1 gg_id:8046 Methylocaldum tepidum str. LK6
AF215633.1 gg_id:73918 Methylocaldum sp. str. r6f
FJ810597.1 gg_id:380204 Subsurface ecosystem resilience: Long-term attenuation subsurface contaminants su
NR_026063.1 gg_id:572916 Methylocaldum gracile str. VKM 14L
NC_002977.6 gg_id:128429 Methylococcus capsulatus str. Bath
NR_029251.1 gg_id:540868 Methylococcus thermophilus str. IMV-B-3037; ACM 3585
X72771.1 gg_id:8036 Methylococcus capsulatus Bath str. ACM 3302 ATCC 33009 NCIBM 1113
X72769.1 gg_id:8040 Methylococcus sp str. JB140
AB354618.1 gg_id:273571 Laminated iron texture iron-oxidizing calcite travertine iron-rich deposit clone FD09

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EU491680.1	269280	4758.1	4572.8	6752.3	6177.6	5693.9	5354.4
AB294957.1	224998	1462.7	499.9	1779.3	1426.7	677.5	944.6
FJ712568.1	525302	8382.3	6080.7	6741.7	8532.4	7960.5	5946.6
FJ712444.1	516890	2649.8	2390.0	3311.2	3086.5	1461.1	1060.6
AB294960.1	218525	1279.2	491.0	1280.5	1885.8	160.3	380.2
EU700156.1	294790	2708.2	2458.6	4576.9	3512.0	5084.8	2423.0
GQ350283.1	578592	9155.9	8879.8	4737.7	7550.7	3652.4	3478.2
AB188770.1	113920	596.6	592.2	1005.5	940.9	171.6	360.4
FJ717255.1	511065	3569.3	4039.2	3654.0	4776.9	6517.6	7784.4
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AB476280.1	549573	3624.1	3682.7	1998.1	534.7	3088.2	1845.0
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FJ717256.1	555227	16056.3	14264.4	6948.1	9159.7	8653.2	7256.8
DQ070797.1	145621	126.5	109.3	103.3	243.5	95.7	105.4
DQ270620.1	144477	143.2	428.5	675.9	262.0	592.8	630.2
GU302420.1	555130	5877.1	6825.7	7177.0	6162.2	11822.5	9540.9
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EU528230.1	286126	6547.0	6625.3	10393.6	8435.1	7337.0	7496.8
DQ270629.1	141697	3283.3	3647.8	4078.6	2663.6	3891.1	3911.4
GQ350218.1	535569	9482.3	9248.8	4984.5	8151.2	7995.3	7669.6
DQ270612.1	142835	2602.8	3781.9	3286.0	3085.9	2342.8	3017.9
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EF203191.1	208702	314.6	990.5	161.2	464.5	198.6	167.0
AJ617834.1	110041	1693.7	1687.4	2564.7	1948.6	1058.3	996.5
U89297.1	8046	1760.2	2060.6	4643.7	2277.0	4443.2	2455.0
AF215633.1	73918	6601.8	8789.4	13728.8	7786.4	11935.6	9001.5
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U05570.1 gg_id:8080 Methylomicrobium pelagicum
AF096091.1 gg_id:8060 Methylobacter alcaliphilus str. 5z
EF495157.1 gg_id:222556 Methylobacter alcaliphilus str. 20Z
AF304194.1 gg_id:38046 Methylomonas rubra str. NCIMB 11913
AF150807.1 gg_id:8055 Methylomonas rubra
AY995198.1 gg_id:119789 Methylomonas rubra str. UCM B-3075; NCIMB 11913; ACM3303; VKM-15m
X72776.1 gg_id:8084 Methylomonas aurantiaca str. JB103 (phenon3)
X72778.1 gg_id:8090 Methylomonas fodinarum str. ACM 3268 JB13 (phenon2)
DQ837263.1 gg_id:245267 Archaeal and pristine National Park Spain Donana coastal aquifer clone 56S_1B_6
GQ340208.1 gg_id:544467 Prokaryotic Marathonas Reservoir Greece water column clone VE07-15-BAC
NR_025040.1 gg_id:550440 Methylosarcina quisquiliarum str. AML-D4; ATCC 700908
AF177296.1 gg_id:8051 Methylosarcina fibrata AML-C10
U67929.1 gg_id:8101 Methylosphaera hansonii str. AM6
DQ337085.1 gg_id:145089 subsurface water clone EV818SWSAP61
DQ001669.1 gg_id:157473 Microbial seeps asphalt seep clone B91-30
AM935153.1 gg_id:534315 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
AB486440.1 gg_id:585666 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC
EU144025.1 gg_id:235630 Methylomicrobium album str. BG8
AM936189.1 gg_id:537819 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
X72775.1 gg_id:8059 Methylomicrobium pelagicum str. ACM 3505 NCIMB 2265
X72773.1 gg_id:8091 Methylobacter whittenburyi str. 3310 NCIMB 11128 ACM 3306
EU328101.1 gg_id:278818 dynamics during bioremediation crude oil contaminated moderate saline soil clone Y
FM242408.1 gg_id:308594 sequences sediment clone 65 T12d-oil
X72772.1 gg_id:8086 Methylobacter luteus str. ACM 3304 NCIMB 11914
AM936083.1 gg_id:539835 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
EF157165.1 gg_id:247809 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon
NR_029240.1 gg_id:594166 Methylomicrobium agile str. A30; ATCC 35068
EU144026.1 gg_id:252662 Methylomicrobium agile str. ATCC 35068
AM936065.1 gg_id:564002 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
EF648094.1 gg_id:254304 dynamics during produced water treatment aerobic activated sludge clone HB102
EU735633.1 gg_id:353064 archaeal structures and pristine soils China oil contaminated soil Jidong Oilfield clone
AY007295.1 gg_id:22040 Methylobacter sp. str. LW12
NR_025955.1 gg_id:555220 Cycloclasticus pugetii str. PS-1; ATCC 51542
AF148215.1 gg_id:7712 Cycloclasticus oligotrophus
AF126548.1 gg_id:7703 Thialkalimicrobium aerophilum str. AL3
AF126549.1 gg_id:7704 Thialkalimicrobium sibericum str. AL7
CP000109.2 gg_id:141093 Thiomicrospira crunogena str. XCL-2
AB166731.1 gg_id:99742 Thiomicrospira thermophila str. I78
FJ792079.1 gg_id:548362 Unexpectedly archaeal species shift between rare and dominant over thousand year

AJ563935.1	100913	2953.2	3728.6	4045.7	3733.9	3964.4	3170.1
AF307138.1	39461	3956.7	3816.5	3687.2	3790.6	1653.1	3021.2
U05570.1	8080	4724.7	3336.4	3806.2	5392.4	2681.8	4216.2
AF096091.1	8060	4617.0	2401.8	3724.2	5044.7	1422.5	1004.5
EF495157.1	222556	3796.2	2826.2	2635.2	3904.9	4727.3	1551.4
AF304194.1	38046	2539.4	1845.6	4264.8	4038.0	1595.7	3424.3
AF150807.1	8055	13630.8	12564.9	11530.5	14786.3	12086.0	12715.7
AY995198.1	119789	11461.4	11751.5	6910.5	11057.9	10178.0	9397.0
X72776.1	8084	1273.5	1454.4	1083.6	3241.7	3410.8	2978.4
X72778.1	8090	10079.6	10090.8	8616.2	8584.0	12340.7	9705.1
DQ837263.1	245267	7964.4	8106.7	2936.5	4161.9	5284.6	4527.0
GQ340208.1	544467	6589.3	6571.3	2580.4	923.1	871.9	4608.9
NR_025040.1	550440	1954.5	1248.2	1305.2	1949.5	3443.8	978.7
AF177296.1	8051	1821.3	2080.9	1753.1	2909.8	3757.9	1792.7
U67929.1	8101	269.2	645.6	370.3	481.3	887.8	265.7
DQ337085.1	145089	2114.7	1915.9	4584.0	7130.8	1961.4	2977.4
DQ001669.1	157473	6297.8	4628.9	5870.9	8019.6	4267.0	6418.1
AM935153.1	534315	5643.9	5556.0	6282.0	5199.6	5515.3	6612.8
AB486440.1	585666	1884.3	2082.2	3164.4	2017.1	4121.5	1338.7
EU144025.1	235630	4344.1	3794.7	6799.8	6727.0	6930.5	4624.9
AM936189.1	537819	4178.9	4980.9	5454.7	8922.2	5265.2	3452.3
X72775.1	8059	4543.4	2010.6	3214.6	3482.0	422.9	315.3
X72773.1	8091	3274.9	1750.6	3354.0	3731.0	1128.4	892.0
EU328101.1	278818	1223.3	1993.1	2755.6	1054.4	2194.1	1869.1
FM242408.1	308594	12678.4	11223.2	13898.8	10468.6	12976.3	11055.2
X72772.1	8086	10189.6	7895.2	9601.4	9615.4	11779.7	10759.7
AM936083.1	539835	4170.6	4443.6	6125.5	5762.8	5062.3	4908.5
EF157165.1	247809	4097.2	4934.4	3881.4	6016.5	4584.5	2169.2
NR_029240.1	594166	5992.6	3646.9	4297.6	6485.0	2486.9	4068.8
EU144026.1	252662	5086.6	3720.4	3313.7	6058.9	6048.6	4774.7
AM936065.1	564002	10981.7	12757.4	14681.8	14964.7	14613.5	11109.1
EF648094.1	254304	3537.3	2902.4	3859.3	7665.5	3926.7	2752.6
EU735633.1	353064	8865.4	8068.6	11932.9	10085.2	13521.4	10253.7
AY007295.1	22040	9595.0	5459.4	6784.3	9084.8	5672.8	6445.6
NR_025955.1	555220	3538.3	2385.9	3776.4	3355.1	4459.6	5988.1
AF148215.1	7712	3315.1	1973.6	2931.8	1639.0	2903.4	4766.5
AF126548.1	7703	9395.1	10011.2	7347.2	7723.6	12471.2	8907.3
AF126549.1	7704	2123.9	3021.3	2306.9	2786.9	3268.9	3024.9
CP000109.2	141093	2378.9	2244.2	3240.6	2351.7	2160.7	2370.3
AB166731.1	99742	50.1	65.1	64.1	67.2	96.3	33.4
FJ792079.1	548362	4843.2	5592.2	3373.6	5139.9	5197.1	6060.1

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NR_029135.1 gg_id:555362 Hydrogenovibrio marinus str. MH-110; JCM7688
AF013978.1 gg_id:7695 Thiomicrospira kuenenii str. JB-A1
EU196336.1 gg_id:252812 Thiomicrospira sp. NP20
FJ791897.1 gg_id:557561 Unexpectedly archaeal species shift between rare and dominant over thousand year
AJ294334.1 gg_id:75896 Thiomicrospira crunogena HY-62
DQ513094.1 gg_id:161678 Microbial life fluids ridge flank crustal fluid clone FS274-19B-03
AY922201.1 gg_id:112990 whalefall clone 131635
FJ792061.1 gg_id:532975 Unexpectedly archaeal species shift between rare and dominant over thousand year
AJ237758.1 gg_id:7698 Thiomicrospira sp. str. Milos-T2
DQ390450.1 gg_id:152006 Thiovibrio halophilus str. HL 5
EF644790.1 gg_id:296669 genes and citrate lyase deep-sea microbial MAR Logatchev hydrothermal vent syster
AF013975.1 gg_id:7696 Thiomicrospira chilensis str. Ch-1
FJ792110.1 gg_id:564352 Unexpectedly archaeal species shift between rare and dominant over thousand year
EU999014.1 gg_id:320018 Predominance Methanolobus and Methanoculleus spp. Archaeal Saline Gas Field Foı
AB176166.1 gg_id:187293 Microbial Hydrothermal System Suiyo Seamount on Izu-Ogasawara Arc vent area wa
FJ792063.1 gg_id:551499 Unexpectedly archaeal species shift between rare and dominant over thousand year
FJ791999.1 gg_id:532862 Unexpectedly archaeal species shift between rare and dominant over thousand year
DQ270630.1 gg_id:142939 hydrothermal carbonate chimney clone LC1446B-39
FJ792260.1 gg_id:512284 Unexpectedly archaeal species shift between rare and dominant over thousand year
FJ791896.1 gg_id:570053 Unexpectedly archaeal species shift between rare and dominant over thousand year
EF687189.1 gg_id:286578 Biogeochemistry iron- and sulfur-precipitating microbial mats (Nile Mediterranean) ir
DQ513107.1 gg_id:160820 Microbial life fluids ridge flank crustal fluid clone FS275-74B-03
AY575776.1 gg_id:106343 Thiomicrospira sp. str. AD03
AM888291.1 gg_id:254539 Thiomicrospira sp. str. NV40C1
FJ792466.1 gg_id:539354 Unexpectedly archaeal species shift between rare and dominant over thousand year
FJ792299.1 gg_id:511672 Unexpectedly archaeal species shift between rare and dominant over thousand year
AF513949.1 gg_id:62496 Piscirickettsia group clone LA7-B48N
FJ792295.1 gg_id:508761 Unexpectedly archaeal species shift between rare and dominant over thousand year
DQ270607.1 gg_id:142087 hydrothermal carbonate chimney clone LC1408B-58
AF069959.1 gg_id:7689 Thiomicrospira crunogena str. MA-3; ATCC700270
AF082327.1 gg_id:7682 Thiomicrospira sp. str. Milos T-1
FJ791989.1 gg_id:511184 Unexpectedly archaeal species shift between rare and dominant over thousand year
AY575777.1 gg_id:106505 Thiomicrospira sp. str. AD07
AF016046.1 gg_id:7702 Thiomicrospira thyasirae str. DSM 5322
EU050820.1 gg_id:245893 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_07_77
EU104341.1 gg_id:340969 Evidence Comamonadaceae determinants settling performance activated sludge clo
EU104176.1 gg_id:311244 Evidence Comamonadaceae determinants settling performance activated sludge clo
CU466829.1 gg_id:344621 Evry wastewater treatment plant anoxic basin clone
DQ463205.1 gg_id:157299 Acid Drainage Tong Lushan Copper Mine China acid mine drainage clone tls3-10
AY493942.1 gg_id:136796 Fingerprinting aggregates soil clone 105
EU134703.1 gg_id:243013 tallgrass prarie soil clone FFCH6306

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AF013978.1	7695	2698.4	1016.1	5018.8	3353.9	2919.1	5145.1
EU196336.1	252812	557.6	310.2	154.8	489.0	194.5	163.1
FJ791897.1	557561	6645.4	7488.0	7202.4	6475.3	9717.9	9287.9
AJ294334.1	75896	1585.1	2672.1	2716.5	1164.8	2492.8	1793.1
DQ513094.1	161678	12447.1	15216.5	10637.9	9790.8	14370.6	11687.3
AY922201.1	112990	2262.7	2056.7	1072.2	2011.0	2737.3	2765.2
FJ792061.1	532975	2822.1	4189.9	3554.9	4477.6	4298.1	3845.6
AJ237758.1	7698	2831.3	1888.5	1789.4	3116.6	1596.4	2799.6
DQ390450.1	152006	895.1	1166.0	1605.3	744.5	4326.0	1801.2
EF644790.1	296669	1778.1	1275.7	2629.0	2231.1	1778.1	2573.1
AF013975.1	7696	87.5	197.4	193.0	202.2	308.6	837.8
FJ792110.1	564352	8373.0	8450.4	6458.8	9014.1	14487.5	7534.0
EU999014.1	320018	3342.7	4370.5	2128.0	4244.7	3860.7	4908.1
AB176166.1	187293	4927.4	3043.7	4243.8	5061.5	7662.8	5298.7
FJ792063.1	551499	6819.1	7542.4	9146.2	8916.3	12435.3	10615.6
FJ791999.1	532862	6456.5	5242.7	3458.6	8481.9	6026.0	5150.8
DQ270630.1	142939	4005.4	5915.3	5990.2	4268.2	5171.2	7576.0
FJ792260.1	512284	12416.7	14764.8	13513.9	11446.8	13857.0	13635.3
FJ791896.1	570053	14395.0	16765.9	19794.1	14566.1	23491.2	22285.3
EF687189.1	286578	3719.7	4008.6	2927.9	4093.1	8935.4	5962.2
DQ513107.1	160820	2625.2	1949.6	3474.8	2995.2	4377.6	2858.8
AY575776.1	106343	1730.7	2637.8	3685.0	1478.0	5587.1	4779.9
AM888291.1	254539	402.0	475.2	1204.7	692.1	1234.4	2607.6
FJ792466.1	539354	6073.0	7097.9	5502.2	4917.4	6886.5	7049.9
FJ792299.1	511672	586.2	733.0	1253.4	994.1	1411.7	2261.4
AF513949.1	62496	364.3	529.4	228.4	596.4	3048.1	1364.2
FJ792295.1	508761	4506.1	2469.4	3284.3	3967.0	2226.9	1559.2
DQ270607.1	142087	1537.5	1558.8	2175.3	2484.0	2191.4	1977.4
AF069959.1	7689	4515.1	3217.2	4291.4	2943.2	3031.2	4834.2
AF082327.1	7682	1067.1	612.3	2848.7	2578.1	2147.6	1841.8
FJ791989.1	511184	6098.4	4697.2	5053.6	6182.9	6783.7	5825.5
AY575777.1	106505	11688.5	14929.5	10313.6	9211.8	12283.0	16901.9
AF016046.1	7702	2112.4	1672.9	1942.2	3230.0	2123.1	2041.1
EU050820.1	245893	654.5	1036.9	2714.8	2242.8	1025.0	900.3
EU104341.1	340969	3619.9	4704.7	7095.8	6243.5	8338.5	6690.3
EU104176.1	311244	3271.8	3240.1	5093.7	5869.9	12772.8	8343.3
CU466829.1	344621	61.4	213.6	1574.8	95.5	87.9	66.4
DQ463205.1	157299	1087.2	2284.9	4736.2	1297.9	4883.3	2718.0
AY493942.1	136796	55.8	152.7	335.4	123.1	334.2	352.7
EU134703.1	243013	51.1	75.2	340.5	62.1	126.9	60.9

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EU647558.1 gg_id:285678 Alcanivorax sp. str. PA2
GQ153648.1 gg_id:581006 Alcanivorax dieselolei str. ANT-2400 S12
EF647617.1 gg_id:270691 Alcanivorax dieselolei P40
AB176073.1 gg_id:195877 Microbial Hydrothermal System Suiyo Seamount on Izu-Ogasawara Arc vent area wa
GU183681.1 gg_id:593585 Alcanivorax dieselolei str. H1673
DQ270698.1 gg_id:143401 Alcanivorax sp. B-3025
DQ768648.1 gg_id:255548 Alcanivorax venustensis MARC4C
AJ244731.1 gg_id:73634 Smegmaraptor porcuscaenosi str. V4.BO.19 = MM_2368
GQ153640.1 gg_id:587714 Alcanivorax sp. str. ANT-2400 S4
EU621895.1 gg_id:278807 Alcanivorax sp. str. LY2
GQ153644.1 gg_id:589864 Alcanivorax dieselolei str. ANT-2400 S8
GQ153643.1 gg_id:541649 Alcanivorax dieselolei str. ANT-2400 S7
DQ234131.2 gg_id:144283 determined library mangrove clone DS047
EU799249.1 gg_id:329506 It's all ranking aquatic Newport Harbour RI clone 1C226826
EF583624.1 gg_id:275378 Alcanivorax indicus str. B114
EF648146.1 gg_id:244272 dynamics during produced water treatment aerobic activated sludge clone XJ93
AY686709.1 gg_id:105070 Uruburuia balearica str. MACL04
FM242351.1 gg_id:325493 sequences sediment clone 52 T9d+oil
FM242291.1 gg_id:314738 sequences sediment clone 12 T9d-oil
AB176167.1 gg_id:187343 Microbial Hydrothermal System Suiyo Seamount on Izu-Ogasawara Arc vent area wa
FM242201.1 gg_id:320352 sequences sediment clone 123 T0h-oil
GQ009749.1 gg_id:499916 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw77
EU440954.1 gg_id:345659 Alcanivorax sp. str. 2PR511-6
AB053125.1 gg_id:32122 Alcanivorax sp. str. I4
EU369139.1 gg_id:340580 libraries oyster shell clone MBIOS-23
NR_027574.1 gg_id:560452 Kangiella koreensis str. SW-125; DSM 16069
EU328013.1 gg_id:279401 dynamics during bioremediation crude oil contaminated moderate saline soil clone B
AY542567.1 gg_id:114206 Gulf Mexico seafloor sediment clone GoM GB425 02B-35
AF382097.1 gg_id:79413 bacterioplankton clone ZA2202c
FJ905711.1 gg_id:551031 s Tonga-Kermadec iron oxide sediments Volcano 1 Tonga Arc clone V1F45b
EF687362.1 gg_id:280438 Biogeochemistry iron- and sulfur-precipitating microbial mats (Nile Mediterranean) s
AY162089.1 gg_id:136096 Cultivating Sargasso Sea clone GMD38D11
EU290714.1 gg_id:249481 microbial structure biogeochemical contrasting shelf sediments Namibian upwelling
FM242204.1 gg_id:313320 sequences sediment clone 317 T0h-oil
EU652570.1 gg_id:278394 Seasonal variation microbial Yel Sea sediment clone B8S-19
EU287139.1 gg_id:241890 Pacific arctic surface sediment clone P13-46
EU050815.1 gg_id:240357 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_06_26
FM242475.1 gg_id:321501 sequences sediment clone 29 T12d+oil
EU037349.2 gg_id:259038 structure landfill sediments receiving long-term augmentations wastes chromium co
EU735618.1 gg_id:346955 archaeal structures and pristine soils China oil contaminated soil Jidong Oilfield clone

EF173354.1	187488	74.3	120.5	203.5	150.6	214.4	95.7
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AB176073.1	195877	4583.2	4931.6	4829.4	6385.3	7816.3	6439.4
GU183681.1	593585	4954.0	5133.9	4689.0	3995.2	6671.9	6549.4
DQ270698.1	143401	2937.1	3627.8	4311.0	3979.1	4941.5	3650.0
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AJ244731.1	73634	1890.8	2497.6	3499.8	3049.8	998.4	1742.1
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GQ153644.1	589864	3748.1	3924.9	5447.6	4177.4	5909.5	6071.0
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EU799249.1	329506	3740.9	3148.9	2305.4	3286.9	3332.1	3244.6
EF583624.1	275378	2755.6	2416.5	2611.6	4540.3	4866.9	5190.2
EF648146.1	244272	3976.6	6414.7	6161.2	3837.4	10185.5	7385.5
AY686709.1	105070	2136.0	3309.1	4114.6	4178.4	5741.8	4601.0
FM242351.1	325493	5587.0	6429.8	4416.5	5210.3	4720.9	5418.5
FM242291.1	314738	3713.8	5078.4	6016.5	4390.3	8973.8	6450.9
AB176167.1	187343	3172.4	4038.5	4944.5	5053.9	7066.3	6421.2
FM242201.1	320352	3171.6	5931.8	5639.9	5173.6	8943.1	7559.8
GQ009749.1	499916	827.5	1884.3	1860.7	519.0	797.6	1920.4
EU440954.1	345659	3592.5	3447.2	3409.4	4380.8	3647.5	5446.1
AB053125.1	32122	55.9	91.7	131.8	85.6	95.9	185.5
EU369139.1	340580	3508.5	4559.7	6867.4	6600.2	6611.8	5289.9
NR_027574.1	560452	4293.7	3436.8	4133.6	4332.0	1855.3	1997.2
EU328013.1	279401	8672.1	9036.4	5285.9	6937.6	7992.9	7683.3
AY542567.1	114206	4737.9	6070.6	3211.0	3642.3	7265.3	4119.0
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FJ905711.1	551031	2229.5	3301.9	2035.4	3488.1	3633.7	4261.4
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EU050815.1	240357	4251.6	4584.1	3765.6	3743.1	7616.1	7937.5
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GQ259322.1 gg_id:579351 Microbial activities coastal marine sediments and water column Svalbard surface se
FM242356.1 gg_id:353945 sequences sediment clone 5 T9d+oil
GU061307.1 gg_id:582472 Evaluation culturing methods cultivate previously Yel Sea intertidal beach seawater
AB015541.1 gg_id:8407 deep-sea sediment clone BD2-13
FJ203036.1 gg_id:316869 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c
FJ202771.1 gg_id:318714 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k
EU491790.1 gg_id:275246 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39
DQ889922.1 gg_id:172811 natural product producing octocoral Erythropodium caribaeorum clone EC52
AJ853538.1 gg_id:110075 landfill leachate clone GZKB44
AF006606.2 gg_id:8204 Candidatus Endobugula sertula str. BnSP
AY532642.1 gg_id:105318 Bugula simplex symbiont
EU287080.1 gg_id:246890 Pacific arctic surface sediment clone B78-116
EU286987.1 gg_id:236857 Pacific arctic surface sediment clone B78-23
NC_010995.1 gg_id:350895 Cellvibrio japonicus str. Ueda107
DQ824661.1 gg_id:186207 human fecal clone RL185_aaj71c06
AJ289164.1 gg_id:30985 Cellvibrio fibrivorans str. R-4079
AF448514.1 gg_id:25527 Cellvibrio fulvus str. NCIMB 8634
EF515971.1 gg_id:222753 grassland soil clone FCPS641
AJ289161.1 gg_id:52677 Cellvibrio sp. str. R-4001
EU528236.1 gg_id:283599 Seasonal Dynamics Mudflat Mouth Major Kentucky Lake Reservoir Tributary sedime
AJ493583.1 gg_id:89552 Cellvibrio ostraviensis str. LMG 19434
GQ263640.1 gg_id:576714 Structure Simulated Level Waste Site simulated level waste site clone FW3_27C
AM935359.1 gg_id:565337 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
AM935949.1 gg_id:537030 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
AB186843.1 gg_id:103183 polychlorinated dioxin dechlorinating microcosm clone TSBX24
EF648042.1 gg_id:257504 dynamics during produced water treatment aerobic activated sludge clone HB32
EF420207.1 gg_id:213653 Mature fine processing harbour methanogenic oil sands tailings pond clone MLSB_3C
EU735695.1 gg_id:316525 archaeal structures oil contaminated and soils China pristine soil Jidong Oilfield clone
FM242423.1 gg_id:331444 sequences sediment clone 66 T12d-oil
AM935832.1 gg_id:535164 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
AM935433.1 gg_id:532686 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
AY033301.1 gg_id:68989 marine bacterioplankton clone MB11B11
EU005741.1 gg_id:277139 Major activity inside and outside natural iron-fertilized phytoplankton bloom 3 micro
EU544831.1 gg_id:267517 free-living particle- aggregate- archaeal and Laptev Sea 1.0-60 um size fraction (susp
AY697919.1 gg_id:103045 Antarctica clone F4C67
GU230303.1 gg_id:585217 Multilevel approach along Rio de la Plata-South Atlantic Ocean coastal water clone A
EU328092.1 gg_id:278620 dynamics during bioremediation crude oil contaminated moderate saline soil clone Y
AY839870.2 gg_id:109919 Marinobacter sp. str. M18
FJ152968.1 gg_id:331146 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX4CE
EU874388.1 gg_id:321327 Marinimicrobium sp. str. ISL-43

AY622252.1	103157	827.7	1678.3	1441.0	1438.2	1565.6	1056.5
GQ259322.1	579351	2514.6	3966.9	3027.1	3446.2	8668.6	7232.1
FM242356.1	353945	7518.1	7456.9	6184.2	6921.2	13070.2	9216.1
GU061307.1	582472	1990.5	1989.5	4153.9	4858.0	8485.8	8870.7
AB015541.1	8407	72.7	120.7	227.8	122.6	256.0	102.3
FJ203036.1	316869	2378.0	2054.4	1360.2	2088.5	3023.0	1578.5
FJ202771.1	318714	503.8	506.0	1562.0	679.2	1615.5	700.9
EU491790.1	275246	538.9	615.1	558.1	482.6	989.8	1390.4
DQ889922.1	172811	146.7	196.1	249.0	151.2	167.8	558.1
AJ853538.1	110075	132.0	284.3	778.6	215.5	3033.9	799.5
AF006606.2	8204	2000.6	2433.6	6043.8	6160.7	6496.4	5209.3
AY532642.1	105318	2304.6	2177.4	3485.2	2555.3	4706.4	2897.2
EU287080.1	246890	6325.0	4577.7	1735.8	783.6	1337.4	950.3
EU286987.1	236857	3708.8	4176.1	3017.2	2370.4	4620.4	5281.1
NC_010995.1	350895	955.5	1831.1	3307.5	1718.7	3371.3	2118.4
DQ824661.1	186207	61.7	65.3	106.5	90.7	107.7	169.1
AJ289164.1	30985	2053.0	1530.8	3970.0	2594.8	5628.6	5667.2
AF448514.1	25527	3348.5	4001.4	6207.2	2390.4	6468.8	7402.8
EF515971.1	222753	1463.3	1275.5	3404.2	1869.4	1170.4	1726.6
AJ289161.1	52677	540.4	880.5	3835.5	1028.7	1415.2	3881.8
EU528236.1	283599	7488.4	6999.1	9381.5	7931.1	13093.0	10363.1
AJ493583.1	89552	75.3	116.1	498.2	69.9	75.7	726.9
GQ263640.1	576714	4220.3	4398.2	4154.6	5226.7	7495.1	6932.8
AM935359.1	565337	5453.1	4618.4	1954.9	5245.9	7332.3	5773.1
AM935949.1	537030	1598.3	1661.2	3459.3	1691.4	2234.7	3320.1
AB186843.1	103183	660.0	720.7	2603.0	472.8	4938.0	860.4
EF648042.1	257504	1799.8	2574.6	3350.5	2501.0	5078.5	4263.4
EF420207.1	213653	9137.0	9724.6	5250.1	4528.2	10689.5	7501.0
EU735695.1	316525	5027.4	4786.4	4082.8	5583.4	4642.0	5096.0
FM242423.1	331444	5946.7	7470.3	8515.6	4975.8	11124.1	6522.1
AM935832.1	535164	13495.7	14275.3	6669.8	10773.3	15389.1	12234.7
AM935433.1	532686	9342.1	7415.6	4342.3	9067.2	12730.2	10516.6
AY033301.1	68989	8969.4	7547.2	6008.1	8238.8	11931.6	7857.0
EU005741.1	277139	55.6	126.0	791.3	355.8	1171.5	875.4
EU544831.1	267517	5525.0	4134.6	1735.0	6509.1	6732.5	6674.3
AY697919.1	103045	7631.2	5134.8	4094.2	5131.9	6738.8	6702.7
GU230303.1	585217	7547.0	7636.3	8714.9	6866.1	11623.2	10411.2
EU328092.1	278620	1802.3	2012.6	1982.7	416.1	2936.2	3369.1
AY839870.2	109919	704.7	719.1	2109.7	353.0	2318.8	1066.6
FJ152968.1	331146	2053.2	2779.5	3950.7	1899.2	5968.6	3761.3
EU874388.1	321327	2017.6	2170.1	3282.4	1874.0	4844.1	7278.9

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EU441002.1 gg_id:332510 Marinobacter bryozoorum str. PR53-11
NR_027192.1 gg_id:541894 Marinobacter bryozoorum str. 50-11; KMM 3840
AF238495.1 gg_id:20696 Marinobacter sp
GQ200189.1 gg_id:548606 Marinobacter hydrocarbonoclasticus str. DQHS-3
FJ984522.1 gg_id:382828 Marinobacter hydrocarbonoclasticus str. NBSL04
NR_028841.1 gg_id:565301 Marinobacter litoralis str. SW-45; JCM 11547
AM945661.1 gg_id:272890 Marinobacter litoralis 2
GU223376.1 gg_id:533417 Marinobacter sp. str. EM497
GQ214550.1 gg_id:556839 Marinobacter mobilis str. B17
AB435646.1 gg_id:396810 Marinobacter sp. str. 2M46
DQ677876.1 gg_id:235549 Marinobacter sp. BF04_CF-4
DQ530479.1 gg_id:168080 Marinobacter sp. str. gap-e-81
DQ521387.1 gg_id:164240 Marinobacter sp. str. ice-oil-325
EF368018.1 gg_id:208660 Marinobacter taiwanensis str. 1645
AB513677.1 gg_id:582394 Marinobacter sp. str. PAD-2
GU183677.1 gg_id:548886 Marinobacter alkaliphilus str. H1711
EU603452.1 gg_id:275327 Marinobacter bryozoorum str. PTG4-16
FJ675262.1 gg_id:517038 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
DQ325514.1 gg_id:149482 Marinobacter koreensis str. DD-M3
NR_025116.1 gg_id:573563 Marinobacter lutaoensis str. T5054; CCRC 17087; JCM 11179
FJ675204.1 gg_id:528351 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
FJ675118.1 gg_id:527584 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
AY592402.1 gg_id:103215 deep-sea mud volcano clone Amsterdam-2B-44; BC20-2B-44
GQ131626.2 gg_id:581833 Marinobacter sp. str. YCSA7
FJ674834.1 gg_id:518091 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
FJ746583.1 gg_id:547174 Marinobacter sp. str. H184B35
EF660754.1 gg_id:240909 Marinobacter goseongensis str. En6
AB305311.1 gg_id:234441 Marinobacter sp. str. IW11-2CT
EF667989.1 gg_id:244324 and biogeochemical influences active heterotrophic prokaryotes off Palmer Peninsula
FJ425903.1 gg_id:590148 Marinobacter zhanjiangensis str. JSM 078120
U14584.1 gg_id:8799 gas vacuolate str. S36-W<gv>1
AF468259.1 gg_id:80533 Arctic pack ice; northern Fram Strait; 80 31.1 N; 01 deg 59.7 min E clone ARKDMS-57
EU287196.1 gg_id:246628 Pacific arctic surface sediment clone S11-13
EU328041.1 gg_id:277828 dynamics during bioremediation crude oil contaminated moderate saline soil clone B
AY180101.1 gg_id:78569 Marinobacter excellens str. KMM 3809
FJ196021.1 gg_id:351303 Marinobacter sp. str. ZS3-32
DQ015835.1 gg_id:139700 Antarctic lake water clone ELB19-223
AM503093.1 gg_id:311877 Marinobacter guineae str. LMG 24048 = M3B
AJ292527.1 gg_id:37115 Marinobacter sp. Trimyema-1 1
AJ439500.1 gg_id:59259 Marinobacter squalenivorans str. 2Asq64
GU223379.1 gg_id:557645 Marinobacter sp. str. EM492

EU441002.1	332510	1002.6	878.4	1576.2	1498.9	4218.0	3124.8
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AB435646.1	396810	654.8	880.4	1315.9	422.8	1976.3	1840.6
DQ677876.1	235549	1418.3	1428.9	1998.0	767.7	3862.1	4000.9
DQ530479.1	168080	795.3	703.6	1221.4	772.2	1650.5	2571.6
DQ521387.1	164240	11070.8	10337.3	4545.1	8082.8	12545.9	11741.4
EF368018.1	208660	251.4	910.8	2575.8	932.7	3768.2	1705.0
AB513677.1	582394	266.3	324.1	741.9	250.3	288.1	717.3
GU183677.1	548886	4968.8	3668.8	4560.8	4714.9	8187.7	5290.9
EU603452.1	275327	3166.1	2194.3	3163.5	4127.9	4518.2	5293.8
FJ675262.1	517038	731.8	999.1	1333.2	548.6	1183.1	1758.9
DQ325514.1	149482	118.0	220.0	371.4	264.6	684.3	1054.8
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FJ675118.1	527584	524.8	1098.5	1709.6	414.7	2121.8	1776.1
AY592402.1	103215	1297.9	1502.6	1244.0	3507.7	5245.7	5264.4
GQ131626.2	581833	619.2	703.4	672.5	561.0	3174.6	3461.7
FJ674834.1	518091	3052.3	2456.4	3672.2	4087.1	3977.0	4471.1
FJ746583.1	547174	257.6	787.5	526.5	209.3	1785.2	2127.5
EF660754.1	240909	855.5	1097.8	2912.6	3881.6	4393.3	4141.0
AB305311.1	234441	2670.9	2826.8	2823.7	5477.7	7602.9	7154.0
EF667989.1	244324	161.7	259.9	190.7	413.2	243.3	858.4
FJ425903.1	590148	190.0	256.8	479.5	184.8	167.4	815.2
U14584.1	8799	365.6	369.7	725.4	198.1	1399.1	1873.8
AF468259.1	80533	960.1	786.9	1707.2	893.2	1894.6	1781.8
EU287196.1	246628	2634.4	2503.0	1657.1	2806.7	2575.7	1683.8
EU328041.1	277828	7418.2	5544.2	3756.8	5075.5	9134.7	9786.7
AY180101.1	78569	325.1	768.1	1416.9	792.3	328.7	603.8
FJ196021.1	351303	333.6	449.1	1250.7	1525.3	3809.8	1626.5
DQ015835.1	139700	1004.0	2171.2	2867.5	2142.9	2845.8	2963.3
AM503093.1	311877	587.6	798.1	1364.5	791.2	2751.9	3932.9
AJ292527.1	37115	1531.9	1017.0	1605.9	1262.3	1634.9	1527.2
AJ439500.1	59259	8588.7	7972.5	3795.9	6456.4	9715.5	7786.8
GU223379.1	557645	1265.2	1766.5	3100.6	2989.7	7141.4	3908.3

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g__Microbulbifer

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FJ675168.1 gg_id:513433 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
EU328057.1 gg_id:278624 dynamics during bioremediation crude oil contaminated moderate saline soil clone Y
AJ871937.1 gg_id:163334 hydrocarbonoclastic Guanabara Bay Brazil mangrove sediments
AB252057.1 gg_id:170550 Brassica napus str. SKA S2
EU440995.1 gg_id:340108 Marinobacter flavimaris str. 2PR54-4
EU293413.1 gg_id:242328 Marinobacter sp. str. cn74
NR_025799.1 gg_id:549391 Marinobacter flavimaris str. SW-145; KCTC 12185
AB026946.1 gg_id:8806 Marinobacter sp. str. NK-1
FJ675374.1 gg_id:528098 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
FJ675429.1 gg_id:526155 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
NR_025671.1 gg_id:557510 Marinobacter lipolyticus str. SM-19; DSM 15157
U85863.1 gg_id:8800 Marinobacter sp. str. IC022
EF428127.1 gg_id:277000 Marinobacter excellens str. LL406
AF237685.1 gg_id:21327 Marinobacter sp
FJ348439.1 gg_id:565377 Investigation microbial soil method saltern 15 cm be surface clone DGGE gel band ntu
DQ097521.1 gg_id:129808 Marinobacter giovannonii str. IS17
DQ530455.1 gg_id:170366 Marinobacter sp. str. gap-d-2
EU718223.1 gg_id:337093 Microbial farmed prawn preservation methods Marinobacter clone HL13
EF632877.1 gg_id:238588 Unique microbial contrasting aquatic altitude Andean Altiplano (northern Chile) wate
DQ097526.1 gg_id:131161 Marinobacter koreensis str. KGB22
NR_029028.1 gg_id:592275 Marinobacter sediminum str. R65; KMM 3657
AY690675.1 gg_id:99388 Marinobacter sp. str. GC101
FJ973518.1 gg_id:454067 Marinobacter alkaliphilus str. NBSL07
FJ674980.1 gg_id:511539 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
AF173969.1 gg_id:21222 Marinobacter aquaeolei str. KT02ds19
EU440994.1 gg_id:353090 Marinobacter alkaliphilus str. 2PR56-13
GU223374.1 gg_id:554900 Marinobacter sp. str. EM491
EU196317.1 gg_id:255215 Marinobacter sp. NP38
EU907917.1 gg_id:326599 Marinobacter sp. str. SKUK MB1002
FJ897726.1 gg_id:547256 Marinobacter sp. str. Set74
DQ235263.1 gg_id:144953 Marinobacter vinulentus str. FB1
GU370116.1 gg_id:517692 Marinobacter hydrocarbonoclasticus str. P721(1)
AB166970.1 gg_id:104848 Marinobacter sp. str. NT N14
AJ557854.1 gg_id:84236 Arctic deep sea Isolation common chemoorganotrophic oxygen-respiring polar current
EU432582.1 gg_id:262300 Marinobacter sp. str. 10050
FJ497670.1 gg_id:509005 Marinobacter sp. str. VS-43
AM990796.1 gg_id:278977 Marinobacter sp. MOLA 20
EU164778.1 gg_id:250476 Marinobacter szutsaonensis str. Halo30-39
AY771710.1 gg_id:108686 Marinobacter lipolyticus str. S2-44
AB304799.1 gg_id:255218 Microbulbifer agarolyticus str. JAMM 0654
GQ334398.1 gg_id:585495 Microbulbifer maritimus str. RV1

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AB252057.1	170550	1483.1	848.9	998.9	279.9	610.1	1101.2
EU440995.1	340108	113.0	295.1	567.8	232.6	470.9	494.6
EU293413.1	242328	476.5	669.9	1283.5	744.3	924.0	879.6
NR_025799.1	549391	68.9	281.1	274.6	180.2	984.7	720.5
AB026946.1	8806	2778.9	4214.7	3951.6	3782.4	5545.2	4540.0
FJ675374.1	528098	1474.9	5077.6	2102.3	3324.4	6529.8	5417.9
FJ675429.1	526155	2024.9	3145.2	1894.8	3198.5	4590.3	3837.1
NR_025671.1	557510	2523.3	2518.5	3385.0	1894.1	8565.9	4467.0
U85863.1	8800	339.5	435.2	97.7	193.2	531.0	715.2
EF428127.1	277000	998.5	673.2	1035.4	2548.9	1534.7	1456.5
AF237685.1	21327	584.0	789.8	217.5	278.0	2277.3	1852.4
FJ348439.1	565377	7604.5	8179.6	4064.2	5698.8	5502.8	6636.9
DQ097521.1	129808	493.0	650.7	2428.9	2897.3	2635.4	3082.4
DQ530455.1	170366	654.2	477.9	1210.2	749.5	997.7	1562.1
EU718223.1	337093	648.5	1382.2	2172.6	943.0	4240.9	2732.8
EF632877.1	238588	247.1	526.2	2100.3	595.1	1745.5	1681.7
DQ097526.1	131161	1707.3	973.6	2102.2	1594.2	3911.5	3208.4
NR_029028.1	592275	450.4	702.9	1690.4	1356.0	3290.7	3077.8
AY690675.1	99388	1153.1	1304.7	3327.4	1141.6	3496.9	1533.1
FJ973518.1	454067	607.2	582.5	2210.4	517.9	927.5	1814.1
FJ674980.1	511539	563.0	1204.3	1105.8	329.4	2425.2	2482.6
AF173969.1	21222	2178.4	2314.7	2014.9	2801.7	2961.7	3859.5
EU440994.1	353090	818.4	704.1	2968.4	800.9	1728.9	2445.6
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EU196317.1	255215	7269.0	6711.0	2191.2	8610.2	9787.2	8906.9
EU907917.1	326599	6340.0	5809.5	3075.4	4376.5	6972.4	7877.2
FJ897726.1	547256	459.6	373.3	1453.0	544.1	426.3	476.6
DQ235263.1	144953	202.8	493.6	1398.2	201.1	650.5	972.1
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AB166970.1	104848	40.7	78.4	244.4	104.7	574.9	135.8
AJ557854.1	84236	3149.8	2998.1	3150.3	3206.2	3782.2	4046.0
EU432582.1	262300	608.6	735.3	1137.4	1950.3	2248.6	2962.6
FJ497670.1	509005	385.0	1113.3	299.5	174.3	2515.5	2047.6
AM990796.1	278977	1985.4	1821.5	1351.0	1475.6	2324.8	3015.3
EU164778.1	250476	121.8	265.7	833.5	218.4	736.6	580.6
AY771710.1	108686	4346.8	6550.9	3047.1	5216.8	6432.3	4611.6
AB304799.1	255218	2476.6	3205.9	3878.3	4615.0	1664.0	4779.2
GQ334398.1	585495	1068.9	1879.1	4537.8	1876.0	3612.2	3091.0

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AB304801.1 gg_id:248696 Microbulbifer thermotolerans str. JAMM 1327
AB167354.2 gg_id:108039 Pelagiobacter variabilis str. Ni2088
AJ510266.1 gg_id:69355 Microbulbifer arenaceous str. RSBr-1
GQ262812.1 gg_id:558634 Microbulbifer sp. str. Y215
FJ169190.1 gg_id:338941 microbial and polyketide biosynthetic potential palmerolide-producing tunicate Synoi
AB500893.1 gg_id:555088 Microbulbifer sp. str. ABABA 23
EF486352.1 gg_id:222510 Microbulbifer celer str. ISL-39
DQ340189.1 gg_id:147845 Dominance Mycoplasma guts Long-Jawed Mudsucker Gillichthys mirabilis five Califo
EF674853.1 gg_id:257184 Microbulbifer halotolerans str. YIM 91118
AY224196.1 gg_id:81821 Microbulbifer sp. str. Th/B/38
AF479688.1 gg_id:51065 Microbulbifer salipaludis str. SM-1
AM180745.1 gg_id:145463 Pseudomonas sp. UC14a
AB500894.1 gg_id:573761 Microbulbifer sp. str. ABABA 212
AB052969.1 gg_id:24308 Pseudomonas sp. PE2
AY862188.1 gg_id:111195 Microbulbifer sp. str. MY05
AB456139.1 gg_id:551285 Microorganisms involved anaerobic phenol degradation treatment synthetic coke-o\
EU491487.1 gg_id:263181 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X4 clone
DQ334644.1 gg_id:194566 Impact metals on sediments heavy metal polluted marine sediment clone HB2-9-21
AB456140.1 gg_id:572166 Microorganisms involved anaerobic phenol degradation treatment synthetic coke-o\
EU491452.1 gg_id:259455 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X4 clone
NC_007912.1 gg_id:153124 Saccharophagus degradans str. 2-40
GQ872422.1 gg_id:569907 Simiduia sp. str. M2-5
EF617350.1 gg_id:234841 Simidua agarivorans str. SA1
FJ202639.1 gg_id:341703 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k
FJ356668.1 gg_id:541691 Intra- Microheterogeneity Multiple Displacement Single-cells Marine Cyanobacteria L
EF092194.1 gg_id:269778 Persistent Axinella corrugata clone Ax29_A1
FJ203003.1 gg_id:317569 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k
GU391220.1 gg_id:530532 Spongiibacter sp. str. JYr4
NR_027564.1 gg_id:565759 Teredinibacter turnerae T7901 str. T7902; ATCC 39867
DQ269073.1 gg_id:198202 marine macro-alga surface clone DPC012
DQ272313.1 gg_id:141068 Lyrodus pedicellatus symbiont RT18
EF061962.1 gg_id:194319 Xiamen China mangrove sediment clone XME54
AB467280.1 gg_id:534461 Umboniibacter marinipuniceus str. KMM 3892
EU236385.1 gg_id:298139 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg92A4
GQ920839.1 gg_id:550044 Marinimicrobium sp. str. SX15
AY845232.1 gg_id:110380 sponge clone 34P38
EU050817.1 gg_id:237439 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_05_77
AY375151.1 gg_id:96709 deep sea sediment clone D78
EU799127.1 gg_id:348578 It's all ranking aquatic Newport Harbour RI clone 1C226690
FJ628337.1 gg_id:555614 transition and zone within near-shore basin: brackish water anoxic fjord Nitinat Lake
EU286983.1 gg_id:256729 Pacific arctic surface sediment clone B78-19

AB304801.1	248696	1889.3	2130.3	2668.3	1090.6	3843.1	3940.7
AB167354.2	108039	1714.6	2431.3	2546.3	2598.1	5297.7	4207.6
AJ510266.1	69355	3022.6	2337.0	5440.6	5226.5	4269.2	4511.6
GQ262812.1	558634	485.0	942.6	1522.1	618.3	2237.6	1639.8
FJ169190.1	338941	1217.4	1255.6	2399.7	1168.8	3167.9	3679.8
AB500893.1	555088	2992.3	3453.3	4307.2	3640.7	5486.7	6075.2
EF486352.1	222510	325.6	498.1	1255.3	351.6	273.9	1059.4
DQ340189.1	147845	3319.9	1757.6	3888.3	5445.0	3277.6	2488.4
EF674853.1	257184	2304.5	3619.8	4406.7	2088.6	9065.6	6519.3
AY224196.1	81821	1207.1	1558.3	1274.8	424.2	4035.9	2714.8
AF479688.1	51065	584.8	479.9	1856.8	818.1	2327.0	2325.4
AM180745.1	145463	2187.7	2235.9	3555.2	3078.9	3733.9	2857.5
AB500894.1	573761	441.7	652.7	1805.5	805.0	2768.5	1400.8
AB052969.1	24308	5718.0	6829.0	4482.2	5168.1	7430.6	6893.2
AY862188.1	111195	646.8	821.4	2534.6	1095.0	9722.7	5571.4
AB456139.1	551285	853.1	1339.0	1190.4	1522.8	2770.5	1717.8
EU491487.1	263181	11543.8	10434.4	12787.7	12377.7	17692.1	13544.9
DQ334644.1	194566	54.2	69.0	199.7	89.3	98.6	128.9
AB456140.1	572166	287.4	280.8	1245.5	349.9	982.8	796.1
EU491452.1	259455	79.6	201.6	628.0	137.7	96.5	534.3
NC_007912.1	153124	23.0	50.9	86.1	73.5	63.6	31.1
GQ872422.1	569907	4545.4	4011.2	6970.1	5505.6	6425.9	5154.4
EF617350.1	234841	129.0	347.1	182.5	281.4	251.0	719.0
FJ202639.1	341703	359.8	754.1	1391.2	531.2	607.6	849.2
FJ356668.1	541691	1446.7	1069.1	1141.6	1001.9	2916.5	2288.1
EF092194.1	269778	1237.6	913.6	1607.9	1072.1	4004.2	1231.4
FJ203003.1	317569	84.3	84.1	112.3	63.9	65.8	79.6
GU391220.1	530532	563.6	358.2	3368.6	1262.2	1532.1	1228.9
NR_027564.1	565759	1505.9	787.8	1689.2	2180.7	3536.0	1503.6
DQ269073.1	198202	564.1	842.2	1325.9	594.6	2807.9	2653.3
DQ272313.1	141068	998.7	976.1	1501.7	1949.8	1605.5	2107.7
EF061962.1	194319	2241.1	787.7	1062.7	3925.1	1391.9	1683.8
AB467280.1	534461	7063.6	4760.0	5536.6	11676.5	3680.8	4989.7
EU236385.1	298139	1898.3	1855.6	5602.2	4190.1	6835.6	2712.1
GQ920839.1	550044	9503.8	8586.2	5565.5	7794.1	10031.8	10413.1
AY845232.1	110380	132.6	109.6	156.4	141.5	68.9	63.7
EU050817.1	237439	1918.8	1277.2	3204.7	2333.9	1815.4	1907.4
AY375151.1	96709	4735.6	3860.4	6658.5	7944.0	5604.1	4420.2
EU799127.1	348578	62.8	84.0	101.5	139.4	208.9	114.1
FJ628337.1	555614	247.5	290.8	366.9	215.3	683.3	452.3
EU286983.1	256729	10558.7	6645.6	7944.7	6631.7	6801.1	8942.3

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FJ347758.1 gg_id:370251 Endozoicomonas sp. str. CL-33
AM259915.1 gg_id:252743 Chondrilla nucula-specific sponge mesohyl clone CN34
AY700601.1 gg_id:109430 Australia: Great Barrier Reef clone PDA-OTU3
AB205011.1 gg_id:113799 Spongiobacter nickelotolerans str. 00P-Ni033-1-1-2
AM990755.1 gg_id:277802 Culturable along NW Mediterranean coast Petrosia ficiformis sponge
FJ202634.1 gg_id:354436 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k
EF516073.1 gg_id:223694 grassland soil clone FCPT525
EU464803.1 gg_id:287677 Hartmann's mountain zebra feces clone AFZEB_aaj71b02
EU104099.1 gg_id:351662 Evidence Comamonadaceae determinants settling performance activated sludge clo
EU464733.1 gg_id:301670 Hartmann's mountain zebra feces clone AFZEB_aaj69h03
EU464904.1 gg_id:301529 Hartmann's mountain zebra feces clone AFZEB_aaj72h05
DQ824554.1 gg_id:183389 human fecal clone RL185_aaj69f03
DQ824608.1 gg_id:180882 human fecal clone RL185_aaj70d02
EU464879.1 gg_id:298205 Hartmann's mountain zebra feces clone AFZEB_aaj72d02
EU104233.1 gg_id:352480 Evidence Comamonadaceae determinants settling performance activated sludge clo
EU464760.1 gg_id:291795 Hartmann's mountain zebra feces clone AFZEB_aaj70c11
DQ824684.1 gg_id:179599 human fecal clone RL185_aaj71f06
EU104152.1 gg_id:319880 Evidence Comamonadaceae determinants settling performance activated sludge clo
DQ824679.1 gg_id:181704 human fecal clone RL185_aaj71e11
CU466815.1 gg_id:307591 Evry wastewater treatment plant anoxic basin clone
AF195410.1 gg_id:24515 Hahella chejuensis str. KCTC 2396
EF495227.1 gg_id:217600 Hahella antarctica str. IMCC3113
AY676463.1 gg_id:107320 Hahella ganghwensis str. FR1050
AY130995.1 gg_id:70229 Zooshikella ganghwensis str. JC2045
AF400466.1 gg_id:36328 Primary endosymbiont Bemisia tabaci clone UG23 aleyrodidarum
Z11928.1 gg_id:8116 symbiont of Trialeurodes vaporariorum (greenhouse whitefly)
AF400467.1 gg_id:46892 Primary endosymbiont Bemisia tabaci clone UG26 aleyrodidarum
Z11927.1 gg_id:8122 symbiont of Siphoninus phillyreae (ash whitefly)
AY266108.1 gg_id:99204 Neomaskellia andropogonis symbiont
AF286123.1 gg_id:51913 symbiont
AY266098.1 gg_id:103124 Aleuroparadoxus arctostaphylli symbiont
AF400469.1 gg_id:54022 Primary endosymbiont Bemisia tabaci clone UG25
AY268081.1 gg_id:88180 Bemisia tabaci symbiont
AY266100.1 gg_id:106952 Aleuroplatus sp. symbiont
AY266107.1 gg_id:99043 Dialeurodes hongkongensis symbiont
AY266096.1 gg_id:102829 Aleurodicus dispersus symbiont
AY266095.1 gg_id:102674 symbiont
AF400462.1 gg_id:19222 Primary endosymbiont Bemisia tabaci clone MEX4 aleyrodidarum
DQ396070.1 gg_id:154863 deep-sea octacoral clone ctg_NISA053
EU799800.1 gg_id:326262 It's all ranking aquatic Newport Harbour RI clone 1C227454

GU118076.1	567768	5170.4	3732.1	4232.2	9644.2	9235.8	8175.8
FJ347758.1	370251	76.1	153.9	164.8	116.0	66.8	477.4
AM259915.1	252743	649.9	894.0	1396.9	3943.7	3542.3	5250.2
AY700601.1	109430	101.0	159.1	164.8	139.5	110.6	205.9
AB205011.1	113799	92.2	200.0	266.4	126.6	131.3	145.2
AM990755.1	277802	2888.7	2640.8	3372.5	2312.7	4285.2	4017.1
FJ202634.1	354436	56.7	68.1	69.2	60.4	200.0	65.4
EF516073.1	223694	40.2	100.2	299.4	79.6	96.9	331.9
EU464803.1	287677	9039.5	7954.6	10922.5	10968.8	11977.6	13779.4
EU104099.1	351662	7032.9	7478.9	10091.2	8859.5	11322.3	9922.6
EU464733.1	301670	4540.1	4737.9	7244.7	6260.3	5413.7	5849.9
EU464904.1	301529	9430.2	12379.3	12075.6	7594.8	16277.2	19431.9
DQ824554.1	183389	10183.3	9381.6	10925.5	11462.1	13750.9	14982.4
DQ824608.1	180882	11465.5	14055.0	12859.7	10872.8	15956.7	17391.5
EU464879.1	298205	3313.3	4435.5	5016.9	3743.5	10239.4	5486.9
EU104233.1	352480	5074.4	6121.6	4982.2	4740.2	6018.2	6194.6
EU464760.1	291795	8531.6	9570.0	11363.6	8195.3	14616.6	14154.7
DQ824684.1	179599	7099.8	7686.2	7928.8	10317.4	11332.4	11010.9
EU104152.1	319880	5060.6	5547.3	6340.4	5218.0	11002.5	10284.0
DQ824679.1	181704	5502.0	5989.8	8522.2	8729.9	9435.9	11878.3
CU466815.1	307591	6832.1	6074.7	9543.4	7414.3	10142.0	9426.8
AF195410.1	24515	242.5	270.7	125.4	151.3	244.0	502.7
EF495227.1	217600	91.6	56.9	99.4	243.4	123.0	128.2
AY676463.1	107320	68.4	296.1	24.2	37.5	50.8	62.4
AY130995.1	70229	29.3	69.8	93.1	84.1	386.9	49.6
AF400466.1	36328	9352.5	8833.3	3613.4	5930.8	9127.0	7874.5
Z11928.1	8116	5757.2	5190.7	4377.4	4450.6	7328.3	5566.2
AF400467.1	46892	5472.4	3937.5	3875.3	3538.5	5207.0	4433.1
Z11927.1	8122	1404.8	1450.0	308.9	2467.3	390.2	1535.0
AY266108.1	99204	189.4	216.4	408.6	114.5	222.5	213.0
AF286123.1	51913	2239.9	2137.5	1695.1	829.1	2467.7	1982.1
AY266098.1	103124	3140.3	4922.9	2245.4	2868.5	4572.8	3947.0
AF400469.1	54022	1386.4	2172.7	774.2	1112.3	1983.5	1649.7
AY268081.1	88180	335.2	473.0	713.3	548.6	1784.7	935.6
AY266100.1	106952	6501.1	5646.6	2446.5	4711.0	5173.2	7616.5
AY266107.1	99043	49.4	58.8	38.1	64.0	57.9	34.4
AY266096.1	102829	4910.7	4316.6	7886.9	9456.1	10823.9	12607.6
AY266095.1	102674	8754.2	6737.4	8937.5	8386.2	10916.4	8857.9
AF400462.1	19222	4198.0	3828.8	3839.6	3771.9	3701.4	3245.7
DQ396070.1	154863	470.8	590.8	745.1	489.2	2066.6	502.7
EU799800.1	326262	9993.0	8532.5	10699.6	10794.0	14375.6	14857.7

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GU061920.1 gg_id:534100 and function microbial mesoscale eddy perturbations South China Sea clone S-5m-3
EU805404.1 gg_id:326883 It's all ranking aquatic 250 miles Panama City clone 6C233413
EF574040.1 gg_id:233586 site S25 near Coco's Island marine clone S25_384
GU230321.1 gg_id:561326 Multilevel approach along Rio de la Plata-South Atlantic Ocean coastal water clone A
EF573891.1 gg_id:239178 site S25 near Coco's Island marine clone S25_235
DQ300590.1 gg_id:145831 microbial ocean's interior amplicon single fosmid library pool 130m depth HOT static
EF572462.1 gg_id:232188 Coco's Island site 23 marine clone S23_561
EU799371.1 gg_id:355943 It's all ranking aquatic Newport Harbour RI clone 1C226958
FJ826408.1 gg_id:510568 Succession during spring diatom bloom Sea filtered surface sea water contrasting nor
AY458632.2 gg_id:101609 marine waters clone EBAC750-02H09
AY907736.1 gg_id:137300 identification picoplankton contrasting waters Arabian Sea water clone A313002
EU805263.1 gg_id:313140 It's all ranking aquatic 250 miles Panama City clone 6C233263
EU237284.1 gg_id:239425 Genes transcripts Eastern and Western Equatorial North Atlantic Ocean microbial as
GQ346911.1 gg_id:593801 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
EU799141.1 gg_id:344498 It's all ranking aquatic Newport Harbour RI clone 1C226706
EU800939.1 gg_id:313914 It's all ranking aquatic Delaware Bay NJ clone 2C229197
EU005838.1 gg_id:276035 Major activity inside and outside natural iron-fertilized phytoplankton bloom 3 micro
AY033317.1 gg_id:55020 marine bacterioplankton clone MB12G11
EF573454.1 gg_id:232533 Coco's Island site 23 marine clone S23_1553
GQ347847.1 gg_id:569985 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
GU061821.1 gg_id:542597 and function microbial mesoscale eddy perturbations South China Sea clone CEP-DC
EF574197.1 gg_id:232349 site S25 near Coco's Island marine clone S25_541
AY354844.1 gg_id:92279 coastal seawater during phytoplankton bloom clone PLY-P1-108
GQ349521.1 gg_id:545321 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
GU230325.1 gg_id:591130 Multilevel approach along Rio de la Plata-South Atlantic Ocean coastal water clone A
AF406526.1 gg_id:60646 bacterioplankton clone AEGEAN_234
EF574293.1 gg_id:233685 site S25 near Coco's Island marine clone S25_637
GQ337298.1 gg_id:593315 Hydrography shapes biogeography deep Arctic Ocean water depth 252m clone NB2
EU035854.2 gg_id:306650 Insight microbial structure Norwegian deep-water water deep-sea coral reef off Nor
DQ071078.1 gg_id:129984 marine surface water clone PB1.39
GU119483.1 gg_id:592804 Threatened Corals Provide Microbial Habitats reef water clone Reef_M13
DQ009457.1 gg_id:125125 bacterioplankton clone SPOTSMAY03_500m13
EU799709.1 gg_id:341723 It's all ranking aquatic Newport Harbour RI clone 1C227344
EF572084.1 gg_id:227627 Coco's Island site 23 marine clone S23_183
GU061923.1 gg_id:532750 and function microbial mesoscale eddy perturbations South China Sea clone S-5m-8
EU804090.1 gg_id:330520 It's all ranking aquatic 250 miles Panama City clone 6C231982
GQ348088.1 gg_id:572910 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
AF406528.1 gg_id:60645 bacterioplankton clone AEGEAN_146
DQ009141.1 gg_id:119608 bacterioplankton clone SPOTSAUG01_5m95
EU805314.1 gg_id:336262 It's all ranking aquatic 250 miles Panama City clone 6C233317

EU259803.1	240733	18410.2	14795.3	12083.2	12857.4	17305.3	14204.3
GU061920.1	534100	596.9	622.8	2061.4	175.2	3230.0	2436.2
EU805404.1	326883	6800.0	7698.1	8012.7	6418.7	6111.8	8984.9
EF574040.1	233586	4223.1	7366.6	4847.8	5979.9	4252.4	3733.0
GU230321.1	561326	4849.8	5333.9	5595.4	4622.6	7623.1	5674.7
EF573891.1	239178	6643.2	5133.0	3848.9	9302.3	7160.2	8854.7
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EU799371.1	355943	32.9	54.3	109.0	85.1	276.0	288.1
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AY907736.1	137300	10107.4	10278.1	4535.7	8174.0	11108.9	11874.7
EU805263.1	313140	955.8	1506.6	2217.7	2565.8	3660.1	2188.7
EU237284.1	239425	2318.8	3390.7	2440.9	2980.8	2483.9	1776.0
GQ346911.1	593801	4687.6	3759.8	5782.0	2370.5	6088.5	4291.7
EU799141.1	344498	3086.8	1888.9	3304.4	4578.8	2163.2	2553.6
EU800939.1	313914	13413.2	12336.5	10348.0	12699.8	15319.0	14309.6
EU005838.1	276035	11591.4	10326.1	4597.2	9076.5	6119.3	7142.5
AY033317.1	55020	511.2	1046.9	1571.2	866.8	1383.2	1023.3
EF573454.1	232533	54.9	98.8	65.4	85.3	421.0	132.6
GQ347847.1	569985	10285.6	7258.5	6725.3	9118.3	5182.8	6309.1
GU061821.1	542597	5643.4	12879.9	7366.5	9275.4	11232.9	9966.3
EF574197.1	232349	9463.0	12291.0	8107.8	8683.2	7561.0	10842.9
AY354844.1	92279	6246.2	6135.7	5892.3	6578.6	7669.3	9308.8
GQ349521.1	545321	7950.4	9380.3	7336.7	4991.3	10012.4	10357.9
GU230325.1	591130	4771.0	5534.6	7002.1	4654.5	8611.3	8063.4
AF406526.1	60646	3244.5	2865.5	4270.9	4389.0	3862.0	4155.4
EF574293.1	233685	8295.2	9606.6	9708.9	7555.1	9775.1	12779.4
GQ337298.1	593315	7459.6	8847.6	5406.4	7749.5	8626.8	8761.6
EU035854.2	306650	938.5	1011.3	1794.0	986.0	896.1	2340.8
DQ071078.1	129984	3937.0	2654.3	2044.0	3933.7	4246.6	3826.6
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DQ009457.1	125125	8618.0	8256.8	6908.9	7858.3	5898.0	5896.0
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EU804869.1 gg_id:344900 It's all ranking aquatic 250 miles Panama City clone 6C232836
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EF573802.1 gg_id:230375 site S25 near Coco's Island marine clone S25_146
EU802942.1 gg_id:323845 It's all ranking aquatic Northeast Colon Panama clone 4C230338
GQ346960.1 gg_id:593450 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
EU802824.1 gg_id:315563 It's all ranking aquatic Northeast Colon Panama clone 4C230203
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AF211861.1 gg_id:43878 Chromohalobacter canadensis str. DSM6769
X87220.1 gg_id:8130 Chromohalobacter marismortui str. -65
X87222.1 gg_id:8128 Chromohalobacter marismortui str. -492
EU122306.1 gg_id:243371 Chromohalobacter salexigens str. TPSV 101
DQ789389.1 gg_id:163006 Chromohalobacter salexigens str. NJ2
AM941743.1 gg_id:273506 Halomonas elongata str. ATCC 33173
EU652046.1 gg_id:276670 Chromohalobacter salexigens str. aa-27
X87221.1 gg_id:8127 Chromohalobacter marismortui str. -100
AY505516.1 gg_id:105302 Chromohalobacter marismortui str. GSP58
AJ277205.2 gg_id:27659 Chromohalobacter nigriandinum str. Taxon 4 4N
AB021386.1 gg_id:8126 Pseudomonas beijerinckii str. ATCC 19372T
AF211862.1 gg_id:43545 Chromohalobacter israelensis str. DSM6768
AJ295146.1 gg_id:48786 Halomonas elongata str. DSM 3043
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DQ375807.1 gg_id:153764 Chromohalobacter israelensis str. TVSP 101
X87219.1 gg_id:8125 Chromohalobacter marismortui str. ATCC 17056-T
AM110924.1 gg_id:140204 Bacillus subtilis B-1040
AM110925.1 gg_id:140613 Bacillus subtilis B-1042
EU652048.1 gg_id:276711 Halomonas salaria str. aa-29
DQ979342.1 gg_id:230168 Salinicola socius str. SMB35
DQ270747.1 gg_id:144625 Halomonas sp. B-1189
AM110928.1 gg_id:140457 Bacillus subtilis B-1064
DQ270696.1 gg_id:142624 Halomonas sp. B-3020
AJ427626.1 gg_id:42325 Chromohalobacter salinarum str. CG 4.1
DQ270679.1 gg_id:144129 Halomonas sp. B-1092
EU937754.1 gg_id:324906 Haererehalobacter sp. str. JG 11 Iti 10
DQ235564.1 gg_id:141553 biofilm water pipeline biofilms steel pipelines Gulf Mexico clone 6
EU175892.1 gg_id:261928 Drop-size lakes: transient microbial habitats soda lake on salt-secreting desert tree c
EF517969.1 gg_id:218181 Halomonas alimentaria str. 6YNAh

AACY01081767.1	103807	2897.5	3195.5	3000.1	4710.8	7174.5	4733.0
EF572959.1	228662	2159.5	1951.0	2828.7	544.4	4238.1	5147.2
EU804869.1	344900	3652.0	5119.6	3257.0	4303.1	4834.8	6158.2
EF572127.1	232511	677.9	461.1	280.2	745.4	1291.6	1483.8
EU804979.1	344649	42.1	33.3	41.0	79.6	69.9	15.2
EF573802.1	230375	12636.9	13263.3	4132.6	9353.7	15311.4	15030.8
EU802942.1	323845	66.4	205.7	2411.5	430.0	1373.3	797.6
GQ346960.1	593450	899.6	1365.7	71.6	1347.3	286.3	50.6
EU802824.1	315563	1948.4	1234.0	1267.1	3914.7	1018.5	1009.8
GU061819.1	535761	7898.1	9602.1	5417.3	5534.0	10202.3	7578.7
EF572665.1	231525	14090.0	13774.0	11643.1	11216.0	11527.7	13147.4
EU268074.1	252291	3337.6	4614.7	4967.8	4523.8	11403.5	12290.9
AF211861.1	43878	124.3	264.5	680.3	322.6	362.3	623.8
X87220.1	8130	2052.4	2869.2	4072.5	1855.0	4018.0	3028.6
X87222.1	8128	527.0	707.8	1432.5	530.4	1031.6	851.4
EU122306.1	243371	6430.7	7528.5	3812.5	3343.9	9550.6	6960.7
DQ789389.1	163006	7653.5	11941.3	5531.4	5841.9	5123.9	6773.2
AM941743.1	273506	2419.8	2424.7	3332.8	3044.0	9176.3	3109.2
EU652046.1	276670	3640.2	5192.2	4104.6	3529.2	5112.7	6636.1
X87221.1	8127	1155.8	1628.1	1869.6	312.2	1911.4	1761.5
AY505516.1	105302	2182.5	3656.7	4198.5	2392.4	3530.2	3168.7
AJ277205.2	27659	1823.7	2512.8	2867.2	2634.8	1250.6	1547.5
AB021386.1	8126	5440.6	7132.3	5263.2	3844.0	6495.1	2204.9
AF211862.1	43545	2415.8	3028.9	5023.7	2933.5	3657.9	4188.1
AJ295146.1	48786	2344.0	3897.6	5524.3	2670.2	5237.3	7699.5
AY373448.1	94374	1176.4	1800.5	2074.2	976.9	5247.6	3266.6
DQ375807.1	153764	1216.7	2019.9	2981.1	1711.5	3067.8	2102.1
X87219.1	8125	2138.1	3147.5	3317.7	3060.1	2899.2	3342.8
AM110924.1	140204	1684.0	1409.0	3333.1	1040.0	2605.1	1814.5
AM110925.1	140613	1381.2	1250.4	1355.3	1128.0	934.5	4570.8
EU652048.1	276711	5211.1	4677.2	4407.9	3959.8	7460.4	5311.4
DQ979342.1	230168	3158.0	2787.4	5454.5	2338.6	1029.8	3013.6
DQ270747.1	144625	5673.6	6616.2	4597.6	6788.2	7064.1	5536.3
AM110928.1	140457	897.9	1300.9	2337.7	2319.4	2892.1	2658.8
DQ270696.1	142624	2026.9	1731.7	1762.3	2942.4	1330.6	1807.5
AJ427626.1	42325	601.1	699.0	1512.3	985.9	612.9	1390.6
DQ270679.1	144129	1950.3	2088.1	1622.1	1326.9	3348.9	2481.8
EU937754.1	324906	3063.7	1362.6	2382.6	2262.4	1140.4	794.7
DQ235564.1	141553	306.3	575.1	460.3	214.3	1751.7	1696.9
EU175892.1	261928	2759.4	2798.3	6185.4	5344.9	1436.7	2688.3
EF517969.1	218181	4821.1	2957.0	3664.6	4560.9	4425.9	3169.5

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AY489405.1 gg_id:101840 Halomonas anticariensis str. FP35
AY245450.1 gg_id:81833 Halomonas boliviensis str. LC2
DQ077911.1 gg_id:160947 Halomonas campisalis str. LL6
X92137.1 gg_id:43696 Lake Magadi isolate 27M1
EF613111.1 gg_id:227593 Halomonas cerina str. 15CR
X67023.1 gg_id:8158 Halomonas elongata str. ATCC 33173
EU085034.1 gg_id:239476 Halomonas korla str. XK2
AJ320530.1 gg_id:70784 Halomonas muralis str. LMG 20969
AY962237.1 gg_id:115026 Halomonas sp. str. AIR-2
AM490137.1 gg_id:203039 Halomonas sp. str. IB-O7-1
E15669.1 gg_id:46054 Deleya sp. ASE1315
X92144.1 gg_id:42889 Lake Nakuru isolate 28N1
X92147.1 gg_id:44380 Lake Elmenteita isolate 35E2
DQ289066.1 gg_id:144891 Halomonas nitritophilus WST 3
DQ289069.1 gg_id:142310 Halomonas nitritophilus WST 6
DQ289070.1 gg_id:143579 Halomonas nitritophilus WST 7
X92146.1 gg_id:22591 Crater Lake isolate 75C4
X92417.1 gg_id:8131 Halomonas desiderata str. FB2
EF121854.1 gg_id:196601 Halomonas daqingensis str. DQD2-30T
X92149.1 gg_id:35481 Lake Nakuru isolate 19N1
L04942.1 gg_id:8170 Halomonas halodenitrificans
AY121436.1 gg_id:63144 Halomonas sp. str. YIM-kkny11
EF101990.1 gg_id:252290 Halomonas sp. EEZMo-14
EU135707.1 gg_id:242748 Halomonas sp. str. YIM C248
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DQ642806.1 gg_id:159766 Halomonas sp. 3
EU432570.1 gg_id:264242 Halomonas sp. str. 10112
EU218533.1 gg_id:239013 Halomonas ilicicola str. SP8
AJ564880.1 gg_id:100009 Halomonas alkantarctica str. CRSS
EF554912.1 gg_id:219933 Halomonas sp. str. G-AMM1
EU848479.1 gg_id:305095 Halomonas sp. str. SP1-3
AF539764.1 gg_id:86698 Halomonas sp. str. R21
AY204638.1 gg_id:81690 Halomonas variabilis str. HTG7
FJ978734.1 gg_id:466034 feces clone CL_F_436
EF421176.1 gg_id:277105 Halomonas sp. ZB-2007
DQ396289.1 gg_id:154439 deep-sea octacoral clone ctg_NISA091
CU914816.1 gg_id:402482 and dynamics adapted microbiota during degradation Tunisian zarzatine enriched se
EF533977.1 gg_id:267271 Halomonas sp. str. L24
EU652039.1 gg_id:274013 Halomonas taeheungii str. aa-1
EU735634.1 gg_id:337872 archaeal structures and pristine soils China oil contaminated soil Jidong Oilfield clone

AY856383.1	111155	2816.0	1974.9	2778.0	1832.8	1547.8	2180.3
AY489405.1	101840	306.6	928.9	483.7	162.9	780.4	1056.5
AY245450.1	81833	2058.5	1641.2	969.9	753.9	385.0	380.7
DQ077911.1	160947	579.9	430.1	604.1	579.1	2017.4	1787.8
X92137.1	43696	2346.1	3159.0	1136.6	1613.6	5979.6	3031.5
EF613111.1	227593	1991.1	3153.3	2567.2	1717.6	4044.2	3731.1
X67023.1	8158	8917.4	9611.3	5978.1	7505.4	11930.9	8491.3
EU085034.1	239476	300.3	371.3	1355.5	561.6	3614.6	2329.2
AJ320530.1	70784	3232.0	3286.5	4774.1	6174.2	1471.5	4012.7
AY962237.1	115026	1384.8	1018.9	2115.7	1579.7	3877.9	3167.4
AM490137.1	203039	1039.2	1080.1	1933.2	1793.2	1011.0	2660.5
E15669.1	46054	4353.8	5087.7	2962.6	1737.7	3655.7	4468.8
X92144.1	42889	1711.7	1515.8	1322.8	2740.9	1957.2	907.1
X92147.1	44380	11531.5	11218.4	8372.2	9037.7	11875.8	10135.6
DQ289066.1	144891	567.3	971.3	1200.6	672.6	3312.8	1750.0
DQ289069.1	142310	7053.5	6851.0	4330.7	6113.1	6352.0	6036.1
DQ289070.1	143579	2493.6	3594.1	2441.3	3177.1	3777.9	2504.5
X92146.1	22591	11811.7	11437.1	12201.5	9635.0	16325.2	14329.3
X92417.1	8131	2337.9	4113.3	4415.3	3462.6	2293.6	2965.9
EF121854.1	196601	1274.9	2272.7	2634.9	2527.2	1040.4	2237.9
X92149.1	35481	767.1	772.1	1319.0	545.1	821.0	681.4
L04942.1	8170	2781.4	3373.9	3632.2	2740.6	4602.1	6460.6
AY121436.1	63144	44.4	317.5	462.3	140.8	248.0	579.4
EF101990.1	252290	4331.5	4343.4	6598.8	4473.3	9739.6	9223.1
EU135707.1	242748	1965.0	1243.7	2797.5	1591.8	327.2	1134.2
EU308354.1	360286	7279.0	4413.3	5872.7	6354.4	8931.7	7432.5
DQ642806.1	159766	4230.1	3205.2	2540.9	2816.3	1772.3	1797.4
EU432570.1	264242	1208.9	1309.0	2400.8	1137.5	4699.9	4277.3
EU218533.1	239013	491.9	535.5	1480.7	868.6	2817.8	2862.4
AJ564880.1	100009	4293.7	2853.8	5959.8	3424.6	2107.8	3404.1
EF554912.1	219933	9463.3	6650.1	5081.5	10836.3	9983.7	12021.7
EU848479.1	305095	4018.7	4115.8	2714.6	3816.5	3079.2	2187.2
AF539764.1	86698	4862.6	6107.4	4789.4	4327.0	2394.6	3696.4
AY204638.1	81690	325.6	470.1	677.4	178.0	126.7	213.8
FJ978734.1	466034	6079.9	1994.7	3517.0	7254.3	3339.2	1598.3
EF421176.1	277105	520.7	388.8	1185.0	731.8	2035.5	2314.4
DQ396289.1	154439	1524.9	1546.2	1392.5	2839.4	1419.4	2816.0
CU914816.1	402482	2412.1	2979.1	3065.7	5114.6	920.4	1495.9
EF533977.1	267271	2867.6	2348.4	3619.4	4478.3	2730.2	5206.6
EU652039.1	274013	2857.5	1897.6	3521.2	2014.3	2501.3	1764.6
EU735634.1	337872	48.1	77.8	98.6	84.0	170.9	249.8

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