FJ873368.1 gg_id:544213 Vertical and archaea methane-rich cold seep located base sediments Okhotsk Sea clo FJ8733
DQ906885.1 gg_id:241976 Oman subsurface soil clone 11B-13 DQ906
AJ347034.1 gg_id:104678 sponge clone TK13 AJ3470
AF026987.1 gg_id:10763 hot spring clone OPB33 AF0269
EU700154.1 gg_id:294756 Study on Shantou Bay Marine Sediments Microorganisms sediment clone STU12 EU7001
EF442978.1 gg_id:257733 Desulforhabdus sp. str. DDT EF4429
EU542438.1 gg_id:262663 Effects chemical structure concentration on pathways microbial during dechlorinatio EU5424
DQ984662.1 gg_id:242560 Anaerobic degradation unsaturated or saturated long chain fatty acids (LCFA) prese DQ984
GQ487978.1 gg_id:542670 Microbial metal soil polluted heavy metals clone G19-236 GQ487
X83274.1 gg_id:10759 Desulforhabdus amnigena str. ASRB1 X83274
AJ237605.1 gg_id:10754 Syntrophobacter sp str. TsuA1 AJ2376
AM176868.1 gg_id:160457 Recovery mangrove sediment clone SZB17 AM176
GU180163.1 gg_id:578505 Impact coplanar PCBs on microbial activity anaerobic estuarine sediments sediment GU180
DQ303457.1 gg_id:151758 Desulfoglaeba alkanexedens str. ALDC DQ303
DQ676446.1 gg_id:219894 Archaeal and plankton freshwater pond suboxic freshwater-pond sediment clone M DQ676
FN646458.1 gg_id:591519 candidate division OP3 cells limonene Limonene degrading methanogenic s clone Li FN6464
GU208388.1 gg_id:587929 Study on Sediment Dongping Lake sediment clone Td2-21 GU208
AJ306776.1 gg_id:66924 DCP-dechlorinating consortium clone SHA-117 AJ3067
AM176858.1 gg_id:161119 Recovery mangrove sediment clone SZB9 AM176
GQ402743.1 gg_id:543482 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
CU919420.1 gg_id:538867 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU9194
AY297973.1 gg_id:89577 thermophilic anaerobic terephthalate-degrading sludge clone TTA_B25 AY2979
CT573926.1 gg_id:153737 Evry municipal wastewater treatment plant clone 012B11_B_SD_P15 CT5739
AB091329.1 gg_id:60011 UASB granular sludge clone UI AB0913
AF229787.1 gg_id:29387 terephthalate-degrading consortium clone TA14 AF2297
CT573826.1 gg_id:152222 Evry municipal wastewater treatment plant clone 013H09_B_SD_P15 CT5738
EU542505.1 gg_id:275595 Effects chemical structure concentration on pathways microbial during dechlorinatio EU5425
EU399669.1 gg_id:262088 and localization microbial consortium full-scale granular activated carbon anaerobic EU3996
EU399678.1 gg_id:275018 and localization microbial consortium full-scale granular activated carbon anaerobic EU3996
AJ009465.1 gg_id:10718 TCB-transforming consortium clone SJA-51 AJ0094
EF198029.1 gg_id:180225 Microbial structures and thermophilic methanogenic consortia anaerobic mesophilic EF1980
AF523969.1 gg_id:63254 forested wetland clone FW121 AF5239
EU399661.1 gg_id:263368 and localization microbial consortium full-scale granular activated carbon anaerobic EU3996
EU399675.1 gg_id:265878 and localization microbial consortium full-scale granular activated carbon anaerobic EU3996
GQ844327.1 gg_id:569150 Microbial full-scale produced water treatment plant biofilm anoxic tank clone BB-B2 GQ844
CT573958.1 gg_id:151218 Evry municipal wastewater treatment plant clone 009F06_B_SD_P15 CT5739
CT574144.1 gg_id:156077 Evry municipal wastewater treatment plant clone 060H12_B_SD_P93 CT5741
CT574201.1 gg_id:151230 Evry municipal wastewater treatment plant clone 060B01_B_SD_P93 CT5742
GU208245.1 gg_id:541892 Study on Sediment Dongping Lake sediment clone 6B1-7 GU208
CT574119.1 gg_id:152546 Evry municipal wastewater treatment plant clone 061D06_B_SD_P93 CT5741
AY862530.1 gg_id:109749 rice slurry clone TPD-48 AY8625

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512.1	3482.1	3973.8	4123.8	3957.7	3727.7	5036.3	3308.3	1336.2	979.9	2522.6
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43.8	225.9	310.3	299.6	251.9	63.0	409.3	92.4	64.4	24.6	106.4
41.5	29.6	36.2	28.0	30.3	29.3	58.3	18.9	20.6	13.1	25.6
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4430.4	1286.0	963.9	1342.7	2218.4	1253.1	1826.7	1687.7	726.1	614.3	1070.8
44.6	95.1	173.6	128.5	119.7	153.0	173.2	135.7	64.1	39.9	69.7
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4697.5	854.7	840.4	998.7	854.7	751.8	1043.4	672.8	1037.3	930.3	813.2
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789.6	1222.1	1090.9	1113.1	1214.3	1097.3	1575.8	1509.4	855.9	580.6	1185.0
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3118.4	5068.6	7435.3
4299.8	3782.4	4299.8
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993.8	840.7	1953.2
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1192.9	1353.9	2038.3
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19.6	17.0	31.0
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709.9	1464.5	1229.7
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5114.3	6446.3	6532.4
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DQ513073.1 gg_id:160937 Microbial life fluids ridge flank crustal fluid clone FS266-12B-03 DQ513
DQ396250.1 gg_id:151404 deep-sea octacoral clone ctg_NISA104 DQ396
GQ348270.1 gg_id:546068 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ348
GQ348264.1 gg_id:590521 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ348
GQ349049.1 gg_id:566231 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ349
GQ348844.1 gg_id:541085 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ348
GQ348190.1 gg_id:583411 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ348
GQ351086.1 gg_id:590469 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ351
GQ337095.1 gg_id:560221 Hydrography shapes biogeography deep Arctic Ocean water depth 1000m clone BB(GQ337
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GQ348641.1 gg_id:571912 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ348
FJ545636.1 gg_id:559552 Diveristy Seawater and Sediment Northern North Yel Sea seawater clone W2-63 FJ5456
GQ337087.1 gg_id:572986 Hydrography shapes biogeography deep Arctic Ocean water depth 1191m clone NB: GQ337
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DQ501327.1 gg_id:198258 Seasonal dynamics free-living and particle- four lakes northeastern Germany freshw DQ501
EU050847.1 gg_id:237789 libraries sediment Kings Bay Svalbard Arctic clone ss1_B_03_45 EU050
EU487900.1 gg_id:574097 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU487
EU491765.1 gg_id:261919 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU491
EF573310.1 gg_id:233830 Coco's Island site 23 marine clone S23_1409 EF5733
FJ155019.1 gg_id:330963 seasonal fluctuation coastal Bohai Bay sequencing and RFLP ocean water clone BX FJ1550
GQ348578.1 gg_id:576386 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ348
AF371949.1 gg_id:23625 swine intestine clone p-4193-6Wa5 AF371
FJ484808.1 gg_id:509157 microbial autonomous rover world's deepest phreatic sinkhole wall biomat El Zacator FJ4848
EU220836.1 gg_id:274794 Spirobacillus cienkowskii EU220
GQ337121.1 gg_id:577297 Hydrography shapes biogeography deep Arctic Ocean water depth 395m clone CB0 GQ337
CU466767.1 gg_id:336493 Evry wastewater treatment plant anoxic basin clone CU466
GU061838.1 gg_id:578641 and function microbial mesoscale eddy perturbations South China Sea clone CEP-DC GU061
U70713.1 gg_id:4709 Cape Hatteras picoplankton clone OM27 U7071
FJ203134.1 gg_id:355193 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c FJ2031
EF574353.1 gg_id:234197 site S25 near Coco's Island marine clone S25_697 EF5743
EU101270.1 gg_id:257793 Sulfide/oxygen supply ratio predicts outcome competition among sulfur-oxidizing wa EU101
DQ330714.1 gg_id:159120 Guerrero Negro hypersaline microbial mat clone 01D1q147 DQ330
EU491257.1 gg_id:269593 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak EU491
DQ395799.1 gg_id:155720 deep-sea octacoral clone ctg_CGOF235 DQ395
EU925894.1 gg_id:346201 sediments sediment station DBS1 northern Bering Sea clone 115G73 EU925
GQ263929.1 gg_id:513958 Structure Simulated Level Waste Site simulated level waste site clone WC2_181 GQ263

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3013.5	5529.2	5657.0	6146.9	8097.5	5636.9	7954.2	5341.8	6156.5	4366.5	5844.5
9101.3	7632.6	6454.5	6779.7	5457.5	6754.5	5648.2	7248.1	7016.1	5757.0	9351.0
60.0	219.7	334.5	206.0	217.4	230.5	666.4	232.0	76.4	56.7	216.8
19802.5	6788.1	6276.4	6201.8	7451.2	6562.9	7527.6	5593.9	9510.8	6680.8	8430.6
10336.5	4333.8	3602.9	5681.9	4042.3	4058.8	6367.6	4908.4	5165.6	6283.7	5482.8
1144.7	3242.1	2928.9	2739.9	5906.3	3930.8	3491.0	3352.4	3273.1	1939.3	2975.8
2888.7	3208.6	3053.5	2804.6	2894.6	2747.1	2947.9	2601.0	4014.7	3394.8	4515.9
49.1	570.1	732.2	785.0	700.3	454.2	342.0	671.1	187.5	111.9	543.1
4797.1	7049.3	7353.5	7930.0	8424.1	7523.3	9459.3	7743.9	6533.1	5906.4	7772.2
448.7	4471.9	5841.4	6791.5	6417.6	5454.1	8597.4	6244.7	2989.2	2861.1	5602.8
45.6	821.7	682.7	1015.3	924.0	602.1	671.4	962.0	864.7	177.3	613.4
50.3	2152.9	1950.6	2671.6	3068.6	1834.0	3148.4	1933.3	1065.1	1919.2	1086.5
8248.6	7456.7	7073.8	7659.0	8364.5	7162.3	8396.7	7033.5	6978.3	7621.5	6832.7
386.7	3524.3	3405.8	3920.2	3670.2	3317.4	4297.0	4195.9	2366.2	2099.2	2409.8
4997.3	8631.1	8012.4	7337.5	7319.7	7548.8	7712.0	7194.9	9403.5	9248.3	7526.0
37.5	32.2	45.6	46.9	59.7	34.9	50.6	27.9	27.5	26.3	26.8
186.0	1180.4	1883.5	1882.9	1979.2	1713.3	2121.8	2171.1	865.6	843.3	738.0
424.7	1699.0	2197.1	2207.9	2011.8	1935.3	2856.8	2304.7	1718.5	731.9	1654.0
116.9	2390.2	2738.0	2928.1	3490.0	2491.3	4501.6	2740.3	1479.1	636.2	1854.8
119.9	1436.5	1906.9	2558.0	1210.2	1333.1	2217.5	1422.6	726.6	216.7	846.9
1074.1	3513.9	6055.7	7866.0	2921.7	3419.0	3155.1	4752.2	3724.7	1671.8	3735.9
91.3	55.7	42.5	77.3	52.0	49.7	59.5	45.1	47.9	40.1	50.6
320.6	5290.6	6002.1	6439.2	6016.9	5581.5	7793.8	6106.5	2490.9	2466.0	4281.6
244.9	1438.5	2084.4	1856.2	1615.2	2026.6	1624.3	2615.2	2004.2	669.9	1137.4
291.1	150.6	243.2	217.1	248.6	179.1	319.7	269.5	61.8	54.0	116.9
721.4	3899.0	4875.6	4931.1	5641.1	3978.6	5981.4	4545.5	2771.5	2399.2	4208.3
205.4	1610.7	1541.1	1546.0	1771.7	1851.4	2193.3	1944.8	876.4	545.7	1219.6
3048.4	6409.3	5844.9	5722.8	5969.6	6514.3	5926.7	6005.9	8220.0	4689.0	4825.9
858.5	3562.4	4353.0	4753.9	5364.6	4090.1	6626.9	4967.5	3039.5	1407.7	3444.8
6183.2	10335.2	9809.9	10699.1	14073.8	10364.1	12871.6	9718.2	8708.9	8422.6	8390.2
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728.4	3949.1	4788.3	4935.2	5502.0	4175.0	6665.7	4473.7	3391.0	1682.3	3604.3
80.0	2924.8	3916.6	4335.8	5030.2	4242.9	5388.8	3275.2	1212.4	558.0	2132.6

8770.0	9748.3	10291.5
6337.2	8105.1	6435.9
6594.5	5999.7	4894.6
5537.1	6618.9	6990.2
8670.3	9940.9	10438.6
8010.7	9063.8	9553.0
3497.4	4965.7	4252.6
7008.1	8360.4	8437.1
5842.1	5826.4	6323.9
5807.3	6210.0	7488.0
359.2	619.1	249.3
5636.7	7716.2	6414.7
4360.6	5499.9	5534.0
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2770.6	3109.3	2613.1
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6280.7	5113.8	6752.4
796.1	565.1	1064.4
1849.8	1876.0	2180.8
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3468.4	4744.0	4614.0
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2409.3	2730.3	3946.3
1059.7	1045.5	1482.1
6664.9	3796.4	4158.4
48.5	57.1	69.9
4852.5	5703.8	7765.8
3380.4	2575.7	2397.0
296.5	251.9	268.3
4367.6	3754.2	4842.8
1807.5	1972.9	2107.8
5612.9	6220.8	5976.2
4792.2	4818.4	5891.2
10353.8	9685.2	10426.3
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EF125414.1 gg_id:190843 soil naked tidal flat sediment near mangrove clone MSB-1F12 EF1254
FJ902004.1 gg_id:573340 phreatic limestone sinkholes northeastern Mexico biomat sediment cenote La Palita (FJ9020
FJ484648.1 gg_id:572347 microbial autonomous rover world's deepest phreatic sinkhole wall biomat El Zacator FJ4846
GQ472419.1 gg_id:547121 Microbial Dongping Lake lake sediment clone 4F2-23 GQ472
AB238778.1 gg_id:147775 shal subsurface Sarobetsu Mire peat soil clone HSM-SS-015 AB238
AM086107.1 gg_id:149503 Abundance and archaea mesotrophic Lake Kinneret lake profundal sediment clone (AM086
AJ519663.1 gg_id:76094 uranium mill tailings soil sample clone GuBH2-AD/TzT-67 proteobacterium AJ5196
FJ716435.1 gg_id:509967 Uncultivated archaea sulfate-reducing biofilm Frasassi cave system anoxic lake water FJ7164
EF590018.2 gg_id:231749 changes structure sediments Songhua River contaminated nitrobenzene -DGGE cloni EF590
FJ484742.1 gg_id:534747 microbial autonomous rover world's deepest phreatic sinkhole wall biomat El Zacator FJ4847
AB300111.1 gg_id:219858 Wide ancient microbial DNAs Quaternary sediments holocene mud sediment clone K AB300
EU589306.1 gg_id:265934 China Ningxia rice paddy field soil clone 2_E4 EU589
FJ902299.1 gg_id:575054 phreatic limestone sinkholes northeastern Mexico biomat rock outcrop cenote La Pal FJ9022
FJ484802.1 gg_id:537592 microbial autonomous rover world's deepest phreatic sinkhole wall biomat El Zacator FJ4848
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AM934934.1 gg_id:549065 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM934
DQ067029.1 gg_id:129752 Lake Washington sediment clone pLW-45 DQ067
FJ538146.1 gg_id:566857 metagenomics study rice treated milk vetch and no-tillage paddy field soil clone MBN FJ5381
EU335163.1 gg_id:239473 Changes microbial metabolic and along hydrogeochemically variable profile saturate EU335
CU922370.1 gg_id:552630 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU922
GU180168.1 gg_id:590108 Impact coplanar PCBs on microbial activity anaerobic estuarine sediments sediment GU180
CU918113.1 gg_id:567976 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU918
CU921396.1 gg_id:561911 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU921
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CU921615.1 gg_id:549289 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU921
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EF574365.1 gg_id:228280 site S25 near Coco's Island marine clone S25_709 EF5743
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EF573912.1 gg_id:228667 site S25 near Coco's Island marine clone S25_256 EF5739
EU592442.1 gg_id:537106 Seasonal changes Salton Sea hypersaline sediment clone SSS66N EU5924
EU592440.1 gg_id:589629 Seasonal changes Salton Sea hypersaline sediment clone SSS64N EU5924
EU488121.1 gg_id:560324 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU488
EU488297.1 gg_id:556385 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU488
DQ463694.2 gg_id:165464 distinct Lake Tanganyika anoxic hypolimnion clone TK-SH10 DQ463
DQ394901.1 gg_id:156343 harbor sediment clone VHS-B1-26 DQ394
GQ261790.1 gg_id:544072 shifts taxa and response localized organic loading deep sea sediment whale falls clo GQ261

72.8	111.9	162.1	195.0	300.2	127.5	259.3	151.4	71.7	53.2	72.0
392.9	3206.6	3790.4	4163.2	4575.1	3655.0	5274.7	4038.6	2754.0	2185.8	3560.2
1520.6	5486.3	6273.5	6624.1	6228.5	6162.4	7293.6	5631.7	3453.8	2687.1	4961.8
14029.0	7336.2	7230.1	8082.1	8439.6	7663.9	9177.9	6741.4	5358.2	4334.5	6834.0
9134.1	3045.4	3732.5	3507.6	3695.1	4219.6	3533.8	3233.4	3296.3	2574.6	3694.7
10269.2	6490.0	6110.3	6867.4	6374.4	6495.9	6875.1	6340.2	8764.5	5798.0	7971.6
46.9	66.6	173.9	166.6	90.2	102.0	101.6	302.3	36.8	27.5	133.0
2201.1	1439.0	1502.7	2154.4	1891.2	1400.5	2823.6	1583.2	2274.5	533.7	904.6
265.2	2099.4	2446.2	1960.3	2123.6	1961.6	2918.9	1982.7	733.0	1853.4	1128.1
1079.7	3281.7	4382.0	4349.6	5195.2	3949.6	5242.7	5256.4	2906.5	1338.7	4228.6
58.0	99.6	110.5	162.8	78.5	157.9	77.0	55.1	35.2	36.2	76.0
1391.1	4433.7	4558.4	5014.8	4740.5	4314.0	5142.6	4237.7	2925.1	1388.4	3481.6
3035.2	4035.2	5528.4	5339.4	5924.1	4736.1	6639.8	4865.1	2957.8	2404.7	3431.3
6031.8	4300.4	4599.0	4421.0	3548.3	3442.0	4397.3	3843.9	3978.2	3734.1	5189.4
118.2	1650.1	1834.7	2146.8	1357.1	1703.2	2293.3	1927.8	472.1	212.4	1178.9
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47.4	982.2	1370.4	1625.2	992.6	896.4	1397.3	989.0	380.1	99.6	606.1
1980.7	2826.9	3575.6	4583.2	4527.3	3005.2	4431.3	3080.7	1287.5	869.6	1775.7
21928.3	11343.2	8993.4	9621.1	9445.2	8699.0	9928.6	8010.6	11317.2	7980.5	11503.5
17576.6	6688.8	7373.6	9251.5	6231.8	6034.9	6316.3	6490.4	7479.4	5866.5	7529.5
57.6	471.5	1277.1	2559.5	405.8	498.3	379.6	593.8	197.3	276.1	215.1
1325.3	7323.4	7287.7	9338.0	10497.2	7606.6	9795.9	7249.1	4997.4	2399.3	5700.4
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123.6	1139.1	1299.9	1397.6	1024.8	1341.1	1061.7	1968.4	763.7	2772.6	814.4
850.5	3941.3	3820.2	3779.3	3871.0	3708.5	4093.8	4518.8	3708.4	3687.8	3437.7
3751.6	2567.7	2552.5	2825.7	2256.7	2773.8	2698.3	2911.7	2560.6	5065.1	2360.5
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317.9	1516.6	1794.6	1927.3	2063.7	1745.9	1700.7	1949.9	1667.8	1394.2	1248.3
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604.7	4522.1	3581.3	3294.3	3179.1	4346.2	3153.4	4086.1	2380.0	1751.6	2098.0
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5521.3	7760.1	5762.9
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9461.7	8824.6	8836.6
5818.2	6515.8	6844.4
338.2	377.6	786.6
6275.5	7673.7	11142.6
7045.0	7724.8	9771.5
4320.7	4433.0	6005.7
5890.5	5957.3	6353.7
3274.2	3993.1	4982.0
5823.5	5187.9	7661.2
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4362.4	5590.8	5093.9
1489.3	1803.0	1259.5
3791.0	4173.7	4604.5
2521.0	2894.0	3819.5
6786.3	7515.8	8252.2
1860.5	1615.3	2548.9
12228.2	12155.4	13925.3
3468.9	3683.2	4754.9
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53.7	61.1	61.3
1967.4	2366.6	5446.1

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DQ394969.1 gg_id:151807 harbor sediment clone VHS-B3-88 DQ394
AB100007.1 gg_id:79461 inactive deep-sea hydrothermal vent chimneys clone IndB3-24 AB100
DQ811792.1 gg_id:167519 mangrove soil clone MSB-3A9 DQ811
EF520534.1 gg_id:232980 structure lakes: what controls ? acid-impacted lake clone ADK-BTe02-06 EF5205
EU861868.1 gg_id:343349 effects chronic fertilization on alpine tundra microbial implications carbon and nitrog EU8618
EU803844.1 gg_id:337066 It's all ranking aquatic Lake Gatun clone 5C231481 EU8038
DQ451526.1 gg_id:156878 forest soil clone FAC87 DQ451
DQ811827.1 gg_id:170103 mangrove soil clone MSB-5C4 DQ811
EF208655.1 gg_id:202296 Vertical and horizontal structure microbial sandy carbonate sediment clone CI35cm.2 EF2086
EF125419.1 gg_id:199002 soil naked tidal flat sediment near mangrove clone MSB-1F8 EF1254
EU491252.1 gg_id:276800 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak EU4912
DQ925889.1 gg_id:255773 Microbes and Thermal Gradients Temperature Hydrothermal Chimneys hydrotherm DQ925
EU050850.1 gg_id:238559 libraries sediment Kings Bay Svalbard Arctic clone ss1_B_09_96 EU0508
FJ535320.1 gg_id:536335 within iron-containing flocculent mats submarine volcanoes along Kermadec Arc sedi FJ5353
AM712338.1 gg_id:255844 detection and ly microbial Brothers Seamount Kermadec Arc New Zealand biofilm h AM712
AF420341.2 gg_id:67796 hydrothermal sediment clone AF420341 AF4203
AJ441235.1 gg_id:57453 hydrothermal vent polychaete mucous clone P. palm A 205 AJ4412
AF420340.1 gg_id:67797 hydrothermal sediment clone AF420340 AF4203
FJ712464.1 gg_id:517432 and Archaea Gas Hydrate Sediments (East Sea) Kazan Mud Volcano Anaximander Mo FJ7124
DQ017948.1 gg_id:136786 upland stream clone S-Btb7_40 DQ017
EU134544.1 gg_id:253026 tallgrass prarie soil clone FFCH2390 EU1345
FJ592579.1 gg_id:509119 Fumarole-supported islands biodiversity within hyperarid -elevation landscape on Pu FJ5925
EF573992.1 gg_id:230171 site S25 near Coco's Island marine clone S25_336 EF5739
EF574948.1 gg_id:230813 site S25 near Coco's Island marine clone S25_1292 EF5749
GQ347789.1 gg_id:541766 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ347
EU048624.1 gg_id:236563 Microbial surface marine sediment Xisha Trough South China Sea clone MD2902-B18 EU0486
EU386045.1 gg_id:274122 Biogeographical and microbes sediments on subseafloor sediment South China Sea c EU3860
EU373913.1 gg_id:275503 southern Cretan margin (eastern Mediterranean Sea) canyon and slope sediment cl EU3739
FJ745210.1 gg_id:570846 Transporter genes expressed coastal response dissolved organic carbon surface wate FJ7452
GQ346753.1 gg_id:568507 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ346
EU134378.1 gg_id:256515 tallgrass prarie soil clone FFCH5621 EU1343
AB486345.1 gg_id:559850 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC AB4863
DQ267495.1 gg_id:149878 Metagenomic group plankton 500m depth mesopelagic Antarctic waters clone DQ267
EF574148.1 gg_id:230908 site S25 near Coco's Island marine clone S25_492 EF5741
DQ154849.1 gg_id:139171 Diel Migration Restructures Hypersaline Microbial Mat hypersaline microbial mat cl DQ154
FJ485412.1 gg_id:558030 microbial autonomous rover world's deepest phreatic sinkhole wall biomat El Zacator FJ4854
AJ241001.1 gg_id:10681 Norway:(Svalbard)Hornsund clone Sva0485 AJ2410
AM882628.1 gg_id:350620 Structure along hydrocarbon contamination coastal sediment oil polluted water pet AM882
EF632708.1 gg_id:256201 Unique microbial contrasting aquatic altitude Andean Altiplano (northern Chile) wate EF6327
DQ103652.1 gg_id:131834 hypersaline endoevaporitic microbial mat clone E6aH12 DQ103
AM040101.1 gg_id:149432 sandy sediments clone Sylt 5 AM040

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35.0	62.6	161.2	136.3	127.8	52.9	171.7	53.8	28.6	24.3	46.8
37.3	974.8	1551.0	1798.5	1050.2	1379.5	2581.0	869.2	238.4	83.4	920.2
35.0	102.6	167.8	147.4	248.4	131.8	200.2	108.8	64.1	40.0	73.7
133.3	1557.0	2335.8	2104.9	2917.1	2109.9	2881.7	2584.0	1337.3	307.1	1264.0
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14100.2	4435.7	5658.1	5732.4	4004.4	4653.0	4706.9	5088.2	5249.6	7705.2	5808.3
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465.7	4441.6	4634.4	5219.0	4888.7	4603.4	5512.7	5293.0	3538.9	2819.8	4143.7
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420.7	4041.6	4341.5	4625.2	4512.4	3721.7	4750.5	3871.1	2730.4	1967.2	2793.3
397.8	5426.5	5761.3	6163.6	6382.1	5005.8	7207.4	5342.7	3713.4	5286.3	5033.0
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84.7	1138.2	1357.3	2536.2	2029.6	1221.1	1909.6	2336.8	544.7	1091.1	835.5
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FJ717005.1 gg_id:553766 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United Kingc FJ7170
AF382143.1 gg_id:79548 bacterioplankton clone ZA3735c AF382
GQ337096.1 gg_id:548348 Hydrography shapes biogeography deep Arctic Ocean water depth 1000m clone BB(GQ337
FM242399.1 gg_id:328281 sequences sediment clone 86 T12d-oil FM242
EU735646.1 gg_id:322881 archaeal structures and pristine soils China oil contaminated soil Jidong Oilfield clone EU735
EU734937.1 gg_id:327296 assemblages sediment station DBSE Northern Bering Sea clone 028C19 EU734
AY375082.1 gg_id:98535 deep sea sediment clone B109 AY375
AJ240985.1 gg_id:10661 Norway:(Svalbard)Hornsund clone Sva0853 AJ2409
AM882631.1 gg_id:306845 Structure along hydrocarbon contamination coastal sediment oil polluted water pet AM882
DQ464344.1 gg_id:157072 Arcobacter skirrowii str. 449/80 DQ464
AY314755.1 gg_id:105549 Arcobacter cryaerophilus CCUG 17802 AY314
EU106662.1 gg_id:260782 Arcobacter nitrofigilis str. F2176 EU106
FJ203148.1 gg_id:334326 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c FJ2031
AB262383.1 gg_id:161324 Microbial Ishigaki-jima Island Japan sea water Ishigaki Port clone IG-1-21 AB2623
AB262379.1 gg_id:160905 Microbial Ishigaki-jima Island Japan sea water Ishigaki Port clone IG-1-16 AB2623
AY922188.1 gg_id:113246 whalefall clone 131599 AY9221
GQ348908.1 gg_id:558608 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ348
FJ497477.1 gg_id:589078 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun FJ4974
AF513455.1 gg_id:60384 Arcobacter sp. str. LA31B AF5134
DQ071284.1 gg_id:139697 dominate filamentous sulfur mat 13 degree north field East Pacific Rise deep-sea hy(DQ071
AF314538.1 gg_id:36386 Arcobacter butzleri oN_107_00 AF3145
AB013832.1 gg_id:11163 NB1-k clone NB1-k AB0138
EU052247.1 gg_id:248438 degradation kinetics and current efficiency cells supplied anode microbial fuel cell fe(EU052
FJ202344.1 gg_id:314840 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2023
EF648116.1 gg_id:251292 dynamics during produced water treatment aerobic activated sludge clone XJ22 EF6481
AY225610.1 gg_id:96366 pumice fragments exposed to Mid-Atlantic Ridge vent clone AT-pp13 AY2256
GU061286.1 gg_id:546186 Evaluation culturing methods cultivate previously Yel Sea intertidal beach seawater GU061
AJ607391.1 gg_id:102614 Arcobacter cibarius str. LMG 21996 AJ6073
EF515495.1 gg_id:222170 Electricigen Enrichment MFC full-scale anaerobic bioreactor sludge treating brewery EF5154
AY922205.1 gg_id:113754 whalefall clone 131644 AY9222
FJ202783.1 gg_id:349369 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2027
FJ403064.1 gg_id:357886 Disease- changes healthy and diseased colonies Caribbean coral Montastrea faveolat FJ4030
EF123613.1 gg_id:239833 Microbial disease microbial mats on Siderastrea siderea three regions wider Caribbea EF1236
AJ271654.1 gg_id:51975 Arcobacter sp. D1a1 AJ2716
AM084124.1 gg_id:140216 Arcobacter sp. str. R-28214 AM084
AY570641.1 gg_id:108516 biodegraded Canadian oil reservoir clone PL-8D4 AY5706
FN429802.1 gg_id:534177 Biogeochemistry -activity cold seep Larsen B area western Weddell Sea Antarctica m FN4298
FJ202326.1 gg_id:315205 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2023
DQ917897.1 gg_id:227146 Microbial profiles bleached and wild-type Muricea elongata Arcobacter clone ME15 DQ917
AY035822.1 gg_id:70950 enriched coastal seawater overlying anoxic marine sediment sulfidicus AY0358
EU050947.1 gg_id:255076 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_02_37 EU0509

2566.2	3442.1	3784.5	3669.7	5868.4	4004.1	5863.9	3769.6	3080.5	1792.6	2650.6
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2672.1	12032.0	14495.4	12271.8	5708.7	11209.0	7317.9	11059.6	6814.8	3513.4	16323.0
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9362.5	11177.2	9440.2
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DQ357825.1 gg_id:150082 Marine Hatchery: Balance Between Pathogenic and Potentially Probiotic Strains adu DQ357
DQ676433.1 gg_id:224791 Archaeal sediment and plankton freshwater pond suboxic freshwater-pond clone M DQ676
AB030594.1 gg_id:50542 groundwater clone 1021 AB0305
EU265967.1 gg_id:567689 transition and zone within near-shore anoxic basin: Nitinat Lake depth 50 m clone Ni EU2659
FJ660508.1 gg_id:561979 Correlation functional stability and dynamics full-scale wastewater treatment plant a FJ6605
EF688595.1 gg_id:284348 Biogeochemistry iron- and sulfur-precipitating microbial mats (Nile Mediterranean) s EF6885
GU061298.1 gg_id:560130 Evaluation culturing methods cultivate previously Yel Sea intertidal beach seawater GU061
FJ717168.1 gg_id:571505 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United King FJ7171
AY621116.1 gg_id:106004 Arcobacter butzleri str. ATCC 49616 AY6211
EF031092.1 gg_id:186810 Prokaryotic Tirez La Macha Spain endorheic hypersaline atalasohaline lake clone SalB EF0310
AY697901.1 gg_id:105639 Antarctica clone F3C43 AY6979
AB234539.1 gg_id:149689 termite gut homogenate clone MgMjD-024 AB2345
FJ203095.1 gg_id:346863 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c FJ2030
AB262386.1 gg_id:159735 Microbial Ishigaki-jima Island Japan sea water Ishigaki Port clone IG-1-27 AB2623
EU236320.1 gg_id:292623 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg1bF7 EU2363
AB015259.1 gg_id:11183 deepest cold-seep area Japan Trench clone JTB360 proteobacterium AB0152
AJ810558.1 gg_id:105006 superficial sediments clone AJ8105
DQ464340.1 gg_id:158050 Arcobacter butzleri str. 520H-2004 DQ464
GQ340204.1 gg_id:583784 Prokaryotic Marathonas Reservoir Greece water column clone VE07-08-BAC GQ340
AB013833.1 gg_id:11181 NB1-l clone NB1-l AB0138
GQ349268.1 gg_id:581309 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ349
EU781617.1 gg_id:322902 Bacteroides ureolyticus 4 EU7816
GQ167663.1 gg_id:581365 Campylobacter concisus str. ATCC 51561 GQ167
EU869312.1 gg_id:334581 Campylobacter cuniculorum str. 119/07 EU8693
NC_009715.1 gg_id:242986 Campylobacter curvus str. 525.92 NC_009
AY621301.1 gg_id:103129 Campylobacter fetus str. 23D AY6213
AF219233.1 gg_id:69901 Campylobacter fetus MGH 97-2126 AF2192
DQ174168.1 gg_id:151146 Campylobacter gracilis str. ATCC 33236 DQ174
DQ174161.1 gg_id:155173 Campylobacter helveticus str. NCTC 12470 DQ174
DQ174163.1 gg_id:154260 Campylobacter helveticus str. NCTC 12472 DQ174
U03022.1 gg_id:11247 Campylobacter helveticus U03022
CP000776.1 gg_id:257761 Campylobacter hominis str. ATCC BAA-381 CP0007
AF043422.1 gg_id:11239 Campylobacter cf. lanienae str. UB 992 AF0434
AF550661.1 gg_id:57347 Campylobacter mucosalis str. ATCC 49353 AF5506
FJ983015.1 gg_id:430191 Aspects Oral Microbiome root canal clone FJ9830
NZ_ACFU01000050.1 gg_id:469893 Campylobacter rectus str. RM3267 NZ_AC
NZ_ACVQ01000030.1 gg_id:470642 Campylobacter showae str. RM3277 NZ_AC
EU781616.1 gg_id:326311 Campylobacter showae 3 EU7816
X67775.1 gg_id:11227 Campylobacter sputorum str. biovar sputorum;LMG 7795 X67775
AB181364.1 gg_id:100818 Campylobacter lari str. A3 AB1813
AB181358.1 gg_id:105325 Campylobacter lari str. NCTC12893 AB1813

901.0	6782.1	6998.1	7543.4	4537.2	7499.3	5505.1	6467.2	4431.4	3117.0	8586.5
6537.7	8408.7	10295.5	11699.1	6371.7	7838.4	7787.5	9467.7	4901.6	2345.2	12287.0
1823.8	7272.8	9370.4	10215.3	6236.8	8417.5	7657.9	8317.5	5245.4	5389.0	10100.0
2420.4	10215.9	9554.3	9619.2	5051.8	8325.6	7292.2	9523.2	6137.5	3611.5	14657.7
500.3	9172.2	11117.6	7761.5	4640.1	7598.2	5723.2	8098.6	5245.4	2450.7	10436.1
2582.5	7151.2	6307.3	7251.5	3005.4	6273.6	5019.7	6514.2	2904.0	1180.0	9265.8
15788.1	7803.8	9225.6	9278.7	6963.4	6162.3	6796.8	6372.1	8950.8	5924.9	11933.7
274.5	1310.2	1346.7	1379.2	546.0	1538.2	1335.3	1637.3	555.5	309.2	1138.6
1346.8	14744.7	17157.2	11863.4	4826.9	11728.2	5297.8	12704.4	7587.3	2693.4	17434.5
10104.4	4599.9	6214.2	8135.3	5285.0	6631.8	5956.8	8944.3	4980.4	4369.6	7759.0
81.1	1459.8	1843.1	2036.9	988.4	2073.4	1545.5	2269.4	575.9	242.5	2199.6
37.6	2704.4	3205.2	1925.5	562.3	2513.2	660.2	3005.4	1333.7	202.7	3128.9
3468.1	9567.5	9767.6	9520.3	5282.6	8640.9	6270.5	9368.3	6856.2	4850.0	14122.5
5511.5	6307.2	6415.7	5927.6	4535.0	5360.9	6392.1	5326.0	6247.1	3929.9	8425.4
152.9	3211.1	4459.9	3617.8	3178.9	3918.3	3012.0	3254.9	1761.4	2323.6	2940.5
39.8	941.3	882.0	976.7	203.5	815.3	484.4	870.7	157.8	27.8	1181.1
533.4	5357.5	8257.7	3551.7	2796.5	4054.8	2872.7	4436.3	2265.1	1929.0	3882.4
25658.2	15740.1	15968.0	13231.4	8854.5	12544.8	9333.9	13665.4	14263.3	8600.2	20638.0
11762.6	12191.3	8926.8	10927.5	5186.5	10331.0	5481.9	10621.3	9282.8	5580.0	18018.5
17134.2	8526.6	7094.7	7165.2	5948.8	6246.7	7268.5	6139.4	8886.7	7725.6	9866.7
1001.4	8417.1	8585.1	8028.2	3977.9	7509.3	6355.7	8623.2	5648.7	3241.2	11586.3
2453.7	4159.3	3935.5	3995.1	3404.5	3602.0	4123.5	3807.5	2666.8	2123.5	4654.1
46.7	3125.2	4274.8	4041.2	1057.3	2572.4	1988.2	3165.5	1166.7	163.2	3325.0
56.9	907.8	905.4	1149.2	608.7	842.5	935.6	965.2	305.0	137.7	561.8
53.0	610.2	681.7	695.5	605.7	569.4	418.6	791.6	206.5	337.8	589.3
1056.7	5531.0	5522.3	6105.2	4955.6	6132.7	5793.4	5342.6	3457.3	6036.3	5837.4
3043.4	5541.4	7057.9	8125.4	3598.0	6502.2	5842.9	6716.6	3613.6	1541.3	7353.4
51.1	90.5	105.6	113.8	84.4	78.3	77.0	134.1	45.2	41.0	86.5
196.3	2644.1	2449.4	2558.0	2712.5	2182.3	3515.6	2390.5	1471.9	866.5	2334.0
529.9	2466.6	3383.1	2924.7	3181.7	2708.4	3912.2	3029.8	1422.8	1093.2	3198.8
5274.6	6533.9	7143.1	6875.4	5072.6	6153.3	6863.1	6441.4	6213.6	3212.9	7818.1
42.7	82.5	179.1	145.2	75.5	67.8	76.4	190.7	31.7	46.7	52.5
190.7	2509.3	2951.5	3386.2	1318.6	683.5	1465.3	2645.1	1223.7	475.7	3441.2
470.9	2405.2	2494.2	2647.3	2128.5	1959.0	2078.9	2485.9	1688.8	451.7	3060.9
9069.0	3219.4	3178.7	3190.6	3395.7	3293.4	3023.0	3066.3	3152.0	3163.2	3893.0
877.8	5152.6	5288.7	5631.5	4554.7	4729.8	5042.2	4860.4	2737.3	2481.9	5512.8
1814.4	5486.0	5758.8	7318.9	4902.0	5566.4	5284.1	6374.1	3210.9	1535.5	6362.4
616.2	2494.6	2734.6	3016.7	2180.5	2438.9	2375.0	2980.0	1389.5	962.6	2907.8
43.6	374.4	1111.5	599.6	76.7	259.5	149.0	610.3	100.9	63.9	375.7
3994.3	5272.0	4091.6	3441.8	3357.4	4486.4	2851.5	3351.1	4967.3	3762.3	3264.5
1435.0	8034.2	9593.9	8026.9	6353.3	7123.6	6509.8	6827.7	9476.0	5705.7	9865.0

5679.6	6092.9	4964.9
6522.8	6554.0	5519.7
6781.2	7477.6	5146.1
7901.0	8482.6	5740.3
7697.0	7151.6	4761.0
4384.5	4163.9	3480.5
5988.4	7065.7	5512.9
970.0	1043.4	648.5
11572.9	9705.0	4427.2
10004.3	8396.5	4089.9
1890.1	4714.3	1261.8
2285.3	2713.1	494.6
8522.9	10421.8	4986.8
4947.7	6522.0	3435.7
3808.1	4252.4	3190.8
639.8	1125.6	174.7
3591.3	3377.5	3245.6
12598.3	11967.1	7847.0
10020.0	10180.4	4517.9
4767.5	7449.8	6160.7
7359.9	7782.3	4286.7
3373.9	3725.1	3282.5
1779.9	2072.4	1042.2
765.1	662.8	807.3
588.5	811.6	725.7
4391.1	5060.4	5211.6
4370.5	3288.4	2860.1
63.4	89.9	75.9
1748.6	2286.2	2284.8
2235.3	2725.4	2443.4
5392.4	6503.9	5223.2
83.3	90.4	69.4
1827.1	2603.8	1746.0
1997.0	2689.5	1213.9
2971.5	4256.5	2898.8
4035.8	3914.8	3886.3
4564.8	5966.6	3207.5
2032.5	2420.5	1265.9
191.7	302.0	139.7
2680.0	3715.2	4070.3
6457.7	8761.0	5452.2

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AB181356.1 gg_id:105014 Campylobacter lari str. CF89-14 AB1813
AB181357.1 gg_id:105165 Campylobacter lari str. NCTC12892 AB1813
AB181359.1 gg_id:105482 Campylobacter lari str. NCTC12894 AB1813
AF550640.1 gg_id:57368 Campylobacter upsaliensis str. LMG 8851 AF5506
AF550632.1 gg_id:102123 Campylobacter lari str. LMG 11251 AF5506
GQ167658.1 gg_id:586732 Campylobacter upsaliensis str. RM3195 GQ167
DQ174156.1 gg_id:154704 Campylobacter showae str. CCUG 11641 DQ174
EU289113.1 gg_id:238608 microbiome cloacal openings urogenital and anal tracts tammar wallaby Macropus e EU2891
FJ832837.1 gg_id:542539 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J3Q301_10B02 FJ8328
AF219235.1 gg_id:70687 Campylobacter hyointestinalis MGH 97-2652 AF2192
AB301962.1 gg_id:219863 Campylobacter subsp. hyointestinalis str. 2831-1 AB3019
AF550641.1 gg_id:57366 Campylobacter upsaliensis str. LMG 8853 AF5506
EU289065.1 gg_id:253584 microbiome cloacal openings urogenital and anal tracts tammar wallaby Macropus e EU2890
AY554142.1 gg_id:113002 Campylobacter sp. str. BTP1 AY5541
AY554144.1 gg_id:113756 Campylobacter sp. str. WB1 AY5541
GQ167676.1 gg_id:542181 Campylobacter coli str. ATCC 33559 GQ167
AF372091.1 gg_id:66989 Campylobacter jejuni str. NCTC 11351 AF3720
EU559332.1 gg_id:549039 Campylobacter sp. str. MIT 97-5311 EU5593
AJ276874.1 gg_id:69947 Campylobacter faecalis str. 1433 stool sample isolate AJ2768
AB301961.1 gg_id:219965 Campylobacter subsp. hyointestinalis str. 2728-1 AB3019
AF550628.1 gg_id:55836 Campylobacter jejuni str. H99/240 AF5506
AF550647.1 gg_id:57361 Campylobacter helveticus str. CCUG 30563 AF5506
DQ174159.1 gg_id:154512 Campylobacter upsaliensis str. NZ5564-94 DQ174
AM933372.1 gg_id:541426 Campylobacter subantarcticus str. LMG 24374 AM933
GQ451185.1 gg_id:533613 Fecal Yunnan snub-nosed monkey feces clone J16 GQ451
AF097688.1 gg_id:11237 Campylobacter hyointestinalis subsp. lawsonii str. CHY8 subsp. AF0976
AB066098.1 gg_id:54599 Campylobacter lari str. CF89-12 Japanese strain AB0660
AJ620504.1 gg_id:108770 Campylobacter insulaenigrae str. NCTC 12927 AJ6205
DQ174164.1 gg_id:152100 Campylobacter helveticus str. E504-90 DQ174
EU623474.1 gg_id:278725 Campylobacter sp. str. 24/06 EU6234
AF550620.1 gg_id:57384 Campylobacter coli str. LMG 9220 AF5506
DQ174146.1 gg_id:151930 Campylobacter lari str. NZ145-95 DQ174
FJ609419.1 gg_id:573432 Campylobacter jejuni str. PRCC-3 FJ6094
EF621895.1 gg_id:243035 Campylobacter canadensis str. L268 EF6218
AF550655.1 gg_id:57353 Campylobacter showae str. LMG 12636 AF5506
EU470464.1 gg_id:302158 Grevy's zebra feces clone GZ_aaa03d07 EU4704
AY288304.1 gg_id:86812 Campylobacter lanienae str. L52 AY2883
EF621896.1 gg_id:240175 Campylobacter canadensis str. L267 EF6218
NR_028692.1 gg_id:561090 Sulfurospirillum barnesii str. SES-3; ATCC 700032 NR_028
EF462744.1 gg_id:295702 meta-genome level extreme microbial symbiosis dorsal surface deep sea hydrotherm EF4627
AB355036.1 gg_id:244687 Monitoring and archaeal two heavy polluted areas lake Egypt based on surface wate AB3550

232.7	1728.8	1764.8	993.4	580.3	1492.2	795.6	1039.2	1094.8	467.9	1286.7
237.7	1885.4	2052.4	1343.0	656.2	1579.1	996.5	1227.7	1075.1	477.1	1433.9
3474.2	3065.9	3321.6	2209.5	1628.7	2550.9	1947.9	1993.3	2337.5	1157.4	3299.3
705.5	4983.4	4755.8	4111.0	3081.0	4250.5	4017.8	3630.1	3118.0	1615.9	3606.7
1006.9	3201.9	3151.9	3428.7	2557.4	2206.1	2984.0	3154.0	2373.6	1362.5	5046.0
77.5	9522.2	7842.8	8707.3	5503.7	7430.2	8269.7	7106.2	5256.8	1975.8	9016.6
346.6	2115.7	2223.5	2513.5	2529.6	2235.3	2126.0	2777.5	1165.4	846.9	2193.2
538.7	5217.3	5864.5	5520.1	4793.8	4126.3	5506.9	5778.5	3290.2	1808.2	5878.9
4166.0	4687.0	5644.6	5478.6	4030.4	4193.1	4845.0	4783.3	4304.2	2247.1	5030.8
2812.5	5211.8	5065.4	5693.5	3883.0	5138.5	4848.2	4476.1	3711.7	1675.3	5651.1
1755.8	494.7	2002.6	1878.9	1205.4	1469.2	1262.2	2067.8	441.8	737.1	1941.5
3414.8	5750.8	6408.8	6630.6	5881.0	5387.8	7100.4	6129.3	5147.2	2490.5	5623.9
429.8	1916.8	2183.3	2667.0	2428.4	1751.8	2237.8	2193.1	2095.5	616.2	1927.5
326.8	4492.1	4226.7	5031.6	4555.0	3644.6	4817.5	3904.1	2244.6	1233.6	4682.4
33.6	852.9	269.9	261.1	237.1	669.2	319.8	387.2	1055.8	62.0	192.7
68.2	1312.4	1298.4	1217.9	794.1	1085.5	905.2	1299.1	626.2	250.8	959.9
244.4	1066.2	1482.5	1049.3	542.6	1076.3	807.1	1052.8	676.6	302.2	1310.1
1725.6	10528.6	12171.9	12506.2	9099.8	9840.8	10130.8	9378.7	7856.0	4634.8	13166.0
37.7	32.1	36.0	48.5	28.7	29.2	31.7	31.1	24.0	12.6	38.3
52.6	462.0	969.0	1100.4	208.4	444.6	327.9	878.3	176.9	53.8	500.3
450.2	3567.7	5871.6	3560.1	3168.3	2856.6	3808.6	3710.5	1962.9	1208.6	5635.8
4222.5	6246.8	5981.8	6561.4	5416.7	5868.9	6438.4	6024.6	4277.4	2987.8	7902.6
508.2	2135.4	3067.7	2692.0	2939.3	2471.8	3506.4	2862.1	1503.7	961.1	2215.0
507.8	2591.8	3558.0	2520.9	1657.1	1505.7	2026.7	2452.2	1954.3	824.1	4070.5
4756.4	3675.3	4471.4	3840.1	3823.8	3987.8	3825.8	4276.6	2645.8	1851.5	4022.3
195.9	1789.1	2208.6	2471.4	1347.5	2489.6	1804.9	2211.7	850.1	389.6	1716.8
1540.4	2708.4	3020.3	2374.8	1599.8	2613.4	2103.4	1903.5	2194.4	1593.6	2689.7
970.8	5056.7	5761.4	4713.8	3078.3	3055.5	3274.1	4976.9	3320.3	1837.3	7106.1
172.4	1908.3	1811.0	1781.6	2161.5	1576.5	2983.7	1758.0	741.7	461.9	1582.3
245.5	4523.4	4903.7	4108.5	3409.8	4221.1	4481.0	4740.8	3350.3	1806.4	4528.7
74.3	1354.5	1697.8	1308.0	934.3	1097.5	1220.7	1434.2	492.9	250.2	1106.2
1648.9	5895.8	6530.8	7212.0	3701.8	4194.0	5262.7	6133.8	3505.1	2322.2	9517.6
5745.9	5884.8	6441.2	5282.4	4250.0	4765.4	4908.7	5141.9	4427.9	2632.4	7568.0
3762.5	7585.6	7339.6	8015.0	5582.5	6833.6	7097.6	5913.1	8356.7	4046.5	7669.4
647.4	3591.7	3388.6	3839.0	2351.5	3244.1	3109.8	3677.6	2130.5	1160.4	4724.0
201.8	5342.2	5075.7	5539.5	3317.3	5231.0	4334.3	4502.9	2988.3	997.5	5168.5
8811.6	8322.5	9408.3	11405.8	5098.6	7022.2	7756.2	7552.3	6312.7	3327.0	11556.3
11832.8	9355.6	8614.0	10105.2	7006.8	8143.4	8640.5	7607.1	8982.4	5478.3	8787.0
10208.7	5963.2	6345.9	7311.5	2657.3	5265.1	5932.7	5741.5	7405.2	4990.7	8298.5
2381.2	4224.9	5202.3	5631.8	4873.8	4543.5	5763.6	4863.0	2956.5	2777.6	4825.5
86.9	6086.4	6067.6	7886.6	2174.9	5819.3	6238.2	6656.1	2314.5	1253.0	7533.3

776.3	984.5	672.9
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1793.6	2437.5	1526.1
2819.8	3446.3	3271.5
2502.8	2938.9	2683.4
6228.6	6275.3	6767.9
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4627.0	5408.7	5244.2
4192.0	4208.9	3874.3
4158.8	3370.1	3565.6
1402.9	1826.5	1499.0
4821.4	5730.0	5679.1
1915.1	1928.0	2765.9
2532.6	3151.3	3161.7
139.2	182.6	151.4
922.0	1637.7	921.8
802.5	991.4	820.9
8645.7	9461.2	8337.8
31.0	58.8	19.5
478.9	259.0	132.1
2616.6	3965.1	2451.6
4948.8	5983.0	5182.9
2295.0	2544.8	2772.3
1924.2	2599.4	1791.6
4060.5	4112.7	3830.8
1740.0	1902.7	2416.7
1780.2	1933.8	1921.1
3598.1	4197.4	3853.0
1194.9	1617.4	1631.6
3643.4	4615.0	4493.1
931.0	1656.9	1092.5
4739.6	5256.7	5090.5
4061.8	6473.6	4246.7
5446.8	5953.0	5477.9
2654.1	3566.2	2249.7
4340.6	4396.9	3745.0
6528.3	6064.0	4573.7
6955.0	6789.2	6544.1
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FJ792436.1 gg_id:546339 Unexpectedly archaeal species shift between rare and dominant over thousand year FJ7924
FJ791877.1 gg_id:573109 Unexpectedly archaeal species shift between rare and dominant over thousand year FJ7918
FJ792027.1 gg_id:534646 Unexpectedly archaeal species shift between rare and dominant over thousand year FJ7920
U85964.1 gg_id:11189 Sulfurospirillum arsenophilum str. MIT-13 U8596
AB286550.1 gg_id:206504 Reducing production and domination comamonadaceae reducing oxygen supply was AB286
AY548994.2 gg_id:103740 marine bone clone boneC3F4 AY548
FJ792107.1 gg_id:534811 Unexpectedly archaeal species shift between rare and dominant over thousand year FJ7921
FJ792301.1 gg_id:562673 Unexpectedly archaeal species shift between rare and dominant over thousand year FJ7923
AY548973.1 gg_id:102465 marine bone clone boneC15D1 AY548
DQ295747.1 gg_id:160847 Epsilonproteobacteria terrestrial caves and springs microbial mat sulfidic Warm spri DQ295
DQ925871.1 gg_id:249367 Microbes and Thermal Gradients Temperature Hydrothermal Chimneys hydrotherm DQ925
DQ228579.1 gg_id:141569 and physiological significance attached microorganisms rock-hosted deep-sea carbo DQ228
AF357199.1 gg_id:22148 Sulfurospirillum sp. str. 18.1 AF357
FJ792478.1 gg_id:534881 Unexpectedly archaeal species shift between rare and dominant over thousand year FJ7924
AY672509.1 gg_id:99157 hydrothermal vent 9 degrees North East Rise Pacific Ocean clone CH1_28_BAC_16SrR AY672
AY327877.2 gg_id:88092 surface vent snail foot clone SF_C11-F3 AY327
FJ640810.1 gg_id:512603 GeoChip-based metabolic microbial hydrothermal vent chimney 4143-1 Mothra field FJ6408
AY280408.1 gg_id:100828 exterior deep-sea hydrothermal vent sulfide chimney Juan de Fuca Ridge Pacific Oce AY280
AB234540.1 gg_id:146284 termite gut homogenate clone MgMjR-060 AB234
AY280434.1 gg_id:106449 exterior deep-sea hydrothermal vent sulfide chimney Juan de Fuca Ridge Pacific Oce AY280
AB192073.1 gg_id:143275 termite gut homogenate clone M2PT2-04 AB192
FN356324.1 gg_id:580201 Prokaryotic structure sulfate reducer activity -temperature reservoirs and without ni FN356
FJ485111.1 gg_id:541385 microbial autonomous rover world's deepest phreatic sinkhole water column El Zacat FJ4851
AY266270.1 gg_id:103575 oil production water clone CT1 AY266
DQ925875.1 gg_id:244236 Microbes and Thermal Gradients Temperature Hydrothermal Chimneys hydrotherm DQ925
FJ156092.1 gg_id:461508 Arcobacter mytili str. T234 FJ1560
AJ969453.1 gg_id:159487 Microbial black smoker s Mid Atlantic Ridge ecological implications rock fragments ch AJ9694
AB231076.1 gg_id:147107 termite gut wall clone NkW01-035 AB231
AJ441214.1 gg_id:106099 hydrothermal vent polychaete mucous clone P. palm C/A 39 AJ4412
AJ576349.1 gg_id:102626 hindgut homogenate Pachnoda ephippiata larva clone PeH32 AJ5763
AY192528.1 gg_id:111196 Flexispira rappini str. 205-2 AY192
AY192526.1 gg_id:109700 Flexispira rappini str. 204-1 AY192
AY126479.1 gg_id:131724 Flexispira rappini str. 205-1 AY1264
AF396078.1 gg_id:20816 Helicobacter cinaedi 30327 AF396
AF396081.1 gg_id:49270 Helicobacter cinaedi 31111 AF396
AB275325.1 gg_id:196588 Helicobacter cinaedi str. PAGU0621 (= 56) AB275
AF302108.1 gg_id:69782 Helicobacter sp. str. HC15880 AF302
AF118017.1 gg_id:11022 Flexispira rappini str. H1353 AF118
AF497810.1 gg_id:56169 Helicobacter cinaedi str. 94105 AF497
AF497807.1 gg_id:60772 Flexispira rappini str. FR106 AF497
AF072471.1 gg_id:10989 Helicobacter mesocricetorum str. MU97-1514 AF0724

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2580.4	2826.0	3250.9	3896.0	2233.5	3465.6	3734.7	3887.0	2836.3	2911.5	3086.8
281.6	2948.1	3269.9	4067.2	1760.5	4093.2	2559.9	3035.9	1418.1	871.0	3328.7
44.9	2731.1	4804.6	7585.0	1162.4	3829.4	5771.7	6052.7	703.5	68.0	4360.4
76.7	770.3	801.7	860.6	429.3	1211.2	1497.8	4250.5	382.3	577.9	3975.5
840.3	4040.4	3749.0	4093.9	3339.4	3493.1	3767.8	3941.2	3338.5	2553.8	3354.7
2516.6	3124.0	3399.0	4321.3	2042.3	3407.9	2457.5	2825.3	2237.5	1453.4	4080.6
10257.4	7081.0	6300.4	8422.7	5484.5	6355.3	6135.7	5697.1	7185.3	6578.6	9298.2
932.8	3646.9	6539.6	4688.6	1901.3	3431.0	2499.2	3541.3	2037.6	3364.7	4766.2
145.0	2831.1	2962.3	4062.2	952.4	2829.0	3454.9	3528.8	1242.5	2279.0	3631.5
129.9	1181.1	2480.3	3012.7	475.4	1002.7	2240.1	2689.2	407.9	221.6	1955.3
1270.9	1925.5	1523.6	1667.3	1394.7	422.8	1628.5	1501.2	1789.1	890.8	1260.2
33.9	3850.9	4932.7	3259.7	584.5	2756.7	1407.6	3340.4	1039.8	427.9	4932.0
7490.4	5050.2	5127.1	6446.6	3973.1	5239.0	4681.6	4209.1	4811.6	3221.1	7234.6
79.0	1633.8	3511.9	2147.1	1036.3	1140.0	1613.7	1683.3	412.2	181.6	1065.9
26.1	521.4	452.7	401.7	81.3	312.3	66.8	117.3	172.9	135.2	103.4
43.5	266.4	356.2	248.1	122.4	191.6	150.4	319.2	109.0	170.9	148.6
43.0	62.0	92.4	101.4	42.6	55.0	69.2	83.0	29.2	16.8	45.7
85.8	3350.5	5541.1	3116.8	1402.6	2346.6	2267.3	4016.2	2730.0	651.3	2635.3
30.4	61.5	112.8	39.5	29.2	44.7	29.3	40.1	46.0	14.0	35.9
45.1	133.7	124.5	144.1	148.4	110.6	112.2	113.6	60.6	52.4	86.9
2963.7	1611.9	1508.3	1585.4	1394.3	1321.0	1613.7	1292.2	1731.6	1619.2	2048.0
52.6	770.0	1547.9	1126.9	710.1	1182.1	649.6	1406.4	266.5	102.5	503.5
1378.5	5487.2	6971.2	8325.7	3341.0	6104.9	6191.1	6262.9	2735.2	2531.3	7404.4
7276.0	10739.2	13459.5	11421.3	7167.0	8607.4	9265.6	9259.4	7970.9	5333.4	14747.9
849.4	11332.9	14365.1	11701.8	3552.4	10779.5	6188.6	10128.2	4805.1	4134.1	15144.7
2989.5	893.7	974.9	734.4	984.7	1245.7	997.4	999.8	775.6	1260.2	690.8
48.7	1983.2	1538.7	1788.9	66.8	147.1	246.1	411.2	517.1	65.0	536.7
60.3	304.0	550.9	517.3	577.4	340.6	526.5	498.6	145.3	102.2	239.4
2234.6	4925.4	7336.7	6328.1	4980.2	5411.1	5223.5	6172.7	2820.1	1868.5	7467.7
788.2	3547.7	4471.0	4374.0	3402.4	4119.5	3679.9	4569.3	3032.7	2793.0	3539.7
647.5	3077.9	3931.2	3694.2	3786.7	3214.7	3404.8	3880.2	2472.0	2266.4	3325.7
1331.5	3512.9	4577.0	4152.4	3142.2	3780.9	3331.0	4275.2	2460.2	2142.2	3965.4
2021.0	5471.3	5629.5	6016.4	2831.7	4630.5	3683.8	4079.2	3520.9	2200.9	5263.3
21610.8	8076.6	8004.0	7831.5	9621.9	7473.0	8754.8	6170.9	9245.8	8215.3	9879.5
191.5	4416.6	4092.4	4419.3	2273.2	3796.4	3249.6	3529.6	2129.8	1784.0	3034.2
1534.0	5656.9	5443.2	3961.5	5125.3	5726.4	4970.5	4234.1	4779.4	5141.1	3542.5
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3236.0	3910.5	2172.8
2059.4	2363.9	2233.2
5503.3	2765.8	1129.1
3149.3	3371.9	785.8
3626.9	3918.4	3824.5
1832.6	3224.3	2209.0
5242.8	6777.4	5482.5
2802.1	4279.0	1307.3
3386.7	2981.8	1260.7
1364.7	993.6	958.4
1197.9	1768.1	1505.3
2324.3	3853.3	668.2
3293.8	5273.4	3843.3
1089.2	870.7	1073.7
141.7	127.5	119.3
201.3	193.1	154.6
53.1	85.1	49.3
2438.1	2902.9	3747.2
36.7	48.7	24.3
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1191.3	1967.8	1185.8
899.5	1342.2	745.9
4987.9	4217.7	2737.6
8317.6	10633.9	6967.9
8314.6	7990.9	3687.7
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241.9	131.6	136.3
401.6	527.5	288.2
5012.0	4960.2	4666.7
3605.7	4070.2	4288.0
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3577.9	4552.3	3478.5
3376.5	3848.4	2841.8
6121.0	7571.3	6311.5
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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
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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

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96.2	2764.6	4018.3	5233.9	1021.7	3220.5	3006.4	5035.3	990.0	875.1	3731.6
603.3	1883.5	2350.6	2294.6	1600.7	1749.2	1914.1	1590.5	1542.1	1333.0	2057.9
2842.6	2825.4	3318.4	3322.4	2577.1	2756.6	3104.2	2518.5	2433.9	2229.3	3217.8
2041.8	2082.1	2232.9	2577.5	1823.2	1993.1	2089.6	1722.3	1943.3	1731.0	2013.3
14279.8	7964.3	7423.1	7296.6	6641.4	7220.3	8103.2	6085.0	8487.5	6884.5	9012.7
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854.7	3413.8	3958.6	4114.4	3025.6	3345.1	3882.7	3194.1	3643.7	3629.7	3142.5
188.2	3526.8	3159.7	3259.1	3447.9	3109.9	3615.2	3587.7	1089.3	1430.8	2691.8
479.9	2856.7	3573.5	3780.0	3392.7	3802.2	3040.4	4402.9	2371.0	4751.9	2952.2
3528.4	3660.9	4706.0	4339.1	3947.2	3676.2	4131.5	3544.0	5575.6	3621.4	4354.0
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91.4	5284.7	2555.2	1766.0	1634.7	3545.9	1313.2	2388.0	5892.9	3233.5	1307.4
11912.5	3609.5	3738.7	3635.2	3979.5	3643.0	3804.3	3425.7	3775.0	2877.3	4486.8
741.2	2325.3	2196.7	2355.1	2275.6	2267.0	2315.4	2461.5	1068.8	545.3	1875.9
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131.0	3486.2	4085.6	4119.9	1822.1	3396.7	3953.1	3763.8	1651.2	1506.3	3671.2
371.6	2268.0	2805.2	3586.5	2023.2	2117.6	2836.1	2844.8	961.1	688.3	3028.1
574.3	2701.4	3375.8	2514.1	2085.7	2414.9	2165.4	2228.3	1647.9	1197.6	2007.7
174.4	1610.4	1872.9	2375.0	1192.5	1503.6	1436.7	1123.0	565.7	334.3	1186.9
65.2	451.9	513.8	409.5	409.6	617.9	405.9	258.5	274.6	207.5	235.1
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3456.1	4973.7	5636.1	6210.2	4325.0	5218.6	4522.5	4483.8	2831.8	1801.9	6410.7

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AF334681.1 gg_id:17771 Helicobacter cf. pullorum str. W.Tee-Cro AF3346
AF333341.1 gg_id:36371 Helicobacter marmotae str. MIT 98-6070 AF3333
AY143177.1 gg_id:76377 Helicobacter cetorum str. MIT 01-6202 AY1431
U96300.1 gg_id:11047 Helicobacter trogontum str. ATCC 43968 U96300
AF237612.1 gg_id:26677 Helicobacter sp. str. Wee Tee AF2376
AY034817.1 gg_id:49918 Helicobacter rappini str. 1 SU AY0348
Y18028.1 gg_id:10969 Helicobacter heilmannii str. AF53 Y18028
AB006148.1 gg_id:11016 Helicobacter suncus str. Kaz-2 AB0061
AJ249858.1 gg_id:41542 Helicobacter sp. blood isolate 964 AJ2498
AF127027.1 gg_id:10980 Candidatus Helicobacter bovis AF1270
AF506778.1 gg_id:64319 Helicobacter heilmannii str. C4E AF5067
AF103880.1 gg_id:11028 Helicobacter felis str. 390-9 AF1038
M88151.2 gg_id:10993 Helicobacter sp. CLO-3 str. CCUG 14564 M8815
DQ415545.1 gg_id:153639 Helicobacter anseris str. MIT 04-9362 DQ415
AY203900.1 gg_id:82216 Helicobacter sp. MIT 02-5519C AY2039
AY634603.1 gg_id:109139 stomach clone AY6346
DQ415546.1 gg_id:153064 Helicobacter brantae str. MIT 04-9366 DQ415
AY686609.1 gg_id:110529 Helicobacter trogontum str. MIT 95-5368 AY6866
AF246986.1 gg_id:16388 Helicobacter winghamensis str. NLEP 98-202 AF2469
AF103883.1 gg_id:11031 Helicobacter bizzozeronii str. 865-2 AF1038
AF142062.1 gg_id:11063 Helicobacter sp. 'feline isolate' AF1420
AF302105.1 gg_id:50310 Helicobacter pametensis str. ATCC51478 AF3021
AF333340.1 gg_id:49735 Helicobacter sp. str. MIT 99-5507 AF3333
AF506780.1 gg_id:72724 Helicobacter heilmannii str. CM1 AF5067
AY634577.1 gg_id:109104 stomach clone AY6345
AY554139.1 gg_id:114285 Helicobacter sp. str. LNB2F AY5541
AF506782.1 gg_id:64314 Helicobacter heilmannii str. MM1 AF5067
AY554140.1 gg_id:113412 Helicobacter sp. str. WB1F AY5541
U46129.1 gg_id:11050 Helicobacter cholecystus str. Hkb-1 U46129
DQ438119.1 gg_id:152253 Helicobacter canadensis str. L222 DQ438
AF297868.1 gg_id:48289 Helicobacter aurati str. MIT 97-5075c AF2978
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AF103881.1 gg_id:11029 Helicobacter felis str. 144-10 AF1038
AB080644.1 gg_id:49390 Sulfuricurvum kujiense str. YK-3 AB0806
DQ295616.1 gg_id:161607 Epsilonproteobacteria terrestrial caves and springs microbial mat sulfidic spring Pah DQ295
EU542457.1 gg_id:267730 Effects chemical structure concentration on pathways microbial during dechlorinatio EU5424
FJ793154.1 gg_id:522980 Archaea and Hot Spring Thailand Tao Dam hot spring clone TDB04 FJ7931
AB080645.1 gg_id:41311 Sulfuricurvum kujiense str. YK-4 AB0806

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268.9	3520.3	4058.0	3449.4	2550.9	3312.7	2513.9	3880.8	2289.7	1290.1	3740.1
6028.0	3475.4	3609.1	3573.4	3960.9	3371.3	3981.9	3104.6	4470.7	3902.1	5496.9
70.4	4310.5	4404.6	6351.9	1943.8	4049.4	4615.4	4668.8	2094.9	915.2	4202.4
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2279.6	4664.8	5077.8	5696.1	3892.6	4405.0	4360.5	4179.7	3777.9	3026.1	5943.0
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83.6	3289.9	3570.9	3961.7	598.7	2248.1	756.6	2312.2	1010.9	621.9	2134.5
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1340.9	3751.6	4066.1	4763.6	1855.8	3722.8	2794.3	3987.4	2347.9	3500.5	3436.2
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597.4	2440.5	2706.3	3465.6	1975.0	2525.7	2679.9	2470.7	2179.2	1521.2	3531.7
97.7	1912.2	2498.8	2600.4	2206.8	1964.7	2226.0	1740.6	821.6	853.7	2281.6
561.5	849.6	1431.8	859.2	598.8	917.0	775.8	860.9	624.4	448.1	801.8
621.6	3288.0	5190.6	6081.7	2642.8	3728.3	4178.5	4954.4	1894.5	1249.0	4823.5
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752.2	5478.4	5976.6	6783.1	3819.1	4945.8	4804.4	5554.2	3475.3	1583.8	6722.3
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2685.7	3012.4	2527.8
2483.3	3247.4	1483.1
1948.6	2412.0	1565.2
3930.5	4873.2	3953.2
1487.4	1453.4	1031.0
4401.0	4936.3	4426.2
816.1	1729.8	1327.9
3426.2	4532.1	3422.9
3754.2	5246.5	4040.9
3560.1	3347.1	2958.1
1989.5	2432.2	886.7
1593.9	1943.7	953.6
4066.8	4631.7	5336.5
900.6	1329.9	1381.0
1068.1	819.3	884.4
3304.7	2523.1	2379.4
6394.0	6970.3	5611.0
4831.3	6190.5	5155.5
91.3	60.7	93.7
2107.7	2694.5	2006.1
1008.1	1236.9	998.7
2142.6	3038.0	2373.8
1062.2	1704.7	2359.4
619.9	866.8	553.0
2997.6	2863.9	3012.3
2926.1	2547.6	3542.5
2850.6	3068.6	1894.1
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4506.6	5613.7	5102.3
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1117.9	1525.5	1129.3
6221.0	7115.1	7427.8
2615.9	2563.2	2451.1
3253.5	3820.0	3863.3
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AB030603.1 gg_id:48041 groundwater clone 1047 AB030
FJ484985.1 gg_id:512690 microbial autonomous rover world's deepest phreatic sinkhole water column El Zacat FJ4849
FJ484902.1 gg_id:563044 microbial autonomous rover world's deepest phreatic sinkhole water column El Zacat FJ4849
FJ484970.1 gg_id:513207 microbial autonomous rover world's deepest phreatic sinkhole water column El Zacat FJ4849
GQ261311.1 gg_id:538468 Study on Sediment sediment Dongping Lake clone 1S3-8 GQ261
DQ295705.1 gg_id:161331 Epsilonproteobacteria terrestrial caves and springs microbial mat sulfidic stream Mil DQ295
AY510188.1 gg_id:109996 microbial mat cave sulfidic spring clone LKC3_57B.17 AY510
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DQ295560.1 gg_id:160845 Epsilonproteobacteria terrestrial caves and springs microbial mat sulfidic cave strea DQ295
EU884105.1 gg_id:326035 Recently Evolved Symbiosis Between Chemoautotrophic and Cave-Dwelling Amphip EU884
AF407391.1 gg_id:30295 MCB-contaminated groundwater-treating reactor clone RA9C8 AF4073
AY191481.1 gg_id:93946 microbial mat sulfidic cave spring clone LKC1.114_6 AY1914
AY191468.1 gg_id:93668 microbial mat sulfidic cave spring clone LKC1.21_5 AY1914
AY510191.1 gg_id:109873 microbial mat cave sulfidic spring clone LKC3_19.39 AY510
DQ295690.1 gg_id:160741 Epsilonproteobacteria terrestrial caves and springs floating microbial mat sulfidic gr DQ295
DQ295702.1 gg_id:160766 Epsilonproteobacteria terrestrial caves and springs microbial mat sulfidic stream Mil DQ295
GQ406165.1 gg_id:512611 Benthic submerged sinkhole ecosystems sediment clone BK-20-18 GQ406
EU101041.1 gg_id:238274 Sulfide/oxygen supply ratio predicts outcome competition among sulfur-oxidizing wa EU101
AB030601.1 gg_id:21738 groundwater clone 1043 AB030
AB030605.1 gg_id:22082 groundwater clone 1028 AB030
EU884110.1 gg_id:329225 Recently Evolved Symbiosis Between Chemoautotrophic and Cave-Dwelling Amphip EU884
AY191482.1 gg_id:93762 microbial mat sulfidic cave spring clone LKC1.114_7 AY1914
GQ390203.1 gg_id:557628 oxic-anoxic interface meromictic crater lake Lac Pavin clone Eub62D4 GQ390
AY510172.1 gg_id:109530 microbial mat cave sulfidic spring clone LKC3_127.39 AY510
DQ787703.1 gg_id:171036 holocene lake sediment clone SLB59 DQ787
EF467565.1 gg_id:203699 situ microelectrode voltammetry sulfur-oxidizing biofilms Frasassi sulfidic cave strear EF4675
AY191466.1 gg_id:103936 microbial mat sulfidic cave spring clone LKC1.21_1 AY1914
AB240521.1 gg_id:143003 microbial structure rhizosphere biofilm Sapporo root-base (80 160 mm) Phragmites S AB240
GQ472372.1 gg_id:553344 Microbial Dongping Lake lake sediment clone 3S2-14 GQ472
DQ787688.1 gg_id:172663 holocene lake sediment clone SLB319 DQ787
DQ295722.1 gg_id:159773 Epsilonproteobacteria terrestrial caves and springs microbial mat sulfidic spring Whi DQ295
AY510167.1 gg_id:110035 microbial mat cave sulfidic spring clone LKC3_22.72 AY510
DQ295745.1 gg_id:159690 Epsilonproteobacteria terrestrial caves and springs microbial mat sulfidic Warm spri DQ295
AY510168.1 gg_id:110808 microbial mat cave sulfidic spring clone LKC3_57B.54 AY510
DQ295557.1 gg_id:160445 Epsilonproteobacteria terrestrial caves and springs microbial mat sulfidic cave strea DQ295
DQ787698.1 gg_id:162117 holocene lake sediment clone SLB422 DQ787
AY532544.1 gg_id:99687 uranium-contaminated aquifer clone 1013-1-CG22 AY5325
AY510194.1 gg_id:111128 microbial mat cave sulfidic spring clone LKC3_57B.49 AY510
AF367495.1 gg_id:43869 deep-sea hydrothermal vent clone VC1.2-cl50 AF3674
AF367492.1 gg_id:70730 deep-sea hydrothermal vent clone VC1.2-cl32 AF3674
GQ433935.1 gg_id:541504 Subseafloor ocean crust microbial observatories: (F-through Osmo Colonization Syst GQ433

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4505.8	8168.9	8361.4	9523.0	3347.8	10021.9	5867.0	6868.5	4331.9	1923.6	10531.4
5826.7	8608.1	8564.2	9770.9	4638.8	10091.4	6795.1	7455.8	5378.8	4104.0	10963.2
2113.2	9627.9	9004.8	11028.1	3048.2	10766.4	6375.4	7738.5	3948.1	2963.7	11525.9
130.7	7814.9	6388.8	7169.4	1624.6	5709.0	3762.6	4613.5	2052.1	718.6	6208.9
133.8	7313.5	8048.5	10487.3	1985.1	9085.5	3748.3	5611.4	1606.5	2558.3	7658.4
28.0	6141.8	7414.2	7938.2	2251.6	5980.2	3232.8	5797.5	2144.7	838.6	7056.1
74.6	7877.8	8337.5	10778.1	1425.4	7248.8	3112.4	5887.5	1798.9	732.2	7508.0
3000.7	8564.2	8888.4	10676.1	4533.1	6578.3	5120.9	6342.3	4165.7	2940.1	8350.0
114.3	13953.7	14279.1	16815.2	4323.9	12622.0	9409.5	10342.6	6314.2	1658.3	14670.1
52.8	12493.0	14575.8	18628.3	3190.8	9193.7	4088.2	12192.6	4741.3	817.5	14330.1
224.4	8256.1	11039.8	10131.0	2744.6	10649.4	5265.0	7388.7	2913.1	1344.3	9912.8
4484.4	6561.9	7493.8	9255.0	4447.9	7377.1	4923.5	6357.2	3292.1	1437.4	6865.4
7250.7	10648.4	12002.9	12593.3	4790.9	10157.5	7046.3	8772.4	5654.1	2270.8	13104.7
4748.2	14214.4	13810.6	16772.4	6163.0	12716.3	10628.5	11831.1	8410.5	4786.3	16177.2
43.8	7869.6	7329.8	9044.5	1690.3	7578.4	4205.4	6017.1	3129.9	553.3	8012.8
4512.5	7888.2	9371.5	11361.9	4969.3	7855.6	6555.2	7742.3	5319.4	3504.2	11316.1
1309.7	10720.3	11980.2	12706.2	8013.9	11380.6	9874.1	9883.1	8202.9	4619.6	12525.0
268.9	9138.5	11278.3	13818.5	3869.2	10906.9	6293.6	9174.6	3510.9	3329.0	12903.1
631.7	11537.0	11530.7	14195.3	5485.6	12058.0	7634.5	9507.8	5008.1	2656.4	13577.9
475.6	10678.2	9577.2	12171.1	6654.3	9011.4	9324.8	6921.7	4281.4	4398.3	9134.6
24690.6	8497.5	8330.5	9379.4	5789.5	8509.7	6510.3	7528.6	9496.3	7437.1	11758.6
301.3	6581.2	7790.6	10134.5	2223.3	6474.8	3885.5	5039.2	2978.9	919.7	6892.1
11149.4	11580.5	12286.5	13806.8	7748.4	11232.4	9897.2	9516.4	12841.1	8717.9	13574.2
15976.9	5025.3	5258.3	5887.0	4302.0	5015.1	4665.1	4139.4	6017.0	5337.9	7415.1
61.1	4735.6	6728.9	7697.0	2252.5	5014.7	3151.6	4005.3	2293.0	1147.2	5318.1
2768.5	5848.2	8469.9	8258.6	2171.8	6362.8	4205.3	6016.3	2878.3	1881.1	9683.0
730.4	11392.9	11290.6	13991.6	5264.0	11380.8	8117.6	8705.9	4867.9	4401.5	12068.6
41.6	4463.7	8383.2	10605.1	207.8	1613.4	82.7	3008.6	467.4	104.8	6896.7
403.7	7232.8	8682.3	11736.8	2097.3	4373.1	3528.4	4968.0	3157.7	1095.2	6363.4
5674.5	8963.5	9658.0	10716.1	6614.9	9516.9	7917.7	7868.0	10835.1	6864.2	10502.2
2647.0	9620.5	11471.1	12935.6	3975.5	9161.8	6092.3	8606.5	4858.5	2292.9	12343.8
75.2	7979.5	10595.1	11954.9	2239.1	7173.0	4766.5	7484.3	3097.4	1062.9	9304.9
7041.8	8453.3	9397.1	10857.7	4890.8	8197.2	6799.2	6916.8	5155.0	4618.5	10306.3
1468.6	11223.5	12828.5	16389.9	5015.1	10172.8	6676.6	9752.0	4887.4	2955.7	14684.2
8297.2	6377.9	6752.1	8185.4	3394.7	6956.5	4614.2	5585.5	3297.7	2378.1	6655.5
1684.5	12210.1	11875.8	14643.6	6591.8	12238.0	8831.2	9076.7	6524.4	3618.5	12747.5
25223.7	8050.1	8557.6	10436.8	6150.2	7672.8	6287.6	8029.8	7150.7	4624.1	9438.9
452.7	1573.4	2385.8	2502.3	990.1	1867.3	1861.0	2136.6	954.1	622.4	2105.5
3364.2	3709.5	4107.6	4193.1	2688.0	3999.3	3111.4	4187.9	4563.4	2524.9	3299.6
5408.8	5013.1	4584.6	5860.1	1758.4	4536.5	3398.5	3970.5	3094.3	1199.9	5554.2

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5416.5	6022.3	5155.6
4255.4	4153.4	3897.7
2431.1	1879.4	1725.0
2583.2	1848.9	2135.8
3671.3	2177.3	2152.2
2283.4	1692.1	1160.6
4731.5	4126.1	3302.5
7084.3	4702.6	4202.4
6047.6	2269.0	1442.8
5369.9	4713.5	2896.7
4144.2	3865.9	3501.6
7214.6	5838.2	4489.7
7216.7	7011.8	6935.1
3238.7	1242.5	1080.3
5487.4	4769.8	4192.2
8312.9	8386.1	7421.2
5692.4	3305.6	3880.9
6376.3	5232.0	5965.2
5904.0	3929.4	3045.1
6215.5	7385.5	5112.7
3198.5	2270.0	2582.9
8069.5	8553.7	8249.7
4191.6	5153.0	4752.8
2822.1	2138.3	1719.5
4406.9	4256.6	2441.5
6039.5	5215.8	5734.8
629.8	117.8	37.4
2776.5	1906.4	1647.8
6794.6	8649.6	6363.8
6557.2	4682.5	3830.1
4644.2	2312.4	1789.2
5369.0	6374.7	4395.2
7157.8	4151.2	3560.8
4045.0	4523.4	4612.6
6325.3	6281.5	6714.6
6219.6	6165.8	5349.0
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3508.3	4324.6	2857.3
2874.1	2605.6	1740.7

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U15101.1 gg_id:11096 hydrothermal vent clone PVB_OTU_2 U1510
NC_007575.1 gg_id:144857 Thiomicrospira denitrificans str. ATCC 33889 NC_00
FJ437888.1 gg_id:547212 Benthic okenone production Fayetteville New York Green Lake 25 m water depth clor FJ4378
AF121884.1 gg_id:11109 phenol-degrading consortium clone Phenol-1 AF1218
DQ295573.1 gg_id:160062 Epsilonproteobacteria terrestrial caves and springs microbial mat sulfidic cave spring DQ295
FJ615170.1 gg_id:593488 Microbial dynamics seasonally fjord: British Columbia Saanich Inlet depth 10m anoxic FJ6151
EU491812.1 gg_id:268142 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU4918
DQ234141.2 gg_id:142794 determined library mangrove clone DS057 DQ234
FJ497618.1 gg_id:563303 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun FJ4976
FJ717090.1 gg_id:551059 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United Kingc FJ7170
DQ676325.1 gg_id:224044 Archaeal and plankton freshwater pond suboxic freshwater-pond sediment clone M DQ676
AY211683.1 gg_id:96203 Gulf Mexico seafloor sediment clone GoM GC234 633E AY2116
AY225615.1 gg_id:97077 iron-rich substrate exposed to Mid-Atlantic Ridge vent clone AT-cs10 AY2256
FN397808.1 gg_id:424252 geomicrobiological investigation sediments Gulf Cadiz GeoB 9072-1 anoxic sub-surfa FN3978
AJ441199.1 gg_id:57482 hydrothermal vent polychaete mucous clone P. palm C/A 78 AJ4411
AF355050.1 gg_id:48010 marine clone Arctic96B-13 AF3550
GQ356982.1 gg_id:592000 Metal Dependent Marine Methane Oxidation methane seep sediment clone FeSO4_ GQ356
AY225612.1 gg_id:97721 organic-rich substrate exposed to Mid-Atlantic Ridge vent clone AT-co23 AY2256
DQ676368.1 gg_id:222158 Archaeal sediment and plankton freshwater pond suboxic freshwater-pond clone M DQ676
FJ497273.1 gg_id:590030 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun FJ4972
EF218993.1 gg_id:215778 and Eukaryotic Hydrothermal Site East Rise Ridge Flank Abyssal Hill hydrothermal site EF2189
DQ228650.1 gg_id:141130 Microbial colonizing mineral surfaces within sulfide-microbial incubator clone CH2b1 DQ228
EF219001.1 gg_id:209624 and Eukaryotic Hydrothermal Site East Rise Ridge Flank Abyssal Hill hydrothermal site EF2190
U15106.1 gg_id:11103 hydrothermal vent clone PVB_OTU_6 U1510
AY280406.1 gg_id:100516 exterior deep-sea hydrothermal vent sulfide chimney Juan de Fuca Ridge Pacific Oce AY2804
GQ848465.1 gg_id:578863 Microbial sediments vents along East Lau Spreading Centre deep sea hydrothermal GQ848
FJ535290.1 gg_id:546926 within iron-containing flocculent mats submarine volcanoes along Kermadec Arc iron FJ5352
FJ717130.1 gg_id:551352 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United Kingc FJ7171
FJ717171.1 gg_id:533593 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United Kingc FJ7171
EF379628.1 gg_id:205139 sea water Victoria Harbor (Hong Kong) area clone VH-PA7-38 EF3796
EU652649.1 gg_id:279233 Seasonal variation microbial Yel Sea sediment clone B8S-4 EU6526
DQ836759.1 gg_id:169835 attached biomass denitrifying bioreactor clone DB-83 DQ836
AY218555.1 gg_id:82461 penguin droppings sediments clone KD1-140 AY2185
EU652651.1 gg_id:278362 Seasonal variation microbial Yel Sea sediment clone A8S-94 EU6526
FM242221.1 gg_id:343001 sequences sediment clone 259 T0h-oil FM242
EU652650.1 gg_id:277911 Seasonal variation microbial Yel Sea sediment clone C8S-4 EU6526
FJ717108.1 gg_id:569301 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United Kingc FJ7171
FJ535347.1 gg_id:510699 within iron-containing flocculent mats submarine volcanoes along Kermadec Arc sedi FJ5353
AB530237.1 gg_id:584301 Monitoring Suez and Tokyo bays based on analyses marine sediment clone Tokyo..B AB5302
AB188787.1 gg_id:113750 cold seep sediment clone SB5-24 AB1887
AB193899.1 gg_id:108823 deep-sea vent clone Mb-NB05 AB1938

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38.4	2656.3	3961.0	4440.0	508.8	3106.5	2985.3	3977.4	915.6	487.7	4536.0
63.5	4199.5	7899.8	10370.4	570.5	3450.9	7769.5	7600.9	1107.7	1975.6	8170.7
43.6	726.1	869.1	1236.7	282.1	1500.0	648.9	1039.8	444.9	68.5	1051.0
6300.7	11888.6	11107.6	13968.9	6816.4	10639.5	10759.3	11310.6	8562.7	6310.2	15407.4
545.2	4333.0	3693.9	4389.6	1747.0	3833.2	4098.1	4326.0	1753.2	1226.7	5240.7
2374.0	6947.5	7042.5	7642.4	5357.8	6830.1	7277.2	7481.3	5350.5	4453.5	7443.7
77.3	2145.3	2974.7	3854.5	211.7	1829.3	2851.1	3224.5	495.3	416.9	3827.8
45.8	540.1	1331.6	1550.8	282.1	424.5	385.5	1193.9	376.0	263.3	1061.7
3437.0	5041.5	6644.9	7532.9	1764.9	5569.5	6239.8	6005.1	2690.6	2419.4	7816.8
101.6	1573.2	2142.9	3218.7	1130.0	2177.8	1592.0	2304.0	555.0	157.3	1703.4
53.8	874.5	1578.2	2501.7	321.8	895.9	907.8	1561.1	181.1	127.1	1366.6
97.2	2632.5	4212.9	4720.8	521.3	3098.5	2405.8	3444.2	810.9	546.3	4152.4
364.0	2550.8	3623.2	5203.4	2431.7	3610.6	3049.8	3871.5	1660.0	1281.5	3556.8
47.0	401.4	864.4	888.8	167.5	479.4	489.8	664.6	220.1	335.6	829.5
34.0	1997.5	2258.9	2921.8	194.5	1345.4	947.6	2058.5	617.6	443.8	3118.2
2024.9	8638.8	8665.3	8885.1	4737.9	7877.5	8224.7	6964.5	6687.3	4275.4	9501.8
74.8	253.0	312.9	430.3	151.4	255.6	147.1	202.7	126.5	42.1	213.7
211.3	5085.4	7590.0	9892.6	1323.6	4968.1	6140.9	8632.7	2196.0	1058.0	9540.7
153.4	3126.4	3707.5	4223.8	1223.0	2293.2	3452.9	3322.9	1720.3	943.5	5238.0
61.1	1124.7	2088.4	3137.6	552.5	908.0	627.5	2092.9	389.3	911.5	1672.1
117.4	4352.8	5256.6	7173.2	1034.3	4628.3	5934.2	6089.8	1891.8	2032.9	7710.4
67.8	837.7	1775.7	2159.3	353.3	1019.5	1190.6	2082.1	431.4	62.6	1901.2
65.2	539.1	1526.1	1543.5	72.4	710.4	1323.7	1919.4	622.2	68.8	2400.5
47.8	4039.1	4499.1	6717.9	1727.8	4334.5	3531.5	3988.0	1470.3	1370.8	4327.9
40.1	2884.5	3307.1	4516.2	573.0	3437.6	3210.8	3846.3	1125.8	451.2	4527.1
110.1	2127.7	4843.8	3555.9	1093.0	2411.1	2539.3	2942.8	989.2	778.3	2587.9
179.9	4784.9	6964.1	8157.9	1412.0	5056.5	6044.0	6702.5	1837.7	1405.3	8027.3
5127.0	7618.1	9095.4	11619.9	4301.3	8054.6	8648.1	9180.4	4902.3	3611.0	11612.8
3519.6	4674.4	6382.0	5787.6	4300.3	4273.2	3827.6	4479.4	3968.1	5251.0	6208.9
265.8	932.5	1276.5	1185.1	936.6	1416.0	1124.1	1419.5	821.4	438.4	1354.6
2117.1	6607.2	9315.2	12028.4	2537.3	6657.6	7180.0	9571.0	3412.0	1667.5	12243.5
1145.8	6773.4	7789.9	9372.9	5060.7	6348.3	6184.1	6980.3	6471.0	3589.8	7930.7
647.5	3050.3	2803.7	2679.4	2195.6	2667.0	2463.5	2774.0	2574.1	2376.5	4157.6
397.6	3409.5	3250.1	3764.4	1961.1	3095.1	4927.0	3045.8	969.7	444.9	3278.6
12568.0	8445.6	8868.5	8817.8	6039.2	8111.9	6669.6	8257.6	8672.1	4562.2	12648.6
919.3	5739.8	6986.2	8420.8	5106.3	6940.7	8325.8	6899.8	3936.6	3110.6	7976.1
6752.1	4538.7	4276.0	4565.9	4155.4	4245.8	6135.4	4972.6	5327.9	3697.8	4667.4
1422.9	3507.4	4874.3	5877.6	4754.7	4725.4	5275.6	4777.8	6087.8	3883.1	6819.9
216.1	744.1	366.6	756.9	473.8	647.4	514.9	602.8	446.0	299.5	1142.9
57.6	1066.6	1863.0	2501.9	409.5	1612.7	1627.1	2377.6	369.4	404.2	2409.5

2367.3	1876.4	1516.0
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4552.8	2243.9	1231.5
445.7	832.0	447.3
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7125.2	5140.6	4563.5
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438.1	597.7	404.6
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1178.5	1446.1	898.0
514.9	503.1	439.7
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1323.5	1425.7	474.9
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145.5	239.8	202.8
3684.4	2442.1	1421.4
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681.1	1123.4	1066.8
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749.6	540.2	216.6
751.4	466.2	85.8
2883.4	2581.2	1678.4
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1933.8	2337.0	1735.4
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7042.1	6227.9	5510.0
4708.9	6754.6	3916.1
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5323.5	4588.1	4510.7
3730.3	2994.5	2665.7
2360.2	1831.8	2065.9
9130.4	8716.3	5644.8
5558.9	6122.3	7148.5
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GQ261804.1 gg_id:560545 shifts taxa and response localized organic loading deep sea sediment whale falls clo GQ261
AY922199.1 gg_id:112883 whalefall clone 131631 AY9221
DQ228651.1 gg_id:142365 Microbial colonizing mineral surfaces within sulfide-microbial incubator clone CH2b1 DQ228
FJ717087.1 gg_id:562754 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United King FJ7170
AY216438.1 gg_id:82215 temperate estuarine mud clone KM51 AY2164
EU491805.1 gg_id:273299 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU4918
AY225613.1 gg_id:98692 pumice fragments exposed to Mid-Atlantic Ridge vent clone AT-pp6 AY2256
AB189375.1 gg_id:113264 cold seep sediment clone JT75-307 AB1893
FJ497428.1 gg_id:572725 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun FJ4974
AY672505.1 gg_id:107511 hydrothermal vent 9 degrees North East Rise Pacific Ocean clone CH1_22_BAC_16Sr AY6725
AB015257.1 gg_id:11113 deepest cold-seep area Japan Trench clone JTB146 proteobacterium AB0152
AJ441200.1 gg_id:57484 hydrothermal vent polychaete mucous clone P. palm C 92 AJ4412
EF999352.1 gg_id:237892 Vertical and Methanotrophs Estuarine Sediments Pearl River Estuary sediments 6cm EF9993
AM982624.1 gg_id:278960 microbial and slurry pig saw dust spent bedding clone PISD-AJC10 AM982
FJ535284.1 gg_id:512607 within iron-containing flocculent mats submarine volcanoes along Kermadec Arc iron FJ5352
EF218991.1 gg_id:206907 and Eukaryotic Hydrothermal Site East Rise Ridge Flank Abyssal Hill hydrothermal site EF2189
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FJ497261.1 gg_id:566005 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun FJ4972
AB235234.1 gg_id:141016 symbiont AB2352
FJ437839.1 gg_id:513719 Benthic okenone production Fayetteville New York Green Lake 25 m water depth clo FJ4378
AB176111.1 gg_id:175999 Microbial Hydrothermal System Suiyo Seamount on Izu-Ogasawara Arc vent area wa AB1761
FM203379.1 gg_id:370488 Biogeography filamentous and epsilonproteobacterial ectosymbionts vent shrimp e FM203
AJ515714.1 gg_id:94683 deep-sea shrimp gut clone 4 AJ5157
FM203398.1 gg_id:371282 Biogeography filamentous and epsilonproteobacterial ectosymbionts vent shrimp e FM203
AP009179.1 gg_id:249880 Sulfurovum sp. str. NBC37-1 AP0091
EF462799.1 gg_id:293907 meta-genome level extreme microbial symbiosis dorsal surface deep sea hydrothern EF4627
AJ515716.1 gg_id:94327 deep-sea shrimp gut clone 15 AJ5157
EU555122.1 gg_id:259007 Microbial Sulfide Hydrothermal Vent Field Juan de Fuca Ridge Dudley hydrothermal EU5551
AY672497.1 gg_id:102782 hydrothermal vent 9 degrees North East Rise Pacific Ocean clone CH1_1_BAC_16SrR AY6724
FJ792125.1 gg_id:510296 Unexpectedly archaeal species shift between rare and dominant over thousand year FJ7921
FJ535278.1 gg_id:554288 within iron-containing flocculent mats submarine volcanoes along Kermadec Arc iron FJ5352
AY531596.1 gg_id:100070 Indian Ocean hydrothermal vent clone SF_C23-C4_shell AY5315
DQ228647.1 gg_id:144474 Microbial colonizing mineral surfaces within sulfide-microbial incubator clone CH2b1 DQ228
AY542560.1 gg_id:113844 Gulf Mexico seafloor sediment clone GoM GB425 02B-28 AY5425
GQ249521.1 gg_id:580475 Microbial anaerobic sediments Bay Cadiz (Spain) marine sediment: 6-8 cm layer clo GQ249
GQ357025.1 gg_id:533206 Metal Dependent Marine Methane Oxidation methane seep sediment clone FeOrig_ GQ357
AF449231.1 gg_id:61878 Riftia pachyptila's tube clone R103-B15 AF4492
AB476184.1 gg_id:536849 Compositional and functional transition epibiotic microbial hydrothermal vent galat AB4761
AY531576.1 gg_id:107839 Indian Ocean hydrothermal vent clone SF_C23-G3 AY5315
FJ535277.1 gg_id:540587 within iron-containing flocculent mats submarine volcanoes along Kermadec Arc iron FJ5352

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1578.6	6401.2	5878.3	6566.5	3768.0	6733.9	5809.1	5981.8	4952.7	4123.5	6873.3
13164.3	12825.0	12560.9	14725.8	9315.5	11574.9	11714.0	10797.4	10957.9	7809.0	15549.8
58.5	110.1	310.9	246.2	37.1	44.8	112.4	76.5	47.8	49.5	259.8
708.1	5683.6	6087.9	7126.3	3128.6	6128.0	6388.6	6120.8	4535.8	3536.1	6823.3
43.4	173.1	332.0	613.2	56.8	138.4	158.3	403.1	97.2	45.6	408.2
494.2	3937.2	4090.7	3101.2	2747.8	3542.8	3467.6	3289.9	3267.7	2938.0	3405.5
66.7	630.4	1009.4	1111.9	493.3	861.7	767.0	1030.6	321.0	383.9	699.3
47.2	438.5	737.9	718.6	312.5	630.0	513.0	854.3	235.3	57.1	436.7
255.7	1541.8	2279.3	2109.7	742.6	1325.3	1370.2	1452.1	969.6	504.8	1806.2
213.3	5839.2	8158.2	8967.0	2581.6	5332.0	5163.8	6332.2	2561.0	1337.5	7370.4
34.6	16.7	19.7	26.8	22.8	15.6	22.2	17.1	25.9	24.4	27.6
41.9	412.8	1147.1	1436.9	46.3	333.2	681.6	1222.6	320.4	60.7	1041.6
5946.6	3577.7	4379.8	5224.3	4036.6	5180.0	4456.1	4445.5	2682.9	1878.0	7001.1
3561.3	4779.1	5273.4	6047.0	4074.2	4920.0	4974.3	5810.8	4430.5	3021.2	5979.3
4411.8	6206.2	6090.5	7785.7	3968.1	6050.4	6397.1	6348.2	7370.4	5083.2	8254.8
285.1	3484.6	3817.5	4388.8	1561.2	3625.1	2946.8	3907.2	1402.1	1285.4	3101.4
135.3	4032.1	6105.5	8187.4	2622.2	3330.6	3952.0	5983.7	1745.5	2333.4	5795.2
544.2	5723.0	7204.8	8323.7	5574.9	6667.2	6445.3	7826.9	5387.1	6453.1	13955.1
42.4	776.2	1472.2	1537.9	94.0	762.2	565.1	1101.1	285.0	89.4	1145.8
5789.3	12051.9	12636.7	15354.7	7876.1	11926.7	12340.9	12127.4	9316.6	8223.7	18148.6
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9026.7	4903.5	4988.8	5515.1	5783.5	6636.4	5867.5	5016.5	7281.2	8195.6	6514.5
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17663.0	6228.4	6393.0	5944.1	5479.1	6123.5	5926.3	7031.8	8682.2	8924.9	10715.9
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9837.1	9584.5	7469.7
597.1	204.2	137.3
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AY225616.1 gg_id:96100 organic-rich substrate exposed to Mid-Atlantic Ridge vent clone AT-co11 AY2256
AB440165.1 gg_id:552622 Farming and harvesting filamentous vent- galatheid crab (Decapoda; Anomura) vent AB4401
EU487998.1 gg_id:570269 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU4879
FJ497296.1 gg_id:541606 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun FJ4972
GU369887.1 gg_id:519900 and mats vents Arc white filamentous microbial mat photic shal hydrothermal vent GU369
FJ535276.1 gg_id:511548 within iron-containing flocculent mats submarine volcanoes along Kermadec Arc iron FJ5352
AY549001.2 gg_id:101316 marine bone clone sacC13A3 AY5490
FJ535285.1 gg_id:554836 within iron-containing flocculent mats submarine volcanoes along Kermadec Arc iron FJ5352
AY225623.1 gg_id:98432 iron-rich substrate exposed to Mid-Atlantic Ridge vent clone AT-cs15 AY2256
AY531587.1 gg_id:104132 Indian Ocean hydrothermal vent clone SF_C23-D11_shell AY5315
AY672538.1 gg_id:105257 hydrothermal vent 9 degrees North East Rise Pacific Ocean clone CH9_1_BAC_16SrR AY6725
AB440171.1 gg_id:569838 Farming and harvesting filamentous vent- galatheid crab (Decapoda; Anomura) vent AB4401
AY531601.1 gg_id:104446 Indian Ocean hydrothermal vent clone SF_C23-C7_shell AY5316
FJ535304.1 gg_id:554479 within iron-containing flocculent mats submarine volcanoes along Kermadec Arc iron FJ5353
EU652643.1 gg_id:278085 Seasonal variation microbial Yel Sea sediment clone B8S-12 EU6526
EU555129.1 gg_id:268986 Microbial Sulfide Hydrothermal Vent Field Juan de Fuca Ridge Dudley hydrothermal EU5551
DQ071277.1 gg_id:139667 dominate filamentous sulfur mat 13 degree north field East Pacific Rise deep-sea hy DQ071
EF462802.1 gg_id:289264 meta-genome level extreme microbial symbiosis dorsal surface deep sea hydrotherm EF4628
AJ441206.1 gg_id:57471 hydrothermal vent polychaete mucous clone P. palm C/A 113 AJ4412
EF462624.1 gg_id:296130 meta-genome level extreme microbial symbiosis dorsal surface deep sea hydrotherm EF4626
AB530172.1 gg_id:559058 Monitoring Suez and Tokyo bays based on analyses marine sediment clone Suez..Ba AB5301
FM165251.1 gg_id:558481 seep chitineous tube vestimentiferan tubeworm Lamellibrachia sp. cold seeps clone FM165
AF420359.1 gg_id:67782 hydrothermal sediment clone AF420359 AF4203
AB205405.1 gg_id:115002 Alviniconcha aff. hessleri gill endosymbiont AB2054
EF462766.1 gg_id:300444 meta-genome level extreme microbial symbiosis dorsal surface deep sea hydrotherm EF4627
AY531572.1 gg_id:107247 Indian Ocean hydrothermal vent clone SF_C23-G9 AY5315
FJ712419.1 gg_id:526671 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) K FJ7124
AF029044.1 gg_id:11139 Benzene mineralizing consortium complete clone SB-17 AF0290
EF462668.1 gg_id:299697 meta-genome level extreme microbial symbiosis dorsal surface deep sea hydrotherm EF4626
AY531593.1 gg_id:99597 Indian Ocean hydrothermal vent clone SF_C23-E5_shell AY5315
AY225618.1 gg_id:98223 organic-rich substrate exposed to Mid-Atlantic Ridge vent clone AT-co12 AY2256
AY672511.1 gg_id:103076 hydrothermal vent 9 degrees North East Rise Pacific Ocean clone CH1_3f_BAC_16SrF AY6725
DQ270643.1 gg_id:142040 hydrothermal carbonate chimney clone LC1133B-58 DQ270
EU107475.1 gg_id:349595 Identification Ectosymbiont on Hair Inhabiting Hydrothermal Vents hair Shinkaia cro EU1074
AY225625.1 gg_id:98807 iron-rich substrate exposed to Mid-Atlantic Ridge vent clone AT-cs7 AY2256
FM165253.1 gg_id:558667 seep chitineous tube vestimentiferan tubeworm Lamellibrachia sp. cold seeps clone FM165
AB099998.1 gg_id:79591 inactive deep-sea hydrothermal vent chimneys clone IndB1-30 AB0999
DQ394973.1 gg_id:153118 harbor sediment clone VHS-B3-94 DQ394
EF462777.1 gg_id:288783 meta-genome level extreme microbial symbiosis dorsal surface deep sea hydrotherm EF4627
AY531595.1 gg_id:99906 Indian Ocean hydrothermal vent clone SF_C23-E10_shell AY5315
EU265786.1 gg_id:258528 epibiotic assemblage recently described Yeti Kiwa hirsuta (Kiwidae) surface crab hyc EU2657

2289.8	897.2	886.3	889.4	783.9	1010.7	853.7	2933.5	668.6	732.9	3098.0
12788.3	3217.9	3474.6	4521.3	3560.3	3467.4	4412.2	5157.2	2305.0	1912.5	4282.1
10430.6	7912.2	8182.0	8859.5	9057.0	7973.8	9643.4	8430.0	12095.2	10907.4	9802.9
259.5	1086.2	1139.5	1266.6	2622.8	1036.6	1196.1	1161.0	1195.3	868.6	1115.6
471.8	4365.1	4502.1	5769.4	3337.3	4539.7	3477.7	5916.2	2583.2	4322.3	5437.1
778.3	1437.4	1726.1	2288.5	653.5	1726.0	1243.8	1259.3	582.0	194.8	1956.9
45.5	1247.5	1203.4	1001.4	346.6	934.2	447.1	1174.5	601.9	180.6	1399.3
3616.5	6666.3	5959.2	7022.0	2510.4	5822.3	5283.1	3344.9	3653.2	2936.4	7006.1
2211.9	569.9	573.3	722.4	576.2	539.5	537.5	699.3	370.2	185.4	286.9
6507.6	1367.9	1930.0	1921.6	1438.9	1256.8	1664.6	1334.5	2943.4	2986.1	2348.0
127.9	379.3	287.9	403.2	125.8	199.5	118.3	215.4	190.6	136.0	207.0
43.5	390.4	561.9	566.4	248.6	392.1	400.4	608.6	285.3	76.2	292.3
2945.8	1959.6	1705.4	2374.2	2074.5	1866.9	1987.6	1678.0	3213.8	1661.3	2426.2
1012.4	2644.5	2828.2	3956.8	1761.8	3200.7	2002.1	2591.4	1508.4	2120.3	3094.7
20242.3	6346.1	4899.6	6003.7	5882.8	5057.0	6020.2	5493.3	8910.7	6273.8	8107.6
57.8	984.8	1758.6	1506.1	522.5	891.7	1163.0	1213.7	184.1	66.0	657.0
495.5	2548.3	2268.0	2515.6	2137.7	2083.6	2104.7	2243.7	2631.1	3710.5	2585.0
20878.4	7923.2	7801.3	8853.8	6517.9	7886.6	7716.4	6897.7	9311.1	8865.5	11144.9
3422.9	4221.9	3699.0	3683.7	3502.6	3240.2	3438.5	3403.0	3559.8	2410.9	3902.1
797.5	2888.2	3031.0	3298.3	2540.0	3465.0	2935.8	3255.4	3045.1	5286.3	4038.0
7086.8	5006.0	4524.0	5440.3	4665.4	4208.2	4858.6	5522.5	4639.0	3158.0	5216.5
10980.8	4126.5	4541.5	4046.3	4881.8	3874.3	4631.1	4670.1	5416.1	3972.7	7521.5
6965.8	2546.4	2465.5	2734.4	2413.6	3183.2	2624.9	4012.2	2607.7	219.6	2805.2
4142.9	3926.9	4282.9	4715.2	4963.8	4583.1	5035.6	6343.5	6491.2	3594.8	7489.8
232.9	670.0	901.4	904.7	552.8	1113.1	802.6	1013.5	304.4	446.8	904.7
46.9	447.8	569.2	647.0	139.5	689.0	364.6	531.2	101.6	69.7	337.0
566.7	4019.9	3892.7	4605.3	1769.8	3607.4	3170.3	6998.5	2190.7	1259.2	7428.2
45.4	497.4	751.4	1058.4	325.5	520.8	500.2	1092.3	135.6	80.5	281.6
9622.9	5474.9	5758.7	7239.4	5656.9	5073.6	5406.2	4768.9	8125.7	6943.9	7149.7
56.5	68.3	173.3	82.9	49.5	88.3	78.2	70.2	54.2	26.7	54.3
842.7	2022.1	2653.6	2630.6	1326.2	1799.1	1614.2	2056.5	716.9	1229.4	1499.6
987.0	4699.1	5368.0	6343.1	4405.0	5519.4	5092.3	4833.1	4366.9	4389.4	5656.8
2778.3	1260.9	1055.4	1219.7	1272.4	1405.4	1351.1	1279.6	542.3	440.6	449.7
80.0	2023.7	2326.1	3058.6	1466.5	2550.1	1969.3	2411.1	1070.6	393.6	1987.3
408.8	2030.8	1980.3	2288.5	560.9	2133.2	1526.9	2646.9	976.4	542.7	4760.7
82.9	332.6	321.7	336.9	1288.4	424.3	356.7	264.5	86.9	62.0	177.7
856.4	2141.1	2051.5	2141.7	1535.2	2327.2	1510.4	2928.1	1780.7	660.8	1911.0
3134.0	8161.7	8063.8	8241.6	7079.2	6776.7	7109.1	8367.4	7082.4	4496.0	9161.0
6498.0	3979.9	4164.0	5577.5	3551.0	3967.7	3992.3	3483.6	4870.1	4115.2	5522.4
120.4	2091.9	2526.8	2572.4	2742.3	2995.5	2495.0	3996.1	2082.1	3045.7	2330.8
157.2	2195.4	1127.7	2300.5	1692.1	2132.7	2213.4	2310.1	1215.6	735.2	2177.9

1526.3	1741.7	875.8
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306.2	590.0	593.1
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6312.8	5892.1	4234.7
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184.7	685.6	327.4
1885.8	2082.0	1871.8
7342.5	6294.7	6921.5
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AY280405.1 gg_id:100364 exterior deep-sea hydrothermal vent sulfide chimney Juan de Fuca Ridge Pacific Oce AY2804
AJ575963.1 gg_id:95437 deep sea hydrothermal vent clone T3-Hot3-706 AJ5759
AY531597.1 gg_id:100222 Indian Ocean hydrothermal vent clone SF_C23-B7_shell AY5315
AM176867.1 gg_id:161081 Recovery mangrove sediment clone SZB13 AM176
EU265795.1 gg_id:262084 epibiotic assemblage recently described Yeti Kiwa hirsuta (Kiwidae) surface crab hyc EU2657
EU662602.1 gg_id:577333 Productivity- Chemolithoautotrophically Based Sulfidic Karst Systems floating microb EU6626
AB476188.1 gg_id:536599 Compositional and functional transition epibiotic microbial hydrothermal vent galath AB4761
AY197378.1 gg_id:83351 Guaymas Basin hydrothermal vent sediments clone B01R006 AY1973
FJ535271.1 gg_id:544300 within iron-containing flocculent mats submarine volcanoes along Kermadec Arc iron FJ5352
EF462600.1 gg_id:303123 meta-genome level extreme microbial symbiosis dorsal surface deep sea hydrotherm EF4626
EU265785.1 gg_id:277410 epibiotic assemblage recently described Yeti Kiwa hirsuta (Kiwidae) surface crab hyc EU2657
DQ394894.1 gg_id:151332 harbor sediment clone VHS-B1-11 DQ394
AY531575.1 gg_id:107689 Indian Ocean hydrothermal vent clone SF_C23-G4 AY5315
AY531585.1 gg_id:103824 Indian Ocean hydrothermal vent clone SF_C23-C11_shell AY5315
AY225614.1 gg_id:96015 iron-rich substrate exposed to Mid-Atlantic Ridge vent clone AT-cs3 AY2256
AB232530.1 gg_id:151369 Prokaryotic gills deep-sea hydrothermal vent shrimp gill Alvinocaris longirostris clone AB2325
DQ270645.1 gg_id:143843 hydrothermal carbonate chimney clone LC1133B-68 DQ270
AY531600.1 gg_id:104287 Indian Ocean hydrothermal vent clone SF_C23-C8_shell AY5316
AY531591.1 gg_id:99285 Indian Ocean hydrothermal vent clone SF_C23-B1_shell AY5315
AY327882.1 gg_id:90455 surface vent snail foot clone SF_C4-D5 AY3278
AY225624.1 gg_id:97289 pumice fragments exposed to Mid-Atlantic Ridge vent clone AT-pp27 AY2256
AF420351.1 gg_id:67787 hydrothermal sediment clone AF420351 AF4203
EU617859.1 gg_id:345356 Seasonal variation microbial Yel Sea sediment clone D13S-42 EU6178
FJ799124.1 gg_id:510696 Microbial Responsible Intermediates Degradation Anaerobic Digestion System Deterr FJ7991
AY225622.1 gg_id:97434 iron-rich substrate exposed to Mid-Atlantic Ridge vent clone AT-cs8 AY2256
EF462801.1 gg_id:299935 meta-genome level extreme microbial symbiosis dorsal surface deep sea hydrotherm EF4628
DQ270655.1 gg_id:141448 hydrothermal carbonate chimney clone LC1404B-6 DQ270
FJ535259.1 gg_id:542712 within iron-containing flocculent mats submarine volcanoes along Kermadec Arc iron FJ5352
GQ167319.1 gg_id:562624 Microbial Life -13C Brine Ice-Sealed Antarctic ice-entrained brine 16.5 m Lake Vida c GQ167
FJ535292.1 gg_id:551198 within iron-containing flocculent mats submarine volcanoes along Kermadec Arc iron FJ5352
AF449253.1 gg_id:61855 Riftia pachyptila's tube clone R76-B151 AF4492
AY672522.1 gg_id:99252 hydrothermal vent 9 degrees North East Rise Pacific Ocean clone CH3_9_BAC_16SrRN AY6725
DQ071276.1 gg_id:140018 dominate filamentous sulfur mat 13 degree north field East Pacific Rise deep-sea hy DQ071
EF462733.1 gg_id:291526 meta-genome level extreme microbial symbiosis dorsal surface deep sea hydrotherm EF4627
AY704398.1 gg_id:112176 oceanic crust clone FS275-77B-03 AY7043
AB440161.1 gg_id:549495 Farming and harvesting filamentous vent- galatheid crab (Decapoda; Anomura) vent AB4401
EF462696.1 gg_id:289073 meta-genome level extreme microbial symbiosis dorsal surface deep sea hydrotherm EF4626
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AB239758.1 gg_id:149235 filamentous epibiont Vulcanolepas osheai AB2397
FJ535270.1 gg_id:533833 within iron-containing flocculent mats submarine volcanoes along Kermadec Arc iron FJ5352

1133.8	5008.2	4753.9	5448.4	2651.2	4511.5	4009.1	3345.4	3823.0	2197.5	5367.3
53.5	1226.9	1407.9	1764.5	662.6	2167.2	1001.1	1590.2	629.0	209.6	1383.3
171.1	6400.9	6157.5	8021.2	5790.4	7021.1	8334.4	8054.8	4949.0	2111.2	8244.3
76.0	149.7	267.1	181.2	118.8	144.8	144.8	192.6	97.5	47.4	114.2
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2950.4	4049.0	3649.4	4653.9	3580.6	3493.4	3674.0	3747.2	3155.5	3010.9	3854.2
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FJ535266.1 gg_id:569006 within iron-containing flocculent mats submarine volcanoes along Kermadec Arc iron FJ5352
EU265789.1 gg_id:258893 epibiotic assemblage recently described Yeti Kiwa hirsuta (Kiwidae) surface crab hyc EU265
AM268719.1 gg_id:232342 Fluid chemistry and microbial southern hydrothermal field (Lilliput) on Mid-Atlantic AM268
AF154091.1 gg_id:11137 hydrocarbon seep clone BPC056 AF154
DQ071288.1 gg_id:139782 dominate filamentous sulfur mat 13 degree north field East Pacific Rise deep-sea hy DQ071
AB440162.1 gg_id:557961 Farming and harvesting filamentous vent- galatheid crab (Decapoda; Anomura) vent AB440
GQ261779.1 gg_id:573816 shifts taxa and response localized organic loading deep sea sediment whale falls clo GQ261
EF462627.1 gg_id:297366 meta-genome level extreme microbial symbiosis dorsal surface deep sea hydrotherm EF4626
EU487914.1 gg_id:538726 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU487
EF462714.1 gg_id:293356 meta-genome level extreme microbial symbiosis dorsal surface deep sea hydrotherm EF4627
AB193955.1 gg_id:108919 deep-sea vent clone Sd-EB04 AB193
EF462827.1 gg_id:292616 meta-genome level extreme microbial symbiosis dorsal surface deep sea hydrotherm EF4628
AY531571.1 gg_id:107097 Indian Ocean hydrothermal vent clone SF_C23-H10 AY5315
FJ535282.1 gg_id:538493 within iron-containing flocculent mats submarine volcanoes along Kermadec Arc iron FJ5352
DQ394936.1 gg_id:153573 harbor sediment clone VHS-B3-29 DQ394
AB188786.1 gg_id:113953 cold seep sediment clone SB5-11 AB188
FJ497361.1 gg_id:542661 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun FJ4973
AB278150.1 gg_id:177809 hydrothermal vent prokaryotes trapped 0.2- and 0.1-micro-m-filtrates obtained Mar AB278
AF121887.1 gg_id:11128 2-bromophenol-dehalogenating consortium clone 2BP-7 AF1218
FM203396.1 gg_id:423805 Biogeography filamentous and epsilonproteobacterial ectosymbionts vent shrimp e FM203
EF061978.1 gg_id:190937 Xiamen China mangrove sediment clone XME34 EF0619
AY327881.1 gg_id:88572 surface vent snail foot clone SF_C4-C4 AY3278
FJ497343.1 gg_id:549911 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun FJ4973
FJ497347.1 gg_id:582544 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun FJ4973
GU180158.1 gg_id:537179 Impact coplanar PCBs on microbial activity anaerobic estuarine sediments sediment GU180
EU107476.1 gg_id:343167 Identification Ectosymbiont on Hair Inhabiting Hydrothermal Vents hair Shinkaia cro EU107
EU662505.1 gg_id:571991 Productivity- Chemolithoautotrophically Based Sulfidic Karst Systems microbial mat EU662
EF462800.1 gg_id:293062 meta-genome level extreme microbial symbiosis dorsal surface deep sea hydrotherm EF4628
FJ497375.1 gg_id:581955 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun FJ4973
GQ249549.1 gg_id:575344 Microbial anaerobic sediments Bay Cadiz (Spain) marine sediment: 12-14 cm layer c GQ249
FJ264679.1 gg_id:328542 Manganese and Iron Dependent Anaerobic Oxidation Methane methane seep sedim FJ2646
EF687491.1 gg_id:284524 Biogeochemistry iron- and sulfur-precipitating microbial mats (Nile Mediterranean) s EF6874
FJ905647.1 gg_id:545620 s Tonga-Kermadec iron oxide chimney-like structure on Volcano 19 Tonga Arc clone V FJ9056
AY531592.1 gg_id:99437 Indian Ocean hydrothermal vent clone SF_C23-B12_shell AY5315
FJ497326.1 gg_id:571424 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun FJ4973
FJ717162.1 gg_id:554142 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United King FJ7171
FJ497317.1 gg_id:574124 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun FJ4973
FJ535287.1 gg_id:544443 within iron-containing flocculent mats submarine volcanoes along Kermadec Arc iron FJ5352
FJ497276.1 gg_id:586842 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun FJ4972
EF061975.1 gg_id:175519 Xiamen China mangrove sediment clone XME6 EF0619
AY672498.1 gg_id:102927 hydrothermal vent 9 degrees North East Rise Pacific Ocean clone CH1_10_BAC_16Sr AY6724

1389.5	458.8	713.8	583.3	358.3	773.8	333.0	492.0	347.4	1126.3	136.8
164.5	405.8	808.5	530.1	403.4	1005.4	369.2	3936.5	404.2	473.7	3984.4
20548.6	5806.7	6378.0	5515.9	5943.5	5357.1	6289.9	5745.0	7419.1	6438.4	6642.6
233.1	1212.5	1480.5	1799.2	1235.4	1806.2	1616.1	1438.2	808.6	637.7	1359.1
49.7	144.5	401.4	211.1	84.2	151.9	111.8	131.6	32.7	45.7	133.8
71.7	125.3	157.3	123.6	101.5	140.7	224.5	93.4	53.3	38.9	40.5
36.2	162.2	176.9	198.1	43.1	193.1	126.6	58.4	79.8	66.0	96.7
2637.0	1870.6	2782.4	2761.9	1674.0	2146.7	1934.7	2082.7	1469.9	1337.7	2378.0
3330.7	5497.6	5809.4	6315.9	2834.7	4629.4	5013.5	5368.5	5578.2	4365.4	9112.3
11787.4	6522.7	6941.8	8026.2	7449.5	7336.3	8552.1	7288.3	7123.1	8686.1	9090.8
512.2	1238.9	2122.1	1658.2	1072.0	1546.5	1479.7	1463.8	968.3	1889.2	1827.9
565.9	5919.1	7573.3	5789.8	3047.3	5360.7	4510.9	4775.7	5228.0	4924.0	8388.7
565.1	3417.1	5192.2	5167.1	2590.3	4934.2	3383.6	2843.6	3908.4	1941.6	4284.2
6147.7	6731.6	5132.0	6201.2	3309.2	4904.6	5007.8	4127.4	3764.0	4434.3	6768.8
40.8	23.7	59.8	79.0	26.7	38.4	33.8	48.5	35.2	30.4	53.1
4955.1	4180.3	4286.8	4217.4	3872.2	4535.4	4426.5	4239.2	4648.7	4784.6	5332.0
1110.0	958.7	792.6	1030.2	756.4	1061.4	723.2	651.0	403.3	266.4	637.7
37.0	360.2	421.9	452.5	262.2	402.9	431.2	434.1	198.0	154.8	231.1
36.6	159.7	179.3	231.8	102.6	118.6	193.3	121.9	66.0	30.6	93.2
169.5	248.8	359.1	447.5	504.5	355.3	290.9	576.6	164.2	209.5	194.7
621.0	1958.2	1742.0	1619.5	1276.5	1531.4	1311.8	1941.2	1302.0	1441.4	1819.7
11684.3	2812.0	2760.4	3009.0	2152.5	2815.3	2767.3	2239.4	3244.4	3167.2	4245.9
376.5	1181.8	1282.2	1830.1	606.9	1373.2	983.2	1128.2	460.9	155.9	1276.9
2397.3	4618.7	5268.4	5953.5	3208.3	5675.2	4378.8	4338.9	4642.2	3079.1	5411.7
3703.3	6713.5	7581.6	7974.2	5432.9	6880.0	7383.7	8198.3	6072.6	5545.8	10679.2
52.2	45.4	45.9	29.5	62.8	42.3	50.5	102.3	22.4	18.3	55.3
51.8	1488.2	1947.1	2276.5	533.8	1314.3	1275.0	1994.4	378.5	273.3	1759.1
3507.4	5262.4	5594.4	5658.2	3119.2	4708.0	3973.8	3839.7	5297.0	2757.0	7084.4
344.9	4691.7	3618.6	5087.7	3844.0	4288.1	4590.1	4639.3	2864.7	1529.0	4659.0
3081.8	5002.8	4870.2	5493.7	5854.5	4843.8	4990.6	5133.1	6069.0	7514.0	7266.7
20882.8	9322.6	8452.9	9526.1	5799.7	8798.0	7897.7	7366.3	8309.2	6461.1	12088.8
57.1	1336.0	1459.1	2036.6	651.7	2036.3	1252.7	1691.5	788.4	295.7	1497.7
48.3	446.0	549.4	772.2	323.3	632.6	555.9	542.8	113.4	82.9	286.5
10100.3	1863.0	2203.4	1963.9	2240.8	2195.7	2719.4	2226.3	2302.7	1896.3	2309.5
257.9	1321.8	1337.6	1728.2	960.2	1682.3	1000.2	1195.8	742.5	716.7	954.3
503.6	4752.3	4701.2	6009.8	1936.8	5113.3	3594.0	4893.7	1974.0	693.3	5637.0
418.3	3189.3	3351.9	3457.1	2065.4	3098.3	2920.8	2519.6	3421.9	3827.9	4361.0
44.1	407.3	406.8	489.7	264.5	420.7	248.6	586.2	144.3	71.6	308.0
1238.9	4639.7	5323.9	4605.1	2312.3	4866.9	3287.6	3954.4	2698.8	1663.8	6006.3
2615.2	2593.6	2367.0	2849.7	1965.6	2290.3	2734.3	2348.6	2607.8	1744.3	2654.1
146.1	515.6	497.9	597.2	339.1	478.4	338.2	599.7	339.6	93.1	304.7

1539.5	1488.1	272.7
1754.7	830.3	768.5
4754.9	6105.8	6154.1
1457.1	1620.1	1548.5
133.0	309.1	234.9
112.9	77.1	149.9
42.3	118.2	132.2
1898.4	1778.6	1876.0
3993.9	4767.9	3308.7
10039.4	8473.7	6229.7
1819.8	2146.1	1009.9
4983.9	4342.5	3595.9
2536.6	2391.8	2465.6
4554.3	4739.9	3238.9
28.1	60.7	24.0
4555.5	5250.0	3883.1
184.3	929.6	753.7
326.2	410.7	255.0
114.2	193.6	203.6
478.1	912.1	382.1
1524.8	1509.4	2866.8
2135.7	3062.1	2117.4
678.3	946.4	680.7
3398.1	4445.4	3749.9
5297.3	6896.1	5171.9
66.9	92.9	58.9
1023.4	840.8	705.2
3167.3	4044.1	2907.7
3866.5	5236.6	4965.9
6082.4	4980.0	5546.4
6397.4	7003.1	5681.7
1117.1	1296.5	964.9
393.2	475.1	739.8
1672.6	3155.8	2483.8
1356.1	1498.1	1111.6
2877.4	2083.9	1914.2
2157.7	2862.6	2366.7
326.0	498.0	455.0
2565.4	2961.9	2943.5
559.6	2293.8	2582.7
348.8	402.1	340.1

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AF449251.1 gg_id:61858 Riftia pachyptila's tube clone R76-B78 AF449
L35520.1 gg_id:11121 Alvinella pompejana L3552
GU369898.1 gg_id:520798 and mats vents Arc white filamentous microbial mat photic shal hydrothermal vent GU369
AY327880.1 gg_id:88951 surface vent snail foot clone SF_C5-F8 AY327
FJ712566.1 gg_id:508922 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) FJ7125
DQ925872.1 gg_id:241522 Microbes and Thermal Gradients Temperature Hydrothermal Chimneys hydrotherm DQ925
EF462629.1 gg_id:295292 meta-genome level extreme microbial symbiosis dorsal surface deep sea hydrotherm EF462
GQ261802.1 gg_id:543184 shifts taxa and response localized organic loading deep sea sediment whale falls clo GQ261
AF420344.1 gg_id:67793 hydrothermal sediment clone AF420344 AF420
DQ295602.2 gg_id:159750 Epsilonproteobacteria terrestrial caves and springs microbial mat sulfidic spring Drin DQ295
FJ497396.1 gg_id:542332 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun FJ4973
EF462824.1 gg_id:302928 meta-genome level extreme microbial symbiosis dorsal surface deep sea hydrotherm EF462
AB187014.1 gg_id:101863 Suiyo seamount hydrothermal vent water 0.2micro-m filterable fraction clone SSM-E AB187
AY542550.1 gg_id:114277 Gulf Mexico seafloor sediment clone GoM GB425 02B-9 AY542
FJ902253.1 gg_id:571547 phreatic limestone sinkholes northeastern Mexico water column 32m deep cenote C FJ9022
FJ264760.1 gg_id:339147 Manganese and Iron Dependent Anaerobic Oxidation Methane methane seep sedim FJ2647
AY355304.2 gg_id:101665 epibiontic clone C11-C9 AY355
AB091292.1 gg_id:84230 Sulfurovum lithotrophicum str. 42BKT AB091
AY672512.1 gg_id:103225 hydrothermal vent 9 degrees North East Rise Pacific Ocean clone CH3_1_BAC_16SrR AY672
AY531604.1 gg_id:104899 Indian Ocean hydrothermal vent clone SF_C23-F6 AY531
AJ132737.1 gg_id:20059 hydrothermal vent clone Top-147 AJ1327
AY672506.1 gg_id:107659 hydrothermal vent 9 degrees North East Rise Pacific Ocean clone CH1_23_BAC_16Sr AY672
EU245507.1 gg_id:252330 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M2-D1 EU245
FJ165504.1 gg_id:539775 Microbially-enhanced Dissolution Karst Carbonates microbial biofilm Sonterra #8 well FJ1655
DQ295697.1 gg_id:160880 Epsilonproteobacteria terrestrial caves and springs floating microbial mat sulfidic gr DQ295
AF449236.1 gg_id:61874 Riftia pachyptila's tube clone R103-B37 AF449
AY672537.1 gg_id:105096 hydrothermal vent 9 degrees North East Rise Pacific Ocean clone CH9_6_BAC_16SrR AY672
AJ969446.1 gg_id:158924 Microbial black smoker s Mid Atlantic Ridge ecological implications rock fragments c AJ9694
GU390848.1 gg_id:530358 Dark hot springs: structure biofilms caves Acquasanta Terme (Italy) sulfidic cave stre GU390
AM745162.1 gg_id:292405 Impact oil er hydrocarbons on microbial and activity Gulf Mexico cold seep marine s AM745
AF420360.1 gg_id:67780 hydrothermal sediment clone AF420360.1 AF420
AF420342.1 gg_id:67795 hydrothermal sediment clone AF420342 AF420
AB105048.1 gg_id:93761 Hydrogenimonas thermophila str. EP1-55-1% AB105
AY261811.1 gg_id:83596 UASB reactor granular sludge clone PD-UASB-2 proteobacterium AY261
DQ295692.1 gg_id:161262 Epsilonproteobacteria terrestrial caves and springs floating microbial mat sulfidic gr DQ295
AY531574.1 gg_id:107543 Indian Ocean hydrothermal vent clone SF_C23-G7 AY531
AB278149.1 gg_id:184732 hydrothermal vent prokaryotes trapped 0.2- and 0.1-micro-m-filtrates obtained Mar AB278
AB175498.1 gg_id:106632 Thioreductor micantisoli str. BKB25Ts-Y AB175
EF467531.1 gg_id:213162 situ microelectrode voltammetry sulfur-oxidizing biofilms Frasassi sulfidic cave strear EF467
FJ497432.1 gg_id:556468 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun FJ4974
EF467559.1 gg_id:211322 situ microelectrode voltammetry sulfur-oxidizing biofilms Frasassi sulfidic cave strear EF467

47.2	838.3	1136.2	1541.1	238.2	2143.5	857.5	884.3	181.7	123.5	721.1
19028.7	5510.8	5462.1	5757.5	5446.9	4319.6	5556.1	5290.5	7317.8	6341.0	7829.8
37.3	787.1	652.5	843.2	383.3	825.6	526.3	1017.4	147.9	126.9	455.2
6032.7	4880.0	5635.2	4816.8	3155.1	3807.9	3791.5	4384.3	4760.2	4554.3	5453.0
265.6	2813.3	2426.6	2957.4	1027.3	2836.1	2197.1	7058.8	991.7	595.9	7713.4
978.4	3540.1	3491.2	3727.6	3653.7	3234.9	3733.7	3466.7	2849.2	2004.7	3011.5
3206.4	6339.3	5832.6	6644.2	5726.7	5528.4	6000.5	6029.8	6315.3	6200.5	7028.1
3221.0	4429.8	3836.4	4476.8	1367.0	3959.6	3662.2	4301.2	1548.2	548.3	5309.1
4532.3	4191.7	4852.5	5286.8	3031.5	4535.8	3300.1	3828.4	6209.8	4926.0	4740.0
2965.8	3566.1	3565.6	4015.3	2884.1	3943.0	3344.7	4523.8	2803.1	1019.6	4468.0
732.3	2503.6	2779.1	3003.8	1833.0	3208.9	2882.7	2441.8	820.9	1093.0	2428.2
1299.4	8047.4	9179.6	9164.2	5835.9	7777.5	7051.3	7374.9	9114.0	6163.3	8948.8
40.9	302.4	333.2	388.5	332.6	549.7	200.1	415.9	197.8	76.0	363.9
1026.9	5188.5	5235.6	4982.1	3339.2	4790.1	3224.9	7408.8	3924.6	2770.9	5930.0
62.3	2923.9	3180.2	2822.9	1147.0	2756.6	1131.3	2855.9	1785.7	3106.4	4501.3
210.5	1982.0	2308.0	2904.6	1561.3	3241.6	2040.6	2615.0	906.9	1071.5	1942.6
28.4	996.6	1398.1	632.6	342.9	630.0	230.2	798.8	216.0	145.0	805.0
219.8	1622.1	2024.1	2701.4	1243.7	2071.1	2254.6	2726.6	1064.7	1154.4	2611.3
38.1	20.9	14.6	23.9	10.1	22.6	15.2	22.4	12.6	8.7	20.1
73.6	350.3	546.5	491.9	354.3	487.5	580.2	590.7	168.2	63.9	228.1
74.9	199.1	399.7	354.7	118.1	229.4	184.7	239.4	84.9	45.8	208.0
501.0	2171.2	2544.7	3093.3	1790.7	2815.0	2348.3	2435.4	1515.9	1622.1	2269.1
37.3	356.7	573.6	365.7	176.4	291.1	336.1	467.9	92.0	46.2	298.1
4004.8	6673.5	8772.5	8093.2	6889.3	6175.6	6575.8	7252.7	11290.6	7347.3	9554.3
9622.3	3724.3	4510.4	3708.1	3663.8	3501.9	4062.6	3648.4	3905.1	3348.1	4510.2
30.7	12.3	17.2	17.4	11.8	13.2	13.0	12.8	10.2	10.4	18.4
3326.5	5046.9	4582.6	5205.6	4830.6	4627.8	4986.6	4470.6	7130.3	4988.0	5975.1
174.2	1986.1	2995.4	1669.2	1253.9	1835.8	1346.3	1871.4	1085.7	825.5	2375.6
1562.5	4975.4	4514.2	4610.3	3405.6	4992.2	4157.9	5295.1	2690.8	4928.0	4765.9
398.9	1591.3	1940.4	1456.4	1357.3	1001.0	1372.1	1395.8	444.5	331.6	1551.8
65.6	621.0	937.9	569.8	330.2	772.4	521.1	629.9	305.8	135.8	578.9
42.8	1085.6	1411.6	1191.3	986.0	1002.8	803.3	1251.5	213.4	105.2	494.5
4830.9	4081.6	4264.1	5288.1	2775.5	3761.4	3190.9	3856.3	2472.1	3163.4	3881.1
5000.2	6458.6	7519.7	9610.1	4131.7	5981.5	5273.4	6420.9	6918.0	5893.3	8652.3
890.4	2614.3	3750.7	3370.8	2790.1	3083.5	2790.7	3610.9	2295.6	896.7	3595.3
95.2	480.2	780.9	878.7	604.1	816.9	501.8	950.4	651.7	157.4	421.3
90.6	359.3	403.7	427.9	374.1	390.0	489.6	375.5	215.2	164.0	295.1
53.2	120.2	104.7	106.4	70.0	118.4	125.0	217.5	82.4	41.5	135.2
3983.0	6236.6	6716.2	7648.5	6195.4	6317.3	6163.1	6454.3	8579.0	4365.9	7497.5
59.0	1825.0	1904.6	2907.9	1181.1	1626.2	964.6	1586.8	470.8	202.2	1622.3
713.5	6677.9	6656.0	8536.7	2682.3	6786.5	3756.7	5821.7	3310.1	1355.3	6259.1

538.9	729.7	943.1
5594.1	6299.8	4856.2
493.3	709.6	709.0
2939.6	4350.6	3739.3
3880.3	1327.9	1436.4
3605.6	3930.9	3653.6
4897.7	6939.8	5386.4
2605.8	2182.2	1435.6
3384.4	5008.7	3706.4
2932.2	3529.3	3563.4
1564.5	1771.5	2288.2
7525.6	7522.8	6189.5
387.6	438.2	510.1
5688.5	5327.8	3017.8
3483.7	2873.8	814.0
2047.6	2440.3	2439.5
518.4	1025.2	495.3
1726.5	1747.9	1595.3
19.0	38.4	9.2
552.0	590.8	758.1
166.1	284.0	201.3
2238.6	2656.9	2511.6
307.4	260.1	153.5
6979.4	8038.2	6329.0
3064.4	4961.5	2437.0
9.7	21.9	12.6
4441.8	6123.1	4373.5
1914.7	2443.2	1685.6
6533.2	5749.6	4948.6
1118.1	1611.9	1520.3
432.2	759.0	274.1
602.3	665.6	437.7
2856.3	3581.6	2632.7
5078.0	6561.2	4416.1
2954.5	2863.6	2584.3
695.4	629.4	524.6
291.4	554.2	395.6
171.3	192.6	113.5
5813.0	6376.6	6046.2
1272.6	1273.0	1402.4
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AY672540.1 gg_id:100136 hydrothermal vent 9 degrees North East Rise Pacific Ocean clone CH9_5_BAC_16SrR AY6725
EF467581.1 gg_id:216198 situ microelectrode voltammetry sulfur-oxidizing biofilms Frasassi sulfidic cave strear EF4675
AM268717.1 gg_id:233206 Fluid chemistry and microbial southern hydrothermal field (Lilliput) on Mid-Atlantic AM268
AY280433.1 gg_id:106294 exterior deep-sea hydrothermal vent sulfide chimney Juan de Fuca Ridge Pacific Oce AY2804
DQ295651.1 gg_id:161606 Epsilonproteobacteria terrestrial caves and springs microbial mat sulfidic cave strea DQ295
EF462765.1 gg_id:299712 meta-genome level extreme microbial symbiosis dorsal surface deep sea hydrotherm EF4627
GU196200.1 gg_id:579980 Bioaugmentation improved recovery digesters after toxicant exposure lab-scale ana GU196
AB278151.1 gg_id:180340 hydrothermal vent prokaryotes trapped 0.2- and 0.1-micro-m-filtrates obtained Mar AB278
AY531573.1 gg_id:107393 Indian Ocean hydrothermal vent clone SF_C23-G8 AY5315
FJ799123.1 gg_id:584284 Microbial Responsible Intermediates Degradation Anaerobic Digestion System Deterr FJ7991
AJ441202.1 gg_id:57475 hydrothermal vent polychaete mucous clone P. palm C 140 AJ4412
DQ295708.1 gg_id:160328 Epsilonproteobacteria terrestrial caves and springs microbial mat sulfidic stream Mil DQ295
EF467511.1 gg_id:215667 situ microelectrode voltammetry sulfur-oxidizing biofilms Frasassi sulfidic cave strear EF4675
FJ485355.1 gg_id:545841 microbial autonomous rover world's deepest phreatic sinkhole wall biomat El Zacator FJ4853
DQ228655.1 gg_id:141137 Microbial colonizing mineral surfaces within sulfide-microbial incubator clone CH2b1 DQ228
EF462722.1 gg_id:296261 meta-genome level extreme microbial symbiosis dorsal surface deep sea hydrotherm EF4627
EU234099.1 gg_id:246280 receiving river and un techniques anaerobic process WWTP treating penicillin G prod EU2340
AJ576002.1 gg_id:98839 deep sea hydrothermal vent clone T6-Ph07-983 AJ5760
GU390742.1 gg_id:517462 Dark hot springs: structure biofilms caves Acquasanta Terme (Italy) sulfidic cave stre GU390
AY082468.1 gg_id:67838 neutral pH mine biofilm clone 44a-B1-40 AY0824
AY280427.1 gg_id:101920 exterior deep-sea hydrothermal vent sulfide chimney Juan de Fuca Ridge Pacific Oce AY2804
EF467460.1 gg_id:205100 situ microelectrode voltammetry sulfur-oxidizing biofilms Frasassi sulfidic cave strear EF4674
AB198587.1 gg_id:135519 termite gut fluid and protists fraction clone RsC01-014 AB1985
DQ295656.1 gg_id:160561 Epsilonproteobacteria terrestrial caves and springs microbial mat sulfidic cave strea DQ295
AF286053.1 gg_id:29701 Helicobacter rappini W.Tee-Yu AF2860
AY571498.1 gg_id:114816 termite gut clone RsaHf427 AY5714
GU369897.1 gg_id:528299 and mats vents Arc white filamentous microbial mat photic shal hydrothermal vent GU369
AY355299.2 gg_id:106198 epibiontic clone C11-E8 AY3552
EU662478.1 gg_id:557968 Productivity- Chemolithoautotrophically Based Sulfidic Karst Systems microbial mat EU6624
AY578096.1 gg_id:105995 Helicobacter bilis str. KI900 AY5780
AY251062.1 gg_id:103492 deep-sea hydrothermal biofilm Edmond vent field on Central Indian Ridge clone FT17 AY2510
EF462645.1 gg_id:297781 meta-genome level extreme microbial symbiosis dorsal surface deep sea hydrotherm EF4626
AF449237.1 gg_id:61872 Riftia pachyptila's tube clone R103-B43 AF4492
EF467591.1 gg_id:214381 situ microelectrode voltammetry sulfur-oxidizing biofilms Frasassi sulfidic cave strear EF4675
AY672507.1 gg_id:107804 hydrothermal vent 9 degrees North East Rise Pacific Ocean clone CH1_25_BAC_16Sr AY6725
EF462782.1 gg_id:290493 meta-genome level extreme microbial symbiosis dorsal surface deep sea hydrotherm EF4627
EU662427.1 gg_id:579840 Productivity- Chemolithoautotrophically Based Sulfidic Karst Systems microbial mat EU6624
U51874.2 gg_id:10979 Helicobacter sp. Dog-4 str. Dog-4; Eaton 1302 U51874
DQ071280.1 gg_id:140620 dominate filamentous sulfur mat 13 degree north field East Pacific Rise deep-sea hy DQ071
AY531583.1 gg_id:103545 Indian Ocean hydrothermal vent clone SF_C23-F3 AY5315
GU390798.1 gg_id:516081 Dark hot springs: structure biofilms caves Acquasanta Terme (Italy) sulfidic cave stre GU390

41.9	208.9	255.4	295.2	323.1	231.8	327.1	197.0	70.5	245.7	120.2
1021.5	3796.6	4681.2	4987.2	3477.5	4096.7	4046.0	4140.4	6225.8	3160.7	5134.1
1468.9	1918.1	2119.2	2037.4	2169.3	1861.9	3174.2	1987.0	1512.7	2140.0	1535.1
31.5	539.6	794.8	493.2	488.9	501.7	417.4	552.8	191.2	60.7	459.3
6174.3	4053.3	4715.3	5709.5	2616.4	3771.3	3221.1	4350.0	4308.4	3236.8	3986.0
7517.9	3658.2	3551.4	3848.1	3825.4	3219.0	3471.7	2922.2	4608.0	3732.3	6347.7
3427.6	2394.9	2855.7	3033.8	2334.2	2162.4	4154.3	2252.4	2978.8	1024.6	2119.1
33.6	194.2	442.2	446.0	147.5	356.8	176.3	186.6	74.4	37.3	221.8
64.8	297.2	321.3	365.6	224.0	518.4	204.0	264.2	83.1	83.9	165.0
418.9	3388.8	3853.6	3057.6	1290.2	2862.2	2187.5	3175.8	1641.5	913.8	3768.7
29.0	18.5	17.3	21.9	12.6	15.6	22.5	20.5	12.7	11.0	19.0
59.0	85.9	147.7	171.0	28.0	61.9	173.3	114.5	29.9	34.9	63.9
773.8	1634.3	2075.1	1970.2	1766.2	3286.8	1504.0	1802.8	953.8	1170.8	1741.4
3221.8	4558.4	5104.8	5572.6	2995.4	4829.3	4025.7	4340.2	5722.8	3996.6	5711.4
7960.4	1876.9	1698.4	1749.1	1926.1	2532.6	1624.7	1632.4	2812.7	1696.5	3209.4
4180.8	2546.8	3292.8	3326.4	3704.0	2638.0	3092.1	3005.5	1741.9	1090.2	3339.8
130.6	3319.4	2695.2	3573.1	3059.5	3258.0	3138.8	3218.1	2566.6	6089.1	2824.9
46.0	2008.1	2572.4	2614.3	1020.2	1959.1	2037.7	2220.4	1022.8	1228.3	2699.0
1877.2	5032.7	2989.7	3802.9	1318.5	4268.7	2279.5	4382.1	2012.2	560.8	5854.4
510.4	5033.2	3828.7	3328.8	3077.1	3961.9	4604.2	3810.9	4585.4	3122.1	3351.7
37.1	359.1	445.7	276.5	130.4	344.8	162.3	199.6	87.1	69.4	216.3
1259.7	4744.1	4354.4	4759.9	3903.9	7663.6	3778.9	4403.7	2516.7	2344.2	3875.1
32.7	51.5	82.3	85.3	42.4	50.2	32.8	52.4	36.3	22.4	35.3
51.5	56.8	40.0	36.4	25.3	81.1	62.2	37.7	11.7	13.4	22.6
409.9	4171.9	5245.7	5511.8	5351.3	4201.9	5037.3	6276.7	3232.8	1733.4	5068.7
30.4	38.6	63.1	74.2	38.3	38.0	33.3	37.1	30.4	16.5	29.6
82.0	5977.4	5477.3	6790.8	2882.3	6463.9	5092.1	5450.2	4020.9	1310.1	6953.6
66.4	442.0	634.7	636.5	189.7	484.9	400.1	451.8	158.4	149.2	547.8
3072.8	4431.0	4964.7	4726.9	3377.6	4621.7	4984.2	4017.6	4228.5	2483.9	5686.5
25878.9	7725.5	7984.6	8294.2	8021.3	7575.5	7937.6	7169.1	12082.9	7238.1	10554.2
50.0	843.1	1138.1	1575.4	443.6	1066.4	333.3	597.6	168.1	113.2	509.4
2822.3	3717.0	3543.4	3826.2	3609.2	4095.1	4425.9	4588.1	3158.3	4971.1	4728.6
150.8	1094.0	1492.0	942.7	539.0	465.6	615.5	872.5	158.5	82.8	1411.7
36.1	160.2	187.3	222.8	441.7	128.1	42.4	141.0	129.4	29.7	119.5
3840.3	4912.8	5017.3	5821.1	4401.2	5258.0	5402.7	5879.3	3751.6	3404.4	6868.3
302.7	2379.0	2459.4	2775.3	2886.1	2554.1	2887.4	2582.1	1564.4	1572.6	2575.0
46.9	155.1	208.4	243.9	120.3	341.2	128.9	180.0	75.9	218.0	42.2
377.3	2691.9	3471.4	4297.8	5503.4	2763.8	5843.0	4035.2	1727.1	1985.6	2931.1
49.2	678.2	465.3	503.3	765.7	562.8	1193.3	611.9	193.3	83.0	228.5
3363.9	7237.8	6974.5	7182.1	4369.7	6433.5	4808.5	6080.3	6375.8	7840.8	6842.5
3210.8	7171.3	6974.1	7108.1	5298.1	6613.4	5334.3	6069.8	6944.8	6533.8	8187.0

121.2	152.7	200.8
3693.6	4784.6	3467.0
2065.0	2832.7	1779.8
422.3	659.4	545.4
2862.6	3764.2	2706.9
2586.7	6036.0	3307.2
2285.3	3421.5	2169.6
167.7	392.7	166.6
138.2	536.7	363.6
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13.7	22.0	14.2
86.4	53.1	170.3
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146.3	238.7	214.5
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4682.4	4774.8	4573.8
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690.7	1128.7	876.7
32.4	374.1	171.5
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2441.8	3337.5	2911.4
233.3	226.3	80.7
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s__Nautilia profundicola	54084
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s__Acidithiobacillus albertensis	3279
s__Acidithiobacillus caldus	2666
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AY510213.1 gg_id:110174 microbial mat cave sulfidic spring clone LKC3_159.12 AY5102
AY578099.1 gg_id:106472 Helicobacter bilis str. KO214 AY578(
AF420347.1 gg_id:67790 hydrothermal sediment clone AF420347.1 AF4203
EF467570.1 gg_id:212152 situ microelectrode voltammetry sulfur-oxidizing biofilms Frasassi sulfidic cave strear EF4675
AF420343.1 gg_id:67794 hydrothermal sediment clone AF420343 AF4203
AF449232.1 gg_id:61877 Riftia pachyptila's tube clone R103-B18 AF4492
GQ355026.1 gg_id:565854 structure between two geochemically distinct springs Alum Rock Park spring clone M GQ355
L35522.1 gg_id:11150 Alvinella pompejana epibiont L35522
AJ969465.1 gg_id:157898 Microbial black smoker s Mid Atlantic Ridge ecological implications rock fragments ch AJ9694
EU864466.1 gg_id:334109 structures under selection pressure levels antibiotics Xiao River receiving treated ox\ EU8644
EF644836.1 gg_id:300292 genes and citrate lyase deep-sea microbial MAR Rainbow hydrothermal vent system EF6448
EF467464.1 gg_id:213273 situ microelectrode voltammetry sulfur-oxidizing biofilms Frasassi sulfidic cave strear EF4674
EF467519.1 gg_id:205825 situ microelectrode voltammetry sulfur-oxidizing biofilms Frasassi sulfidic cave strear EF4675
GU390782.1 gg_id:516622 Dark hot springs: structure biofilms caves Acquasanta Terme (Italy) sulfidic cave stre GU390
AY766315.1 gg_id:108123 VC2.2 hydrothermal chimney Snake Pit site on mid Atlantic ridge clone 3 AY7663
GU390711.1 gg_id:515047 Dark hot springs: structure biofilms caves Acquasanta Terme (Italy) sulfidic cave stre GU390
AY280435.1 gg_id:106612 exterior deep-sea hydrothermal vent sulfide chimney Juan de Fuca Ridge Pacific Oce: AY2804
NC_005090.1 gg_id:93903 Wolinella succinogenes str. DSM 1740 NC_005
AF273252.1 gg_id:29152 Wolinella succinogenes str. SeR-1 AF2732
AF068812.2 gg_id:11156 hydrothermal vent clone VC2.1 Bac12 AF0688
AY691429.1 gg_id:106012 Caminibacter sp. str. TB-1 AY6914
NR_028943.1 gg_id:571654 Caminibacter hydrogeniphilus str. AM1116; DSM 14510 NR_028
AF299128.1 gg_id:40818 S17sBac34 complete clone AF2991
AF068804.2 gg_id:11155 hydrothermal vent clone VC2.1 Bac30 AF0688
ABCJ01000004.1 gg_id:243079 Caminibacter mediatlanticus str. TB-2 ABCJ01
NR_028999.1 gg_id:579615 Caminibacter profundus str. CR; DSM 15016 NR_028
CP001279.1 gg_id:528797 Nautilia profundicola str. AmH CP0012
NR_025497.1 gg_id:566284 Nautilia lithotrophica str. 525; DSM 13520 NR_025
AM937002.1 gg_id:260087 Nautilia abyssi str. PH1209 AM937
AP009178.1 gg_id:247747 Nitratiruptor sp. str. SB155-2 AP0091
AB175499.1 gg_id:106788 Nitratiruptor tergarcus str. MI55-1 AB1754
AB167820.1 gg_id:136358 Lebetimonas acidiphila str. Pd55 AB1678
EF462830.1 gg_id:302768 meta-genome level extreme microbial symbiosis dorsal surface deep sea hydrotherm EF4628
AY830901.1 gg_id:109592 Acidithiobacillus thiooxidans str. OYCS3 AY8309
DQ431197.1 gg_id:156297 Acidithiobacillus caldus str. YN06 DQ431
FJ154522.1 gg_id:556258 Acidithiobacillus caldus str. Da FJ1545
AF329205.1 gg_id:33408 Acidithiobacillus ferrooxidans str. ATCC23270 AF3292
DQ646482.1 gg_id:257953 Acidithiobacillus ferrooxidans str. DX-AF-1 DQ646
DQ646485.1 gg_id:238863 Acidithiobacillus ferrooxidans str. DX-AF-4 DQ646
EU079375.1 gg_id:243219 Acidithiobacillus ferrooxidans str. NF-01 EU0793
AB039820.1 gg_id:19750 Acidithiobacillus ferrooxidans str. NASF-1 AB0398

51.1	217.5	289.2	259.2	304.0	401.2	286.3	400.3	101.5	71.2	179.3
309.4	3081.6	3332.1	3717.2	4851.2	3026.1	4206.5	3585.3	2102.2	1270.8	3930.7
46.2	54.8	114.9	127.8	95.5	103.7	921.2	103.0	28.8	31.8	50.8
21801.9	7245.1	7638.6	7521.8	7074.8	7018.6	7321.9	6977.9	11913.5	7671.0	10789.6
36.5	137.1	286.9	305.6	70.1	165.9	247.2	192.1	41.6	17.3	144.4
87.6	2174.2	3839.8	4463.9	349.7	1656.2	1173.4	3022.1	533.8	360.8	3030.7
1814.7	2075.6	2531.1	2532.7	1532.5	2967.2	2283.7	1716.0	2098.0	1794.3	2299.3
1851.4	5563.9	5333.5	5849.2	6209.6	4966.5	6510.9	5085.6	4818.7	3447.0	5619.0
42.0	318.2	669.1	974.7	256.5	377.9	279.7	624.7	171.8	68.4	398.3
2568.5	3673.6	3190.1	3197.6	2868.0	2780.8	3728.2	2670.6	4492.0	3376.6	4127.7
419.7	2424.9	3226.4	3124.7	1900.8	2549.4	1987.0	2690.9	1571.2	2432.9	2403.3
131.3	1185.9	1698.9	2061.5	604.0	3266.8	1430.5	1947.9	528.4	438.1	1988.4
1405.2	6005.2	6326.5	5998.2	6122.1	7561.3	5693.7	5967.3	5651.3	4625.4	6711.6
1175.2	6039.8	9184.3	6739.7	4433.1	6060.9	5269.3	6614.4	5936.3	5143.8	6652.8
65.8	82.2	130.0	88.5	59.5	60.2	74.6	102.2	82.3	137.4	114.4
3546.4	3912.6	5336.0	6223.8	1817.3	3341.7	2439.4	4571.7	2674.4	1446.2	2627.7
88.8	1575.6	1939.8	2471.6	985.6	1508.3	1182.2	2089.7	745.1	350.9	1717.2
64.7	1407.2	2244.7	2506.8	860.3	1571.5	1536.9	1683.9	469.7	129.0	1590.2
8442.3	2219.4	5973.8	4645.1	3611.0	3831.7	4179.9	3716.7	4783.5	3783.1	4780.8
4729.3	4386.2	4359.0	4759.8	5476.7	3842.4	8559.9	4455.5	3194.4	3435.5	4637.4
1073.6	3258.5	3148.6	3418.0	3654.0	2693.9	6475.8	3105.5	2194.9	2300.3	3256.3
1658.6	2279.1	2332.3	2701.1	3754.8	2572.4	3258.4	2897.8	1778.6	880.8	2232.2
5450.1	4661.2	4393.9	5242.9	5511.0	5094.4	5562.0	4908.5	4600.7	4194.9	5525.6
33707.7	10404.1	13504.1	13228.9	10200.9	10294.3	13341.5	11234.7	15752.1	17430.3	14976.5
583.2	3175.7	5659.7	5179.6	5548.2	4694.5	7116.0	4121.5	1938.7	2414.7	2723.5
103.3	3830.4	4049.7	4308.0	3806.4	4353.5	5478.8	4382.1	1581.0	1050.2	3500.8
19744.7	5530.1	5187.6	6370.5	5958.4	5383.3	6614.4	7206.6	6854.5	4694.7	8551.6
8418.6	3498.1	3213.2	4493.6	3668.6	3487.3	4453.2	5085.8	2025.2	1254.7	3588.4
67.3	4102.4	4017.9	4506.2	3890.8	3800.8	4512.1	5310.1	2212.5	1218.0	4274.7
59.8	465.7	772.8	622.7	507.1	634.0	698.1	630.8	294.8	585.8	375.1
37.1	462.3	418.9	415.6	190.9	496.8	160.9	200.8	136.2	98.5	179.2
52.8	409.2	419.2	423.3	447.6	370.7	399.2	461.6	211.2	192.5	303.3
3546.9	4873.9	5448.9	5779.1	7014.8	5582.3	6780.2	5319.4	2638.3	3153.8	4253.2
32.8	147.3	118.0	194.9	227.5	166.4	200.4	108.2	49.0	18.9	61.3
3172.2	1722.2	2238.8	2325.6	4532.9	2660.8	1858.3	6198.2	1436.9	386.8	4210.9
50.1	926.7	474.9	164.0	122.2	459.6	76.8	225.4	541.2	133.5	110.8
11189.8	6541.2	6416.2	7516.4	6544.0	6547.1	7027.8	6912.1	13472.9	10694.8	10770.2
65.9	947.3	1013.5	1329.6	1380.7	1137.7	1914.2	1389.5	321.6	174.7	992.1
4612.1	3158.6	3317.0	3679.5	3691.8	3480.5	4093.7	3514.5	2232.0	1898.0	3297.7
10662.9	5044.7	4913.9	4866.7	4955.8	5260.3	4685.6	4862.6	4928.4	4764.2	4717.1
4196.1	5205.3	5258.7	5125.1	6704.6	5206.0	6216.6	5585.9	6067.7	5246.4	5261.9

294.6	260.1	199.9
2607.4	2881.5	3219.1
301.2	248.3	66.7
6659.0	8502.7	6430.0
169.7	198.8	268.1
1268.8	710.9	934.3
1785.7	1791.3	2342.4
4703.5	6755.6	6805.0
247.7	603.5	151.7
2534.9	3659.3	2163.2
2602.7	2783.5	1394.9
1139.1	1697.8	1721.2
5253.9	6261.8	5670.8
5649.2	7778.2	5358.0
70.8	117.5	49.5
3125.5	3019.2	2694.5
1445.8	1634.1	2314.2
1089.7	1019.3	1546.2
3568.6	4350.7	4182.6
4578.3	4926.0	4978.7
2808.1	3173.4	4185.5
1939.8	3530.4	3012.9
4465.1	5013.1	6646.9
9778.9	13566.5	9265.5
3514.5	6751.6	6926.0
3232.2	3360.5	4632.5
6203.3	6137.9	6884.3
4027.0	4061.6	5070.7
3422.6	3218.0	4278.7
565.2	588.1	1410.5
337.1	508.2	329.8
393.6	632.5	463.4
5122.6	5605.7	6831.4
304.6	213.0	382.5
2492.5	2986.5	1758.4
198.2	258.8	214.5
6205.0	7940.0	5917.2
1131.2	1035.0	1196.5
3440.4	3576.2	3838.7
6146.2	6233.3	5399.9
5566.4	6059.8	6671.3

k__Bacteria	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria
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o__Acidithiobacillales	f__Acidithiobacillaceae
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s__Acidithiobacillus ferrooxidans	2941
s__Acidithiobacillus ferrooxidans	2961
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s__Acidithiobacillus ferrooxidans	3200
s__Acidithiobacillus ferrooxidans	3292
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s__Aeromonas encheleia	6892
s__Aeromonas encheleia	7038
s__Aeromonas enteropelogenes	6533
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s__Aeromonas enteropelogenes	7629
s__Aeromonas jandaei	6444
s__Aeromonas jandaei	7060
s__Aeromonas jandaei	7269
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s__Aeromonas media	6837
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AF362022.1 gg_id:53544 Acidithiobacillus ferrooxidans str. ATCC 19859 AF362
EF015577.1 gg_id:177741 Acidithiobacillus ferrooxidans str. SRHGR EF0155
DQ321746.1 gg_id:148463 Acidithiobacillus ferrooxidans str. yunnan1 DQ321
DQ909079.1 gg_id:170265 Acidithiobacillus ferrooxidans str. c DQ909
GU167981.1 gg_id:583008 Acidithiobacillus ferrooxidans GU167
AF359940.1 gg_id:21015 Acidithiobacillus thiooxidans str. KCTC 8929P AF3599
AJ879995.1 gg_id:127417 Acidithiobacillus ferrooxidans str. B4 AJ8799
DQ529311.1 gg_id:301400 Acidithiobacillus ferrooxidans str. DBS-1 DQ529
EU250259.1 gg_id:241484 acid mine drainage clone GXDC-45 EU250
EF446188.1 gg_id:210453 Prokaryotic and Ecology Floating Macroscopic Filaments Extreme Acidic River Rio Tint EF4461
FJ946877.1 gg_id:567607 Acidithiobacillus ferrooxidans str. NK-16 FJ9468
AY552091.1 gg_id:147725 Acidithiobacillus sp. str. CASQ22 AY552
FJ890908.1 gg_id:574423 Microbial heap: implications model and control process -grade copper bioleaching he FJ8909
EF612419.1 gg_id:248238 historic semiarid lead-zinc site mine tailings clone K6-C19 EF6124
EF059761.1 gg_id:188237 Acidithiobacillus ferrooxidans str. CHMS EF0597
X75266.1 gg_id:7484 Acidithiobacillus ferrooxidans X75266
FJ154519.1 gg_id:539257 Acidithiobacillus ferrooxidans str. F6 FJ1545
AM502930.1 gg_id:241149 Acidithiobacillus ferrooxidans str. LMT1 AM502
EU084698.1 gg_id:254158 Acidithiobacillus ferrooxidans str. DGS EU084
DQ159176.1 gg_id:139484 Wetland System Treating Acid Coal Mine Drainage wetland clone AMD 636 DQ159
EU250217.1 gg_id:253906 acid mine drainage clone GXDC-3 EU250
AJ459801.1 gg_id:66601 Thermithiobacillus tepidarius str. DSM 3134 AJ4598
AJ458408.1 gg_id:67017 Aeromonas encheleia str. LMG 16328 AJ4584
AJ458416.1 gg_id:67011 Aeromonas encheleia str. E195 = S 191 AJ4584
FJ940842.1 gg_id:419066 Aeromonas enteropelogenes str. CRX104 FJ9408
FJ940843.1 gg_id:465898 Aeromonas enteropelogenes str. CRX105 FJ9408
FJ940844.1 gg_id:457890 Aeromonas enteropelogenes str. CRX203 FJ9408
FJ940845.1 gg_id:394895 Aeromonas enteropelogenes str. CRX207 FJ9408
FJ966347.1 gg_id:411204 Aeromonas veronii str. 5CB1 FJ9663
FJ940820.1 gg_id:455969 Aeromonas veronii str. LNC205 FJ9408
FJ940816.1 gg_id:401894 Aeromonas jandaei str. LC208 FJ9408
EU770282.1 gg_id:320191 Aeromonas veronii str. IH118 EU770
AB032088.1 gg_id:9365 Aeromonas hydrophila str. Ef1L1 AB032
AF157690.1 gg_id:9454 Aeromonas media str. 86352 AF157
AY900170.1 gg_id:143274 Aeromonas hydrophila str. PCA0081 AY900
FJ940831.1 gg_id:449999 Aeromonas media str. pW28 FJ9408
EU488683.1 gg_id:545213 Aeromonas media str. 974a EU488
FJ168773.1 gg_id:559246 Aeromonas media str. 480a FJ1687
AF418218.1 gg_id:59117 Aeromonas media 5 AF418
GQ470996.1 gg_id:546104 Aeromonas hydrophila str. HQ070610B-1 GQ470
AM262152.1 gg_id:158666 Aeromonas media str. CDC 0862-83 AM262

54.6	677.1	642.6	660.7	479.9	793.4	547.8	797.1	439.7	173.3	400.3
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2244.9	3003.8	3014.5	3091.1	2556.2	2739.3	3268.7	4645.2	3373.0	3218.4	4479.3
7130.8	2795.2	2603.7	2606.7	1718.6	2632.7	2345.9	2584.1	3242.2	2331.9	3291.8
69.4	1381.8	1218.7	1453.9	1340.6	1465.4	1400.7	2604.0	870.4	914.3	1675.3
50.4	265.7	245.2	225.0	409.0	324.2	180.5	422.2	340.6	93.3	104.3
6667.0	1710.8	1563.7	1452.7	1382.3	1785.8	1404.1	1525.4	1842.9	709.9	1478.9
1638.0	1509.7	1481.4	1917.6	1890.2	1870.6	1301.9	1955.6	745.4	839.9	4412.6
2636.2	3088.4	3191.2	3302.1	2593.0	2854.8	3066.1	2610.5	6292.1	3202.5	4497.8
7206.4	6498.7	5718.3	7049.5	7624.6	6263.0	6627.3	5872.1	6803.0	4410.7	11353.3
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9303.8	6808.6	6594.7	7191.3	6663.4	6648.5	6599.5	6046.4	10866.0	8537.5	9473.9
212.1	767.8	906.8	1071.3	1094.0	853.2	1406.0	779.9	507.0	248.9	741.5
2899.7	2732.4	2332.3	2362.2	3333.8	2424.9	3456.0	2747.5	2982.8	1199.8	2280.3
5293.9	2828.6	2590.1	2603.1	2769.3	2911.2	2226.3	3016.5	2218.9	1193.8	3951.2
9194.9	6377.8	6729.5	6222.1	6727.5	6158.8	5812.2	5890.8	9764.4	7284.2	10888.3
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5356.8	5876.3	5486.1	6081.9	6090.5	5247.4	6800.4	6116.2	5995.0	5984.7	7073.9
13153.3	6955.3	6490.9	6447.3	7047.2	5565.8	6426.8	5689.8	7536.2	7556.1	14109.9
8607.5	2124.9	1804.4	2012.0	1677.3	2171.0	1885.2	1783.7	3530.1	2132.6	2664.1
3630.7	7112.9	7294.9	8199.8	8652.4	6674.5	8682.2	6206.1	8400.5	6822.1	12209.5
465.0	358.3	431.4	396.8	760.1	506.8	785.5	516.8	173.1	225.1	219.0
445.1	7823.8	7277.7	9442.7	6669.2	8832.2	3945.1	11335.2	8111.3	18382.7	6454.6
667.0	7866.6	7378.7	9272.0	5692.1	8548.8	3039.9	10889.6	8088.7	17474.9	6578.7
193.0	5308.9	4027.3	4634.3	3352.0	6073.0	1996.4	5725.9	6350.6	14201.3	3236.9
1511.0	8257.2	7795.6	9024.1	6986.7	10047.0	3567.8	9144.8	8807.7	17409.5	6633.3
161.1	4419.1	3119.9	3456.4	2207.6	5403.6	1104.7	4506.6	5620.1	13733.4	2467.5
101.3	3755.1	2649.4	2598.2	1680.6	4775.3	591.8	3567.2	4374.1	12828.4	1620.3
450.9	9187.9	8000.3	9659.8	6575.7	9618.2	4330.4	10762.5	9819.3	19113.5	7124.7
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158.5	4542.7	3053.4	3084.3	2553.2	5986.5	2223.2	4742.7	4079.8	16098.9	2393.7
888.8	9929.9	8470.2	10083.2	7640.4	10362.4	5108.6	10767.1	10515.4	19249.4	8363.1
385.0	9203.6	8541.1	9609.5	8750.3	12505.4	3056.8	9648.0	7906.5	21817.8	6037.5
429.2	8078.7	7778.7	8887.8	8266.2	11355.7	3502.6	9632.7	7366.1	20517.6	5456.7
587.0	8718.9	8384.8	9551.6	8634.0	11829.1	3903.0	10184.3	8222.4	21188.1	6129.7
531.4	8659.5	8193.7	9486.1	8578.4	11695.1	3862.5	10038.7	8293.0	21173.7	6163.1
331.2	7296.3	6810.3	7651.6	6862.6	9760.2	2401.8	8227.1	7507.7	18505.6	5160.1
468.1	9189.6	8479.1	9751.0	8473.1	12058.0	3272.8	9975.8	8591.2	21473.9	6456.6
85.3	3763.7	4619.9	6026.7	4626.8	6723.2	1144.2	6338.0	3620.1	13906.3	2642.5
337.7	8921.9	8209.4	9304.0	8143.8	12106.7	2726.9	9247.5	7139.0	20928.1	5612.4
589.3	9078.0	8728.7	9952.4	8666.3	12245.0	3463.3	10307.7	8369.3	22214.5	6542.5

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5307.8	6108.1	6289.3
4462.6	4781.8	2788.7
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2311.6	2467.5	2003.5
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2792.9	3720.4	2730.4
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3191.0	3596.8	3637.0
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648.8	1169.5	1247.1
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2843.7	3128.2	3622.2
5407.3	6317.0	5708.5
4779.5	5344.6	5761.9
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1467.5	3445.5	1851.2
5603.5	6880.4	6767.8
439.8	591.6	624.2
9944.0	9551.4	8041.2
9457.5	9879.5	7574.2
4810.2	5307.0	4158.7
9303.8	9454.6	6488.5
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2630.8	3375.8	1994.3
9938.9	9634.6	6646.6
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3529.0	2985.6	2462.2
10090.9	9811.1	7048.1
10163.9	8942.6	6301.0
9747.9	8572.9	6241.4
10426.3	9217.0	7037.6
10241.6	9203.9	6921.8
8466.4	6436.1	4492.0
10199.7	9273.5	6609.4
6974.1	6966.7	5468.8
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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
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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
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EU770278.1 gg_id:327136 Aeromonas veronii str. IH101
EU770304.1 gg_id:316400 Aeromonas veronii str. MW17
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AY987741.1 gg_id:198899 Aeromonas hydrophila str. -32
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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
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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

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AY5326
GQ845
GQ844
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FJ9407

1396.9	10122.4	9560.8	11404.7	9440.6	12134.8	5706.7	11571.1	10670.5	21263.1	8994.0
242.0	7090.6	7617.5	8482.9	5128.7	9604.9	2086.2	8348.6	7656.1	16334.3	5069.4
1337.2	9210.9	8760.0	10235.2	8526.1	11358.9	4999.4	10577.4	9294.5	20385.8	7756.2
515.9	8664.8	8113.7	9500.0	8470.2	11745.2	3605.4	10089.0	8310.3	21169.7	6158.0
212.9	7751.7	6814.2	8056.3	7357.0	9644.7	2968.8	8889.0	7635.0	18846.9	5271.7
617.8	9147.0	9143.6	10552.8	8735.6	12346.1	3877.3	10954.5	9454.1	22463.2	7120.4
465.7	9116.9	8564.1	9531.3	8304.8	12290.2	3186.1	9366.6	7566.1	21009.4	6046.0
7343.5	6729.6	6686.9	7396.2	7569.1	8241.7	5894.9	7569.2	8080.8	15207.2	6563.0
565.3	6089.3	6406.3	6987.7	6423.8	7701.2	3802.6	7915.9	6325.9	12704.2	5560.9
630.2	8031.8	7165.2	9351.7	6623.3	8809.6	4066.8	11178.0	8502.2	17871.0	6910.4
518.2	6903.6	6435.9	7319.7	4490.9	7233.2	3035.5	8094.0	7751.1	13826.2	5356.8
554.5	7450.0	6786.4	7861.0	5319.1	7803.9	3678.5	8572.1	8169.6	14837.5	5957.6
623.7	7933.5	6917.2	5820.2	5617.3	6867.8	4383.3	6342.4	8825.2	11875.4	4828.8
2617.3	4597.0	4544.6	5326.0	3720.9	5574.8	2043.9	6522.5	6494.4	11258.3	3507.4
979.9	9851.1	8875.3	10183.3	7850.1	10847.4	5248.4	11057.7	10513.0	20435.8	8317.5
341.4	9326.1	7290.4	9797.1	6343.2	8803.5	4689.8	10463.9	9992.5	19264.3	7088.0
631.8	9851.1	8712.1	10140.1	7145.7	10177.4	4624.8	11142.2	11136.8	19360.9	8257.0
481.3	9390.8	8206.6	9626.6	6864.3	9730.1	4379.4	10715.4	10608.4	18770.0	7735.5
487.5	10088.5	8996.4	10771.2	7821.6	10578.7	5214.9	11875.6	10831.2	20433.0	8212.2
1190.0	8616.9	7410.6	8048.8	6633.1	8410.5	6630.3	8735.9	9645.3	14762.8	6995.8
19914.5	7387.1	7933.4	9573.2	6600.7	8704.2	7405.4	8684.1	8711.2	13609.7	9591.0
148.5	4619.2	2646.3	3175.5	3064.2	6458.5	2244.1	4808.3	3933.1	16311.4	2646.3
285.7	5480.2	5875.8	6767.3	3859.9	8594.1	2040.2	7228.5	5810.3	13129.6	4230.8
6560.0	6025.5	6181.9	7295.5	6119.1	6540.1	4349.9	6989.0	6246.5	9967.3	5494.7
1613.5	10170.2	9050.0	10954.4	8345.8	11014.8	5629.4	11627.9	11080.6	20170.7	9314.1
888.8	9605.0	8324.5	9823.1	7613.0	10199.5	4987.7	10433.6	10149.4	18540.3	8158.8
233.6	4714.8	4693.5	5811.9	3769.2	6558.1	1600.5	5924.1	4327.6	11550.8	3286.4
513.0	8168.0	7541.1	8688.5	8155.8	11113.8	3462.6	9442.2	7317.1	20306.1	5536.3
92.8	8162.2	6579.4	7589.2	5042.2	8344.3	2094.8	8419.6	7915.0	17215.3	5002.3
475.4	7963.6	7357.6	9485.0	6770.0	8829.7	4206.3	11289.3	8163.5	17924.3	6708.1
676.6	4947.0	4176.9	5648.0	4964.9	5471.8	4552.5	5171.3	4685.5	9802.0	4532.0
268.0	7782.9	6362.9	7370.6	4605.5	7308.4	3587.4	9221.3	8563.4	16665.0	5663.4
251.6	4988.2	4659.0	6231.5	4043.8	6316.0	3315.2	5307.0	3436.8	11890.5	3900.2
842.0	11001.2	9720.4	11816.8	8372.8	11110.1	5712.2	12591.1	12458.7	22282.8	9551.5
2168.2	3255.0	3410.9	3694.8	3278.0	4822.5	2123.9	4283.0	2974.0	10479.8	2695.0
794.6	9310.1	7920.3	9346.1	6988.6	9661.0	4783.6	10096.7	9619.7	18026.7	7690.7
221.0	4978.2	4534.4	5290.3	4081.2	5417.4	4095.0	6239.5	5286.0	13469.1	4642.9
443.5	10431.8	9242.7	11165.2	7964.0	10853.2	5318.9	12051.9	10510.7	21552.4	8121.9
384.4	9721.8	8420.2	10339.3	6854.8	9682.9	4387.9	11420.7	10601.4	20317.8	7701.6
15326.3	8397.8	7805.8	8743.5	6903.1	8466.6	5896.2	8789.2	9478.0	16179.5	7676.2
320.8	4989.5	4931.0	5925.6	3564.9	7208.8	1674.8	6191.8	4440.1	14038.1	3429.3

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FJ940839.1 gg_id:447408 Aeromonas hydrophila str. CLX208
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FJ940830.1 gg_id:371339 Aeromonas jandaei str. pW23
EF077527.1 gg_id:193001 Aeromonas hydrophila

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106.7	3865.4	2656.4	2659.9	2538.2	6147.8	1619.0	4113.3	2881.2	15765.6	1953.6
320.1	5875.2	5435.3	6420.5	4756.7	7551.3	2728.5	7540.3	5642.2	15525.9	4540.3
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256.7	7125.1	6515.0	7296.3	5480.4	8744.6	1787.9	7624.0	6159.3	15755.1	4454.1
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109.6	2750.5	2275.6	2610.9	1668.8	4468.1	799.2	3057.0	2327.8	10260.0	1848.7
257.3	5748.1	5125.8	5719.8	4613.5	7673.1	3225.3	6068.6	4851.6	17754.2	4714.3
3873.8	8201.0	7789.0	9646.7	7403.4	9361.5	5625.3	10892.0	10536.2	16304.8	8293.7
828.9	10608.4	9134.0	10892.7	8084.2	10833.4	5576.8	11288.0	11034.1	20206.4	8911.0
442.1	9042.1	8198.4	9430.7	8218.7	12157.5	2914.8	9336.4	7695.0	20694.7	5952.9
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4399.8	8707.1	7580.8	9054.2	7708.4	8730.7	6359.8	9875.2	9744.4	15971.1	8653.0
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192.8	7274.7	7166.9	8788.2	7213.5	9495.1	2945.1	8555.7	5893.8	17833.7	4647.4
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937.2	6656.6	5759.1	6244.2	4891.7	6696.4	4355.0	6758.4	7300.7	13385.0	5488.4
26844.7	10105.3	10636.8	10815.6	12358.2	10720.4	10959.1	10383.2	15329.8	15505.3	10078.7
824.4	9809.7	8481.3	9956.4	7565.5	10311.7	4907.4	10703.9	9959.4	19482.8	8022.6
163.2	6675.8	6429.0	7065.0	6592.9	9516.7	2416.5	7277.5	5264.7	16129.2	3874.7
559.5	7446.3	6715.9	8035.7	5572.4	7981.1	3593.8	8880.1	8564.1	15664.1	6148.6
92.2	3274.0	2440.8	3090.7	1936.3	2875.3	1741.6	4289.7	3008.6	7350.9	2199.8
138.0	6811.7	5425.2	6407.8	3650.4	7241.2	1540.1	7620.5	6063.3	16064.5	4121.8
527.7	4749.6	4557.4	5566.6	4162.9	6382.7	3090.9	6082.3	8078.9	11835.3	4677.4
24343.2	10915.4	10447.6	12092.9	11908.6	12057.0	10939.8	11729.7	11089.9	18347.4	10924.6
815.8	9756.5	8107.2	9874.2	7477.9	10345.4	4880.7	10708.9	10184.3	19031.4	8106.9
163.7	6554.4	6970.1	7681.8	6024.2	8378.4	3688.8	8235.4	5905.3	14091.2	4517.1
1408.8	10160.3	9623.6	11570.8	9292.8	12187.3	5652.5	11764.6	10826.7	21942.2	8774.3
859.7	7991.0	8080.5	8923.5	6052.9	9425.0	3848.5	8800.3	8047.3	15295.8	7411.4
2388.5	6747.1	6084.0	8050.0	6408.8	7007.4	4586.6	9021.4	6113.7	13983.7	5543.0
3231.3	7044.2	5774.5	6182.9	4623.4	6106.2	4643.1	6704.0	7284.6	11920.3	5848.5
156.3	6312.5	4581.4	5082.6	3371.9	5374.9	3108.8	6402.7	7110.2	13019.0	3873.7
302.8	5698.8	4676.5	5304.7	3732.7	8055.4	1661.0	6489.3	5202.7	18121.5	3626.1
101.1	2439.7	2107.3	2399.7	1654.1	4020.6	768.7	2699.4	2174.3	10040.8	1499.5
71.2	8239.7	6545.5	7615.1	5010.3	7795.1	2620.9	8837.6	7871.6	18644.7	5281.3
185.2	5721.4	5719.4	5855.6	2781.9	5980.4	1783.5	6393.4	7939.3	11214.7	4251.2
246.4	6537.0	4934.8	6679.3	4699.1	7218.2	3488.9	7735.8	6599.5	16242.5	4901.6
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2399.2	2406.2	1618.9
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DQ539497.1 gg_id:169858 Aeromonas hydrophila SBRD9
DQ816568.1 gg_id:161901 mouse cecum clone aab19g05

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428.9	9274.8	8237.0	9800.8	6912.1	9675.1	4173.9	11159.5	10783.2	19594.8	7643.0
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1742.4	10608.0	9293.4	10977.9	8625.9	11269.1	6200.4	11593.8	11498.3	20532.8	9546.0
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161.2	4798.9	3767.1	4542.0	2710.2	5454.2	1257.5	4995.7	5836.0	12066.4	3161.6
138.7	3389.8	2429.3	2679.0	1788.1	3902.8	1530.2	3180.8	3207.3	8661.0	2575.2
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384.9	8875.8	7891.5	9380.8	6357.3	9388.1	3935.5	10524.7	9428.3	18485.8	6876.3
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164.4	4765.6	3752.1	4260.3	2695.0	5365.4	1339.3	5258.7	5811.1	11899.3	2970.8
214.2	4754.5	4690.8	6245.7	4295.4	5011.6	2300.5	5517.4	4132.8	11632.1	2669.8
524.2	7098.0	6378.9	7584.1	5236.9	7689.3	3189.8	8545.1	8084.6	16356.9	5529.4
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GU205196.1 gg_id:585209 Aeromonas popoffii str. JW08
GU205192.1 gg_id:534484 Aeromonas allosaccharophila str. JNC912

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1989.6	7440.5	5689.5	7169.9	6208.3	6520.1	4945.3	8958.0	8971.6	15318.6	5561.3
565.5	7291.0	6521.6	7631.0	5047.0	7945.6	2864.9	8794.4	7606.5	16255.8	5720.1
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265.9	3738.0	2768.3	2763.3	2103.6	6041.6	1082.9	3967.3	3144.5	15326.9	2177.6
564.7	9720.3	8712.7	10249.1	7577.6	10445.8	5040.0	11252.9	10484.3	20222.1	7879.1
2938.3	8387.2	8356.7	9411.6	7596.8	9481.6	5653.4	10185.3	9805.0	17736.6	7605.9
113.6	6878.4	5769.0	6413.7	5330.1	8063.2	2093.4	7023.6	6722.7	15435.6	3938.8
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210.6	4884.3	3791.8	4012.7	2894.3	7362.0	1390.4	5104.3	4106.5	17020.2	2808.2
2696.1	8451.4	7422.3	8427.2	6226.3	10225.1	4002.7	9307.9	8335.2	16045.5	6925.2
2799.4	7528.9	6803.8	7886.1	5902.0	7534.4	6055.1	8354.8	8235.3	14688.8	7521.9
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539.7	8537.0	7984.3	10086.3	6642.5	9738.4	3566.9	11353.5	9671.0	19610.9	7334.1
79.7	6054.2	6038.1	7295.3	7067.9	8752.8	2182.3	6889.8	4310.2	16495.1	3341.8
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320.5	6427.8	6219.2	7152.1	5415.6	8507.1	2624.2	8070.2	6118.8	16358.8	4646.4
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g__Oceanimonas
g__Oceanisphaera
g__Tolumonas
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g__Zobellella
g__Anaerobiospirillum
g__Anaerobiospirillum
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g__Ruminobacter
g__Ruminobacter
g__Ruminobacter
g__Ruminobacter
g__Succinivibrio
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s__Tolumonas auensis	6616
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s__Anaerobiospirillum succiniciproducens	16050
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EF428988.1 gg_id:205966 Aeromonas veronii EF4289
EU770305.1 gg_id:306230 Aeromonas veronii str. WE02 EU770
AM945539.1 gg_id:554884 Aeromonas hydrophila ayu-Ah0201 AM945
DQ814092.1 gg_id:162823 zebrafish digestive tract clone aab59f09 DQ814
AY347679.1 gg_id:110092 Aeromonas culicicola str. 03037TRG AY3476
FJ966348.1 gg_id:411481 Aeromonas veronii str. QB205 FJ9663
EF371904.1 gg_id:208133 Aeromonas veronii str. TF15 EF3719
AY987759.1 gg_id:189821 Aeromonas punctata str. RK 25447 AY9877
AF094724.1 gg_id:73145 Oceanimonas doudoroffii str. ATCC 27123 AF0947
AB019390.1 gg_id:9401 Oceanimonas doudoroffii str. MBIC1298 (=ATCC27123) AB0193
DQ416806.1 gg_id:263963 Oceanimonas sp. G2DM-26 DQ416
AY562194.1 gg_id:113893 Oceanimonas sp. str. Be07 AY5621
GU183679.1 gg_id:567474 Marinomonas sp. str. H1693 GU183
EU530640.1 gg_id:270644 Oceanimonas sp. str. GK1 EU5306
AJ550470.1 gg_id:84842 Oceanisphaera litoralis str. DSM 15406 AJ5504
CP001616.1 gg_id:526816 Tolumonas auensis str. DSM 9187 CP0016
EU569287.1 gg_id:274900 Zobellella denitrificans str. MW1 EU5692
EU109731.1 gg_id:237124 Shewanella sp. str. NH21 EU1097
FJ230836.1 gg_id:346053 Serratia sp. str. AN4 FJ2308
DQ195676.1 gg_id:140125 Zobellella taiwanensis str. ZT1T DQ195
NR_026075.1 gg_id:560865 Anaerobiospirillum succiniciproducens str. S411; ATCC 29305 NR_026
EF428122.1 gg_id:206236 Anaerobiospirillum sp. str. 78/9/02 EF4281
GQ867410.1 gg_id:538586 and prevalence blaTEM genes Arctic seals colon content clone S7_13 GQ867
GQ867419.1 gg_id:587570 and prevalence blaTEM genes Arctic seals colon content clone S7_31 GQ867
EU776462.1 gg_id:320643 Red Kangaroo feces clone KO2_aai17h02 EU7764
EU794084.1 gg_id:309826 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_E16 EU7940
GU303104.1 gg_id:577587 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU303
AB004908.1 gg_id:9350 Ruminobacter amylophilus str. NIAH-3 Bovine rumen AB0049
FJ684530.1 gg_id:511689 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6845
FJ673136.1 gg_id:513301 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6731
FJ681014.1 gg_id:514935 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6810
FJ678936.1 gg_id:529684 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6789
FJ680138.1 gg_id:514703 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6801
FJ673291.1 gg_id:522804 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6732
FJ681705.1 gg_id:517924 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6817
FJ680474.1 gg_id:517852 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6804
EU532009.1 gg_id:259131 Predominant role host genetics controlling gut microbiota FMF remission stool clone EU5320
FJ680476.1 gg_id:521800 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6804
FJ679937.1 gg_id:525643 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6799
FJ676890.1 gg_id:530694 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6768
FJ681292.1 gg_id:530658 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6812

328.6	8237.2	6256.8	7429.3	3948.9	6402.3	3442.4	9050.5	9297.9	17316.5	5859.1
705.4	8746.5	6668.7	8187.8	6491.4	8406.5	5288.4	9344.2	9121.1	16825.0	6471.9
2721.5	8844.8	8921.2	10587.4	9994.9	10282.1	6731.9	10532.2	8858.8	16896.1	7170.3
1531.6	3746.3	3741.3	4950.9	2665.5	4462.0	3626.5	4192.3	4585.0	5315.6	3523.5
535.7	9729.5	8530.8	10293.0	7257.1	10172.1	4868.8	11378.0	10755.1	20198.1	7857.9
583.8	7227.7	6449.2	8219.6	5053.1	7772.5	2963.3	8536.7	7350.1	14769.1	5968.6
17918.6	8952.5	8139.4	9091.4	7379.9	8780.2	7701.9	9662.4	11033.5	14667.3	10803.3
466.1	9477.1	8664.9	10080.8	7963.2	12029.1	3279.8	10377.4	8575.0	21023.6	6677.6
32670.2	9273.7	9037.3	10577.3	6324.1	9565.9	8171.4	9774.8	12651.8	16909.1	11913.7
57.7	2614.3	2819.6	3635.2	1699.4	2827.4	1322.1	4602.3	1894.7	7305.7	1352.0
224.3	2995.6	3375.3	3658.5	2929.2	4426.1	2972.6	4546.4	2199.9	7468.6	2672.2
197.2	2291.0	2473.3	2715.4	1986.5	4030.1	2017.3	2514.0	1570.0	8923.7	2621.5
478.8	1382.3	1618.2	1957.6	1825.0	1701.8	2128.5	1974.2	1101.3	1396.9	979.6
39.1	766.5	1468.2	2492.4	330.2	1266.6	253.8	2173.0	683.6	3360.7	747.8
52.6	416.6	767.6	1142.0	86.1	734.2	289.6	1097.4	313.2	1669.2	209.3
673.3	7087.1	7011.2	7914.0	6243.0	8477.0	5846.3	7780.9	7684.5	10131.5	7209.3
167.7	4050.7	6107.2	6890.2	3170.1	5815.2	2533.0	6726.9	5235.7	9154.7	4590.1
3111.8	2209.4	2758.4	2676.8	1832.2	2957.8	1606.9	3156.4	1894.8	2975.7	1634.7
112.7	2066.4	3055.5	3386.5	1778.9	2382.9	1669.3	3692.5	3506.4	2136.0	2198.2
641.4	2751.0	2916.4	3105.4	2042.1	3406.0	2145.9	2946.7	2511.7	3405.0	2229.6
934.9	3179.6	3767.3	3946.9	3553.4	3729.6	3535.5	4049.7	3690.7	5455.2	3121.5
113.0	671.1	1089.4	971.7	910.5	1058.9	625.6	1115.9	913.6	3225.0	458.9
1347.3	3072.9	3252.0	3676.6	3122.5	3487.3	3125.4	3698.6	3211.1	3753.9	3707.2
291.7	2535.3	2597.4	2561.9	2265.8	2651.5	2688.1	7339.8	3194.2	2758.2	8095.8
11518.1	5920.9	6534.9	6339.4	7545.1	6385.0	7289.4	6591.9	7559.8	7799.3	6682.4
9328.0	5012.9	5057.3	5189.7	5169.2	4962.4	5798.7	5170.7	5593.5	6476.5	5303.9
221.6	3277.7	4222.6	3623.0	3101.6	3642.1	2835.6	3383.1	3027.8	5429.9	3898.9
52.6	111.9	165.1	175.0	196.8	169.4	188.8	125.9	171.4	170.1	203.7
856.6	3970.5	5446.4	6229.0	4222.9	6242.5	3892.9	5904.0	4887.4	6182.9	4076.0
1441.4	2810.6	2816.0	2999.6	2373.7	3312.6	2691.9	3985.9	2830.6	3664.2	1947.2
4714.1	4891.1	7285.0	7606.7	6660.2	6602.8	6298.7	7195.3	5227.6	5488.0	6288.1
2367.8	7064.3	9033.9	8430.0	5737.0	7524.0	5809.0	6744.8	7271.6	13595.1	9140.9
17058.6	8894.6	9522.8	10819.8	8988.0	9850.7	9793.3	10220.2	10861.1	10607.0	11290.0
10381.1	6863.9	8968.3	8076.8	7129.5	8047.9	7243.6	8233.4	8947.7	11526.3	9059.4
8520.8	6474.2	6225.3	7194.0	7515.2	6156.1	7438.8	6870.8	6496.8	5719.9	7220.1
7190.9	6964.5	7670.3	8480.2	7366.4	7303.3	7521.6	7341.1	7704.7	9436.4	8715.4
11775.2	4487.4	4751.7	5444.8	4831.7	4741.9	5266.5	5271.1	6488.2	5242.7	4870.3
33098.9	10360.5	10029.0	11425.7	10450.6	10069.9	11782.3	10378.2	15903.9	13500.4	17372.9
6401.0	5869.7	5617.3	6234.9	5728.2	5777.5	4981.6	5851.3	7944.0	8242.5	7127.1
2674.7	4848.6	4951.2	5748.7	5639.9	5172.7	5469.8	5356.0	5173.2	7949.4	6064.2
8387.6	5879.6	7166.1	7540.5	6256.2	7277.6	6471.0	7836.7	7311.0	11877.6	9647.2

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11061.7	9674.0	6903.3
3497.8	4050.3	3112.9
10717.8	9824.2	7207.3
7852.2	7359.7	5551.8
9091.6	9975.9	7003.5
10333.2	10322.9	6916.6
9389.1	11841.0	6979.4
3514.9	2802.7	1447.0
4142.5	4278.1	2479.0
3055.2	2748.4	1559.5
2077.7	1617.9	1572.9
984.2	187.7	189.0
548.9	364.5	168.8
9526.2	8995.0	7309.0
6786.3	5002.4	3535.7
2774.0	3803.4	1531.7
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4336.4	4005.9	1932.7
4596.1	4062.1	2802.9
1410.3	1642.7	1522.3
3294.1	3929.1	2707.0
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7006.0	7296.8	6569.5
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3335.9	4667.8	2312.1
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3705.7	4140.8	3407.9
7152.0	7439.6	6300.2
7236.3	9094.6	5661.5
10877.3	11842.5	11055.1
8246.8	10170.8	7138.6
6967.0	7785.3	7559.3
7151.2	9746.9	7404.7
4676.6	6443.1	5160.3
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FJ681318.1 gg_id:519035 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6813
FJ673806.1 gg_id:519747 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6738
FJ685189.1 gg_id:515645 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6851
FJ683080.1 gg_id:526775 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6830
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FJ684018.1 gg_id:529769 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6840
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FJ673346.1 gg_id:514406 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6733
FJ673002.1 gg_id:524997 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6730
FJ678905.1 gg_id:530101 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6789
FJ684508.1 gg_id:525389 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6845
FJ673381.1 gg_id:516159 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6733
FJ680565.1 gg_id:519066 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6805
FJ679553.1 gg_id:531893 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6795
FJ676324.1 gg_id:517601 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6763
FJ679041.1 gg_id:530617 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6790
DQ904673.1 gg_id:163857 human fecal clone 001-d11 DQ904
FJ680750.1 gg_id:518347 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6807
FJ678215.1 gg_id:520650 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6782
FJ679230.1 gg_id:520332 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6792
FJ676809.1 gg_id:530331 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6768
FJ673289.1 gg_id:513756 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6732
FJ679155.1 gg_id:528625 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6791
FJ683157.1 gg_id:521108 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6831
FJ678890.1 gg_id:521551 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6788
FJ679040.1 gg_id:528737 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6790
FJ672134.1 gg_id:518385 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6721
FJ673998.1 gg_id:532469 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6739
FJ682525.1 gg_id:521818 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6825
FJ681785.1 gg_id:531974 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6817
FJ676261.1 gg_id:529152 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6762
FJ678600.1 gg_id:524710 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6786
EF445277.1 gg_id:205408 dairy cow rumen clone NED4F7 EF4452

4650.7	7509.8	8291.0	8643.1	6728.8	8982.7	6206.2	9027.1	10940.9	15465.2	9628.0
5328.6	5646.9	6076.7	6486.5	5081.0	6993.7	4386.3	7247.9	7642.1	11916.1	7286.7
8061.7	5470.9	6541.3	7090.2	6291.7	6435.7	6580.8	6834.4	7128.7	6249.9	6268.2
1695.0	5332.4	6318.8	7702.5	5959.4	7437.0	5699.6	7543.5	4903.3	12739.9	8992.5
16110.6	6186.7	6934.5	7080.6	5668.5	7376.5	5136.9	6794.2	10030.2	9924.1	8495.3
6865.0	6237.1	7208.3	6964.7	5870.4	7219.9	5450.8	7114.5	8671.3	9005.2	7091.1
2926.0	3263.7	4383.7	4361.1	4196.4	4298.9	3793.0	4749.5	3497.7	2274.2	3113.5
2565.6	7448.7	8648.4	9407.8	7129.0	8637.3	6214.2	8821.0	11774.4	14835.2	9240.2
3645.8	3631.2	5527.9	5599.6	3007.7	5342.8	2637.3	5395.1	5978.9	8839.2	4418.0
10048.2	3574.4	4385.9	4510.8	4045.8	3916.3	4689.4	4171.3	5551.2	4512.4	4364.8
2532.5	3656.9	4541.1	4966.0	3470.6	4968.2	2783.5	4956.5	5115.5	5592.3	3402.7
2990.7	3688.2	6531.0	6812.3	4336.1	6778.0	3960.2	7127.2	5296.0	9798.0	5976.7
11604.3	5610.5	6561.1	7072.0	4539.8	7500.2	4660.4	7331.4	9588.4	12372.8	6818.0
3034.7	2385.3	3890.9	3836.9	3501.3	3257.2	3904.5	3389.4	3028.1	3615.0	5004.4
698.4	4452.8	6258.9	7341.1	4613.1	7061.7	3385.9	7241.7	6894.8	9748.2	4976.4
7895.5	5169.5	5380.0	6380.9	5894.0	6661.4	5348.8	6118.3	5972.4	10280.5	5425.6
12406.4	3862.6	5073.1	5203.5	4644.7	4869.5	4509.2	5242.1	3939.0	2413.0	4328.9
549.1	4926.8	6398.6	6717.2	4928.3	7201.0	3322.7	7095.1	8073.6	11960.5	4971.1
6522.1	1823.1	2112.9	2042.0	2186.5	2329.5	1792.4	2579.3	2103.6	3283.6	1265.7
16774.0	4907.8	3763.5	5348.5	5445.7	5044.3	5611.3	4727.8	6850.4	5225.5	7038.6
10759.5	6408.7	6442.7	6780.3	6767.2	6753.0	6133.2	8124.8	6504.9	7496.3	6484.1
5033.8	3579.1	3405.9	4281.8	3807.0	3181.2	4010.0	3722.1	3608.1	2654.4	3933.7
23509.3	8165.2	7511.0	8810.8	7828.3	7801.4	5638.8	7893.6	12460.5	10360.2	11364.8
6378.3	4281.0	5764.2	6592.7	4816.0	6674.6	4549.1	7087.3	6399.2	8965.9	5363.1
10607.4	6005.8	6456.2	7060.3	6318.8	6275.8	6944.1	5969.4	9726.3	9960.9	8937.8
6412.4	4967.7	6532.0	6735.6	5523.1	5876.8	5504.4	5972.5	5777.8	8566.1	9162.4
8493.5	4061.8	4833.5	4956.9	3778.5	5119.6	3892.1	4724.9	6620.7	6691.3	5213.1
5526.7	5439.2	5989.6	6496.4	5746.7	6255.8	5392.7	6339.4	6644.5	9165.8	7215.3
3207.4	3552.9	4761.5	5510.3	3727.6	5296.1	3522.5	5562.4	4424.4	5524.6	3625.8
451.8	6037.5	8048.6	8343.2	5105.0	8092.4	3845.9	8242.8	8535.6	12962.3	6408.6
2104.5	6454.6	8077.0	8700.7	5857.4	8934.1	4561.3	9384.9	9893.8	16599.1	8696.7
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2943.5	4502.0	5174.5	4829.4	4132.1	4553.4	4411.6	4545.3	4137.9	7092.8	5488.1
15122.0	7532.6	6549.8	7573.5	7431.2	7078.4	7995.2	7080.5	10113.2	8804.9	8054.8
301.6	4442.0	5926.4	6259.6	3162.4	6083.0	2072.5	6978.8	5869.7	11294.1	4405.5
1491.9	4278.6	6122.3	6745.5	3527.4	6103.4	3149.1	6568.6	6336.6	8126.7	9678.0
7615.1	6563.8	6601.3	7335.0	6968.7	6639.1	6083.1	6515.1	9256.2	10190.6	7391.0
2370.6	7019.7	8377.0	9329.5	6259.6	8544.2	5574.1	8654.3	9245.3	14169.7	7748.3
12977.2	5198.2	5371.8	5338.0	4436.1	5795.3	4881.6	5734.3	8034.0	8502.4	5960.3
2705.6	4524.3	7174.1	7451.5	5820.8	5881.5	6913.2	6688.9	5517.5	5539.2	7394.6
487.4	3543.3	4574.0	5054.9	4217.8	4731.1	3960.5	5173.4	3632.6	6329.2	3821.2

10971.6	10493.0	6003.4
7972.0	8601.2	4536.8
8209.2	7915.1	6424.6
8991.4	7678.3	6712.0
8863.0	8652.8	5324.0
8645.9	9189.8	6298.9
5519.4	4791.7	3893.8
11054.3	10743.4	7586.8
7012.5	6862.0	2969.2
3410.8	4931.5	4850.8
5640.8	5643.8	2652.7
7703.1	7392.9	4036.9
9275.4	9806.3	4994.6
2958.2	4587.4	3079.1
9142.1	7598.0	5260.2
6220.5	8403.8	5617.1
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8667.2	7094.9	5516.7
3363.9	4096.2	1473.0
4499.1	6157.3	5058.8
7118.8	7710.3	6435.3
2910.0	5126.2	4903.1
8742.4	10025.4	8048.0
9461.7	8962.4	3722.5
6166.2	7501.0	6407.7
7103.1	8226.7	4973.9
5846.3	6003.7	3980.4
6973.3	8054.3	5147.0
6674.6	5861.5	3791.7
9712.1	8769.8	5464.1
12020.8	10363.4	6595.9
7671.4	6401.3	3338.2
4869.4	5322.0	4886.2
6806.2	9385.0	8008.7
9497.4	7533.5	3974.9
6254.9	7497.4	4359.3
7899.5	8688.0	7182.7
8525.8	8810.9	7367.4
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5579.1	6567.6	7421.1
5002.3	4992.5	4121.7

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o__Aeromonadales	f__Succinivibrionaceae
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s__unclassified	6302
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s__unclassified	7142
s__Alteromonas genovensis	1393
s__Alteromonas marina	1103
s__Alteromonas marina	1282
s__Alteromonas marina	1471
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s__Alteromonas marina	154
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s__Alteromonas marina	1962
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s__Alteromonas marina	665
s__Alteromonas marina	686
s__unclassified	1312

FJ680116.1 gg_id:526488 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6801
FJ679573.1 gg_id:530904 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6795
EU794184.1 gg_id:344867 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_B23 EU794
FJ679565.1 gg_id:527828 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6795
FJ679188.1 gg_id:520121 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6791
FJ673005.1 gg_id:530535 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6730
Y17599.1 gg_id:9351 Succinimonas amylolytica str. DSM 2873 Y17599
EF445219.1 gg_id:207757 dairy cow rumen clone NED4C12 EF4452
FJ440064.1 gg_id:511871 Megamonas hypermegale colonization correlates Campylobacter jejuni exclusion pou FJ4400
AJ420985.1 gg_id:29865 Anaerobiospirillum thomasii str. DSM 11806T AJ4209
FJ832419.1 gg_id:577393 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P1Q401_75C10 FJ8324
GU303829.1 gg_id:539467 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU303
AF018457.1 gg_id:9354 Aeromonas subgroup subdivision clone 12-11 AF0184
FJ832403.1 gg_id:548716 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P1Q401_45E06 FJ8324
FJ832430.1 gg_id:559309 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P1Q401_91C12 FJ8324
DQ456106.1 gg_id:158543 pre-adolescent turkey cecum clone CFT114E2 DQ456
EU381934.1 gg_id:271179 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU381
FJ952818.1 gg_id:443894 Alteromonas sp. str. 2tb4 FJ9528
GQ391974.1 gg_id:519442 Aestuariibacter sp. str. PaD1.02 GQ391
AB076557.1 gg_id:60317 Agarivorans albus str. MKT 82 AB0765
GQ200591.1 gg_id:544653 Agarivorans sp. str. WH0801 GQ200
DQ416550.1 gg_id:153331 s1cb18 DQ416
AF290480.1 gg_id:27315 cf. Alishewanella fetalis clone Llangefni 75 mite AF2904
AF144407.1 gg_id:33192 Alishewanella fetalis str. CCUG 30811 AF1444
AY093457.1 gg_id:55811 deep marine sediment clone MB-A2-102 AY0934
DQ256339.1 gg_id:142481 subsurface water clone EV818BHEB5102702SAS10 DQ256
AY820719.1 gg_id:109054 drilling fluid clone CCSD_DF2030_B15 AY8207
FJ040187.1 gg_id:347660 Alteromonas genoviensis str. I96 FJ0401
EU189225.1 gg_id:239877 Alteromonas marina str. MB 3 EU189
AY881234.1 gg_id:145384 Alteromonas marina SCH0402 AY8812
AF288360.1 gg_id:71626 Alteromonas alvinellae str. HY757 AF2883
AF386742.1 gg_id:44702 Alteromonas sp. str. 4BT AF3867
AJ319537.1 gg_id:71568 Alteromonas macleodii subsp. abyssi str. HYD657 subsp. AJ3195
AM931040.1 gg_id:239418 Alteromonas sp. str. BUS 07-8 AM931
DQ836766.1 gg_id:163484 Alteromonas simiduii str. BCRC 17572 DQ836
AF114499.1 gg_id:8878 attached marine recovered surface clone 17 proteobacterium AF1144
EF061429.1 gg_id:190836 Alteromonas sp. NJSX37 EF0614
EU982324.1 gg_id:322486 Alteromonas sp. str. UST010723-013 EU9823
FJ210814.1 gg_id:309174 Alteromonas sp. str. QDHT-19 FJ2108
DQ486510.1 gg_id:227411 Alteromonas sp. str. DG1302 DQ486
AF114505.1 gg_id:8883 attached marine recovered deep chlorophyll maximum depth clone 2 proteobacterium AF1145

6155.8	4657.2	5534.1	5954.8	4112.4	5155.8	4804.1	5783.9	5573.9	6961.7	5638.2
15355.7	7767.1	7244.5	7172.5	6599.0	6953.5	7438.4	6781.6	9679.7	9297.7	8595.9
8806.3	3894.0	4657.9	5298.9	3463.4	5619.6	3088.5	6117.7	4125.6	5947.8	3651.5
3131.1	2633.5	2603.4	2843.2	2701.1	2719.0	3032.2	2667.1	2236.3	1756.9	3359.3
2619.0	5722.3	7146.0	8241.1	4735.2	8278.4	3961.9	8491.7	9785.9	13520.3	6779.5
12693.5	4553.8	4328.1	5033.6	4551.6	4909.5	4463.2	4813.9	5877.3	5081.2	5817.6
381.8	4474.8	4539.4	4707.8	4303.7	5326.5	4510.1	5890.3	3528.8	4229.9	3030.7
4310.6	3163.9	3020.5	3513.7	3335.0	3060.3	3612.2	2917.3	4310.0	3515.4	3196.2
7289.4	3387.8	4469.9	4098.8	4686.2	3530.8	3532.5	3633.6	6588.2	5200.1	4963.3
187.5	1395.2	1550.7	1085.6	621.0	1308.4	1216.5	853.6	1132.0	300.8	746.0
2477.4	5770.6	6021.4	6708.4	5666.2	7007.2	5749.2	7768.4	6109.0	10120.9	5525.8
300.4	2247.2	2253.6	1787.8	2202.9	2404.8	1548.6	2297.5	1238.1	3848.6	1392.5
1620.7	2243.7	2571.0	2959.7	2615.3	2828.0	2455.9	3065.5	2831.6	2418.0	2231.4
560.7	4294.0	4967.9	6807.9	4312.7	5640.7	5029.5	6238.1	4647.6	7758.4	3915.8
1242.8	3321.4	3678.3	4330.4	4801.8	5295.3	5146.1	5524.9	3232.7	8005.8	4208.5
133.6	1731.8	1848.9	1703.3	3228.6	2503.5	1878.9	2273.3	1415.1	2008.8	1436.2
330.7	907.7	1386.4	801.7	988.3	988.1	764.8	1052.8	1481.9	1161.7	2419.1
57.4	748.3	1680.1	1557.7	724.8	1592.1	518.0	1722.1	1492.8	2260.6	761.9
247.1	2712.6	3754.5	3242.9	2486.6	4124.4	2687.5	5147.6	3001.3	5607.6	3009.4
802.8	2321.6	2827.3	3147.5	2901.1	2492.9	2957.0	2609.7	1492.5	1761.9	3027.5
1380.8	3255.7	4460.0	4820.6	3430.0	4104.4	4321.9	5776.6	8892.8	5704.4	3180.5
3491.7	5116.7	5881.3	6379.0	5242.5	5624.0	5731.6	6163.9	6960.9	6688.3	5734.7
146.1	2399.0	3329.0	3349.4	1986.6	3752.8	1130.7	4195.9	5264.2	4159.6	2668.0
439.5	3185.7	5923.9	6281.3	2028.9	4125.1	1687.2	7143.2	9138.8	3629.4	4795.3
7159.1	5655.8	8102.7	8650.1	5498.6	7481.5	5004.7	9055.4	9637.6	7280.1	7015.9
2481.7	3133.9	4541.5	5375.8	3267.7	3616.2	3273.9	5213.7	6232.0	2441.3	3745.2
7495.0	6130.1	6866.6	8012.8	5678.4	7069.2	6322.3	8491.9	10425.3	11521.1	7447.2
54.5	102.8	154.0	173.5	143.4	114.5	96.5	169.7	44.9	64.1	85.4
302.9	1805.2	2060.6	2439.4	2030.4	3037.5	1776.6	2979.3	1756.6	4076.9	1869.4
141.9	1289.1	1728.6	2068.2	1625.3	2087.4	1195.6	2374.4	1356.7	1865.7	1367.0
48.2	55.8	63.6	80.6	71.3	72.4	23.6	121.6	61.1	52.3	71.7
3254.3	2910.2	2797.2	3540.6	4096.6	4527.3	3198.9	3916.6	3693.7	2849.1	4835.3
86.2	939.9	1232.7	1355.9	1177.0	1488.7	649.8	1708.1	980.2	1520.6	1080.0
88.9	1064.7	1388.8	1600.0	1341.3	1547.7	870.4	1821.8	1046.0	1628.2	1183.0
88.4	1037.5	1526.7	1546.9	1243.2	1495.4	1008.2	2016.9	1067.7	1623.1	1292.1
115.5	234.1	303.9	230.4	412.4	1049.2	150.9	1286.1	131.0	958.7	824.3
81.3	908.2	1241.6	1387.7	1310.4	1260.6	1013.8	1543.5	1186.5	1267.3	692.8
124.3	480.8	906.1	1112.2	738.2	1072.9	459.1	1300.5	583.6	735.9	511.6
800.5	1117.9	1446.4	2057.8	1375.3	1341.7	1097.6	2146.6	1308.3	535.2	1430.8
150.4	1245.7	1951.0	1997.5	1735.9	3214.7	1146.8	3399.8	1657.2	2945.7	2197.3
12565.1	5493.2	6187.3	7384.6	4539.1	5927.5	5601.3	5928.5	5733.5	5746.5	7659.4

5855.2	7122.1	5644.2
6470.4	8032.1	6896.9
6467.1	6634.2	4423.9
2472.4	3036.1	3022.1
10588.5	9096.9	5923.3
3943.1	6718.9	4026.5
6822.5	5827.6	7187.8
2835.0	3964.7	3652.0
2962.7	3906.8	2903.1
697.9	681.6	1100.0
7138.8	8979.6	7210.4
2533.0	1221.6	2147.9
2352.9	2944.9	2293.0
5524.4	7156.8	5309.2
6256.2	6371.0	4666.9
2627.5	2066.8	1783.1
755.7	960.2	464.7
2007.1	2258.2	1189.8
4493.1	4255.6	2853.4
2401.7	2667.4	1707.7
4611.4	5742.9	3634.8
6449.0	6606.9	4883.5
4551.9	4735.0	1957.7
7213.8	4763.1	2676.0
9946.4	7592.8	5458.9
4917.6	4496.3	3733.4
8014.5	8594.0	6026.4
136.3	172.0	89.8
3223.9	2992.9	1988.4
2338.6	2484.9	1528.5
146.2	207.9	108.0
3016.8	4310.2	2339.2
1799.4	1590.1	1031.6
1925.7	1658.4	1113.5
1856.4	1719.0	1148.6
601.5	709.0	230.2
1266.1	1609.3	1081.3
1142.0	1558.4	892.9
1613.4	1338.5	1575.7
2540.5	2823.4	1778.2
6527.7	4959.9	4088.0

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s__Glaciecola punicea	1281
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AF114498.1 gg_id:8877 attached marine recovered surface clone 14 proteobacterium AF1144
AF114504.1 gg_id:8882 attached marine recovered depth 400m clone 25 proteobacterium AF1145
AF114508.1 gg_id:8886 attached marine recovered surface clone 8 AF1145
AY428573.1 gg_id:105550 Alteromonas litorea str. TF-22 AY4285
Y18232.1 gg_id:19130 Alteromonas macleodii str. CH-518 Y18232
AY344429.1 gg_id:91492 Lake Kauhako 30 m clone K2-30-18 AY3444
AM885869.1 gg_id:240896 Alteromonas macleodii R-28696 AM885
AF114501.1 gg_id:8880 attached marine recovered surface clone 18 proteobacterium AF1145
AF114496.1 gg_id:8875 attached marine recovered deep chlorophyll maximum depth clone proteobacterium AF1144
EF574195.1 gg_id:228587 site S25 near Coco's Island marine clone S25_539 EF5741
DQ071162.1 gg_id:136631 marine surface water clone Surf1.42 DQ071
AM882576.1 gg_id:311934 Structure along hydrocarbon contamination coastal sediment oil polluted water pet AM882
AY165578.1 gg_id:81399 Antarctic pack ice Lasarev Sea Southern Ocean clone ANTXI/4_14-11 AY1655
AF468279.1 gg_id:80086 Arctic pack ice; northern Fram Strait; 80 31.1 N; 01 deg 59.7 min E clone ARKIA-118 AF4682
CP000388.1 gg_id:160590 Pseudoalteromonas atlantica str. T6c CP0003
AY697880.1 gg_id:104267 Antarctica clone F2C28 AY6978
U85854.1 gg_id:8873 Glaciecola pallidula str. ACAM 615T IC079 U85854
AY167284.2 gg_id:81210 Glaciecola sp. str. ANT9142 AY1672
AB238790.1 gg_id:140832 Glaciecola sp. #105 AB2387
AM941178.1 gg_id:284078 Microbes enriched seawater after addition coral mucus and reef waters mixture1-8 AM941
AM913910.1 gg_id:439090 antibiotic-active brown alga Laminaria saccharina Baltic Sea Saccharina latissima AM913
AJ240915.1 gg_id:73940 5' clone CHAB-XII-8 AJ2409
AY771709.1 gg_id:108683 Glaciecola mesophila str. S2-38 AY7717
AJ488501.1 gg_id:65357 Glaciecola mesophila str. KMM 241 AJ4885
Y18230.1 gg_id:202397 macleodii- and cellular rDNAs Mediterranean seawater mesocosm experiment Alterom Y18230
AJ548479.1 gg_id:89023 Glaciecola mesophila str. LMG 21855 AJ5484
AF173965.1 gg_id:71399 Alteromonas macleodii str. KT1113 AF1739
AY349463.1 gg_id:91221 Glaciecola sp. WHOI JT-6b AY3494
U73724.1 gg_id:8898 gas vacuolate str. 214.6 U73724
AJ293820.1 gg_id:39858 Glaciecola polaris str. LMG 21857 AJ2938
DQ784575.1 gg_id:162089 Glaciecola agarolytica str. NO2 DQ784
AY553295.1 gg_id:106840 Salinimonas chungwhensis str. BH030046 AY5532
EU583725.1 gg_id:272031 Alteromonas sp. str. JSM 073008 EU5837
AJ240916.1 gg_id:74015 5' clone CHAB-V-29 AJ2409
AB040465.1 gg_id:38060 Alteromonas sp. str. K AB0404
FJ024319.1 gg_id:368249 Prokaryotic and their role biogeochemical cycling marine basalts basalt Juan de Fuca I FJ0243
AB473549.1 gg_id:419632 Aestuariibacter sp. NT-2008 str. Sd 2-38 (= KMM 3894) AB4735
AY207502.1 gg_id:84007 Aestuariibacter salexigens str. JC2042 AY2075
AY207503.1 gg_id:83231 Aestuariibacter halophilus str. JC2043 AY2075
AB040466.1 gg_id:45496 Alteromonas sp. str. D AB0404
FJ202664.1 gg_id:350427 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2026

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2451.9	745.1	621.5	1025.2	968.9	697.5	593.7	1008.3	478.1	491.8	825.6
353.7	413.3	486.3	581.5	390.9	548.1	339.4	822.0	481.9	988.8	384.6
258.1	2092.4	2287.0	2340.7	2116.6	3295.8	1876.9	3825.8	1674.2	5736.9	2342.8
1160.5	3446.8	5527.8	6761.0	5380.1	7472.7	5742.0	7324.4	5167.7	8091.9	7565.2
242.2	930.9	1442.3	1397.1	745.0	928.7	829.0	1325.0	730.1	2257.5	1000.5
123.5	482.0	600.2	914.3	743.4	780.6	528.4	886.0	434.5	493.7	420.9
6467.3	3966.0	5239.8	5020.5	4634.5	5108.2	5533.1	4997.1	5435.4	5327.1	5955.0
419.4	1454.4	1483.4	1599.2	1639.5	2836.8	1134.4	3621.7	886.2	3316.5	3245.5
4324.8	2020.1	3229.9	2554.8	2963.7	2303.4	2618.6	2951.2	2911.2	1350.2	2657.1
788.6	4364.7	5146.0	6026.2	6195.5	5851.4	4134.3	5602.8	4772.7	4679.3	4589.9
420.6	2058.9	2251.1	2128.5	1694.1	2522.3	1715.8	3174.1	2199.4	1832.9	2424.2
612.3	2164.7	2462.7	3173.6	2801.6	2278.8	4389.7	2596.6	2559.9	2068.1	951.8
80.8	1479.4	1852.1	2416.9	1335.6	1908.8	2932.2	2134.0	1903.6	3707.5	1633.4
796.0	3385.3	3933.9	4753.6	4094.9	4901.0	4191.7	5018.8	5115.0	6133.2	3008.7
1760.8	3730.3	4464.5	4789.4	4035.9	3570.3	4087.2	4584.8	4369.6	2775.0	3069.8
36.1	172.9	324.7	312.3	206.7	193.8	220.4	342.3	86.5	131.2	150.9
752.6	3352.1	3432.7	3402.5	3959.7	3402.1	2870.0	3894.0	3386.6	3166.5	2106.2
21374.7	5808.9	5610.7	7133.3	5774.3	5727.4	7795.4	5358.1	7682.7	7550.6	8580.9
3877.6	6068.7	6067.7	7122.6	7256.9	8948.0	5869.0	6750.1	6353.3	9781.6	6219.2
7109.9	2487.6	3458.9	4018.1	2961.7	3792.7	2483.0	4184.5	5757.8	4106.3	3734.8
12916.5	5203.5	5138.7	5523.0	5168.8	5257.2	6322.7	4874.0	7711.8	5828.9	7326.0
2848.3	1352.9	1678.8	1558.5	1471.9	1980.0	1242.3	2192.1	1699.7	2940.7	1634.8
803.4	3520.5	4100.6	5014.6	4359.5	5067.8	4483.0	5261.1	4825.3	6239.5	3126.6
186.7	2409.6	2868.5	3896.8	2357.6	2718.5	2293.5	3573.6	1980.0	1573.9	2483.9
798.4	3012.3	3256.7	3972.3	4171.8	3931.8	4209.4	4025.2	4011.9	4357.2	2421.0
157.5	495.0	898.4	904.6	470.0	698.4	457.6	898.0	554.7	611.5	1084.7
3735.6	3951.4	4339.3	5676.0	4688.6	4708.0	5139.5	4256.2	4923.5	5403.0	3451.6
137.0	452.8	674.6	697.7	247.7	966.8	249.3	991.2	738.0	1745.3	414.9
2476.6	474.9	546.7	418.2	251.4	810.5	184.2	718.6	500.9	492.6	334.7
105.1	1934.8	1880.9	2025.0	1528.2	3364.3	1009.8	2096.4	1654.1	5392.8	1226.9
49.4	239.0	458.6	355.9	254.5	569.9	321.2	376.9	174.4	658.9	199.2
386.8	3687.9	4957.4	6412.6	3393.3	4999.9	2482.9	5902.1	4137.6	7663.3	4115.4
31.3	650.6	1252.0	1247.9	1095.1	1337.3	695.2	948.6	401.6	560.3	339.5
2406.4	1655.5	2141.4	3661.7	1393.0	1913.0	2626.5	2860.2	1501.7	3270.7	2955.0
99.5	142.1	288.0	289.6	275.8	177.4	202.3	214.0	149.1	232.4	113.4
3976.0	4036.8	4552.3	5726.1	4578.4	4751.2	4716.8	4766.0	4293.1	7423.3	4906.8
164.0	1788.6	2092.0	2511.9	1640.7	2300.9	1160.6	1952.1	2487.1	3028.2	2023.7
7194.4	3863.9	4242.5	4936.6	3586.8	4686.3	3299.8	5918.4	3455.0	5906.5	7652.8
3082.3	2039.3	2193.9	2273.6	1978.9	2561.8	2246.5	3111.4	2525.5	3329.7	1724.4
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1528.3	1639.3	706.8
798.8	1372.2	632.8
846.1	983.9	462.5
3648.3	2574.2	2220.4
6722.5	6206.6	4627.6
1144.1	1442.8	779.2
798.9	1156.3	566.7
4052.8	5398.2	4549.9
1998.7	2569.5	1380.3
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2902.5	3369.9	2617.7
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3758.0	5049.4	3670.8
270.1	529.4	504.4
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2065.4	2643.3	1793.5
4805.7	6060.2	3951.6
3432.4	4525.2	2824.4
3696.5	4634.4	3440.8
851.1	934.0	583.3
5321.1	5411.4	3749.8
1223.0	1631.4	763.9
999.7	1366.0	869.2
3352.1	2982.1	2246.8
613.6	745.6	188.5
5732.3	5407.3	3841.0
1995.9	1584.3	812.8
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264.8	416.8	344.9
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EU188146.1 gg_id:347006 Uncultivated oceanic unicellular N2-fixing cyanobacteria are picoplankton unusual 7(EU188
FJ425616.1 gg_id:366875 communnities healthy and diseased colonies Caribbean coral Montastrea faveolata A FJ4256
GU289642.1 gg_id:552344 Alteromonas sp. str. MEBiC06033 GU289
EU907922.1 gg_id:304111 Alteromonas sp. str. SKUK MB1007 EU907
DQ343294.1 gg_id:149488 Bowmanella denitrificans str. BD1 DQ343
EF092177.1 gg_id:275572 Persistent Axinella corrugata Alteromonas clone AC3_H2 EF0921
AJ295715.1 gg_id:73259 Alteromonas stellipolaris str. LMG 21861 AJ2957
AM882575.1 gg_id:316071 Structure along hydrocarbon contamination coastal sediment oil polluted water pet AM882
EU287412.1 gg_id:256595 Pacific arctic surface sediment clone S26-112 EU287
AM990642.1 gg_id:277954 Alteromonas sp. MOLA 365 AM990
AY926461.1 gg_id:113825 Alteromonas hispanica str. B-35 AY9264
AB040464.1 gg_id:137101 Alteromonas sp. str. S AB0404
AB526336.1 gg_id:573848 Alteromonas sp. str. JAM-GA13 AB5263
Y18233.1 gg_id:8895 Alteromonas macleodii str. CH-460 Y18233
EU188189.1 gg_id:317008 Uncultivated oceanic unicellular N2-fixing cyanobacteria are picoplankton unusual 7(EU188
GQ495024.1 gg_id:581173 Pseudoalteromonas sp. str. W-14-2 GQ495
AM183347.1 gg_id:155988 Alishewanella baltica str. BA131 AM183
EU841485.1 gg_id:310357 Alishewanella sp. str. 205 EU8414
AB295494.1 gg_id:216998 Alteromonas sp. str. A14 AB2954
NR_027234.1 gg_id:540876 Algicola sagamiensis str. B-10-31; DSM 14643 NR_02
GU108538.1 gg_id:591045 active chemolithoautotrophic prokaryotes sulfidic zone Black pelagic redoxcline dete GU108
EU714266.1 gg_id:332103 Alteromonas sp. str. BG20 EU714
DQ913886.1 gg_id:276341 Celerinatantimonas diazotrophica J-G1-2 DQ913
AJ002006.1 gg_id:8823 Rheinheimera baltica str. OS140 Baltic # 166 AJ0020
DQ985066.1 gg_id:177157 Rheinheimera sp. str. JL1145 DQ985
GQ009534.1 gg_id:500133 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw77 GQ009
GQ280117.1 gg_id:570209 Rheinheimera aquimaris str. JS-47 GQ280
FJ170027.1 gg_id:325282 Rheinheimera sp. str. CF12-10 FJ1700
FJ821606.1 gg_id:569335 Rheinheimera sp. str. TPS16 FJ8216
DQ298025.2 gg_id:143812 Rheinheimera chironomi str. K19414 DQ298
FJ902308.1 gg_id:509338 phreatic limestone sinkholes northeastern Mexico biomat rock outcrop cenote La Pal FJ9023
AM117933.1 gg_id:143326 marine boreal sponge Geodia baretti Norway:Korsfjord AM117
GQ240227.1 gg_id:576918 Rheinheimera sp. str. BZ19 GQ240
EU662623.1 gg_id:594183 Productivity- Chemolithoautotrophically Based Sulfidic Karst Systems floating microb EU6626
GQ130023.1 gg_id:440958 Genetic inventory 'JPL-SAF' during MSL mission spacecraft assembly clean room floc GQ130
AY887010.1 gg_id:114447 fresh water clone 1.34.5 AY8870
FJ902639.1 gg_id:593719 phreatic limestone sinkholes northeastern Mexico biofilm 1m deep hydrothermal ver FJ9026
AY701891.1 gg_id:140048 Rheinheimera texana str. A62-14B AY7018
GU108532.1 gg_id:548750 active chemolithoautotrophic prokaryotes sulfidic zone Black pelagic redoxcline dete GU108
FN397813.1 gg_id:405654 geomicrobiological investigation sediments Gulf Cadiz GeoB 9072-1 anoxic sub-surfa FN3978
AY167340.1 gg_id:81146 Psychrobacter sp. str. ARK10133 AY1673

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209.9	1201.7	2227.8	1301.4	811.0	1359.7	765.7	1418.1	907.2	2260.8	887.7
802.7	2290.4	2537.8	2877.0	2040.8	2547.5	2063.3	2908.4	1920.7	4034.1	2483.9
36.3	49.2	108.5	222.6	53.5	85.3	43.0	225.2	108.6	85.8	134.0
960.9	2561.7	3227.0	4381.4	2708.9	3734.8	2886.1	3669.9	1932.9	7071.2	3995.0
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1881.1	4284.7	5742.2	6955.8	5727.2	5728.3	5443.4	4899.6	4092.0	6012.4	4680.5
6220.0	3805.4	5595.8	5667.0	3586.1	4892.1	4990.4	5914.6	3163.5	2529.9	5494.5
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217.4	1008.3	1540.9	1865.6	1056.0	1567.7	2244.2	1873.8	1145.4	889.5	972.6
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89.8	679.7	1721.1	613.7	313.1	1213.2	262.6	569.4	483.7	1002.0	625.3
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s__unclassified	990
s__Thalassomonas agarivorans	1374

AF173964.1 gg_id:36120 Colwellia psychrerythraea str. KT0919 AF173
EU236321.1 gg_id:299112 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg1bG1 EU236
AB011364.1 gg_id:8843 Colwellia psychrerythraea str. ATCC27364 AB011
FN397812.1 gg_id:392867 geomicrobiological investigation sediments Gulf Cadiz GeoB 9072-1 anoxic sub-surfa FN397
GU061308.1 gg_id:560509 Evaluation culturing methods cultivate previously Yel Sea intertidal beach seawater GU061
U85841.1 gg_id:8840 Colwellia psychrerythraea str. ACAM 604 U8584
AF001375.1 gg_id:8836 Colwellia psychrerythraea str. ATCC27364; ACAM 550T AF001
AF530145.1 gg_id:61116 Colwellia psychrerythraea str. MGP-41 AF530
AY167332.1 gg_id:82309 Colwellia rossensis str. ANT9271 AY167
AY167269.1 gg_id:82300 Colwellia rossensis str. ANT8283 AY167
FJ905674.1 gg_id:560989 s Tonga-Kermadec iron oxide chimney-like structure on Volcano 19 Tonga Arc clone V FJ9056
DQ027051.1 gg_id:130223 Colwellia sp. str. MT41 DQ027
EF551378.1 gg_id:225725 Colwellia sp. str. BSw20516 EF5513
EU050773.1 gg_id:257619 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_01_78 EU050
DQ837294.1 gg_id:235556 Archaeal and pristine National Park Spain Donana coastal aquifer clone 49S1_1B_55 DQ837
DQ490038.1 gg_id:158539 Microbial life ridge flank crustal fluids clone ODP-70B-02 DQ490
AY167330.1 gg_id:81643 Colwellia sp. str. ANT9407 AY167
DQ351740.1 gg_id:146764 Microbial Adherent Sediment Particles Heavy Metal Contaminated North Sea Surfac DQ351
GQ350647.1 gg_id:559927 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ350
GQ848466.1 gg_id:581903 Microbial sediments vents along East Lau Spreading Centre deep sea hydrothermal GQ848
L10950.1 gg_id:8854 marine snow clone agg53 L10950
AY829231.2 gg_id:179606 Colwellia sp. IE7-5 AY829
EU394582.1 gg_id:309555 Coccolithophore bloom dynamics shape (NE-Atl) northern Bay Biscay pelagic particle EU394
DQ027052.1 gg_id:131520 Colwellia sp. str. KT27 DQ027
GU391219.1 gg_id:531807 Thalassomonas sp. str. JYr2 GU391
AY165571.1 gg_id:81437 Antarctic pack ice Lasarev Sea Southern Ocean clone ANTXI/4_14-151 sea AY165
AB094412.1 gg_id:97603 Colwellia piezophila str. Y223G AB094
AF419350.1 gg_id:74479 Colwellia sp. str. Ant5-9 AF419
EU491932.1 gg_id:271119 Abundance and microbial life ocean crust deep seawater East Pacific Rise clone EPR4 EU491
EU599214.3 gg_id:319654 Colwellia sp. str. KMD002 EU599
EU491916.1 gg_id:258657 Abundance and microbial life ocean crust deep seawater East Pacific Rise clone EPR4 EU491
DQ492707.1 gg_id:158794 Colwellia sp. str. BSi20061 DQ492
NR_024635.1 gg_id:548903 Colwellia maris str. ABE-1 NR_02
EU491896.1 gg_id:259552 Abundance and microbial life ocean crust deep seawater East Pacific Rise clone EPR4 EU491
AY165566.1 gg_id:81127 Antarctic pack ice Lasarev Sea Southern Ocean clone ANTXI/13-90 sea AY165
AF530146.1 gg_id:103969 Colwellia sp. str. MGP-59 AF530
GU108544.1 gg_id:589927 active chemolithoautotrophic prokaryotes sulfidic zone Black pelagic redoxcline dete GU108
AY167264.1 gg_id:81818 Colwellia sp. str. ANT8203 AY167
DQ923440.1 gg_id:179604 Alteromonas sp. W-6 DQ923
DQ228659.1 gg_id:141317 Microbial colonizing mineral surfaces within sulfide-microbial incubator clone CH2b7 DQ228
DQ212914.1 gg_id:140089 Thalassomonas agarivorans str. TMA1 DQ212

59.5	341.2	435.5	372.6	552.8	343.5	1185.8	565.6	281.7	519.1	288.5
41.3	560.7	662.5	719.6	1142.0	792.1	783.1	1137.6	527.2	244.1	351.5
7321.4	3570.0	3292.1	3550.2	4057.3	3476.0	4438.0	3763.9	5136.3	3369.5	4576.6
23820.8	8219.1	7175.2	8007.3	7948.0	7829.3	8432.8	7400.2	12732.7	10993.6	12356.3
412.8	2352.9	2787.9	2356.2	2820.3	2728.5	3202.9	2741.0	1688.6	1350.6	2634.1
54.5	67.3	86.3	77.4	75.3	48.5	586.8	77.8	69.6	135.1	47.6
195.6	1153.8	1168.3	1281.7	1805.5	1499.7	2114.5	1611.8	1476.1	588.0	719.0
11904.6	5114.8	4707.6	5317.9	5071.9	4648.4	6579.4	5883.6	6749.0	5491.5	5884.1
4830.6	2105.2	1686.8	1656.5	2096.3	1685.1	1599.6	2120.3	3204.8	2757.2	1173.1
43.0	167.8	186.1	190.4	418.8	231.1	1199.3	194.8	106.3	39.8	95.1
10443.1	6599.4	6223.4	6837.7	5159.3	6532.6	4518.3	8446.8	7629.1	10141.9	6989.8
2031.6	1453.6	1921.3	1725.8	1634.3	1706.4	1198.4	1665.8	1221.7	805.5	1007.4
62.8	1261.1	1074.2	923.0	848.3	1367.7	2529.0	1901.6	681.3	910.2	807.9
441.1	3642.2	3001.6	4051.3	2924.2	4093.5	3566.5	4326.5	2125.3	2564.4	3273.9
152.9	834.6	1031.0	982.0	1469.0	1096.7	2119.6	1380.0	588.0	482.7	627.9
2834.2	5057.4	5437.6	5717.8	4968.5	5071.2	3772.3	5978.2	7355.8	5400.1	4792.6
1320.3	1704.7	1957.4	2095.5	3507.2	2308.5	4378.7	2502.8	834.5	1455.4	1681.5
902.0	1877.0	2339.3	2524.7	2854.3	2151.7	2416.2	3221.3	2348.8	1413.0	1473.0
196.7	1905.1	1636.7	1736.7	1381.6	1449.1	1397.1	1397.2	1364.5	1606.9	1055.4
2908.8	3668.5	4571.2	4918.8	4271.4	4787.9	4508.1	5643.5	4542.6	6982.2	4307.6
44.2	51.1	77.7	68.3	62.7	78.4	60.3	264.0	63.6	18.4	63.5
2762.0	4786.9	4873.9	4851.8	5051.0	4965.3	5982.8	4838.0	6163.3	4723.0	3702.2
53.6	420.7	787.7	889.2	526.2	554.8	1721.7	796.9	677.4	303.3	409.9
6917.7	2497.9	3649.7	3638.7	2328.5	2817.0	2319.2	2733.0	4302.5	2812.9	3574.1
42.1	1248.6	1339.1	1828.9	1385.5	1318.9	2163.6	2454.6	1014.2	701.6	916.1
896.7	3524.4	4083.4	4803.3	4416.4	4563.4	3746.7	4408.6	5517.4	1944.9	3835.4
3565.3	2950.9	3520.3	3395.1	4242.4	2586.9	5119.4	3363.2	4063.5	3117.1	2610.2
16306.7	3408.4	3207.9	3268.6	3434.9	4157.3	4107.8	3868.5	4839.2	5402.1	4353.7
68.4	1003.4	948.6	1194.2	733.0	613.9	1794.1	1526.1	621.9	437.0	872.4
140.0	1861.8	2276.1	2174.6	1407.9	2388.1	1501.1	1954.7	3603.6	1988.8	1484.6
3542.8	2277.8	2850.9	2985.6	3130.2	2230.4	3000.9	2842.2	3473.4	1920.7	2169.4
240.1	4502.5	4145.4	3597.7	2189.4	4108.9	3596.1	6110.4	3744.7	2563.8	4448.8
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4428.8	7017.9	6211.3	6293.3	6748.4	6364.8	7093.6	6797.5	7865.2	5352.2	5397.0
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6042.6	4424.7	4698.9	4198.7	3306.6	3569.3	3325.4	4322.0	5426.7	5269.6	7345.6
64.6	497.0	770.8	686.4	274.3	458.3	749.2	627.4	387.3	213.9	135.3
241.3	1657.6	1767.4	1472.1	1803.8	1459.7	1577.8	3373.0	1009.6	785.9	1752.2
1733.1	2373.6	2190.4	2522.7	2961.3	2278.1	4745.2	2431.3	286.3	2008.0	2437.1
139.4	3025.5	3268.4	3911.8	2981.8	3808.9	4007.8	4044.3	2514.2	2226.0	2757.5

834.8	663.4	547.2
1219.0	859.2	805.1
4367.3	3840.2	3138.8
7480.4	9400.5	7622.3
2803.2	2854.7	2872.8
89.2	111.5	35.0
1364.1	1300.1	920.7
4929.9	4887.5	4464.9
1396.0	2295.6	1740.3
232.2	134.3	181.4
6931.5	7165.7	4779.0
1510.4	2612.1	2058.1
1443.8	1615.3	1060.8
4459.4	4450.2	3433.0
1296.3	1210.1	1075.2
5823.8	5346.2	4068.9
1801.4	1998.3	2166.2
3146.1	2365.8	2147.2
1688.2	2139.5	2337.3
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97.4	39.3	78.7
4602.1	5433.0	3402.2
816.5	1048.9	867.8
2559.5	5001.7	2207.3
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1051.8	1155.5	470.5
2388.1	2685.3	1157.1
2566.3	2852.0	2492.8
5370.6	4595.8	4015.8
831.8	788.8	516.6
6810.3	6360.1	5346.6
1846.2	1129.7	1054.6
6319.6	7429.7	6146.9
3609.5	4141.7	3588.0
729.3	865.5	380.6
1645.1	2035.1	1610.0
2694.1	2380.9	2867.4
3621.2	3473.9	3725.9

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s__Pseudidiomarina homiensis	806
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GQ848478.1 gg_id:584370 Microbial sediments vents along East Lau Spreading Centre deep sea hydrothermal GQ848
FJ717227.1 gg_id:553622 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United King FJ7172
FJ202297.1 gg_id:322290 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2022
GU230351.1 gg_id:594414 Multilevel approach along Rio de la Plata-South Atlantic Ocean coastal sediment clo GU230
FJ203045.1 gg_id:322845 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c FJ2030
AY643537.2 gg_id:131602 White plague like disease Eilat coral reef AY6435
AY194066.1 gg_id:81968 Thalassomonas ganghwensis str. JC2041 AY1940
FJ203217.1 gg_id:306276 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c FJ2032
EU491328.1 gg_id:269454 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak EU4913
U15115.1 gg_id:8864 hydrothermal vent clone PVB_OTU_12 U15115
FJ791872.1 gg_id:513615 Unexpectedly archaeal species shift between rare and dominant over thousand year FJ7918
FJ203091.1 gg_id:324976 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c FJ2030
AJ294747.1 gg_id:26868 Thalassomonas viridans str. XOM5 CECT 5082 DSM 13753 AJ2947
AY770724.1 gg_id:110997 sea urchin Paracentrotus lividus clone PIS53 AY7707
FJ952826.1 gg_id:382239 Colwellia sp. str. 1tb5 FJ9528
AB193748.1 gg_id:111458 Ferrimonas marina str. A2A-30 AB1937
AB252733.1 gg_id:243052 Paraferrimonas sedimenticola str. Mok-142 AB2527
GU391222.1 gg_id:528038 Ferrimonas sp. str. JYr13 GU391
FJ203654.1 gg_id:341133 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h FJ2036
EU620413.1 gg_id:278677 Ferrimonas balearica str. S8-05 EU6204
AB193752.1 gg_id:112098 Ferrimonas balearica str. A2A-18 AB1937
AB193755.1 gg_id:111912 Ferrimonas sp. str. A3B-58 AB1937
NR_027560.1 gg_id:549106 Idiomarina baltica OS145 str. OS145; DSM 15154 NR_027
NC_006512.1 gg_id:128686 Idiomarina loihiensis str. L2TR NC_006
AE017340.1 gg_id:128915 Idiomarina loihiensis str. L2TR AE0173
AY092077.1 gg_id:67499 Idiomarina loihiensis str. 53 AY0920
AY635468.1 gg_id:107632 Idiomarina seosinensis str. CL-SP19 AY6354
EU603445.1 gg_id:275762 Idiomarina seosinensis str. PTG4-5 EU6034
AY553081.1 gg_id:107227 Idiomarina loihiensis str. GSP41 AY5530
NR_029115.1 gg_id:557590 Idiomarina fontislapidosi str. F23; LMG 22169 NR_029
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DQ235566.1 gg_id:142194 biofilm water pipeline biofilms steel pipelines Gulf Mexico clone 20 DQ235
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AY505529.1 gg_id:101950 Idiomarina loihiensis str. GSP13 AY5055
FM877003.1 gg_id:574998 Idiomarina sp. IT-2008 str. CVS-6 FM877
DQ234155.2 gg_id:144284 determined library mangrove clone DS071 DQ234
EF486355.1 gg_id:222466 Idiomarina salinae str. ISL-52 EF4863
GQ180187.1 gg_id:591011 Pseudidiomarina sp. str. SW5 GQ180
GQ246209.1 gg_id:577128 Pseudidiomarina sp. str. YCSA4 GQ246
DQ416777.1 gg_id:268666 Idiomarina sp. G2DM-8 DQ416
DQ118948.1 gg_id:131585 Pseudoidiomarina taiwanensis str. PIT1 DQ118

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106.2	1242.1	1803.1	2023.9	765.9	991.7	1400.1	1525.5	514.8	879.0	1442.4
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492.1	691.1	508.4
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5237.1	6005.7	3748.7
796.4	762.7	364.9
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3424.2	3591.1	3468.7
282.1	453.2	233.1
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3644.7	3325.3	2804.7
7111.5	6420.8	4581.4
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189.4	159.5	139.5
1671.1	2115.3	1449.9
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s__Pseudoalteromonas aurantia	480
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s__Pseudoalteromonas issachenkonii	438
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s__Pseudoalteromonas luteoviolacea	830
s__Pseudoalteromonas marina	1674
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s__Pseudoalteromonas piscicida	1093
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FJ581032.1 gg_id:541977 Idiomarina sp. str. IITRM14 FJ5810
EF212001.1 gg_id:214514 Pseudidiomarina sp. str. c121 EF2120
EU600202.2 gg_id:260949 Pseudidiomarina sp. str. 8C EU600
EU722654.1 gg_id:327394 Microbial athalassohaline Tirez lagoon (Spain) sediment clone SB43 EU722
EF554907.1 gg_id:222862 Idiomarina sp. str. G-He8 EF5549
GU458902.1 gg_id:562858 microbiota human male female forehead forearm and influence make-up skin clone GU458
X92129.1 gg_id:44150 Crater Lake isolate 11C1 X92129
GU471247.1 gg_id:517013 Idiomarina sp. str. 10-D-4 GU471
EF554896.1 gg_id:226059 Idiomarina sp. str. JK38 EF5548
FJ152984.1 gg_id:347471 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX4CI FJ1529
EF554906.1 gg_id:223511 Idiomarina sp. str. G-He7 EF5549
X92128.1 gg_id:32525 Lake Nakuru isolate 20N1 X92128
D21224.1 gg_id:8975 Moritella japonica str. DSK1 D21224
AF530133.1 gg_id:70982 Moritella sp. str. MGP-6 AF5301
AJ132226.1 gg_id:8977 Moritella viscosa str. NVI 88/478T AJ1322
AB189343.1 gg_id:112983 cold seep sediment clone JT58-18 AB1893
AJ297540.1 gg_id:48310 Moritella marina str. NCIMB 2263 AJ2975
AY700605.1 gg_id:109434 Australia: Great Barrier Reef clone PDA-OTU7 AY7006
AB183504.1 gg_id:105913 Moritella sp. str. 47A1 AB1835
AB008797.1 gg_id:8989 Moritella yayanosii str. DB21MT-5 AB0087
AY382585.1 gg_id:96373 Moritella sp. str. 2-2-2-1 AY3825
AB038033.1 gg_id:33284 Moritella marina str. ATCC15381T AB0380
NR_025380.1 gg_id:573974 Moritella abyssi str. 2693; JCM 11436 NR_025
AJ252023.2 gg_id:72172 Moritella profunda str. 2674 AJ2520
AB183499.1 gg_id:101616 Moritella sp. str. 38C1 AB1834
AB183496.1 gg_id:101122 Moritella sp. str. 36C1 AB1834
AB013841.1 gg_id:8993 Moritella sp. 9-11.F AB0138
AB013842.1 gg_id:8994 Shewanella sp. 7-1.E AB0138
AB040467.1 gg_id:20333 Pseudoalteromonas sp. str. R AB0404
DQ349123.1 gg_id:147282 Pseudoalteromonas aurantia DQ349
CR954246.1 gg_id:140486 Pseudoalteromonas haloplanktis str. TAC125 CR9542
CR954246.1 gg_id:140406 Pseudoalteromonas haloplanktis str. TAC125 CR9542
AY040230.1 gg_id:21879 Pseudoalteromonas translucida str. KMM520 AY0402
AF316144.1 gg_id:52879 Pseudoalteromonas issachenkonii str. KMM 3549; F13 AF3161
EU880522.1 gg_id:351145 Pseudoalteromonas elyakovii str. P18 EU8805
AF316142.1 gg_id:37455 Pseudoalteromonas issachenkonii str. KMM 3558; F2 AF3161
FJ457238.1 gg_id:568943 Pseudoalteromonas luteoviolacea str. S4060 FJ4572
FJ952795.1 gg_id:446774 Pseudoalteromonas sp. str. 1tc11 FJ9527
FJ200646.1 gg_id:308744 Pseudoalteromonas haloplanktis str. I 6 FJ2006
EF584051.1 gg_id:228654 Pseudoalteromonas sp. str. GAS9 EF5840
EF584064.1 gg_id:227631 Pseudoalteromonas sp. str. LS3 EF5840

2818.7	2357.1	2672.6	2835.4	2200.0	2805.4	2358.3	3168.5	2112.2	2732.4	2112.6
63.5	2003.0	1940.5	2207.2	2131.7	3371.4	1986.9	2253.8	1280.9	2247.2	1692.8
92.0	1331.2	1697.3	1810.5	1090.2	1940.1	1032.4	2326.8	1355.8	3317.4	1253.3
397.1	1735.3	2572.8	2483.9	2292.7	1790.7	2686.4	2409.0	1461.9	2189.2	1664.3
12541.0	3526.8	4659.7	4467.6	5207.1	4608.8	4793.6	4904.1	4690.1	6111.5	4848.4
13708.1	4852.9	5789.1	6169.1	6888.0	5138.2	5173.4	7083.4	8646.6	4849.2	8724.4
66.5	631.3	849.1	889.7	660.1	1068.3	636.4	924.4	582.1	1920.7	461.3
118.8	3825.7	1993.0	1829.3	1687.0	1841.7	2037.0	4344.3	1819.7	4792.4	1926.0
740.2	2015.2	2990.5	2669.2	2084.0	2618.0	1797.0	3462.2	3339.3	2640.7	2347.5
1016.0	2288.8	2990.1	3111.8	2834.5	3155.7	2804.7	4025.6	3349.3	2664.1	2775.2
3593.0	2005.7	2284.0	2226.8	3543.2	2522.8	2725.4	2418.6	1634.1	1589.6	2186.4
58.1	98.8	117.8	125.4	87.3	113.8	95.7	216.2	111.2	137.1	63.9
3273.7	3174.7	3823.6	4265.8	3855.1	4466.2	3617.0	3913.7	3221.3	5506.5	3327.5
232.4	1681.0	2189.7	2378.4	2083.9	2064.8	2125.5	2816.7	2227.4	2529.0	1661.0
177.4	3434.5	3732.9	3575.5	3281.2	4493.4	3027.4	4853.7	4028.8	6118.0	3249.5
1876.3	2644.2	3506.5	2939.7	2624.9	2997.1	2773.4	2865.6	3671.2	4046.2	3129.3
1214.9	4328.5	5073.6	5397.3	3959.1	5157.6	4700.1	4950.0	6521.7	5434.3	4425.3
3488.7	3717.8	3606.8	3840.7	4157.0	4471.2	3464.1	4483.7	5159.5	6805.5	3484.6
500.0	2008.8	2169.8	2351.0	1812.0	2301.1	2041.1	1904.9	2779.5	2528.6	2442.2
2704.3	2445.0	3113.5	3271.4	3278.7	3042.0	3320.7	3058.9	2592.1	2893.4	2727.0
18445.9	5376.1	6232.8	6542.9	5351.2	6031.0	5915.0	6197.5	8554.3	8185.4	6135.1
2939.9	2758.2	3500.3	3799.3	3667.2	3713.0	3364.3	3561.0	2966.1	4285.6	3014.6
3229.1	2494.2	3075.5	3257.7	3326.6	3262.9	3205.2	2891.0	2352.2	3410.1	2706.1
152.2	2320.1	2365.3	2598.9	2291.5	2714.8	2298.3	2957.6	1978.4	3853.4	2044.3
77.0	1260.6	1663.3	1902.5	1395.6	2071.3	1198.9	2083.4	1506.2	2911.1	1318.3
159.7	2697.5	2669.5	2918.0	2160.2	3600.9	1827.9	3242.6	3542.0	5520.5	2157.9
4547.5	1023.4	1062.5	1189.9	1284.4	1375.9	1118.5	1435.5	1445.7	1879.9	1101.2
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65.5	914.8	714.4	503.4	658.1	919.0	509.4	675.8	997.6	1668.3	463.2
96.0	308.7	606.4	798.5	140.2	238.4	210.4	683.4	161.5	366.6	275.9
182.0	963.0	1511.4	1453.2	546.3	1126.9	816.7	1796.9	955.2	1547.1	1438.9
2192.7	3234.6	2873.0	2920.0	2980.6	3280.8	2045.8	3574.4	3034.9	4581.1	3973.7
232.8	1609.9	2113.4	2605.9	1200.7	1909.6	1572.5	2275.1	1127.9	3060.0	1715.1
176.6	3421.4	2605.9	2870.6	2506.7	3923.4	1398.6	3403.4	3597.2	6048.5	2286.5
44.7	142.7	129.4	98.4	218.9	99.0	190.0	105.2	102.9	69.5	35.8
23906.3	13797.1	13433.1	16403.5	14077.2	14386.1	14941.0	13923.8	21500.1	12148.4	19185.5
84.5	2498.8	3003.5	2802.0	2447.0	2959.1	1931.7	3748.8	2440.8	4687.6	3181.7
96.5	1351.3	1881.9	2279.6	1611.8	1458.0	901.4	2615.8	2017.1	2272.3	1267.3
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2613.2	2824.3	3027.6
4903.9	5165.0	4083.3
6296.3	5777.1	4845.0
966.6	1816.7	732.9
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3846.1	3533.8	3201.1
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3798.9	4225.8	2940.8
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2640.2	3756.0	2280.3
4261.3	6873.2	3986.0
4189.8	4302.8	3168.2
1869.1	2756.8	2301.5
2940.5	2913.6	2394.1
5513.8	7399.9	5593.7
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2655.0	3157.9	2893.4
2036.2	2073.1	1335.4
2872.4	3040.8	2327.7
1368.8	1753.3	1002.0
2604.3	2995.3	1558.0
3386.3	4535.9	2866.7
1006.1	1389.3	634.4
944.5	807.2	583.8
369.9	518.4	178.1
1520.9	914.9	461.1
3167.9	3335.0	1816.8
1878.8	1906.3	936.6
4129.3	3538.2	2634.8
90.3	180.3	120.3
14300.1	15701.7	12820.6
3592.6	3676.6	1954.1
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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
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DQ492780.1 gg_id:157463 Pseudoalteromonas sp. str. BSi20598
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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
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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
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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

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529.0	2015.8	2580.4	2839.2	2065.8	2230.2	1972.8	3315.6	3264.7	3054.5	1895.7
9056.2	3002.4	3971.4	4150.3	3623.4	2909.7	3810.1	3468.8	5796.9	3542.2	4132.4
503.3	1039.2	1445.9	1619.6	1588.4	1320.3	1363.3	1820.4	1213.6	1941.3	912.9
350.4	908.4	1150.3	1444.3	1163.7	1079.7	1314.6	1544.9	1004.2	1001.1	663.0
3250.6	1608.0	1434.1	1934.5	1694.9	1883.0	1400.2	1630.4	1865.3	1710.7	1558.3
3261.0	1679.1	1531.1	2019.3	1802.5	1970.6	1408.8	1662.4	1791.8	1816.8	1592.4
59.0	1254.8	1544.3	1468.7	1262.4	1986.2	1119.0	1593.7	526.9	1655.7	687.0
63.7	1230.0	1885.0	2099.2	693.4	1146.7	570.1	2742.2	2519.5	1642.4	1211.0
1799.5	3455.7	3388.6	3858.4	2874.4	3515.3	2746.5	3817.7	4010.6	4249.5	3945.7
3253.7	5058.1	5575.1	6370.4	5830.9	6805.3	5611.0	6327.1	5131.5	9610.3	4143.6
68.6	872.8	1451.0	663.7	660.0	1184.5	550.3	1539.9	522.8	1434.8	1636.9
2645.4	5022.3	5542.8	5815.9	5944.9	5341.8	6409.5	5139.2	5558.6	8145.6	5587.9
2215.6	2310.2	2232.1	1412.2	1655.0	2357.8	1547.4	1780.0	2917.0	1733.5	1099.4
3877.3	4612.0	5545.3	5595.2	4640.4	5541.7	5375.6	5737.6	5275.7	8384.1	6084.7
148.2	521.7	535.4	559.1	396.7	745.6	263.7	965.7	405.9	1064.4	571.3
14321.9	6665.0	6863.9	6760.7	7464.5	6316.6	7123.5	7580.2	9132.3	9144.5	6983.2
3267.0	1990.9	1948.9	2501.8	2028.3	2559.4	1578.7	2290.8	2343.3	2770.8	1847.8
222.5	1778.6	2426.0	2588.6	1434.1	2066.6	1661.2	2822.1	1253.2	3682.0	2080.9
306.9	1653.4	2954.1	3328.9	870.1	1759.5	1722.4	2923.3	997.5	2909.8	2264.7
6788.7	1765.6	2149.2	1891.1	2063.8	2149.8	3354.2	1854.6	2403.1	1900.5	2004.8
125.5	53.5	54.9	56.9	55.6	47.8	39.0	58.2	58.6	68.7	50.9
93.2	110.9	427.6	635.1	125.7	287.6	140.1	153.7	60.8	52.9	136.5
50.6	521.3	495.4	362.4	376.4	491.1	404.7	956.0	288.2	671.3	837.1
2902.8	3723.7	4957.1	4545.5	4293.1	4422.0	4287.3	4370.6	4867.9	5639.4	4285.6
144.2	1660.7	1474.4	1479.2	1804.0	1770.6	1758.0	1534.2	1419.7	1847.5	1139.3
2281.9	3254.3	3203.1	3456.1	4338.5	4088.0	3104.0	4168.1	3108.0	6207.3	3790.8
70.5	598.7	773.0	768.6	1083.3	1276.3	755.9	672.5	578.5	2146.7	544.7
15152.7	5421.7	5373.3	6325.9	5174.5	4770.4	6418.8	4568.4	7535.8	7129.5	9625.5
6602.0	5952.6	5591.0	6826.6	6579.0	6466.4	6149.9	7352.6	6434.3	5466.6	10458.9
1742.6	482.6	637.7	322.2	553.6	288.1	111.4	399.4	494.4	409.2	1554.3
51.1	626.7	717.6	743.3	1195.4	1039.9	743.1	752.8	680.0	2107.3	613.3
105.3	2395.6	2848.8	2763.5	2715.4	2670.4	1665.2	5060.9	2943.1	3109.1	2435.7
2296.3	2212.8	2217.5	2853.7	2240.7	2499.5	3218.4	2840.3	2227.1	3738.8	1670.0
2750.4	3124.6	3639.4	3217.5	3140.3	3064.9	3692.3	3720.1	3419.4	3706.0	3814.6
32766.9	9498.4	8278.3	9117.3	8269.0	9395.8	10313.1	7532.3	15055.7	10034.2	12676.3
6469.5	4870.4	5087.0	5322.9	5496.3	5622.2	6017.4	5467.4	6388.1	5076.2	5289.8
170.0	3044.6	3275.2	3255.4	2727.2	3097.9	2197.5	3615.3	2866.4	3779.8	3505.8
30.3	85.4	138.0	91.2	139.4	101.2	101.5	86.7	40.2	45.9	62.5
112.9	1374.9	1807.6	2176.5	1458.0	1784.9	986.1	2406.1	1376.9	2304.2	1708.8

2464.5	2471.0	2066.3
1678.6	1586.5	1316.9
3065.8	3458.7	2259.9
2905.5	5401.7	3350.4
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1872.6	2189.1	1588.6
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3531.1	4169.3	3022.4
6963.9	7592.8	5235.4
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505.0	413.2	156.7
4989.1	5262.1	3855.2
1934.6	1866.2	1334.5
4913.4	4127.7	2642.2
1082.0	1310.9	552.2
4569.3	6287.6	4987.0
6761.8	6352.3	5886.9
217.3	578.3	151.5
1245.1	1386.0	520.4
3643.4	3840.3	2620.6
2966.3	3189.6	3061.0
3346.5	5093.3	3736.6
7685.6	10944.7	8040.0
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3078.6	3235.8	1874.0
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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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EU807989.1 gg_id:310988 Pseudoalteromonas haloplanktis str. AFMB-008041
DQ492753.1 gg_id:157167 Pseudoalteromonas sp. str. BSi20333
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FJ494890.1 gg_id:419752 Pseudoalteromonas sp. str. B10
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DQ517866.1 gg_id:161247 Pseudoalteromonas elyakovii str. BSi20428
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DQ537517.1 gg_id:161333 Pseudoalteromonas haloplanktis str. BSi20585
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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

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X82134
DQ537

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35.0	461.8	1089.8	381.5	151.6	487.8	174.5	756.7	277.1	228.1	290.3
55.2	56.3	82.5	56.3	58.3	79.5	44.8	62.6	53.5	90.2	27.2
224.1	1571.7	2133.0	2634.5	1209.3	1789.5	1655.8	2126.8	1028.4	3087.1	1692.3
1121.7	4517.1	3895.4	2868.2	3076.9	4429.8	2528.9	3149.2	3649.5	3954.6	2137.7
2193.8	2561.4	2172.2	2173.9	1718.5	2242.5	1217.9	2737.6	2404.8	2634.8	3244.0
37.1	126.6	147.6	108.5	76.7	277.1	47.5	292.1	98.8	842.2	162.1
65.1	1890.5	2203.3	2086.1	2201.5	1994.2	1308.2	4237.8	2367.1	2477.8	1978.3
30426.1	11685.0	10810.6	11513.5	10928.7	12500.8	14132.7	10636.7	17482.3	14584.9	15392.9
299.1	3280.6	3458.1	2940.4	3074.7	3772.8	2503.7	3101.1	3506.8	6756.5	4288.1
279.6	3523.8	6156.2	2723.5	2365.8	2227.6	2286.9	3800.5	3515.3	4927.0	7370.1
10173.7	4934.7	5364.6	6060.0	4891.4	5288.8	5308.1	6277.9	7562.1	7872.0	6743.6
6287.1	4959.4	5343.7	5525.5	4757.2	4966.6	3755.0	6107.3	6780.2	4695.3	7835.3
43.5	137.2	123.6	111.8	79.5	126.5	53.6	110.9	78.5	317.1	47.2
3094.1	1797.6	2075.3	2648.6	1518.4	3046.3	1329.5	3190.8	2396.2	5903.8	1912.8
9248.3	5969.3	6039.8	6546.2	7182.7	6628.1	6642.2	6048.2	7234.6	9883.8	8461.0
4141.2	2402.6	2208.5	2946.0	2016.6	2656.1	2529.2	2490.7	2575.4	2576.5	2877.6
455.8	2761.8	3692.4	4170.3	2110.8	4054.3	1612.8	4231.5	3847.5	6443.5	2684.4
47.4	1927.9	2415.6	2304.1	1822.7	2228.9	1398.9	3588.6	2531.9	2548.0	1986.2
2290.8	3432.4	3538.6	3982.6	3363.8	3922.8	3368.8	3385.3	3843.5	5226.9	4745.8
87.9	318.6	507.1	497.2	174.1	393.9	179.5	740.5	202.5	389.3	279.9
148.5	1164.0	1341.6	1551.7	923.0	1443.4	374.8	1884.1	986.7	2338.7	2325.1
10762.4	5307.7	4756.1	5288.7	6082.4	5924.6	5801.1	5652.0	5653.3	7781.4	6800.7
208.7	1751.2	2408.0	2569.6	1429.5	2048.9	1656.5	2789.0	1234.1	3612.0	2070.5
143.8	230.8	245.8	295.3	193.6	386.9	139.4	412.8	163.5	421.8	216.1
3944.5	1461.9	1817.0	1791.6	1664.5	2104.4	1386.7	2233.0	2294.6	4639.8	2003.9
2739.2	3404.1	3246.7	3274.7	3615.0	3734.4	3377.2	3665.1	4562.7	5167.1	2911.3
426.3	1469.0	1456.7	1782.3	949.4	2475.9	1011.2	2452.7	1452.6	4252.9	1356.6
32.9	49.0	59.3	43.0	42.7	44.8	23.6	23.2	19.9	62.9	18.3
218.8	1389.8	1602.9	1515.0	2398.6	2017.4	2360.1	1747.7	877.0	4299.0	1312.4
341.0	869.8	1344.3	1668.9	779.3	1236.6	1240.7	1629.9	560.1	2443.5	904.0
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414.5	2231.0	2578.0	3143.7	2726.6	2944.5	2952.9	2842.0	2966.8	5277.0	2538.8
557.8	2609.4	3259.4	3804.8	3719.5	3838.2	2183.1	3747.4	3553.4	6896.3	2512.4
163.9	2873.6	2682.2	2687.1	2178.5	2759.4	1383.5	3127.0	2729.0	3471.0	3282.3
10707.5	3545.9	4192.2	5424.2	4272.5	5284.3	5612.2	4294.7	6018.2	7170.4	7529.3
60.2	579.2	626.0	421.2	447.6	658.0	448.0	1227.4	278.9	761.7	865.0
3370.5	4078.8	3915.1	4738.8	3961.0	4853.0	4809.8	4401.6	3920.3	4480.1	5392.4
2593.9	2941.1	3590.2	3545.8	3024.0	3576.9	3352.8	3977.2	3194.5	6169.3	3883.5
29235.3	9856.1	8717.7	10552.7	9468.0	9301.8	9117.0	10020.3	10804.4	12045.3	13927.2

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631.7	488.4	304.1
117.6	47.7	86.3
1770.5	1750.5	850.3
3581.7	3926.7	3329.5
2257.5	2309.6	1376.8
144.1	562.1	97.7
3060.1	3011.8	2305.7
11124.1	14427.5	10622.9
4495.4	3751.9	2188.7
2846.5	2609.5	2175.5
5927.2	7282.8	4502.0
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210.5	332.9	76.1
2559.6	4218.4	2107.3
7392.1	7067.0	5291.8
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4665.3	4391.7	2201.0
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3272.0	3584.9	2318.8
423.4	547.3	240.2
1387.5	1540.4	721.8
6007.9	7773.6	5081.1
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3618.9	5094.5	3761.7
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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
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EU849123.1 gg_id:348634 Pseudoalteromonas sp. str. LP621
AY682201.1 gg_id:107552 Pseudoalteromonas chazhmella str. R10SW10
DQ517879.1 gg_id:161373 Pseudoalteromonas elyakovii str. BSi20670
AB518970.1 gg_id:543117 Pseudoalteromonas sp. str. MB55
DQ492738.1 gg_id:158140 Pseudoalteromonas sp. str. BSi20316
AF313497.1 gg_id:111481 Pseudoalteromonas sp. str. A3
DQ923439.1 gg_id:187538 Pseudoalteromonas sp. W-5
AB257336.2 gg_id:182468 Pseudoalteromonas mariniglutinosa str. Do-52
AM110978.1 gg_id:140823 Pseudoalteromonas sp. str. 3023
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
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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

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FJ1720

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82.4	1010.2	1488.7	1638.0	1486.6	1894.6	886.0	1546.1	1064.9	1852.2	1304.3
7002.5	2916.4	3122.0	3282.7	2636.2	4582.5	2734.7	3421.1	3475.3	3630.8	3848.2
34.3	51.0	63.6	30.7	46.9	45.0	27.4	25.4	23.4	55.4	15.3
2417.9	3136.5	3599.1	3792.5	3227.6	3827.8	3617.1	3712.6	3410.2	5752.5	3630.7
165.4	738.8	1305.8	1425.6	456.0	1080.7	347.2	1576.2	1580.8	1055.9	1266.5
71.3	750.1	935.3	1100.6	1027.4	1017.9	852.3	1318.2	648.1	489.2	522.5
2039.0	4546.7	4361.4	5129.4	5058.3	5179.7	6266.0	4767.7	4948.8	7202.0	4348.3
550.7	853.3	1044.9	1732.9	1050.1	1452.0	440.4	1633.6	625.2	2952.0	975.0
57.4	144.7	255.8	191.6	300.5	230.0	195.7	299.8	170.1	118.5	123.9
659.8	2696.4	2654.6	2914.6	2696.5	3801.9	1878.0	3054.8	3164.9	3011.8	1737.1
1806.0	3790.5	5042.0	4711.2	3576.3	6321.2	4338.7	4678.4	5993.5	5988.0	4315.5
225.7	1242.7	1092.7	1267.3	1413.6	2034.7	890.9	1412.1	1902.9	1232.4	1372.1
111.1	2010.7	2704.6	2703.4	2091.5	2435.2	1645.9	4662.7	1888.3	2770.4	2033.6
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54.6	252.0	453.8	399.1	297.4	465.1	333.3	762.8	449.6	669.6	319.0
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2197.5	2416.2	2335.3	2550.8	2801.9	2855.0	2881.3	2675.1	2154.7	3670.1	2057.9
108.1	1981.9	2119.3	1809.1	1423.3	1749.8	732.2	1838.3	2376.5	2646.4	2267.0
1833.2	1805.2	1567.0	1463.1	1835.2	2260.5	1449.3	1870.7	1951.8	3250.4	1378.4
3820.0	2997.0	2975.0	3282.3	2738.7	3612.9	3357.6	3581.8	3264.0	4613.6	3525.0
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275.3	3845.0	3282.4	2567.1	2070.5	2495.3	1181.8	3230.2	4912.8	4310.0	3857.9
1013.9	2184.3	2157.1	2128.0	2147.8	2095.7	2256.9	2015.7	2640.4	3807.5	2347.4
173.8	1710.3	2272.0	2263.4	1937.3	2579.3	1114.3	3937.9	2875.3	3168.0	1469.0
6453.4	3832.8	3842.1	4559.0	5029.2	4139.9	7429.0	4896.0	4548.9	2136.1	4648.0
38.3	21.1	32.4	34.6	23.1	20.3	31.5	19.2	23.5	24.7	25.5
65.0	810.6	1509.5	1284.6	1069.0	958.9	869.7	1183.0	449.7	1644.4	658.6
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7292.2	4140.6	3048.5	4380.6	4233.6	4069.8	3754.3	3794.2	4335.2	4144.3	312.0
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61.1	805.7	2104.6	793.6	226.1	601.0	358.8	1143.6	358.2	207.6	342.2
25547.3	6723.6	6060.6	6751.1	5469.6	6929.0	7144.9	5350.5	8829.7	8120.7	9001.6
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9127.3	7346.6	7251.1	7910.6	7123.6	7568.4	7923.0	7670.5	13586.6	12579.5	10044.1
4143.2	2914.9	3126.0	3203.1	3956.7	2929.9	3464.7	4242.0	5188.7	3032.5	2291.9
52.2	16.3	18.8	27.7	20.2	14.1	17.6	16.7	16.1	17.8	16.4

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3250.1	4079.4	3070.5
112.1	109.0	38.3
3704.0	3991.7	2517.1
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1753.5	1285.6	823.6
5744.9	6035.4	5302.3
1127.8	1382.9	881.4
362.3	521.0	215.7
3308.6	4242.6	1580.4
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1612.8	1704.1	1435.8
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1898.1	1650.9	962.9
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o__Alteromonadales	f__Shewanellaceae

g__Pseudoalteromonas
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g__Psychromonas
g__Shewanella

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s__Shewanella algae	6759

DQ642828.1 gg_id:159691 Pseudoalteromonas sp. 28 DQ642
DQ665792.1 gg_id:163917 Pseudoalteromonas elyakovii str. BSi20426 DQ665
AM913936.1 gg_id:403449 Pseudoalteromonas sp. L232a AM913
EU330363.1 gg_id:252092 Pseudoalteromonas sp. str. BSi20602 EU3303
DQ492784.1 gg_id:158866 Pseudoalteromonas sp. str. BSi20612 DQ492
AY563031.1 gg_id:100315 Pseudoalteromonas marina str. Mano4 AY5630
AB049728.1 gg_id:51317 Pseudoalteromonas atlantica str. AR06 AB0497
DQ011614.1 gg_id:125030 Pseudoalteromonas ganghwensis str. FR1302 DQ011
FN554588.1 gg_id:566577 Pseudoalteromonas sp. str. HL4 FN5545
AM111074.1 gg_id:140761 Pseudoalteromonas sp. str. 8039 AM111
FJ425222.1 gg_id:367067 Pseudoalteromonas sp. str. K1-14 FJ4252
AF173963.1 gg_id:18661 Pseudoalteromonas atlantica str. KT0910 AF1739
DQ787199.1 gg_id:165819 Pseudoalteromonas arctica str. 37-1-2 DQ787
DQ492758.1 gg_id:157718 Pseudoalteromonas sp. str. BSi20343 DQ492
AM111078.1 gg_id:140967 Pseudoalteromonas sp. str. 8043 AM111
AF043742.1 gg_id:22902 Pseudoalteromonas distincta str. KMM 638T; ATCC700518 AF0437
FJ202088.1 gg_id:326316 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2020
EU050781.1 gg_id:246147 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_02_66 EU0507
FJ403097.1 gg_id:359108 Disease- changes healthy and diseased colonies Caribbean coral Montastrea faveolat FJ4030
EU930871.1 gg_id:342076 Pseudoalteromonas sp. str. KDW4 EU9308
EF101548.1 gg_id:192719 Psychromonas arctica str. KOPRI24930 EF1015
AB365349.1 gg_id:275002 Psychromonas heitensis str. 04HE-4-40 (= MBIC 08331) AB3653
NZ_AAQS01000017.1 gg_id:160611 Psychromonas ingrahamii str. 37 NZ_AA
U14582.1 gg_id:9115 gas vacuolate str.90-P<gv>1 U14582
AJ969456.1 gg_id:157483 Microbial black smoker s Mid Atlantic Ridge ecological implications rock fragments ch AJ9694
AF374385.1 gg_id:38990 Psychromonas arctica str. Pull 5.3 AF3743
AY548987.2 gg_id:99098 marine bone clone sacC3D3 AY5489
U85849.1 gg_id:9117 Psychromonas sp. str. IC004 U85849
AB304804.1 gg_id:236309 Psychromonas sp. str. JAMM 0394 AB3048
DQ009471.1 gg_id:126016 bacterioplankton clone SPOTSMAY03_890m29 DQ009
AB374544.1 gg_id:264272 Psychromonas sp. str. J42-3A AB3745
U73722.1 gg_id:9120 gas vacuolate str. 174 U73722
DQ027056.1 gg_id:133700 Psychromonas sp. str. CNPT3 DQ027
AB304807.1 gg_id:252707 Psychromonas sp. str. JAMM 0700 AB3048
AY167326.1 gg_id:81340 Psychromonas sp. str. ANT9265 AY1673
AJ519627.1 gg_id:76528 uranium mill tailings soil clone Sh765B-TzT-48 AJ5196
AF235108.1 gg_id:71948 Alteromonas sp. str. KT1114 AF2351
DQ530480.1 gg_id:166114 Psychromonas sp. str. gape-82 DQ530
AJ416756.1 gg_id:25724 Psychromonas profunda str. 2825 AJ4167
FM994680.1 gg_id:561093 gill and deep-sea limpet Pectinodonta sp. digestive tract host on sunken wood deptl FM994
EF542799.1 gg_id:224364 Shewanella algae str. YJ06114 EF5427

40.7	204.3	204.9	187.8	72.1	257.9	88.2	274.4	106.6	401.8	134.8
69.2	941.7	1162.0	1116.4	1022.5	1278.3	599.7	1433.0	1113.2	1633.6	1000.6
258.7	1687.5	2767.7	1721.1	760.9	1598.8	1062.7	2689.4	798.1	1171.3	1521.6
358.6	321.6	359.4	259.5	432.1	432.4	151.1	527.8	219.8	1068.4	206.4
139.3	835.9	870.9	949.5	1177.8	1364.6	719.6	1242.9	701.9	2179.4	806.0
8018.2	4473.5	4303.0	5070.4	3754.6	4340.7	4718.3	4634.1	5144.0	4717.2	5606.6
1629.1	3160.2	4309.0	5045.6	2449.5	3545.2	3052.4	3936.5	2193.0	3229.3	3626.2
2669.5	2327.3	3111.3	2714.1	2056.2	2690.8	2414.0	3549.6	4075.7	2685.8	2723.7
2064.9	4735.5	4410.1	5069.6	4272.0	5266.3	5009.5	5259.3	7277.1	7210.2	3982.2
13015.0	7542.9	8413.5	9264.3	8027.1	9297.6	8547.2	9205.8	12255.3	11317.0	10203.9
3788.7	3137.6	3020.3	2978.2	3390.9	3001.2	3094.6	3923.8	2676.4	3658.1	2500.5
4495.2	5563.0	5379.2	6027.3	6210.3	6841.5	5620.3	6585.0	5772.3	10047.4	6391.6
132.3	2085.0	1967.2	2085.8	2686.5	2737.3	2217.8	2898.9	1700.8	3484.1	2505.8
121.3	516.8	511.5	611.0	416.5	779.2	267.7	926.2	384.1	962.1	559.5
688.6	494.0	317.0	234.9	298.2	497.8	279.5	369.5	406.1	714.4	212.9
44.3	1838.2	2617.2	2018.1	2359.7	2340.1	1475.0	4428.2	3086.2	2631.7	1900.5
32.9	63.0	83.5	119.0	50.2	196.7	55.0	188.4	55.3	217.7	66.7
8477.9	6532.1	7057.5	7126.5	7235.1	7468.4	11945.1	7149.4	9073.6	6947.5	7381.7
53.4	1193.0	2287.7	1529.5	2336.3	1473.2	2383.4	1552.7	535.3	425.9	1156.8
54.0	363.6	516.7	435.5	489.4	676.8	294.8	501.2	471.6	79.4	193.2
355.0	5487.5	5870.2	6407.3	5917.6	6876.3	5841.5	6311.9	5215.3	9542.9	5321.3
5881.3	6156.6	6665.1	6951.8	8262.5	7232.4	5695.7	7788.1	6984.3	8197.0	5965.2
382.7	4801.6	5788.3	6437.3	5041.0	6526.1	3968.9	7086.1	5994.7	9565.4	4709.8
112.0	2370.0	3199.7	3741.8	2789.7	3068.4	2918.0	3585.9	3048.6	2741.5	2170.5
2370.8	3888.5	3946.2	4390.5	3542.9	4257.2	3971.0	4932.5	4994.6	5477.1	3553.8
54.3	2996.7	2556.7	3112.7	2738.2	3396.1	2114.6	3035.2	2786.6	2741.5	2368.1
180.7	2151.2	2773.4	3347.2	2136.8	2151.2	2538.3	3669.1	3943.7	2028.4	2259.5
439.6	4046.2	5336.9	5811.2	5257.6	4223.7	7444.8	4519.2	3711.4	2740.6	4326.3
220.6	2554.2	3635.4	4290.3	4500.1	3045.3	5371.3	3413.5	1396.4	2265.3	2109.3
1232.7	4196.2	4704.9	5025.7	5652.1	4913.0	4996.8	5601.9	4234.3	5759.6	4198.9
271.7	3177.0	4096.7	4302.6	4841.0	4671.0	3234.7	4134.2	3256.4	3447.5	3243.8
205.8	3009.8	4722.8	5438.3	3203.4	3891.3	4401.7	5010.3	2878.6	2803.6	4030.9
448.5	3270.9	3498.6	3787.6	3206.8	4579.0	2348.3	4577.3	3998.5	5989.0	3490.3
2114.5	5084.0	6272.8	7172.7	7588.4	5946.6	5408.6	7439.4	7875.7	6364.1	5066.1
2993.1	4464.6	5784.5	6679.5	7754.0	5353.2	5684.2	5893.7	6758.7	4271.3	4304.2
7577.8	8716.9	9347.4	10345.6	10132.6	9925.5	8245.3	9839.5	10625.2	15094.6	7819.8
427.8	6138.9	6405.8	6621.6	6708.8	7878.3	3858.7	7190.3	6665.4	9861.7	4740.5
68.3	2079.9	2374.9	2258.5	4562.2	4121.3	2005.6	2544.5	1054.9	980.3	1083.8
428.9	2651.2	3059.2	3141.3	3363.7	3928.8	2750.5	3999.8	2225.9	4683.2	2462.3
6124.2	5081.2	5581.5	6227.2	6009.7	6098.2	5776.3	6036.5	6520.3	6666.2	5405.4
368.7	1883.4	2243.5	1963.5	1672.6	2867.9	1712.1	2213.8	1629.4	3639.4	1390.7

217.8	480.8	184.7
1612.1	1626.6	792.2
1949.2	1339.2	802.3
440.8	666.4	410.0
1707.3	2173.8	816.6
4685.8	4938.5	3754.1
3585.2	3511.1	2600.9
3996.5	4147.4	2458.3
4504.7	6422.3	3221.4
9908.3	10470.5	8037.2
3256.2	3257.7	3206.1
6896.2	7236.8	4564.5
2862.6	3096.5	1159.6
658.6	764.0	358.5
514.0	450.8	284.6
3229.2	3891.0	2957.4
189.3	218.9	114.7
7815.8	8115.4	7300.6
1648.9	2024.6	1475.6
378.9	658.1	241.5
6896.6	7491.9	5902.2
6517.7	8348.2	6129.4
7287.1	7357.7	5463.7
3480.0	3489.7	2953.4
4543.6	5785.6	4089.1
2978.4	3743.8	2783.9
2974.3	2908.1	3776.9
4087.8	4331.3	3176.2
2963.6	3479.9	3096.4
5689.3	6812.7	5449.0
3228.7	4266.9	4001.9
4478.5	3840.2	3347.4
4383.0	5421.0	2863.5
7492.8	6763.0	6995.2
4783.0	6114.0	6604.8
9954.2	10626.8	8111.8
6750.5	8653.3	5348.4
1708.5	2181.4	3402.0
4087.6	4939.9	3864.3
5469.6	7057.8	4658.3
2153.8	3035.3	1341.9

k__Bacteria	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria
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s__Shewanella algae	7034
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s__Shewanella amazonensis	7273
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s__Shewanella frigidimarina	7148
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s__Shewanella halifaxensis	6552
s__Shewanella hanedai	6667
s__Shewanella kaireitica	7591
s__Shewanella loihica	6688
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s__Shewanella marinintestina	6463
s__Shewanella oneidensis	6635
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s__Shewanella pacifica	7623
s__Shewanella pealeana	6853
s__Shewanella piezotolerans	6475
s__Shewanella piezotolerans	7362
s__Shewanella schlegeliana	6681
s__Shewanella sediminis	7281
s__Shewanella sediminis	7355
s__Shewanella sp. ANA-3	6646
s__Shewanella woodyi	6637

DQ883817.1 gg_id:164354 Shewanella algae 62
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
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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

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1640.8	3923.6	4533.9	4867.2	4620.5	5371.1	4147.2	5178.7	5361.7	7801.1	3967.7
12620.3	4394.6	4975.0	5652.2	5513.6	5462.3	4531.5	6041.6	4609.1	6567.7	6419.2
1363.9	2245.7	2247.7	2414.2	2264.7	2922.9	1640.5	3381.7	1850.7	3307.0	2227.6
418.6	2743.2	3225.9	3392.7	2513.9	3589.0	1595.7	4481.8	2447.3	3865.2	2112.3
76.0	1005.0	1375.9	1398.5	814.8	1806.7	425.6	2091.9	1284.8	2853.9	857.5
131.1	1608.1	2621.4	2781.6	974.0	3113.5	633.7	2029.4	1905.9	5007.6	1393.3
260.7	3094.5	3233.6	3028.1	2382.2	4135.2	1395.5	4331.9	2886.1	5992.4	2099.4
1690.8	4607.0	4873.9	5635.0	5793.9	5279.5	5107.7	5486.4	4489.9	5961.5	4500.2
1859.1	3538.7	3775.7	4052.7	3278.5	4224.6	2941.9	5318.3	3216.2	3728.1	2971.8
2547.6	5875.1	6966.8	7879.1	6468.0	7531.5	5409.1	7961.4	6989.7	10026.2	6407.5
297.7	2066.4	2112.8	2104.1	1283.6	2667.1	972.9	3755.5	1373.0	2385.5	1167.7
457.9	2614.6	3148.8	3718.0	2895.2	3607.9	2076.5	3926.9	2886.2	4720.7	2826.3
1701.4	5014.3	5599.9	6314.3	6160.8	6323.6	5032.5	6426.9	4643.8	7124.2	4486.5
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42.2	975.8	1568.2	1607.3	1717.9	2095.2	937.6	1701.9	1049.1	3599.0	963.9
4126.1	1347.0	989.2	1592.3	1271.0	1509.9	1398.6	1458.1	1438.1	1234.8	1057.9
34524.4	10421.6	10013.9	11814.6	12786.5	10101.0	13107.5	9665.1	14863.5	12170.9	13402.2
2181.9	1305.2	1521.9	1668.8	1410.8	1735.2	1426.2	2992.6	1651.8	858.4	1714.3
84.6	550.3	564.5	482.4	761.6	663.6	448.2	694.3	240.4	251.7	237.8
538.1	2060.9	1766.4	2538.3	2677.2	2558.4	2169.7	2546.5	1718.1	3347.1	1850.2
563.6	2620.3	2578.3	3395.8	3137.6	3108.8	2829.4	3563.0	2427.6	3641.5	2420.5
254.4	2528.1	2407.7	2558.8	2230.4	3306.1	1403.3	2839.9	2898.7	4564.1	1748.8
545.6	3421.4	3836.7	4104.2	4362.0	4014.7	4112.0	4790.3	3305.1	4685.1	3608.9
913.8	2266.7	2470.8	2728.2	1301.9	3604.9	1019.3	3614.3	2191.3	6044.8	1799.9
3344.5	2084.9	2388.3	2683.3	2191.7	2383.3	2611.1	2683.2	2633.8	3414.1	2029.1
4038.1	4190.7	5189.0	5818.3	3811.2	4405.7	4730.3	5411.8	3487.3	5876.8	4321.3
533.7	3659.7	3512.0	3726.4	3461.2	4328.1	2381.6	3581.0	4281.4	4360.2	2568.5
2628.1	4679.6	4776.3	5359.0	4648.3	4934.8	4436.9	6314.6	5447.1	5076.2	5362.8
188.2	2922.8	3269.3	3367.4	2845.4	3305.7	2829.7	5444.4	3742.0	4806.3	2683.8
4619.0	2006.1	2836.5	2709.8	3888.6	2739.8	2698.4	2701.0	2801.8	1497.0	2479.5
267.4	3616.9	3361.3	3385.4	3119.7	4112.2	2145.2	3497.9	4311.7	4330.0	2215.6
1045.3	2195.7	2530.7	2718.7	1838.9	3811.1	1424.1	3654.1	2527.8	7219.0	2183.0
984.1	4263.9	4795.3	5096.9	4234.5	6507.1	3120.9	6807.4	4698.2	11893.1	4397.8
101.6	1499.4	1548.2	1545.5	533.7	1993.9	247.0	2796.1	1005.1	2817.7	840.9
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6221.0	4941.5	5042.7	5523.5	5131.2	5013.1	6016.5	5269.8	5715.6	5888.0	4995.4
16223.2	5307.0	4820.9	5890.1	7695.2	6664.2	5416.4	5526.2	6290.8	5032.6	5706.6
3441.3	3433.8	3619.7	4039.9	2908.5	3653.1	2968.2	4073.7	2758.8	6296.1	3035.4

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3515.8	2949.2	2798.3
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1677.3	1353.0	588.9
1309.5	1869.2	1150.3
10233.8	11157.6	10023.3
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697.5	883.2	552.0
2589.1	3290.1	1942.7
3532.4	4188.4	2572.6
3032.1	3624.0	1469.8
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3965.9	4463.2	2492.0
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4100.3	4399.6	2001.7
6424.5	6794.8	4559.8
5008.1	5294.7	3508.2
2178.2	3028.1	1895.7
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6972.4	7489.5	5050.1
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U91551.1 gg_id:9106 Shewanella putrefaciens str. NCIMB 12577 U9155
AF530149.1 gg_id:61112 Shewanella gelidimarina str. MGP-71 AF530
AF005255.1 gg_id:9108 Shewanella putrefaciens str. MR-30 AF005
AF170300.1 gg_id:70300 Shewanella putrefaciens str. IR-1 AF170
DQ010165.1 gg_id:119545 Shewanella sp. str. HN-41 DQ010
FJ952791.1 gg_id:372983 Shewanella sp. str. 3tb16 FJ9527
AF039055.1 gg_id:9060 Shewanella oneidensis str. SP-22 AF039
AY902211.1 gg_id:113783 Shewanella sp. str. BR2 AY902
AM269901.1 gg_id:159850 Shewanella sp. str. ES-5 AM269
AM180742.1 gg_id:146524 Shewanella gaetbuli UL19 AM180
DQ537513.1 gg_id:161502 Shewanella frigidimarina str. BSi20544 DQ537
NR_025794.1 gg_id:561965 Shewanella aquimarina str. SW-120; KCCM 41821 NR_02
NC_009831.1 gg_id:246711 Shewanella sediminis str. HAW-EB3 NC_00
DQ325517.1 gg_id:148004 Shewanella sp. str. 62 DQ325
EF105398.1 gg_id:175874 Shewanella sp. str. IE9-3 EF1053
AF022402.1 gg_id:9027 Shewanella sp. ANG.209 str. ANG.strain 209 ANG.209 AF0224
DQ677025.1 gg_id:173087 Shewanella sp. Iso-W8 DQ677
AB205571.1 gg_id:113604 Shewanella putrefaciens str. T147 AB205
EF584058.1 gg_id:234701 Shewanella sp. str. HE5 EF5840
AF189696.1 gg_id:111615 Shewanella sp. str. BC47 AF1896
DQ665797.1 gg_id:173544 Shewanella frigidimarina str. BSi20542 DQ665
EU979479.1 gg_id:352968 Shewanella sp. str. CR07-A1 EU979
AF039056.1 gg_id:9061 Shewanella oneidensis str. SP-32 AF039
FJ497707.1 gg_id:589412 Shewanella sp. str. VS-7 FJ4977
AY170369.1 gg_id:69583 Shewanella fidelis str. KMM 3589 AY1703
DQ307731.1 gg_id:147165 Shewanella putrefaciens str. Hac411 DQ307
AF387347.1 gg_id:33931 Shewanella oneidensis str. DML7 AF3873
U91553.1 gg_id:9071 Shewanella putrefaciens str. NCTC 10695 U9155
FJ456679.1 gg_id:581729 microbiota two Antarctic notothenioid fish species intestinal flora clone A221_NCI FJ4566
U85903.1 gg_id:128222 Shewanella frigidimarina str. ACAM 591T ICP1 U8590
AB205567.1 gg_id:114271 Shewanella colwelliana str. Q-06 AB205
AB205578.1 gg_id:114304 Shewanella baltica str. W145 AB205
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NZ_AATK01000145.1 gg_id:166958 Shewanella baltica str. OS195 NZ_AA
NR_029070.1 gg_id:575480 Shewanella gaetbuli str. TF-27; JCM 11814 NR_02
FJ210800.1 gg_id:328373 Shewanella algae str. QDHT-04 FJ2108
AF132874.1 gg_id:113095 Shewanella frigidimarina str. ACAM 517 AF1328
AY485224.1 gg_id:106352 Shewanella marisflavi str. SW-117 AY485
AF500079.1 gg_id:88004 Shewanella japonica KMM 3582 AF500

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2090.0	2840.0	2647.9	2988.8	2744.3	3424.3	2783.9	3477.4	2528.7	5117.6	2961.6
7570.9	3092.0	2643.3	3249.6	2873.0	2866.9	2651.5	3984.5	3288.6	3306.6	3563.8
1270.9	3188.6	3726.1	4125.6	3498.5	4256.5	2804.6	5460.9	4195.7	4585.3	3251.5
3442.3	7695.2	7541.5	8551.2	7789.3	8143.8	6929.5	9607.4	8702.3	9938.5	6758.8
14134.3	4794.0	6588.2	7639.1	5031.2	6395.9	5409.7	5949.1	5919.6	7207.0	5309.7
65.4	335.5	706.5	686.5	423.2	970.8	209.7	1565.3	531.5	327.4	373.1
448.6	3680.1	3373.0	4171.3	4295.3	3966.3	3751.1	3999.8	3617.6	5176.2	3975.1
358.5	3495.7	3883.1	4566.2	4469.6	4554.7	3104.9	4846.5	2822.5	5206.7	2907.4
135.1	1239.0	1509.7	2056.0	1377.5	1572.3	883.4	3466.7	1465.6	2721.6	1258.4
615.4	2957.8	3718.0	4801.5	3739.8	4100.2	4199.1	4219.4	3384.4	6447.7	2924.3
3338.9	2992.6	3396.2	3644.4	3087.1	3560.7	3840.4	4021.1	4063.4	5542.0	3115.2
6132.2	4598.5	4545.8	4757.1	3995.4	4809.5	4517.2	5016.0	5225.9	5761.0	4279.8
792.5	721.9	1155.2	1361.8	739.6	1327.3	751.5	2135.1	417.8	1415.3	679.1
33.3	502.7	918.2	546.5	751.9	1180.4	102.7	2186.0	773.4	282.2	393.8
141.6	1166.7	1351.1	1206.5	765.2	1790.6	337.6	1659.9	1078.4	2312.5	884.2
1008.0	4963.8	5160.6	5975.0	5949.8	6017.5	5204.1	6747.2	4566.4	9180.3	4958.4
4077.3	4504.7	4836.5	5599.8	4961.4	4700.5	4584.6	6956.7	4634.7	4808.9	4939.6
579.4	2128.0	2254.6	2691.1	2011.3	2488.0	2108.7	2764.5	2507.7	1811.3	3000.5
9057.9	6289.8	7240.0	7619.7	6365.7	8127.8	6210.9	8439.1	9642.1	10963.0	8200.2
865.6	2243.6	2584.0	2925.8	2368.2	2806.3	2658.3	3139.0	2874.7	3190.6	2025.4
200.3	2927.4	3315.9	4162.2	2220.1	4143.0	1861.8	4391.4	4265.1	8193.2	3017.4
266.7	1809.7	2314.3	2444.1	1310.4	2777.1	1270.0	2754.5	2532.7	5222.8	1897.8
16602.4	6909.2	7369.9	7698.2	7182.0	8422.6	8209.5	7398.9	7710.8	8863.1	6901.0
150.0	751.3	957.9	1056.7	563.3	1223.8	260.5	2020.9	1088.6	2018.6	695.8
137.3	1273.1	2207.4	2459.7	1607.8	2820.6	1215.3	5905.0	2310.7	4164.3	1940.2
2041.6	4261.3	4624.5	4868.7	4229.2	4763.6	4168.3	5891.6	4647.2	5153.1	5067.1
103.7	1546.2	1582.8	1694.6	891.2	1658.0	986.4	2840.3	1458.1	2578.9	1186.8
5077.9	5138.1	4557.9	4898.4	4374.0	5503.6	4574.6	5637.0	5947.6	5708.0	4716.5
466.0	4608.9	4524.2	4551.5	4919.1	4702.6	5980.6	5095.7	6072.1	3774.3	3390.7
21629.8	7796.9	8200.4	8858.8	7515.9	9052.4	8068.3	8341.3	11986.7	12658.8	10748.3
36.5	736.2	839.9	820.2	290.7	1273.2	135.5	864.7	246.5	1544.8	153.8
61.7	1946.6	2507.0	2478.0	1639.8	2923.8	1104.5	5191.1	3036.6	4204.6	1574.3
1915.2	4467.0	5250.0	6054.2	5208.1	5654.8	3972.9	6358.2	4909.6	6323.8	4553.4
258.5	2303.5	3296.5	3585.2	2884.8	4635.7	1685.3	4203.9	3044.7	6938.3	2153.7
403.7	944.5	1076.9	1002.3	1269.4	1078.1	1218.7	1123.8	753.5	952.6	569.3
1346.0	1910.9	2964.8	2504.7	1751.2	4179.5	1657.4	3845.7	1928.0	5645.3	2556.2
140.8	1942.6	1681.0	2101.7	2552.3	2503.5	2169.1	2541.7	1899.3	2779.5	1591.9
8680.0	4539.8	4798.9	5218.4	4632.6	4982.7	5125.6	5302.7	4634.1	5816.2	4352.5
84.5	1733.5	2345.4	3052.6	1744.2	2908.5	1675.9	3578.7	2640.9	4104.6	2190.4

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2756.6	3180.5	2489.9
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2806.2	3257.2	1851.4
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8119.1	10039.5	6802.7
1118.1	766.1	217.5
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7310.5	6231.0	5046.9
5624.3	4549.3	2387.8
1233.9	1299.9	1370.5
3160.7	4767.4	2170.2
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DQ514298.1 gg_id:160423 Shewanella frigidimarina str. BSs20181 DQ514
AB204519.1 gg_id:137352 Shewanella pneumatophori str. SCRC-2738 AB204
AF132878.1 gg_id:38945 Shewanella frigidimarina str. ACAM 557 AF1328
EU290154.1 gg_id:256999 Shewanella marinus str. C4 EU290
DQ167234.1 gg_id:139040 Shewanella sp. str. HJ039 DQ167
DQ520894.1 gg_id:159825 Shewanella frigidimarina str. BSi20531 DQ520
EF105397.1 gg_id:179131 Shewanella sp. str. IE9-1 EF1053
AJ288152.1 gg_id:22553 Shewanella sp. Bok-1-30-2 AJ2881
DQ351772.1 gg_id:147472 Microbial Adherent Sediment Particles Heavy Metal Contaminated North Sea Surfac DQ351
EU427307.1 gg_id:265579 Shewanella sp. MSI04 EU4273
FJ169987.1 gg_id:323759 Shewanella sp. str. E505-14 FJ1699
CP001252.1 gg_id:527693 Shewanella baltica str. OS223 CP0012
EF584096.1 gg_id:231545 Shewanella sp. str. WA3 EF5840
FM887036.1 gg_id:459403 Shewanella sp. str. JC19 FM887
U85905.1 gg_id:137215 Shewanella frigidimarina str. ACAM 588 ICP4 U85905
AJ288153.1 gg_id:19933 Shewanella sp. SK-3-30-1 AJ2881
DQ334633.1 gg_id:196033 Impact metals on sediments heavy metal polluted marine sediment clone HB2-42-1 DQ334
EF584069.1 gg_id:231993 Shewanella sp. str. LS9 EF5840
AB201782.1 gg_id:137622 Shewanella sedimentalis str. d943 AB2017
NC_009997.1 gg_id:238071 Shewanella baltica str. OS195 NC_009
FJ154999.1 gg_id:320502 seasonal fluctuation coastal Bohai Bay sequencing and RFLP soil clone G5 FJ1549
U91552.1 gg_id:9070 Shewanella putrefaciens str. F137 U91552
AF011335.1 gg_id:9032 Shewanella pealeana str. ANG-SQ1 AF0113
CP000931.1 gg_id:270483 Shewanella halifaxensis str. HAW-EB4 CP0009
GU362097.1 gg_id:575055 Shewanella sp. str. KTSW-7 GU362
EU073095.1 gg_id:335676 Shewanella sp. str. TS29 EU0730
AF039054.1 gg_id:24664 Shewanella oneidensis str. SP-7 AF0390
EU434392.1 gg_id:260399 Shewanella putrefaciens str. a324 EU4343
DQ819373.1 gg_id:173702 Shewanella sp. T1E1C05 DQ819
EU000239.1 gg_id:324409 Shewanella livingstonensis str. KOPRI_22225 EU000
AY515438.1 gg_id:101407 Shewanella sp. str. GWS-BW-H27M AY5154
EU543691.1 gg_id:268317 Shewanella putrefaciens str. DL4 EU5436
EU180603.1 gg_id:242880 Shewanella putrefaciens str. S002 EU1806
GU289647.1 gg_id:586719 Shewanella sp. str. MEBiC05444T GU289
AF295592.1 gg_id:52642 Shewanella olleyana str. ACEM-9 AF2955
AB306516.1 gg_id:247972 Shewanella sp. str. MIB015 AB3065
AM990834.1 gg_id:278789 Shewanella sp. MOLA 59 AM990
AY170366.1 gg_id:69757 Shewanella waksmanii str. KMM 3823 AY1703
EU000237.1 gg_id:309277 Shewanella donghaensis str. KOPRI_22224 EU000
EF584057.1 gg_id:234216 Shewanella sp. str. HE4 EF5840

543.5	2194.1	2338.4	2578.6	2377.3	2496.6	2089.4	3926.0	1960.7	2870.1	1543.4
12908.7	4884.9	4675.7	5288.6	5186.1	4592.3	5818.4	4297.3	7510.6	7270.3	6188.5
241.1	2162.9	2637.4	2911.4	1924.0	3009.9	1513.1	4387.4	2477.9	4202.6	1939.7
1492.1	2490.0	2833.7	3119.8	3594.4	3275.6	3151.9	3828.8	2854.9	4859.7	2146.0
530.1	2156.2	2641.8	2093.7	1414.8	2692.1	2154.1	3072.6	2052.6	2079.8	1744.2
3017.2	4249.3	4425.2	4275.2	4289.8	4867.7	3674.0	4884.0	4410.0	5513.1	6640.3
634.9	2118.7	1870.2	2489.4	2873.1	2713.0	2272.9	2558.7	1738.3	3349.0	1906.6
59.3	419.6	397.1	283.4	419.4	453.6	237.6	521.0	242.0	156.7	128.1
23853.0	7104.6	6822.9	7581.3	7608.2	7188.7	7812.7	6497.1	10688.1	7922.5	10140.7
267.3	4203.0	5152.2	5155.9	2553.0	4887.9	2643.2	5724.9	4102.9	7372.9	3542.5
648.6	2389.3	2124.0	2803.7	2840.8	2918.4	2378.6	3291.0	2107.3	3395.0	2113.8
5076.3	3904.9	4225.7	4981.4	4362.8	4180.0	5492.2	4959.5	3446.5	4007.8	4156.4
411.1	3287.1	3646.9	4327.7	5246.4	3844.0	3931.4	4569.1	2903.8	4705.8	2989.5
16719.4	3975.1	3620.9	5394.9	4824.8	4371.1	4194.3	4310.2	6737.5	6768.4	5177.4
10114.0	5617.6	5770.6	5679.6	5408.0	6626.2	4844.9	5333.5	6303.7	9305.4	4813.4
580.0	2118.1	1866.4	2647.0	2891.7	2712.4	2136.3	2713.9	1737.5	3348.3	1905.0
16098.7	6033.7	6244.6	6607.6	6887.9	6520.6	6920.4	6371.9	7645.0	8395.1	6994.9
2432.9	5425.7	5890.1	6901.7	5396.6	5663.0	6083.7	6075.1	5537.5	5630.1	5345.6
89.5	907.5	1005.9	1317.0	868.5	1111.4	479.3	1370.6	1175.3	2204.1	834.9
1298.3	2734.7	2901.4	2959.6	2786.6	3444.6	2655.0	3961.4	2843.5	4286.4	2135.0
284.8	1388.9	1543.8	1547.5	1228.2	1962.0	865.8	2669.1	1127.0	2115.2	843.6
5787.2	4127.3	4440.6	4734.4	4207.2	4763.7	4165.4	5308.6	5790.3	6394.9	4586.6
1757.5	3687.7	4358.4	4751.3	4007.0	5008.1	3703.5	5112.5	4177.7	5689.3	3825.3
2308.5	2806.2	3060.9	3050.7	2415.1	3254.6	2640.1	2848.6	3795.4	5721.1	2796.6
480.3	3077.2	3049.9	3201.0	2669.9	4067.6	2009.8	3426.5	3720.7	4670.1	2204.2
1630.7	2761.3	2820.5	3446.8	2416.4	2955.4	2711.8	3089.8	3131.0	4395.7	2850.6
725.1	3432.3	2765.2	3918.6	4234.1	3871.6	2983.0	3997.5	2612.2	3385.1	2190.1
1943.4	4651.3	5101.7	5342.8	4702.8	5375.3	3853.8	6094.5	5332.1	9096.4	4272.0
1858.2	2023.8	1811.2	1874.7	1704.7	2591.4	1319.0	4318.1	2433.0	4822.9	1921.9
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435.6	1812.9	1862.0	1912.8	2525.9	1859.2	2371.9	1820.5	1334.1	2105.3	1297.0
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866.0	2544.8	2608.9	2926.9	2125.2	2598.8	2124.2	4380.1	2900.0	3998.9	2523.4
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806.2	2653.1	3291.0	3125.0	3306.1	2804.8	5583.3	3235.3	2461.8	2441.7	2692.1
2020.1	3352.5	3371.8	3482.9	3425.8	3730.7	3355.4	3124.0	3868.5	2824.0	4792.0
3803.5	5864.4	5540.7	5965.3	4576.6	6006.7	5472.0	6700.8	5764.0	7530.4	5665.2
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128.6	996.1	1689.8	1583.8	1510.8	1830.6	858.2	2071.6	1607.2	3020.2	1088.1
735.4	4895.1	4619.1	5557.4	5146.4	6153.8	4956.1	5259.3	4702.9	6124.9	5585.3
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3725.6	3671.0	3985.8
4596.0	5526.1	4839.2
4102.3	4394.5	2476.7
4062.2	4029.1	3004.0
1467.9	2975.7	1494.2
5641.1	7420.0	5464.1
2746.8	3501.5	2033.4
1057.0	714.3	307.0
7165.0	8166.2	6904.8
3895.4	4719.8	1743.9
3163.3	4126.3	2465.9
4534.2	5240.9	3917.7
4051.4	4365.4	3686.4
4357.5	5321.9	3826.8
7191.7	6444.1	4890.4
2740.1	3471.8	1909.2
6506.3	8373.3	5978.2
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1095.8	1498.4	764.1
3781.9	4566.5	2576.6
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4264.9	4783.7	2961.9
5936.2	5985.7	3894.1
3643.7	3504.4	4197.9
3581.8	4244.4	2155.6
6228.6	6248.2	4496.3
4651.1	3613.6	3967.4
1683.4	1225.0	569.2
5661.4	6168.8	4139.8
1917.9	2928.4	1714.4

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s__Nitrosococcus oceani	2440

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AF173966.1 gg_id:54246 Shewanella baltica str. KT0246 AF173
AB094597.1 gg_id:83672 Shewanella surugaensis str. c959 AB094
AY445591.1 gg_id:103376 Shewanella profunda str. LT13a AY445
NC_009665.1 gg_id:255224 Shewanella baltica str. OS185 NC_00
AF132873.1 gg_id:37061 Shewanella frigidimarina str. ACAM 516 AF132
Y13699.1 gg_id:9053 Shewanella frigidimarina str. NCIMB 400 Y13699
AY351983.1 gg_id:92948 Shewanella affinis str. KMM 3587 AY351
GQ869534.1 gg_id:569132 Shewanella sp. str. KCCM 42936 GQ869
NC_009831.1 gg_id:246705 Shewanella sediminis str. HAW-EB3 NC_00
AB013839.1 gg_id:9017 Shewanella sp. 3-8.C AB013
NR_025934.1 gg_id:540854 Cardiobacterium hominis str. 6573; ATCC 15826 NR_02
AY596470.1 gg_id:104981 Cardiobacterium valvarum str. CCUG12990 AY596
DQ645464.1 gg_id:160756 Cardiobacterium valvarum VA1941 DQ645
CP000513.1 gg_id:226003 Dichelobacter nodosus str. VCS1703A CP000
AJ717394.1 gg_id:149350 Suttonella ornithocola str. B6/99/2 AJ717
X92131.1 gg_id:46026 Lake Elmenteita isolate 2E1 X92131
AF384209.1 gg_id:25151 Chromatium sp. str. NZ AF384
AM712619.1 gg_id:237043 Allochromatium phaeobacterium str. JA144 AM712
FJ716332.1 gg_id:508808 Chlorobi dominate shal chemocline Bahamas Sawmill Sink column 10.3 m water dept FJ7163
AF384208.1 gg_id:22729 Chromatium sp. str. NM2 AF384
NR_025315.1 gg_id:559119 Chromatium okenii str. DSM 169 NR_02
FJ437816.1 gg_id:541203 Benthic okenone production Fayetteville New York Green Lake chemocline 20.5 m wa FJ4378
AB478662.1 gg_id:548000 SSU sequences Alps Cadagno di Fuori submerged biofilm mats montane wetland clo AB478
DQ330802.1 gg_id:159452 Guerrero Negro hypersaline microbial mat clone 02D2Z45 DQ330
AJ223235.1 gg_id:7564 Lamprocystis purpurea str. DSM 4197 AJ2232
AM941378.1 gg_id:344367 Marichromatium indicum str. JA122 AM941
AM941379.1 gg_id:304631 Marichromatium indicum str. JA210 AM941
AM179449.1 gg_id:190862 Marichromatium imhoffii str. JA120 1 AM179
AM941377.1 gg_id:325577 Marichromatium indicum str. JA214 AM941
AM941046.1 gg_id:369706 Marichromatium indicum JA347 AM941
AJ889020.1 gg_id:112951 Marichromatium chilcum str. CH8 AJ889
FJ376391.1 gg_id:360805 Marichromatium purpuratum str. DSM 1711 FJ3763
FM177512.1 gg_id:344391 Marichromatium indicum str. JA290 FM177
AM179448.1 gg_id:191066 Marichromatium imhoffii str. JA120 2 AM179
AF294030.1 gg_id:135580 Marichromatium purpuratum str. TAR AF294
FM177510.1 gg_id:333563 Marichromatium bheemlicum str. JA284 FM177
EU850807.1 gg_id:342759 Marichromatium purpuratum str. DSM 1591 EU850
AM180952.1 gg_id:148217 Marichromatium bheemlicum str. JA124 AM180
AJ543328.1 gg_id:111805 Marichromatium indicum str. JA100 AJ5433
AF508991.1 gg_id:71278 Nitrosococcus oceani str. SWC19 AF508

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329.7	1462.9	1882.2	2168.6	1505.6	1822.9	1688.0	2146.6	892.0	3217.2	1303.9
204.5	2444.3	3128.2	3687.2	2481.1	4244.3	1846.0	4396.6	3725.2	5827.9	2513.3
706.1	5574.3	5976.5	6564.6	8087.0	6593.1	5860.7	7182.4	5483.9	8566.4	4816.2
119.1	1663.4	1472.2	2131.5	2169.3	2038.1	1887.5	2600.8	1562.8	2727.7	1392.2
634.8	2227.8	2100.8	2967.6	2668.2	2889.4	2367.2	3415.7	2079.1	3174.9	2105.8
516.8	3671.7	3676.9	3294.4	3480.7	3863.5	3146.6	3926.2	4162.5	4361.2	2340.9
9919.8	6086.9	6577.0	7352.8	8259.4	5823.6	8288.6	6638.7	7254.8	7359.5	6584.1
1005.3	2034.5	2503.2	3044.8	3516.8	2558.6	3626.1	3292.0	1409.5	1470.3	2212.5
329.3	2694.9	3133.4	3583.8	3834.9	2871.6	4053.5	3770.0	3462.4	2649.4	2594.4
50.8	346.7	556.3	524.4	477.5	404.2	392.6	376.9	200.4	232.5	197.2
3165.9	6237.3	6394.4	7583.9	7863.9	6854.7	9018.8	6773.9	3846.6	7468.5	5801.4
11666.4	4216.9	4696.0	5460.1	5078.3	5378.4	3821.5	4721.7	2382.6	5228.8	2889.4
1846.6	7209.9	7358.6	6626.4	10167.0	8114.3	9448.7	8387.1	8034.0	4014.8	6984.2
1904.6	3672.9	4062.9	3941.5	5514.1	4926.3	3388.8	5133.0	3395.6	6199.9	3576.7
53.9	348.5	2863.6	2701.3	556.0	1582.8	219.7	3175.7	3707.4	816.2	1832.8
70.5	200.2	126.9	161.2	539.1	191.5	1353.8	248.7	99.3	53.3	76.8
6715.5	4180.8	4309.2	5078.3	4481.6	4295.7	5913.8	5138.7	3941.2	3373.9	4644.8
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60.0	636.6	616.5	715.9	1151.8	793.8	1366.1	996.6	366.3	687.6	414.8
505.3	3910.5	4040.6	4208.2	6776.0	4038.3	9708.8	5435.8	3074.4	1712.9	4611.6
4339.2	5038.5	4567.0	4390.1	5410.9	4057.1	8305.6	5129.1	5454.9	2213.0	3391.5
8689.5	8410.9	8009.6	9488.9	9003.4	8356.7	11241.8	9389.6	7285.1	8159.0	8673.1
430.1	3367.0	3562.6	3928.9	3840.7	4294.2	5442.0	4485.0	2938.0	3524.0	1891.0
63.5	361.8	250.8	241.3	310.9	528.5	7418.2	563.4	117.7	75.9	150.8
6074.9	2722.0	2607.1	2980.0	4133.2	3060.2	3829.9	3146.2	3183.7	3431.4	3198.8
120.1	2090.2	2215.9	2568.6	3016.9	2497.3	2813.7	3225.3	1962.7	1973.7	1568.1
112.9	2382.0	2566.5	2793.0	4132.8	2873.0	3509.9	3803.8	2212.1	2025.6	1585.3
247.0	4471.5	4503.9	5110.3	7932.7	5594.4	5876.5	6292.8	3610.8	5672.7	3011.1
240.1	3355.6	3387.9	3911.5	4099.2	4267.6	4251.8	4549.4	3139.8	4341.1	3048.8
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144.6	1584.9	1992.5	2001.4	2921.4	2054.5	2931.8	2505.5	1091.3	1458.7	1456.5
117.0	2118.8	2217.2	2522.8	3142.9	2501.4	2639.9	3352.6	1947.7	1870.7	1464.9
210.4	3476.0	3771.8	4172.0	7743.4	4362.1	5739.7	5325.2	2568.1	3637.3	2358.4
15006.9	6555.5	7264.8	7575.1	7723.7	6976.6	8968.4	6422.6	8135.9	6334.9	7624.9
203.0	4166.4	4130.5	5001.8	4475.1	4298.6	4535.7	4620.9	2756.4	3295.7	3082.4
87.2	1446.6	1983.1	2008.0	2298.3	2068.3	1927.5	2895.2	1553.8	1883.6	1111.0
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5848.6	6859.4	6783.9	7656.1	8266.1	7092.1	8769.8	7901.1	6335.4	5874.4	7033.3
18881.1	8732.6	7314.6	9860.7	9288.8	7916.2	10010.2	10078.4	10339.8	8089.0	11609.2

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7522.5	6596.6	4228.8
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7042.0	5677.8	4912.2
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g__Nitrosococcus
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g__Thiocapsa
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AF508990.1 gg_id:73060 Nitrosococcus oceani str. AFC5P AF5089
AF508992.1 gg_id:56278 Nitrosococcus oceani str. AFC3 AF5089
AJ298748.1 gg_id:77717 Nitrosococcus halophilus AJ2987
NR_025356.1 gg_id:573506 Thiocapsa litoralis str. BM5; ATCC 700894 NR_025
AF112999.1 gg_id:7533 Thiocapsa roseopersicina str. M11 AF1129
AM779060.1 gg_id:261543 Thiocapsa subramanianii str. JA146 AM779
AJ581994.1 gg_id:141744 Thiocapsa marina str. BM-3 AJ5819
AF112998.1 gg_id:7532 Thiocapsa roseopersicina str. 5811 AF1129
EF581005.1 gg_id:278653 Thiocapsa roseopersicina str. KS1 EF5810
AJ277022.1 gg_id:71426 Thiococcus sp. str. A31 AJ2770
Y12373.3 gg_id:71248 Thiococcus pfennigii str. 4250 Y12373
FN293055.1 gg_id:570678 Thiococcus pfennigii str. 4252 = DSM 228 FN2930
FN293058.1 gg_id:536936 Thiocystis gelatinosa str. 4310 = DSM 215 FN2930
D50655.1 gg_id:7517 Thiocystis gelatinosa D50655
AJ224438.1 gg_id:7518 Thiocystis violascens str. DSM 168T AJ2244
EF149014.1 gg_id:188673 Thiocystis sp. str. Mog3 EF1490
AM086640.1 gg_id:139588 Thiocystis sp. str. 448.10 AM086
AJ971090.1 gg_id:172979 Thiorhodococcus mannitophagus str. WS AJ9710
Y11316.1 gg_id:7526 Thiorhodococcus minor str. CE2203 Y11316
AM748925.1 gg_id:245986 Thiophaeococcus mangrovi str. JA304 AM748
AB016986.1 gg_id:7570 Thiorhodovibrio winogradskyi str. MBIC2776T AB0169
AB294924.1 gg_id:225518 -dependent & analyses hydrothermal system off Taketomi Island Japan microbial ma AB2949
DQ867045.1 gg_id:196530 Microbial and methanogenic potential temperature water Japan natural gas field clo DQ867
FJ535065.1 gg_id:545461 microbial colonizing walls Karstic Slovenia cave wall biofilm clone 2PJM13 FJ5350
AF420353.1 gg_id:55790 hydrothermal sediment clone AF420353 AF4203
DQ811841.1 gg_id:166871 mangrove soil clone MSB-4C11 DQ811
DQ395021.1 gg_id:152376 harbor sediment clone VHS-B5-48 DQ395
FJ712412.1 gg_id:516020 and Archaea Gas Hydrate Sediments (East Sea) Kazan Mud Volcano Anaximander Mo FJ7124
AY225634.1 gg_id:95183 Mid-Atlantic Ridge hydrothermal sediment clone AT-s26 AY2256
EU373841.1 gg_id:265007 southern Cretan margin (eastern Mediterranean Sea) canyon and slope sediment clo EU3738
AM882514.1 gg_id:309379 Structure along hydrocarbon contamination coastal sediment oil polluted water pet AM882
GU369919.1 gg_id:524281 and mats vents Arc white microbial film on pebble aphotic zone shal hydrothermal v GU369
FJ203535.1 gg_id:340951 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h FJ2035
EU617747.1 gg_id:337743 Seasonal variation microbial Yel Sea sediment clone C13S-68 EU617
FM877665.1 gg_id:362822 Microbial several mining wastes Bulgaria vicinity uranium mine Sliven clone Sliv-109 FM877
DQ499304.1 gg_id:159535 acidic cave snottite biofilm clone CV55 DQ499
EU050785.1 gg_id:254811 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_01_66 EU050
GU061986.1 gg_id:593500 and function microbial mesoscale eddy perturbations South China Sea clone S-DCM- GU061
AY225631.1 gg_id:96909 Mid-Atlantic Ridge hydrothermal sediment clone AT-s2-13 AY2256
EU652572.1 gg_id:278349 Seasonal variation microbial Yel Sea sediment clone B8S-132 EU6525
DQ269059.1 gg_id:182899 marine macro-alga surface clone UA09 DQ269

13185.7	8155.8	7551.4	8079.2	8400.5	8378.3	9711.2	9526.5	11316.8	8778.2	9402.3
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45.1	263.3	253.1	257.3	503.0	278.8	200.7	282.2	108.3	72.6	113.8
17833.1	6106.0	6827.7	7145.1	7049.5	6868.2	8001.1	6336.4	7923.8	5765.9	11541.0
2500.7	4869.7	4150.4	4292.7	5601.7	3966.9	7084.3	5086.1	3299.8	3993.2	4453.5
13222.7	4893.2	4660.4	5212.7	4828.7	4814.4	8327.4	3727.3	7080.1	7157.4	6365.1
80.9	4555.2	4155.9	5412.3	5285.6	4355.0	6651.4	4921.4	3226.0	4614.5	4052.8
118.8	2180.9	1767.9	2599.1	3557.0	1981.4	6081.9	2445.3	975.6	390.1	929.4
3231.5	4416.8	4928.6	4689.4	6140.2	4416.3	9226.9	4661.8	3620.4	4318.8	3655.3
447.5	292.4	312.9	387.6	330.4	329.8	577.6	377.5	200.9	95.1	335.0
567.1	2671.1	2504.8	2882.6	3612.4	2664.9	6425.3	3019.5	1548.5	1500.1	1990.3
344.6	2377.2	2683.7	2355.1	3078.6	2696.7	6164.6	3192.7	1722.6	1134.3	1458.5
209.7	1482.5	1477.5	1378.4	1936.6	1566.6	2845.6	1768.9	1080.0	1307.1	759.9
8301.8	4203.7	4548.2	4155.4	4053.4	4501.4	5548.8	4290.7	4731.5	5807.0	5144.1
11388.7	5923.4	5691.8	6389.2	8008.9	6232.9	7745.2	6147.0	7450.0	5975.6	9452.5
114.5	802.1	737.2	767.4	1343.4	1161.8	2545.6	944.4	498.9	1060.3	506.4
3306.7	1869.1	2195.3	2676.0	2991.3	2623.8	8236.9	3115.9	1230.4	608.0	1076.4
1552.3	3920.8	4564.5	5461.3	5786.9	3811.3	6593.3	4995.3	2604.6	1832.8	2937.6
797.4	3059.2	2659.4	2958.6	3388.0	2759.1	10521.9	2641.9	2187.7	1386.4	1998.8
2398.9	4174.3	3501.2	4307.2	4553.1	5420.1	4971.3	4673.8	2771.7	6153.4	3117.6
57.6	186.7	105.1	120.6	100.5	187.1	165.5	168.8	65.0	55.2	113.4
2651.7	3171.6	2951.7	3818.9	4143.9	2846.1	3456.7	3471.5	4339.3	3295.2	2646.5
60.0	800.2	697.0	823.5	1182.2	875.6	853.3	1179.0	287.7	135.9	303.1
4643.2	4843.8	4306.9	5380.1	7792.2	4792.2	7153.2	4779.3	3683.1	5191.9	3876.7
4347.2	3707.2	3677.2	3561.0	4557.1	3758.0	1973.7	2970.6	5312.4	4002.8	5681.9
128.8	4305.8	4080.3	4900.0	7527.4	3791.2	8154.8	3021.1	1302.2	1199.5	2266.8
57.2	3266.1	2736.5	1438.5	1394.8	2700.0	1294.6	1439.6	3507.9	1561.9	1125.4
1185.6	6802.6	7577.7	7169.0	8276.6	7616.9	6820.5	6504.7	6058.3	5502.3	6469.7
8810.2	8013.6	7977.6	8626.3	8421.6	8378.1	9312.0	7811.9	9307.6	9461.7	9342.9
5574.9	3604.2	3835.5	3437.4	3949.6	3372.0	4258.4	3094.0	3423.6	3532.5	2843.1
2911.7	2833.9	3302.3	4435.0	3847.1	4329.2	4453.4	3571.1	2943.3	8617.0	2364.2
111.5	413.7	657.8	710.3	1013.3	513.9	466.3	897.0	188.8	316.9	275.2
363.1	6586.1	7110.7	7634.0	7363.8	7451.2	8074.4	7298.7	6643.4	6360.5	5254.8
12892.6	6555.6	4965.1	5373.7	5166.0	7457.7	4946.4	6685.7	6367.0	5607.8	5807.1
1224.1	3431.8	3841.2	4193.2	6863.1	4269.7	8427.4	3949.7	2498.4	3444.1	3212.8
1128.8	1214.7	1270.7	1564.1	1323.6	1347.7	1234.4	991.7	1168.0	313.1	1804.6
121.3	2400.7	2273.9	2104.8	3828.7	2818.4	2464.6	2869.8	2154.3	1248.8	1040.1
872.2	4738.3	4694.8	4680.6	5879.6	5875.0	4775.1	5030.0	3504.1	4580.5	3539.9
74.9	1328.2	1156.5	1290.7	1219.2	1312.5	833.5	1569.5	722.0	375.0	498.7
526.5	3718.8	4207.7	3754.6	4941.8	4520.0	4392.9	5766.6	2680.2	2423.5	4007.6
1897.2	2589.9	3486.2	2316.5	2385.7	2562.8	2273.0	2446.0	1824.0	1063.6	1664.7

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9019.3	9237.4	9690.4
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6300.8	6288.2	6010.2
3604.9	4626.4	3332.5
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4465.9	3573.3	3864.7
1957.5	1756.1	2135.9
4683.2	4303.2	4368.5
406.8	596.5	431.5
2314.2	3359.7	2820.0
2368.2	2993.8	2605.1
1565.3	1808.6	1133.3
3733.1	5564.3	3922.5
6447.3	7426.3	7037.1
982.9	1184.8	1047.8
2834.5	2934.9	2923.9
4975.8	4405.9	4029.0
2778.5	2596.8	2747.7
4067.7	5148.6	3584.9
134.8	193.5	172.4
3115.5	3494.9	3655.7
834.0	1030.1	1708.1
4338.4	5109.0	4897.0
3077.0	4821.4	3706.0
2810.6	3668.5	6698.5
1739.4	1726.5	1286.4
5749.4	7011.0	6571.7
8451.2	8374.7	7858.9
4003.7	4266.7	3864.7
4631.1	3511.7	2814.0
476.5	1065.4	474.1
7912.4	7119.9	7185.2
5836.6	7946.7	5123.8
3700.1	4715.0	4238.5
982.0	1728.8	1132.8
1907.9	2467.7	2595.7
4841.7	4745.6	3511.2
1535.9	1636.9	1703.8
5347.1	5780.8	5193.3
2767.1	2305.3	1748.4

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EU799991.1 gg_id:341773 It's all ranking aquatic Newport Harbour RI clone 1C227671 EU799
AY592343.1 gg_id:99715 deep-sea mud volcano clone Amsterdam-1B-40; BC20-1B-40 AY5923
FJ712551.1 gg_id:519028 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) k FJ7125
AY796036.1 gg_id:108755 gold mine bore hole clone 47mm23 AY7960
EU700150.1 gg_id:298462 Study on Shantou Bay Marine Sediments Microorganisms sediment clone STU8 EU7001
FJ545527.1 gg_id:533202 Diveristy Seawater and Sediment Northern North Yel Sea seawater clone W1-36 FJ5455
DQ289941.1 gg_id:173031 Microbial Carbon and Nitrogen Cycling Sediments South Atlantic Bight Permeable Sh DQ289
AY225628.1 gg_id:96854 Mid-Atlantic Ridge hydrothermal sediment clone AT-s3-68 AY2256
EF644798.1 gg_id:299470 genes and citrate lyase deep-sea microbial MAR Logatchev hydrothermal vent syster EF6447
EU491553.1 gg_id:268415 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR4C EU4915
DQ303270.1 gg_id:141619 Microbial ecology macroscopic filaments extreme Tinto River acidic river clone fa7 DQ303
GU061300.1 gg_id:574531 Evaluation culturing methods cultivate previously Yel Sea intertidal beach seawater GU061
DQ394966.1 gg_id:153375 harbor sediment clone VHS-B3-85 DQ394
FN396767.1 gg_id:555049 constant flux thermophilic cold seabed Arctic marine surface sediment clone s5_8_I_ FN3967
FJ484458.1 gg_id:553048 microbial autonomous rover world's deepest phreatic sinkhole wall biomat El Zacator FJ4844
DQ351781.1 gg_id:147516 Microbial Adherent Sediment Particles Heavy Metal Contaminated North Sea Surfac DQ351
AM040135.1 gg_id:145316 sandy sediments clone Sylt 39 AM040
GQ351146.1 gg_id:586541 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Eastern GQ351
EF646139.1 gg_id:247661 Potential interactions particle- anammox and archaeal partners namibian Namibian u EF6461
FJ205341.1 gg_id:551312 Prokaryotic deep-sea hydrothermal region East Lau Spreading Centre deep marine se FJ2053
AM889168.1 gg_id:584938 structure superficial sediments Bizerte (Tunisia) southern Mediterranean coastal an AM889
FM877664.1 gg_id:367915 Microbial several mining wastes Bulgaria vicinity uranium mine Sliven clone Sliv-80 FM877
FJ529318.1 gg_id:512678 Evidence vertical transmission symbionts adult embryo Caribbean sponge Svenzea ze FJ5293
AB099937.1 gg_id:79212 inactive deep-sea hydrothermal vent chimneys clone IheB2-13 AB0999
DQ469234.1 gg_id:158638 Microbial and ecology water Zhong Tiaoshan mine Shanxi province China AMD clone DQ469
GU118309.1 gg_id:589714 Threatened Corals Provide Microbial Habitats clone Dstr_I04 GU118
EU801093.1 gg_id:336892 It's all ranking aquatic Delaware Bay NJ clone 2C229409 EU8010
FJ205285.1 gg_id:564511 Prokaryotic deep-sea region East Lau Spreading Centre active hydrothermal field sedi FJ2052
DQ833482.1 gg_id:164256 detected analyses depth sediment Guanting Reservoir clone 35-8 DQ833
AJ536881.1 gg_id:78477 uranium waste soil clone JG30-KF-AS32 AJ5368
DQ234241.2 gg_id:143226 determined library mangrove clone DS159 DQ234
EF613006.1 gg_id:234358 acid mine drainage clone YSK16S-43 EF6130
FJ535355.1 gg_id:556389 Granulosicoccus sp. str. Z271 FJ5353
EU394558.1 gg_id:342967 Coccolithophore bloom dynamics shape (NE-Atl) northern Bay Biscay pelagic free-livi EU3945
EU439003.1 gg_id:540861 symbiont EU4390
FJ228294.1 gg_id:324503 sulfate-reducing enriched during bioremediation experiment sediments (Brandenburg FJ2282
DQ070793.1 gg_id:147722 Prokaryotic Structures Seafloor Basalts Varying Age and Juan de Fuca Ridge basalt gl DQ070
DQ396312.1 gg_id:154441 deep-sea octacoral clone ctg_NISA188 DQ396
EU491600.1 gg_id:270104 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU4916
EU617752.1 gg_id:341837 Seasonal variation microbial Yel Sea sediment clone C13S-45 EU6177
EU491687.1 gg_id:276375 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU4916

909.6	3184.5	2695.7	3186.8	2943.8	2841.6	4234.8	2973.5	2177.9	1054.0	2303.7
29537.0	8626.7	8368.2	9005.3	10281.0	8576.4	11743.5	8023.6	11567.9	10581.4	13202.6
1467.7	4418.7	6071.2	6919.2	5565.5	6358.0	6593.7	6461.1	4316.2	5442.1	4149.9
134.9	1017.2	1571.6	1381.9	1234.2	1327.2	1692.2	1327.0	541.2	529.3	893.0
4995.9	4790.2	4871.6	5573.7	7088.9	4932.9	7938.4	5414.4	2801.9	3748.5	3162.6
4887.4	5738.8	5431.9	6091.0	7060.0	5827.8	7897.4	6440.9	6019.6	6068.1	7730.3
77.0	1846.9	1315.1	1446.3	1725.3	1445.9	2214.6	2171.6	900.5	425.2	1207.0
272.4	110.7	201.7	206.2	267.9	252.1	192.9	170.0	62.5	317.8	55.4
283.1	4436.6	4310.9	4104.4	4217.6	4711.5	6312.3	7036.4	3691.5	2990.9	6331.5
58.7	1252.0	1404.6	1057.0	1274.8	1234.0	1072.9	1286.1	1687.3	779.1	857.7
414.8	2914.0	3514.4	3531.7	4151.1	3063.4	3649.6	3153.0	1735.2	1292.0	2899.1
1286.0	6154.1	5747.7	5445.2	5468.6	5288.4	5611.0	5281.5	4335.4	5459.2	5168.5
19143.7	8439.2	6956.4	7162.4	9079.3	7513.5	9509.1	8519.3	7633.9	10843.0	7331.8
1151.3	1730.1	1486.8	1622.0	2026.0	1789.0	1348.9	1861.7	1515.7	1923.0	1489.1
5528.1	5047.8	6188.7	6734.9	8363.2	5585.3	8130.3	6389.2	5424.8	3352.5	5246.7
3341.0	4141.5	3850.8	3753.1	4689.3	3989.0	4148.7	3803.7	4129.1	6885.4	4341.9
222.5	2263.4	2498.1	2416.9	2661.5	2029.5	3029.6	2182.0	1113.4	2574.7	1533.3
8365.7	8951.5	8255.4	9609.7	10614.0	8829.2	11026.3	9310.1	9865.5	9627.0	11089.0
16149.5	3488.7	3763.0	4902.3	3968.4	3667.3	3989.6	4110.1	5660.3	3714.4	5339.9
4730.2	7495.7	7007.4	6481.2	6313.0	7145.4	5858.9	7234.8	7151.5	8148.5	5905.6
261.3	649.0	836.5	1010.5	1143.2	510.7	1352.8	723.7	317.1	202.7	308.5
7295.4	8858.3	9295.6	10160.4	10361.2	8513.9	10797.1	8573.9	9129.8	6241.0	9717.5
43742.7	14636.0	13033.2	14594.7	15851.6	13060.5	16085.5	11975.8	17528.7	13608.4	16493.1
53.6	187.9	422.8	426.8	280.6	291.4	186.9	383.8	259.6	107.7	243.4
771.8	1781.6	1153.5	1784.4	2044.5	1843.1	2515.6	1963.8	1626.0	2904.0	1430.2
3382.8	4109.7	3376.4	3735.7	3462.7	3692.5	3423.1	3872.6	3145.7	4387.8	1999.6
9177.8	6525.6	6971.1	7792.6	8787.7	7413.5	9301.9	7354.5	4739.7	5842.1	7221.2
1925.8	7120.8	7751.3	8113.1	7160.5	6769.1	7237.0	7337.1	7420.7	3727.9	7205.5
437.0	3458.1	4514.5	5414.1	5560.2	4229.7	5961.4	4231.7	2915.3	1319.1	3202.8
2730.8	1862.6	2334.6	2048.1	2157.7	2295.1	2308.4	1907.1	2066.9	2485.7	2282.4
64.9	161.6	359.5	376.6	203.0	225.3	244.6	463.5	116.4	32.5	280.4
99.6	297.2	346.7	284.4	438.4	390.9	453.0	972.3	274.2	79.5	242.0
69.8	557.5	569.3	196.2	198.8	448.8	213.1	495.6	181.4	71.2	186.3
624.1	1750.7	1880.8	1834.2	1816.0	1927.8	1839.9	2121.2	1386.5	5180.3	1739.3
311.7	622.8	858.2	1031.6	722.5	667.2	568.3	700.1	574.6	412.0	207.5
5136.6	2737.5	4228.4	4314.2	4898.2	4398.3	5196.6	5103.9	3616.1	2522.8	5916.7
1450.6	3867.9	3816.8	3281.8	3450.9	3920.9	3718.4	3090.7	3448.2	4642.3	3582.9
3347.5	5855.8	4794.1	5318.1	5355.2	5090.4	5269.7	5068.0	7453.4	5476.2	5445.8
1065.5	3438.5	3545.2	4260.3	3831.2	3556.5	4805.7	4120.1	2244.9	3650.4	2510.5
210.8	2530.3	3164.8	2866.1	2629.6	2858.1	2653.0	2575.8	1167.7	1325.7	1795.6
7998.7	8739.4	7185.4	7555.1	8652.3	7215.4	9458.7	7269.4	6890.6	8884.1	6954.3

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5585.6	6553.0	5044.1
1718.5	1466.3	2386.6
333.5	222.6	150.7
6059.9	5539.5	3817.5
1952.3	1575.3	1326.7
2777.6	2716.9	2443.8
5788.4	5942.6	6904.7
10226.9	9396.1	8807.0
1924.9	1669.7	1230.3
7302.7	5973.6	6292.3
4337.2	4957.1	4856.1
2298.7	2873.6	2480.2
9785.7	9489.5	8192.1
3195.9	4028.6	4110.8
7032.3	7949.2	6143.4
956.7	854.3	711.5
8594.7	8897.1	11470.7
13183.9	13633.3	13766.9
369.1	537.7	348.4
2094.8	2826.3	3033.3
3810.2	4259.3	2911.2
7375.0	6459.5	6093.3
7024.3	6763.7	7128.5
3752.2	4519.8	7423.0
1861.0	1923.8	1967.1
252.4	193.5	245.9
457.4	337.1	484.3
364.6	347.6	484.0
1805.2	2538.3	1847.4
769.2	731.7	655.6
4106.9	4205.7	3678.1
4063.9	4255.4	3488.7
4612.0	6021.8	5271.3
5167.3	4049.4	3221.0
2468.4	2401.3	2513.4
8358.2	7330.2	7473.5

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EU035934.2 gg_id:316421 Insight microbial structure Norwegian deep-water Desmacidon sponge deep-sea cor EU035
GU208368.1 gg_id:577626 Study on Sediment Dongping Lake sediment clone Td1-10 GU208
FM213426.1 gg_id:354483 Chemosynthetic Bivalvia species mud volcanoes Gulf Cadiz host gill tissue clone Mer FM213
EU491699.1 gg_id:268263 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU491
EU491199.1 gg_id:275872 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak EU491
DQ396273.1 gg_id:156456 deep-sea octacoral clone ctg_NISA021 DQ396
AJ567545.1 gg_id:89831 deep-sea sediment clone MBMPE27 AJ5675
AM882524.1 gg_id:313486 Structure along hydrocarbon contamination coastal sediment oil polluted water pet AM882
EF540405.1 gg_id:220661 oil-shale semi-coke solid waste clone 4_4MK EF5404
GQ351258.1 gg_id:570178 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Eastern GQ351
EU491112.1 gg_id:258311 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak EU491
DQ070809.1 gg_id:149398 Prokaryotic Structures Seafloor Basalts Varying Age and Juan de Fuca Ridge basalt gl DQ070
DQ289928.1 gg_id:168507 Microbial Carbon and Nitrogen Cycling Sediments South Atlantic Bight Permeable Sh DQ289
EU491667.1 gg_id:262608 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU491
AY328730.1 gg_id:89553 drinking water system simulator clone DSSD31 AY3287
AY532575.1 gg_id:106089 uranium-contaminated aquifer clone 1013-28-CG34 AY5325
EF612420.1 gg_id:244634 historic semiarid lead-zinc site mine tailings clone K6-C62 EF6124
EU246808.1 gg_id:241908 polyphasic description Pocillopora meandrina Palmyra Atoll Calcinus obscurus abdon EU2468
EU735667.1 gg_id:307033 archaeal structures oil contaminated and soils China pristine soil Jidong Oilfield clone EU735
FJ535071.1 gg_id:571233 microbial colonizing walls Karstic Slovenia cave wall biofilm clone 3PJM14 FJ5350
DQ811846.1 gg_id:165797 mangrove soil clone MSB-4G2 DQ811
GQ348058.1 gg_id:533527 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ348
FM877661.1 gg_id:357872 Microbial several mining wastes Bulgaria vicinity uranium mine Sliven clone Sliv-13 FM877
EU491253.1 gg_id:274139 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak EU491
AB252438.1 gg_id:154019 Microbial extremely CO2 rich deep-sea sediment Marine sediments Yonaguni Knoll I AB252
GU198380.1 gg_id:546867 Metagenomic denitrifying sulfur-oxidizing consortium enriched marine sediment clo GU198
FJ205202.1 gg_id:563890 Prokaryotic deep-sea region East Lau Spreading Centre inactive hydrothermal field se FJ2052
GQ397041.1 gg_id:539039 Functional unvegetated perhumid recently-deglaciated soils do not correlate shifts s GQ397
FJ529263.1 gg_id:590516 Evidence vertical transmission symbionts adult embryo Caribbean sponge Svenzea ze FJ5292
DQ925902.1 gg_id:255109 Microbes and Thermal Gradients Temperature Hydrothermal Chimneys hydrotherm DQ925
DQ269101.1 gg_id:180233 marine macro-alga surface clone DPC112 DQ269
GQ495417.1 gg_id:575230 terrestrial volcanic rocks Iceland Hnausahraun lava f clone Bas-7-60 GQ495
GU230383.1 gg_id:561498 Multilevel approach along Rio de la Plata-South Atlantic Ocean coastal water clone A GU230
DQ334625.1 gg_id:186898 Impact metals on sediments heavy metal polluted marine sediment clone HB2-20-8 DQ334
EU700176.1 gg_id:296708 Study on Shantou Bay Marine Sediments Microorganisms sediment clone STU34 EU700
EU800034.1 gg_id:307663 It's all ranking aquatic Newport Harbour RI clone 1C227721 EU800
GU118033.1 gg_id:579643 Threatened Corals Provide Microbial Habitats clone Apal_F02 GU118
GQ263152.1 gg_id:541400 Structure Simulated Level Waste Site simulated level waste site clone F3_08X GQ263
AF223298.1 gg_id:37006 marine sediment clone B2M54 AF2232
FJ712427.1 gg_id:519729 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) K FJ7124
DQ836756.1 gg_id:172425 attached biomass denitrifying bioreactor clone DB-47 DQ836

9493.8	9378.5	7916.7	9124.2	10252.0	8772.4	10457.8	10068.1	6980.0	5429.0	10222.6
8834.7	8658.1	8660.1	9765.1	10929.4	8951.6	11066.7	8377.8	7327.5	6660.2	12165.2
67.3	127.3	241.2	154.9	228.5	196.8	273.5	143.9	81.9	29.9	105.7
1057.1	2444.4	2624.9	2604.6	3726.2	3068.1	3493.0	3102.9	2069.0	2696.7	1811.8
558.5	3718.7	3908.0	4501.7	5390.3	4377.0	5170.4	3723.3	3220.7	1344.4	2953.9
18125.8	7921.4	6143.7	6783.5	7613.5	6437.6	8379.1	6718.1	5249.9	6382.8	5220.6
120.6	2878.7	2211.2	1879.7	2252.8	2098.0	3261.7	2212.3	1789.7	1492.3	1192.5
7938.3	4991.4	4661.3	5492.2	6054.2	5716.7	6563.1	6407.5	4299.7	2885.8	5466.5
8533.3	6828.7	5983.2	6592.6	7101.9	6645.4	7550.5	6034.7	6620.9	7994.3	9100.4
53.0	160.0	171.8	150.0	264.8	183.4	828.4	185.7	98.3	65.0	78.5
1913.6	4505.3	4444.1	4890.4	5148.5	4703.6	5477.7	4824.1	2929.8	3621.3	3197.8
9531.3	6436.9	5878.4	6355.4	7485.1	6660.8	6751.2	6189.0	7996.9	6949.3	6761.6
36.6	177.6	286.0	331.9	458.9	431.4	535.0	338.8	127.5	732.4	102.1
6988.5	4455.7	4636.6	4964.9	5186.8	4884.6	6810.0	5082.9	4561.0	7934.4	4703.4
181.4	3569.1	3990.3	4455.8	3499.7	4083.1	4406.7	5112.4	2817.4	2800.9	4147.1
1139.9	5108.5	4975.5	6096.0	6441.3	5130.4	7473.2	5949.2	3590.9	2923.9	4158.0
1367.3	5800.7	4358.8	3168.3	2896.9	4494.6	3476.7	4084.7	6922.7	4429.7	2933.9
3034.6	4069.0	4262.2	4938.7	4469.9	4368.6	3987.3	5099.3	4149.0	4392.7	4334.0
93.1	1227.2	1203.4	1215.4	1337.7	986.6	1242.3	1838.3	590.1	278.9	734.6
1034.4	3716.1	3699.5	4520.4	5122.2	4685.8	5138.0	5060.3	2705.3	3823.1	3199.7
102.4	1055.4	1141.5	1169.7	414.4	1515.9	488.0	1664.9	1142.9	670.0	968.8
3201.5	5426.0	5612.3	6340.2	5696.6	5471.5	6902.3	5584.7	5731.2	4179.9	6438.2
3415.4	7002.8	7347.5	8343.0	10678.0	7653.9	9394.0	7787.1	6074.9	5424.5	7603.5
467.2	3391.1	2985.6	3279.5	3564.9	3433.7	3360.3	3754.6	4730.5	2106.9	2697.1
20919.3	10451.1	9697.4	11221.6	13629.5	10708.1	14178.3	11515.3	9876.2	9466.1	10869.6
24334.8	9670.1	8701.2	9594.9	9670.0	10568.8	9234.7	9866.8	10902.4	11834.8	13073.4
51.1	500.1	561.5	500.8	754.4	499.6	1097.4	392.0	50.1	327.2	180.1
567.9	3733.3	3350.0	3737.4	5461.7	4129.0	4410.3	4190.5	1730.7	1852.5	3305.4
8033.7	6950.7	7215.0	7984.4	9540.8	7288.8	9598.6	8364.4	5730.2	5333.2	6173.1
5900.0	3030.9	3328.3	3901.1	3185.1	4058.5	4024.3	3618.8	2858.1	6603.5	2890.5
32.8	74.8	118.3	118.9	139.9	71.7	154.2	84.1	36.9	31.9	48.0
108.3	2446.6	2245.5	2580.9	3230.9	2170.5	2553.3	2815.2	953.9	2783.9	1598.0
3763.7	2126.5	1878.0	1622.7	1678.4	1152.2	1839.9	1673.5	2120.9	2013.4	1850.1
52.8	155.1	185.3	181.0	249.8	147.7	341.4	184.9	35.1	27.5	190.6
382.0	2747.0	3278.5	3734.6	2214.7	3254.9	2295.0	4913.6	3552.1	2050.2	2787.4
1950.1	4892.1	4487.6	5158.6	5029.2	4604.8	5232.7	4803.8	4798.8	4483.5	4574.0
593.5	3814.6	3397.6	4065.1	5405.4	4076.3	6331.7	4921.5	2335.1	2506.3	2200.3
2392.2	5435.0	5168.2	4577.8	5828.7	4779.0	5310.7	3341.8	5043.7	3873.8	2115.7
21743.2	7970.9	7531.5	8456.2	9519.6	7650.9	10369.5	7917.8	10354.2	7658.1	9138.9
8622.0	6410.5	5897.3	5803.6	4388.6	6260.8	3944.2	5161.7	5983.1	5084.1	5093.1
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1895.2	2581.5	2412.6
5613.2	5521.8	6442.6
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8327.9	6978.2	7056.1
471.6	580.9	241.5
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5721.3	5682.5	7510.6
3444.4	2994.0	4157.3
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12833.3	12034.8	13811.9
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3143.9	4167.9	4670.8
8024.1	7393.3	7766.3
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1494.6	2476.4	2063.0
105.9	79.3	166.9
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4743.9	5331.4	5999.3
7315.0	4441.9	4628.0
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7804.1	8834.2	8791.7
6496.0	6753.0	7898.0
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GU302446.1 gg_id:538297 Spatial structure and activity sedimentary microbial underlying Beggiatoa spp. mat h GU302
EU286994.1 gg_id:254165 Pacific arctic surface sediment clone B78-30 EU286
EU491103.1 gg_id:271777 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak EU491
DQ328618.1 gg_id:148733 microorganisms populating site extreme acid mine drainage sediment clone H6 DQ328
GQ262946.1 gg_id:511219 Structure Simulated Level Waste Site simulated level waste site clone F1_84X_2 GQ262
AM997814.1 gg_id:543652 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A AM997
GQ348554.1 gg_id:554477 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ348
GQ866093.1 gg_id:553108 Seasonal changes Norway lobster (Nephrops norvegicus) gut clone F1-2 GQ866
FM178271.1 gg_id:310885 Thiolamprovum pedioforme str. 4470 = DSM 3802(T) FM178
GQ346946.1 gg_id:555763 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ346
FJ497646.1 gg_id:587676 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun FJ4976
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DQ070817.1 gg_id:149753 Prokaryotic Structures Seafloor Basalts Varying Age East Pacific Rise and Ridge basal DQ070
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FM242262.1 gg_id:329501 sequences sediment clone 93 T0h-oil FM242
EU491843.1 gg_id:260428 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU491
AM882535.1 gg_id:316871 Structure along hydrocarbon contamination coastal sediment oil polluted water pet AM882
FJ152611.1 gg_id:355416 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX1A_ FJ1526
AM086641.1 gg_id:139719 Thiocystis sp. str. H1.1 AM086
EF644807.1 gg_id:297894 genes and citrate lyase deep-sea microbial MAR Logatchev hydrothermal vent syster EF6448
DQ431906.1 gg_id:213821 microorganisms catalyzing nitrogen removal and organic matter metabolism perme DQ431
FN397816.1 gg_id:429948 geomicrobiological investigation sediments Gulf Cadiz GeoB 9072-1 anoxic sub-surfa FN3978
GQ246407.1 gg_id:551973 Temporal and spatial China North Yel Sea sediments clone Ld1-12 GQ246
AM882545.1 gg_id:347412 Structure along hydrocarbon contamination coastal sediment oil polluted water pet AM882
AM997582.1 gg_id:542870 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A AM997
AM882565.1 gg_id:312010 Structure along hydrocarbon contamination coastal sediment oil polluted water pet AM882
FJ437960.1 gg_id:512465 Benthic okenone production Fayetteville New York Green Lake surface sediments 16. FJ4379
GU454932.1 gg_id:530809 Understanding short-chain fatty acids accumulation enhanced alkaline digestion: kir GU454
DQ498828.1 gg_id:160903 Thiocapsa sp. str. SC5 DQ498
EF125462.1 gg_id:177523 mangrove soil clone MSB-2H6 EF1254
EU491333.1 gg_id:261470 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak EU491
FJ535330.1 gg_id:511313 within iron-containing flocculent mats submarine volcanoes along Kermadec Arc sedi FJ5353
EF999348.1 gg_id:250082 Vertical and Methanotrophs Estuarine Sediments Pearl River Estuary sediments 6cm EF9993
FJ745203.1 gg_id:553528 Transporter genes expressed coastal response dissolved organic carbon surface wate FJ7452
GQ495440.1 gg_id:543963 terrestrial volcanic rocks Iceland Hnausahraun lava f clone Bas-7-84 GQ495
EU050786.1 gg_id:245663 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_07_19 EU050
FJ712524.1 gg_id:513647 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) k FJ7125
AF406546.1 gg_id:60630 bacterioplankton clone AEGEAN_245 AF4065
FJ497635.1 gg_id:558137 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun FJ4976
FM242359.1 gg_id:317250 sequences sediment clone 16 T9d+oil FM242
FJ717238.1 gg_id:538780 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United Kingc FJ7172

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687.4	2186.7	3211.6	2705.1	5450.2	2938.5	2652.6	3513.0	2760.6	737.7	1813.3
11380.0	9712.2	7774.7	8064.5	8296.1	8048.1	8048.1	7200.9	11674.2	7834.0	11191.0
6662.1	258.0	169.7	302.1	354.5	399.1	2771.8	760.9	3336.8	3257.2	160.3
7719.0	6788.7	6618.9	8722.2	8723.6	7268.9	9326.0	7925.3	6646.8	3991.8	7579.8
13823.1	3994.6	4771.5	4440.3	4705.8	4039.3	6176.7	5100.8	3404.0	2885.9	4170.2
4849.3	6142.0	5543.8	5128.0	6229.4	5922.7	7158.7	5405.6	6787.2	3321.1	4574.9
1958.3	3987.4	4330.4	4801.1	4714.4	4102.1	4937.8	4740.9	3537.8	4384.4	4904.3
212.5	3988.7	4055.0	4622.9	6184.5	4339.2	7069.7	4889.9	3171.5	2962.2	2905.0
489.2	4332.7	5178.7	5579.0	5885.0	4744.2	5751.7	6405.6	3234.3	4840.0	4580.1
111.3	1462.8	1749.3	1770.5	1821.9	1456.8	2185.1	1996.6	1007.2	441.0	1085.1
3159.6	6681.9	6071.4	6383.0	6290.6	6430.9	7061.6	6159.3	8553.0	9956.8	5484.1
103.4	838.0	1482.6	1309.6	807.5	898.2	1318.7	1557.9	896.3	472.4	588.0
2601.0	2448.9	2189.6	2010.1	3383.7	2567.8	2886.6	2347.7	2304.1	2118.3	2394.3
629.3	5202.3	4489.6	4489.4	4343.0	4962.8	4761.3	4521.1	5263.6	4521.3	3830.3
3316.4	3956.5	4050.6	5043.6	3628.8	5253.1	3084.4	4478.2	2153.4	9400.1	1991.7
842.7	2280.1	2565.0	2907.4	3202.2	2748.1	3942.1	3026.2	1205.5	997.7	1348.4
1975.3	2439.7	2032.6	2476.3	3465.1	2340.1	2550.8	3128.7	1045.5	3135.1	1336.4
279.1	1723.9	1647.1	1739.9	2509.5	1965.9	5152.1	2057.9	1097.7	1773.2	977.4
6075.4	4892.2	5243.0	5982.6	4884.9	5477.3	6384.7	7132.4	3955.8	2924.7	5900.2
1496.0	4541.7	6055.6	6666.3	7056.8	6503.6	8772.5	6902.2	2494.4	5538.8	6029.2
2455.6	8050.9	8420.0	8381.0	8568.6	8951.4	7733.9	7153.1	6315.9	8203.2	8007.1
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63.4	2043.2	2391.8	2182.5	2932.7	3110.4	2952.8	2492.0	1587.1	2137.8	1269.6
170.5	1838.0	1842.9	1916.2	2166.2	2072.0	2296.4	2368.9	939.6	464.4	1053.0
2361.1	4238.4	4623.1	5536.6	4975.4	4699.7	6119.1	5400.6	3683.7	5194.8	3904.8
2392.6	2614.6	2642.0	2748.2	3709.8	2615.7	5753.0	2745.2	2056.5	1583.7	2780.1
2353.5	6198.0	6882.9	8282.9	9399.8	6565.9	11273.9	6556.6	4764.8	4784.5	5642.1
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308.7	2295.8	1997.2	2133.6	2196.9	2410.9	1691.4	2537.3	2531.3	1756.6	1220.7
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4618.2	6229.4	5216.3	6102.3	7053.6	5659.3	6703.9	6487.0	3197.9	6420.0	5701.1
11692.4	5697.5	6111.8	5791.7	7048.2	6880.5	7362.0	6139.8	6012.3	7787.5	5864.9
3142.9	5239.8	5538.2	6293.5	4567.3	5926.3	5597.6	6181.2	5145.1	5619.1	4719.9

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3226.9	3123.0	2263.7
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2483.2	2470.3	2215.4
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1214.6	1987.9	1565.2
6570.9	5774.8	6808.4
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1944.5	2460.4	1971.6
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3008.5	3271.9	2816.3
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FM210274.1 gg_id:528855 Marichromatium fluminis str. JA418 FM210
GQ141761.1 gg_id:435569 Microbial thriving -pH Rincon de la Vieja Volcano National Park Costa Rica superficia GQ141
EF076070.1 gg_id:256660 Sponge- microorganisms: ecology and biotechnological potential Bahamas: Little San EF076
AB426192.1 gg_id:267544 -situ identification study benzene-degrading s under methanogenic condition anaerc AB426
DQ925905.1 gg_id:254195 Microbes and Thermal Gradients Temperature Hydrothermal Chimneys hydrotherm DQ925
GQ406158.1 gg_id:593544 Benthic submerged sinkhole ecosystems sediment clone TS-45-9 GQ406
EF654696.1 gg_id:242116 mixed granule anammox reactor clone KIST-JJY027 EF6546
U24110.1 gg_id:7550 Gamma-proteobacterial endosymbiont U2411
DQ408758.1 gg_id:241921 endosymbionts gutless marine nematode Astomonema sp. sediments coral reef sed DQ408
EU555131.1 gg_id:265444 Microbial Sulfide Hydrothermal Vent Field Juan de Fuca Ridge Dudley hydrothermal EU555
DQ925881.1 gg_id:242627 Microbes and Thermal Gradients Temperature Hydrothermal Chimneys hydrotherm DQ925
EF125401.1 gg_id:193004 soil naked tidal flat sediment near mangrove clone MSB-1D8 EF1254
AB100006.1 gg_id:79132 inactive deep-sea hydrothermal vent chimneys clone IndB3-17 AB100
AM882566.1 gg_id:314376 Structure along hydrocarbon contamination coastal sediment oil polluted water pet AM882
EU050809.1 gg_id:253074 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_01_83 EU0508
AJ006212.1 gg_id:7572 Lamprocystis purpurea str. ML1 AJ0062
AB252426.1 gg_id:153466 Microbial extremely CO2 rich deep-sea sediment Marine sediments Yonaguni Knoll I' AB2524
EU491139.1 gg_id:272596 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak EU491
AB294972.1 gg_id:225408 -dependent & analyses hydrothermal system off Taketomi Island Japan microbial ma AB2949
DQ458038.1 gg_id:157435 acid mine drainage clone DX41 DQ458
AM282561.1 gg_id:193170 Thiorhodococcus kakinadaii str. JA130 AM282
AACY01032263.1 gg_id:105207 Sargasso Sea AACY0
EU491349.1 gg_id:260349 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X3 clone EU491
DQ676419.1 gg_id:223736 Archaeal and plankton freshwater pond suboxic freshwater-pond sediment clone M DQ676
AM997970.1 gg_id:541611 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A AM997
EU491101.1 gg_id:271612 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak EU491
EF208706.1 gg_id:202468 Vertical and horizontal structure microbial sandy carbonate sediment clone CI75cm.2 EF2087
EU617749.1 gg_id:332804 Seasonal variation microbial Yel Sea sediment clone D13S-16 EU617
NR_029333.1 gg_id:589849 Thiocystis violacea str. N. Pfennig 2711; DSM 207 NR_02
DQ676383.1 gg_id:219789 Archaeal sediment and plankton freshwater pond suboxic freshwater-pond clone M DQ676
EU491810.1 gg_id:261375 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU4918
AM491592.1 gg_id:274061 Thiohalocapsa marina str. JA142 AM491
AJ002796.2 gg_id:7556 Thiohalocapsa halophila str. SG3202 AJ0027
DQ330805.1 gg_id:159272 Guerrero Negro hypersaline microbial mat clone 02D2Z63 DQ330
EU236358.1 gg_id:295840 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg91C2 EU2363
FM242313.1 gg_id:328728 sequences sediment clone 25 T9d-oil FM242
FJ264656.1 gg_id:346479 Manganese and Iron Dependent Anaerobic Oxidation Methane methane seep sedim FJ2646
AF328856.1 gg_id:43810 Olavius algarvensis sulfur-oxidizing endosymbiont sulfur-oxidizing AF3288
AJ620507.1 gg_id:108086 Olavius crassitunicatus endosymbiont AJ6205
AM934861.1 gg_id:560973 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM934
AY953181.1 gg_id:114439 anaerobic swine lagoon clone B-1O AY953

2745.7	2976.2	2926.5	3476.8	3819.2	3934.2	5607.6	3562.5	4507.6	3194.9	2602.8
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11931.5	6302.2	6899.0	7196.8	7333.1	6586.9	8528.8	6691.8	5668.3	4673.8	7793.9
840.5	2307.3	2573.3	2568.1	3720.3	2628.0	3938.1	2208.3	1407.7	986.8	1222.6
758.1	3386.8	3159.8	3250.5	3100.9	2787.5	3696.5	3323.7	2062.9	2552.2	2181.0
1133.0	2881.9	2711.9	2943.5	3735.8	3065.4	4237.9	3350.1	1340.2	1498.5	2299.9
577.1	3614.0	4007.1	4087.5	4684.1	4357.3	5538.4	4835.8	2259.7	3882.6	3878.6
342.7	3595.5	3510.2	3455.9	4735.7	4011.7	4048.4	4187.8	3364.0	3732.1	2960.6
302.2	2066.2	2064.2	2080.5	2184.9	2069.2	3349.1	2493.2	1470.2	3080.8	1369.1
766.3	3510.8	3455.5	3630.6	4819.2	3671.5	4680.7	4039.0	1619.3	1997.3	2659.7
10748.6	5908.6	5643.6	6634.4	6003.3	6143.3	6782.7	7186.0	6520.5	7563.7	6850.8
151.1	2177.0	2532.8	2950.7	3445.9	2557.8	3505.8	2816.4	914.9	1367.3	1227.1
35.9	232.9	310.1	176.6	114.6	174.2	164.7	193.3	130.0	366.2	154.4
93.5	3051.6	3988.0	4747.5	3456.9	4041.1	2792.7	5593.3	2796.4	2282.2	2615.1
158.9	2292.0	2493.8	2399.7	3057.1	2256.7	3540.5	2309.5	1250.4	2063.6	1326.5
5995.2	5273.2	5471.1	5578.1	8192.7	5940.8	8052.2	5678.9	4358.2	1823.0	5906.3
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275.0	3531.8	3748.2	4407.0	4310.0	4289.1	6086.2	4287.1	2037.9	2599.1	5127.2
54.2	205.9	373.8	276.0	238.3	285.4	132.3	302.3	146.5	124.4	142.5
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8246.2	7196.3	6778.1	8481.5	6378.4	7921.6	8397.6	8780.9	7045.7	8983.1	5904.9
171.3	4885.5	4761.4	5261.0	4497.0	5613.9	5384.9	4847.8	3833.9	4809.0	4331.5
1187.0	3444.1	3036.2	3192.8	2996.3	3118.0	3779.8	3830.8	3251.1	2464.2	2059.6
987.1	3061.4	3346.5	2927.1	3282.4	3114.3	3700.6	2586.4	4524.6	4391.8	3514.7
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1486.7	2213.9	1936.7	2061.6	2021.9	2374.9	2696.7	3049.2	1711.0	1314.1	1547.4
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EU491595.1 gg_id:277061 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU4915
AJ404006.1 gg_id:67655 Thiobaca trueperi str. BCH AJ4040
AF468306.1 gg_id:80943 Arctic sea ice; northern Fram Strait clone ARKICE-74 AF4683
EU035919.2 gg_id:305967 Insight microbial structure Norwegian deep-water Desmacidon sponge deep-sea cor EU0359
FM242312.1 gg_id:323358 sequences sediment clone 62 T9d-oil FM242
AY225632.1 gg_id:98768 Mid-Atlantic Ridge hydrothermal sediment clone AT-s3-1 AY2256
FM242217.1 gg_id:352618 sequences sediment clone 9 T0h-oil FM242
GU061223.1 gg_id:560363 Evaluation culturing methods cultivate previously Yel Sea intertidal beach seawater . GU061
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EF157171.1 gg_id:246738 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon EF1571
FM242216.1 gg_id:315780 sequences sediment clone 328 T0h-oil FM242
AM942764.1 gg_id:259432 Thiorhodococcus kakinadensis str. JA326 AM942
AB247483.1 gg_id:149328 lab-scale EBPR sludge clone Run-SP84 AB2474
DQ834966.1 gg_id:239144 Methylohalomonas lacustra DQ834
GU061216.1 gg_id:561480 Evaluation culturing methods cultivate previously Yel Sea intertidal beach seawater . GU061
EF644813.1 gg_id:288087 genes and citrate lyase deep-sea microbial MAR Logatchev hydrothermal vent syster EF6448
EU734910.1 gg_id:313480 assemblages sediment station DBSE Northern Bering Sea clone 001A1 EU7349
AJ620498.1 gg_id:353788 Olavius 1 endosymbiont O. ilvae Individual 2 AJ6204
FJ971729.1 gg_id:415655 microbial autrotrophic denitrification granular sludge clone R1-B5 FJ9717
FM955329.1 gg_id:546246 nematodes marine sediment FM955
AM282559.1 gg_id:192789 Thiorhodococcus bheemlicum str. JA132 AM282
DQ408757.1 gg_id:211956 morphological between endosymbionts and marine nematode Astomonema sp. Bal DQ408
EU617748.1 gg_id:327160 Seasonal variation microbial Yel Sea sediment clone D13S-78 EU617
FJ971740.1 gg_id:437967 microbial autrotrophic denitrification granular sludge clone R2-B11 FJ9717
EF999974.1 gg_id:245668 Thiodictyon bacillosum str. DSM 234T EF9999
FJ712507.1 gg_id:529626 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) K FJ7125
EF999973.1 gg_id:257959 Thiodictyon elegans str. DSM 232T EF9999
AB186842.1 gg_id:103037 polychlorinated dioxin dechlorinating microcosm clone TSBX13 AB1868
GQ249599.1 gg_id:509542 Microbial anaerobic sediments Bay Cadiz (Spain) marine sediment: 12-14 cm layer cl GQ249
GQ347493.1 gg_id:540052 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ347
AF223299.1 gg_id:31454 marine sediment clone B2M60 AF2232
EU652571.1 gg_id:279434 Seasonal variation microbial Yel Sea sediment clone A8S-46 EU6525
FJ358866.1 gg_id:580890 and redox-stratified sediments marine reef sandy sediment clone OX79 FJ3588
FJ264672.1 gg_id:348014 Manganese and Iron Dependent Anaerobic Oxidation Methane methane seep sedim FJ2646
DQ867047.1 gg_id:186089 Microbial and methanogenic potential temperature water Japan natural gas field cl DQ867
GQ246364.1 gg_id:593033 Temporal and spatial China North Yel Sea sediments clone Cm1-27 GQ246
GU056102.1 gg_id:571289 Biologic Techniques Applied Microbial Prospecting China: Ban 876 Gas Oil Field Bein GU056
AB530206.1 gg_id:586045 Monitoring Suez and Tokyo bays based on analyses marine sediment clone Tokyo..B AB5302
AB530192.1 gg_id:549648 Monitoring Suez and Tokyo bays based on analyses marine sediment clone Suez..Ba AB5301
DQ269062.1 gg_id:190822 marine macro-alga surface clone DPC061 DQ269
EU134786.1 gg_id:243086 tallgrass prarie soil clone FFCH2627 EU1347

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46.9	144.0	224.0	183.2	428.6	210.3	1609.9	184.8	65.1	39.0	136.2
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13908.7	7286.3	7133.3	7933.7	7872.0	7717.4	8410.8	7916.4	10276.5	5890.2	10685.1
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705.1	489.1	502.0	514.4	876.8	740.7	3113.7	1060.8	664.7	578.5	423.7
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196.7	1860.0	1567.2	1941.3	1882.9	1556.9	2592.3	2727.2	890.5	709.1	1545.5
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45.7	1899.2	2238.1	2258.6	2147.0	2811.5	2443.7	2482.8	1762.2	3631.5	1564.7
1565.3	5572.7	5096.0	5208.8	7024.5	5392.5	7924.4	4963.5	4605.5	5358.8	7089.5
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5317.2	5806.5	4800.6
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3749.1	4319.4	3795.1
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AJ853601.1 gg_id:110147 landfill leachate clone GZKB108 AJ8536
EU236373.1 gg_id:297512 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg91G3 EU2363
AY225627.1 gg_id:96329 Mid-Atlantic Ridge hydrothermal sediment clone AT-s68 AY2256
FJ497388.1 gg_id:579158 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun FJ4973
EF632940.1 gg_id:242102 Unique microbial contrasting aquatic altitude Andean Altiplano (northern Chile) fresh EF6329
EU491429.1 gg_id:261838 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X4 clone EU4914
DQ811847.1 gg_id:164335 mangrove soil clone MSB-5C2 DQ811
DQ811843.1 gg_id:172303 mangrove soil clone MSB-4E4 DQ811
EF203207.1 gg_id:207236 phylotypes sediments Lake Kastoria Greece sediment clone Kas176B EF2032
FM877666.1 gg_id:366930 Microbial several mining wastes Bulgaria vicinity uranium mine Sliven clone Sliv-112 FM877
AY225635.1 gg_id:98613 Mid-Atlantic Ridge hydrothermal sediment clone AT-s80 AY2256
DQ811842.1 gg_id:171222 mangrove soil clone MSB-4D7 DQ811
AY328773.1 gg_id:88634 drinking water system simulator clone DSSD75 AY3287
DQ351776.1 gg_id:146277 Microbial Adherent Sediment Particles Heavy Metal Contaminated North Sea Surfac DQ351
FJ937836.1 gg_id:397082 Marine Sponge Gelliodes carnosa coastal waters Lingshui Bay Hainan Island South Ch FJ9378
EU236293.1 gg_id:290042 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg9Co20 EU2362
GU208274.1 gg_id:568003 Study on Sediment Dongping Lake sediment clone 6F3-6 GU208
GU118056.1 gg_id:580801 Threatened Corals Provide Microbial Habitats clone Apal_E11 GU118
AB188772.1 gg_id:114044 cold seep sediment clone SB1-7 AB1887
FJ205206.1 gg_id:559269 Prokaryotic deep-sea region East Lau Spreading Centre inactive hydrothermal field se FJ2052
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GU369933.1 gg_id:527507 and mats vents Arc white microbial film on pebble aphotic zone shal hydrothermal v GU369
EF612432.1 gg_id:244758 historic semiarid lead-zinc site mine tailings clone Fe-K6-C35 EF6124
EU491147.1 gg_id:261461 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak EU4911
DQ823153.1 gg_id:167115 Techniques Microbial Studies Oregon Caves National Monument Quad 3 off trail clo DQ823
AB189342.1 gg_id:113899 cold seep sediment clone JT58-17 AB1893
CP000453.1 gg_id:171890 Alkalilimnicola ehrlichei str. MLHE-1 CP0004
AJ404972.1 gg_id:46869 Alkalilimnicola halodurans 34Alc AJ4049
DQ217918.1 gg_id:142576 Alkalispirillum sp. str. AGDZ DQ217
DQ217919.1 gg_id:142198 Alkalispirillum sp. str. ALPs 2 DQ217
EU308278.1 gg_id:358039 Arhodomonas sp. str. 50B226a_1 EU3082
EU653291.1 gg_id:280943 Thiobacillus prosperus str. DSM 5130 EU6532
EU653290.1 gg_id:282074 Thiobacillus prosperus str. V6 EU6532
AY298904.1 gg_id:89646 Ectothiorhodosinus mongolicum str. M9 AY2989
EU590916.1 gg_id:265489 Ectothiorhodospira sp. str. PHS-1 EU5909
AM943124.1 gg_id:556051 Ectothiorhodospira variabilis str. WN21R AM943
AM902494.1 gg_id:571311 Ectothiorhodospira imhoffii str. JA319 AM902
FN293051.1 gg_id:562547 Halorhodospira halophila str. 9622 FN2930
AJ318525.1 gg_id:62637 Halorhodospira neutrophila str. SG 3301 AJ3185
FJ153016.1 gg_id:323860 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX4CI FJ1530
NZ_ABYM01000001.1 gg_id:349593 Thioalkalivibrio sp. str. HL-EbGR7 NZ_AB

2884.3	4095.7	4688.6	5490.9	6086.7	4929.1	6338.3	5474.9	4683.7	2628.0	3982.8
8448.9	5490.3	5148.0	5052.1	5845.0	5801.7	5970.4	5420.1	5141.4	3349.4	4673.5
2206.2	1093.8	1030.1	898.7	899.1	742.4	1077.6	1058.5	913.2	1355.5	1151.3
981.3	909.4	1066.8	1227.2	1969.5	1105.9	1534.3	1543.1	526.1	486.9	618.2
2421.5	3927.6	3407.1	5809.3	5865.3	4442.4	6202.0	4048.7	2457.6	2854.6	4152.1
131.1	2336.6	2040.9	1875.4	2841.0	2665.8	2234.4	2831.5	904.6	2028.8	1364.0
43.5	1021.8	1033.9	968.6	1798.3	1130.4	1144.8	1683.1	676.3	176.5	608.4
565.5	4514.5	4586.8	5198.3	3805.1	4655.2	4082.4	7427.3	4541.6	1527.6	5739.9
2962.9	4385.8	4694.7	4528.3	5606.9	4296.3	6302.9	4553.5	3239.8	2073.4	3316.6
4008.6	6993.2	7237.8	8057.3	7172.8	7152.9	8487.1	7359.8	6217.0	7126.7	7271.1
115.3	2019.7	2009.8	2113.7	2383.5	1835.4	1995.2	2271.5	862.4	2122.5	894.3
2396.0	4158.3	3736.7	4821.5	5640.9	4295.3	4720.8	4029.4	3745.6	3808.6	3550.3
128.6	987.3	1336.3	1481.0	898.2	950.1	1076.6	2158.3	770.9	645.0	604.7
1112.2	2534.2	2897.2	1875.8	3033.0	2581.0	2802.3	1317.0	2074.9	3191.3	2890.7
2521.7	7519.1	8124.1	8337.2	10905.4	6985.1	11084.4	6867.0	5970.6	4932.8	9063.4
2507.2	5480.4	6051.1	4405.4	6579.4	5485.6	4062.7	5255.9	4460.4	9711.9	5206.4
1569.0	4956.8	4781.1	5516.6	5704.4	4835.0	6079.2	4505.5	3331.0	3468.3	4354.3
97.8	728.7	880.0	893.7	962.6	865.2	1530.1	1148.6	421.4	131.3	592.2
25168.5	7137.9	6441.2	8045.5	8298.8	6841.1	8886.6	7112.0	9099.2	7884.2	9444.6
1239.3	4735.4	5166.9	5618.7	5459.3	5559.0	6109.3	5138.1	4895.8	6300.8	4007.5
1154.2	3945.4	3500.9	2438.8	3662.6	3655.0	4399.6	3160.1	4880.8	3938.4	3942.4
2172.4	3228.2	3009.8	3281.9	2764.7	2756.8	3929.1	3054.8	2747.3	2555.6	1750.7
1166.7	3135.8	3357.2	3860.9	5713.8	3889.6	5314.2	4321.6	2496.1	1407.5	2744.4
181.3	4128.8	4018.3	4096.0	4095.8	4367.3	4778.4	4583.4	3134.9	3675.7	3570.8
56.0	237.6	175.5	218.0	164.6	101.5	264.4	177.2	63.0	130.1	77.5
2358.6	2781.7	3292.1	3462.5	4123.4	4195.9	3057.2	4896.7	3982.4	5946.0	2977.3
157.3	1201.4	1100.8	1342.1	1879.9	1247.4	1357.0	898.8	566.9	219.4	612.2
16361.8	7467.5	6615.7	7535.4	7942.2	6934.4	8051.6	7273.3	6521.8	5889.3	9637.0
35.0	1167.2	955.7	1148.9	1769.9	1045.9	1117.1	689.9	449.3	153.4	438.3
11601.9	8374.8	8217.2	8869.0	8690.1	7501.0	9229.1	7158.5	11301.0	8945.3	9069.2
4836.0	4761.9	4664.4	5065.7	6059.1	4787.3	6271.2	4651.9	5741.6	5879.1	4880.9
1946.2	3570.1	3177.5	3303.0	3791.3	4219.9	3334.2	4862.8	4635.8	2112.9	3276.8
2421.1	2365.5	2601.6	2687.2	3477.6	3254.7	4030.9	3712.6	2450.3	728.0	2000.7
7283.3	6549.3	8373.8	7657.3	7916.5	7191.8	8280.5	8765.1	6926.2	6131.3	7296.1
181.3	2274.2	1827.8	1984.3	2137.9	3042.9	1721.0	2729.7	1131.9	993.1	1318.9
34.1	24.4	27.9	20.4	19.7	17.4	27.0	21.3	16.3	10.4	26.0
388.9	2874.9	3186.1	3367.6	4313.4	3737.4	3710.8	4490.6	1300.5	847.1	1516.9
1604.4	2998.3	2742.6	2416.0	3004.8	4128.7	2573.5	3380.3	5145.8	4368.2	2489.2
98.1	118.7	220.9	257.0	277.5	219.6	326.8	389.5	112.4	134.8	190.6
6216.3	6725.3	7405.9	7660.2	7515.9	6904.8	8477.4	7071.7	7033.0	5497.5	6515.1
1396.8	3134.8	3191.1	3140.1	3579.7	3253.8	5170.7	4658.3	2833.4	1555.1	1585.5

6117.3	4710.5	5636.4
4783.1	5327.5	4893.0
783.2	1313.7	846.7
1531.9	1492.4	846.2
4527.0	5217.4	8615.3
1976.6	2885.5	2908.3
979.2	1352.6	1256.9
6036.0	5033.9	3480.2
3932.0	3948.9	4059.1
7990.8	8120.1	7753.3
3627.9	2583.5	2308.0
5869.1	4039.6	4087.0
1632.0	900.0	1132.2
2435.5	3074.0	2652.5
6486.3	7216.2	8148.2
5943.4	4290.4	3798.1
4172.8	5349.7	6759.1
878.5	1014.6	764.9
7660.8	7763.2	6041.2
5207.2	5755.3	4643.7
3494.6	3942.3	3550.5
3268.3	3477.6	2576.5
3506.1	3848.6	4157.7
3978.9	5320.7	3835.0
216.2	221.3	235.4
4589.6	6001.0	2942.0
973.7	1185.6	1036.3
6359.2	7653.0	7528.4
686.0	753.9	670.7
6954.0	7917.0	7701.0
5291.2	4766.4	5617.5
3635.4	4078.9	3466.7
3222.5	3723.9	3880.6
7994.7	7064.6	7627.2
2573.8	2780.1	3916.3
16.0	29.8	19.5
3048.7	3312.4	5340.5
3037.4	3592.9	2332.5
242.1	319.8	259.6
7021.8	6972.9	6661.0
4757.6	3654.5	4680.3

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EU709869.1 gg_id:354793 Thioalkalivibrio sp. str. ALMg14 EU709
GU083686.1 gg_id:581381 Microorganism Xiarinur soda lake sediment clone x307 GU083
DQ103664.1 gg_id:130099 hypersaline endoevaporitic microbial mat clone E2aA03 DQ103
GU083688.1 gg_id:568686 Microorganism Xiarinur soda lake sediment clone x309 GU083
AF126545.1 gg_id:73895 Thialkalivibrio denitrificans AF126
EU709878.1 gg_id:341189 Thioalkalivibrio sp. HL-EbGR7 str. HL-EbGr7 EU709
AY360060.1 gg_id:93813 Thialkalivibrio thiocyanodenitrificans str. ARhD AY360
EU368849.1 gg_id:260942 Thiohalospira halophila str. HL18 EU368
EU169227.1 gg_id:245592 Thiohalospira alkaliphila str. ALgr 6sp EU169
EU908045.1 gg_id:341286 Thiorhodospira sp. str. SLG EU908
AJ006530.2 gg_id:7548 Thiorhodospira sibirica A12 AJ0065
EF157110.1 gg_id:244243 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon EF1571
EF105756.1 gg_id:202113 microbial two endoevaporitic salt crusts evaporitic crust Lindsey Lake New Mexico cl EF1057
DQ001657.1 gg_id:158793 Microbial seeps asphalt seep clone B91-13 DQ001
AM935440.1 gg_id:539161 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM935
AF339744.1 gg_id:40387 thermal vent clone V3 AF339
FM209168.1 gg_id:543583 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd FM209
AJ581598.1 gg_id:93189 soil near uranium mill tailings clone KCM-B-23 AJ5815
EF157167.1 gg_id:245899 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon EF1571
EU735681.1 gg_id:349780 archaeal structures oil contaminated and soils China pristine soil Jidong Oilfield clone EU735
FM242405.1 gg_id:309866 sequences sediment clone 1 T12d-oil FM242
FM209058.1 gg_id:541794 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd FM209
EF157096.1 gg_id:256594 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon EF1570
AJ581597.1 gg_id:94093 soil near uranium mill tailings clone KCM-B-112 AJ5815
AM935143.1 gg_id:536607 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM935
EF105729.1 gg_id:202055 microbial two endoevaporitic salt crusts evaporitic crust Lindsey Lake New Mexico cl EF1057
FJ152988.1 gg_id:321932 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX4C FJ1529
EF157181.1 gg_id:251900 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon EF1571
FJ153022.1 gg_id:306675 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX4C FJ1530
CU467452.1 gg_id:315091 Prokaryotic Tunisian saltern Saltern solar multipond clone CU467
EF103128.1 gg_id:186404 Natronocella acetinitrilica str. ANL 6-2 EF1031
EF105732.1 gg_id:203311 microbial two endoevaporitic salt crusts evaporitic crust Lindsey Lake New Mexico cl EF1057
DQ001686.1 gg_id:157622 Microbial seeps asphalt seep clone B101-25 DQ001
CU467468.1 gg_id:328117 Prokaryotic Tunisian saltern Saltern solar multipond clone CU467
AF513947.1 gg_id:62495 Ectothiorhodospiraceae clone LA7-B9 AF513
EF157075.1 gg_id:255083 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon EF1570
AB240322.1 gg_id:142319 microbial structure Phragmites rhizosphere biofilm reed bed reactor laboratory clon AB240
AF507818.1 gg_id:62740 Mono Lake at depth 2 m station 6 July 2000 clone ML602J-47 proteobacterium AF507
AM936356.1 gg_id:562653 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM936
EF105746.1 gg_id:203128 microbial two endoevaporitic salt crusts evaporitic crust Lindsey Lake New Mexico cl EF1057
EF157092.1 gg_id:256908 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon EF1570

6557.8	7789.8	7796.1	8262.2	9523.3	7008.0	9126.0	7229.4	6014.9	4597.7	8037.4
1156.6	3267.9	2816.9	3592.1	4460.2	3356.0	4200.2	6156.1	2330.3	1259.0	5304.5
198.1	1988.1	2547.0	2568.9	2738.0	2172.3	2336.4	2712.3	1233.8	657.7	3538.5
648.4	2648.9	2887.6	2770.9	3065.5	3257.0	3007.8	3919.1	1900.2	2716.9	2413.0
329.7	3719.6	3848.4	3747.5	3995.9	3729.0	4618.8	4707.9	4618.2	1680.8	2395.6
336.5	2126.5	2087.7	2080.7	2506.5	1867.4	2253.0	2318.4	1566.4	553.8	1343.3
2360.6	4206.1	4342.9	4620.8	4776.3	4874.3	5521.2	6422.8	4051.7	1858.2	4575.4
18.1	66.7	46.1	50.9	114.8	39.5	55.4	73.7	41.3	32.0	26.7
11924.3	6680.6	5949.9	6638.7	6483.0	6037.6	6872.0	6438.0	6204.1	5738.2	4947.8
286.4	2630.4	2415.3	2493.5	3492.0	2897.6	3558.8	3556.8	1613.7	935.8	1337.5
45.1	38.9	61.8	58.8	50.2	31.0	95.5	47.2	42.7	36.0	35.2
19059.9	9385.3	8844.3	9834.9	9841.1	8847.3	13451.3	9515.4	11036.7	8702.0	14653.3
7228.2	3494.0	4082.7	4139.7	4637.0	3908.8	5450.2	3978.4	4076.5	3617.1	3979.0
19279.5	7312.7	6194.3	6569.7	6577.1	6297.3	7985.8	6317.0	7010.4	6148.9	8644.5
3627.4	5868.8	6040.9	6404.3	7524.3	5449.8	9255.2	6461.7	3674.4	3322.8	6077.2
16822.9	7603.9	6384.4	8670.2	8633.0	8203.0	9654.7	8660.0	7282.7	5647.2	7350.5
5382.3	6377.1	6417.6	6919.0	7033.0	6597.7	7359.0	6852.4	10265.1	8076.1	6785.3
33251.4	9627.6	8730.4	10384.5	9997.6	8953.8	11809.0	9613.8	10720.9	9335.0	15215.1
25018.9	8504.1	7432.8	8378.4	8721.4	8278.1	9903.9	7910.5	8688.7	8738.4	13851.7
376.7	2156.0	1969.8	1869.4	2009.7	2221.8	2375.6	2052.3	1824.1	1457.2	2687.9
4602.0	5741.6	5931.3	6815.6	7243.7	5970.5	8335.5	6604.1	5392.8	5456.8	5504.6
1822.4	6698.4	6127.7	6483.0	7404.6	6398.3	7180.7	9370.7	4044.1	3369.4	9277.9
13810.2	6952.8	6764.6	7359.0	6966.9	7480.2	9668.3	6906.0	8817.8	10790.5	7910.1
19436.3	6656.6	6234.8	6585.6	6488.3	6380.0	7253.9	5911.4	7946.0	5981.4	9268.4
3098.2	3826.7	3933.7	3963.5	3864.9	3894.4	5389.5	4262.0	3307.3	3208.2	4473.5
692.0	403.7	200.2	243.8	467.9	252.5	375.8	338.7	96.2	110.9	162.3
4725.9	8508.8	7985.4	8026.7	9477.2	7669.4	10047.2	9311.1	6280.0	6151.0	8329.6
4494.7	9853.5	9094.0	9371.9	10031.4	9139.1	11756.7	8414.3	10496.8	7952.5	9572.4
5741.0	2675.1	2892.9	3147.6	4117.9	2871.2	3902.7	2775.5	2569.9	1644.0	2122.9
249.2	3652.9	3843.1	3931.7	3021.5	4266.6	5504.3	3883.2	4342.6	3749.5	3101.8
53.5	833.7	1007.2	1075.5	1263.0	1139.3	1209.8	841.5	215.3	72.5	383.8
45.1	38.3	96.1	88.5	166.0	46.5	127.1	56.9	19.1	20.3	36.0
1275.2	3576.2	4042.2	3937.5	3675.0	3936.9	5109.2	3472.7	2793.2	3235.5	2494.1
5091.7	7660.1	7984.5	8855.2	9636.2	7801.5	9118.8	7901.9	9837.6	5564.2	7539.2
2749.2	3691.9	3640.7	3568.8	4843.6	3686.4	5008.6	4413.4	5702.0	2611.5	2613.9
8385.3	7587.5	6110.0	5895.1	6270.2	6140.3	8458.8	6570.5	5787.9	3665.1	6137.4
40.3	220.3	394.7	535.9	970.7	1282.2	582.2	306.6	100.0	520.2	100.1
52.2	93.4	103.5	35.2	133.8	89.8	128.1	127.7	65.2	56.3	56.8
11160.9	8490.9	7582.9	7799.5	8412.9	8047.2	9897.5	8011.0	8329.4	8029.2	12775.7
16317.0	5793.8	5410.0	5497.7	5376.3	5492.4	5669.7	5959.0	7542.6	5691.7	7213.8
490.5	3899.5	3885.9	4166.9	5736.1	4099.5	6067.8	4699.9	4164.4	3658.6	3593.2

7246.6	6914.2	6776.2
2783.0	3218.0	5447.2
1922.9	2858.4	3176.5
3246.4	3808.2	5488.8
3443.9	4382.4	3601.4
1899.3	1971.7	2061.7
5556.3	4882.8	5106.3
77.4	86.3	66.0
6862.7	6819.1	6751.9
3337.0	3403.7	3166.6
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9876.0	9994.9	9054.6
4500.4	4369.4	4551.3
6356.1	7499.2	5777.5
5924.5	5083.5	6083.5
7741.4	7394.4	6724.1
6082.3	6829.2	6415.0
9301.9	9712.0	9519.7
7996.1	9202.8	8601.0
2239.3	2172.8	1929.4
6401.0	5694.1	4860.9
8550.2	5901.8	6425.6
6740.4	7713.8	6818.4
5778.2	7665.3	6316.0
3900.2	4297.2	3753.4
425.7	227.7	504.8
10606.0	7377.0	9012.7
8522.0	8986.5	7656.9
3308.0	3362.9	2723.7
3733.6	4522.9	4707.0
782.4	728.3	1095.8
63.9	80.1	76.4
3487.8	3034.8	3589.4
7567.3	8525.3	8429.3
4540.1	4577.3	5659.0
7025.6	6792.3	7988.1
473.0	1316.1	2496.4
45.3	48.3	41.1
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4494.1	4503.4	4909.5

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EF157077.1 gg_id:256826 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon EF157C
AM935364.1 gg_id:548480 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM935
EF157150.1 gg_id:245575 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon EF1571
AM936329.1 gg_id:560668 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM936
DQ378188.1 gg_id:153768 oil-polluted soil clone F24_Pitesti DQ378
M90662.1 gg_id:7758 Halothiobacillus hydrothermalis str. r3 M9066
AJ294337.1 gg_id:76987 Halothiobacillus hydrothermalis HY-66 AJ2943
AF170419.1 gg_id:19288 Halothiobacillus kellyi str. BII-1 AF1704
EU124668.1 gg_id:242036 Thioalkalibacter halophilus str. ALCO1 EU1246
AF173169.1 gg_id:44985 Halothiobacillus neapolitanus str. DSM 581 AF1731
EU196318.1 gg_id:239328 Halothiobacillus sp. NP37 EU1963
EU245085.1 gg_id:256790 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-H1-G02 EU245C
EU101029.1 gg_id:246599 Sulfide/oxygen supply ratio predicts outcome competition among sulfur-oxidizing wa EU101C
EU101026.1 gg_id:246095 Sulfide/oxygen supply ratio predicts outcome competition among sulfur-oxidizing wa EU101C
EU101090.1 gg_id:239627 Sulfide/oxygen supply ratio predicts outcome competition among sulfur-oxidizing wa EU101C
AF154088.1 gg_id:7760 hydrocarbon seep clone BPC028 AF154C
EU101065.1 gg_id:238117 Sulfide/oxygen supply ratio predicts outcome competition among sulfur-oxidizing wa EU101C
EU101080.1 gg_id:251622 Sulfide/oxygen supply ratio predicts outcome competition among sulfur-oxidizing wa EU101C
GU196195.1 gg_id:587626 Bioaugmentation improved recovery digesters after toxicant exposure lab-scale ana GU196
AM950234.1 gg_id:554439 Sulphide oxidation elemental sulphur membrane bioreactor: Performance and selec AM950
AB473891.1 gg_id:549132 sequences Cadagno di Fuori biofilm mat alpine wetland varying conductivities clone AB4738
EU037214.1 gg_id:252299 Hot Spring Microbial Mat Khir Ganga India hot spring microbial mat clone MO20 EU0372
GU390833.1 gg_id:530086 Dark hot springs: structure biofilms caves Acquasanta Terme (Italy) sulfidic cave stre GU390
GU390794.1 gg_id:519254 Dark hot springs: structure biofilms caves Acquasanta Terme (Italy) sulfidic cave stre GU390
GU390789.1 gg_id:517389 Dark hot springs: structure biofilms caves Acquasanta Terme (Italy) sulfidic cave stre GU390
GU196237.1 gg_id:577717 Bioaugmentation improved recovery digesters after toxicant exposure lab-scale ana GU196
EU101158.1 gg_id:236588 Sulfide/oxygen supply ratio predicts outcome competition among sulfur-oxidizing wa EU1011
GU390879.1 gg_id:515900 Dark hot springs: structure biofilms caves Acquasanta Terme (Italy) sulfidic cave stre GU390
DQ354745.1 gg_id:154107 subsurface water clone MS149BH1062003_5 DQ354
EU101063.1 gg_id:237262 Sulfide/oxygen supply ratio predicts outcome competition among sulfur-oxidizing wa EU101C
EF467492.1 gg_id:214022 situ microelectrode voltammetry sulfur-oxidizing biofilms Frasassi sulfidic cave strear EF4674
DQ459215.1 gg_id:160856 Microbial consortia involved anaerobic degradation unsaturated and saturated LCFA DQ459
EU101162.1 gg_id:245464 Sulfide/oxygen supply ratio predicts outcome competition among sulfur-oxidizing wa EU1011
AY493939.1 gg_id:136667 Fingerprinting aggregates soil clone 455 AY4939
EU134704.1 gg_id:248771 tallgrass prarie soil clone FFCH11229 EU1347
GQ264259.1 gg_id:513055 Structure Simulated Level Waste Site simulated level waste site clone WW1_b62 GQ264
FJ535077.1 gg_id:584489 microbial colonizing walls Karstic Slovenia cave wall biofilm clone 3PJM60 FJ5350
DQ123669.1 gg_id:137171 'Division Labor' Degradation Polycyclic Aromatic Hydrocarbons Bioreactor Treating C DQ123
EU449562.1 gg_id:568421 Soil are Changed Agricultural Practices agricultural soil clone Plot4-D11 EU4495
EF605262.1 gg_id:262257 Steroidobacter denitrificans str. FS EF6052
EU202849.1 gg_id:313985 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo EU2028

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5266.8	9781.3	8068.3	7388.5	8137.4	8358.0	8830.4	7748.9	9253.2	6048.8	8441.6
1022.3	3713.2	3880.0	3962.1	4029.3	4025.0	5611.9	3798.7	2625.5	2844.6	2705.7
12374.5	10482.9	9257.7	10556.5	10454.6	9765.2	11549.7	11701.2	9987.5	9224.3	18668.3
39.2	202.7	213.9	297.0	259.0	207.6	257.2	313.5	116.1	38.4	98.3
157.5	737.5	1105.1	1631.1	928.6	1638.8	780.6	1370.3	775.6	1263.1	677.7
2847.5	3103.7	3097.4	3481.3	2490.3	3297.9	2571.0	2801.8	2917.9	2572.7	3892.7
36.0	125.4	146.1	159.7	169.3	90.9	64.7	766.2	439.2	71.1	248.9
3446.5	3636.9	3884.8	4127.1	3754.9	3687.1	4151.7	4722.0	4975.2	6566.9	2995.6
3658.2	5633.8	6187.0	7167.7	6220.6	5993.6	6608.2	5593.3	6107.0	5586.7	8347.0
273.9	1712.1	2580.2	2317.2	2183.6	1771.9	2851.9	1807.4	1858.5	804.4	1389.8
64.7	2073.6	2214.7	2685.7	2974.6	2283.7	3016.3	1780.9	1746.9	1638.5	1520.1
14281.5	5821.9	5954.1	6589.5	5893.0	5786.5	7709.8	5961.6	7832.6	6514.1	8528.2
238.1	2386.9	2658.6	3175.8	2882.0	3046.8	3569.0	3213.2	1638.9	6377.4	2301.9
24390.2	6430.8	6235.0	7347.1	6882.3	6839.4	6381.4	7638.2	7665.2	5913.4	6313.3
563.4	4507.8	4761.8	5007.7	4670.8	4263.0	4623.7	4208.3	2552.8	3712.8	4547.5
2797.4	1769.7	1705.3	1674.1	1650.7	1632.3	2619.3	1722.1	2294.9	1628.9	1777.0
5175.9	3387.3	3401.2	3581.0	3963.8	3457.3	4697.2	3271.3	4512.2	4497.7	4774.2
4322.6	4020.8	3932.1	4338.4	4605.2	4355.8	5556.0	4527.4	4425.4	2652.5	5476.9
869.7	3476.3	4022.2	4433.9	3374.2	3431.6	3675.0	3594.0	5637.5	4024.1	3465.0
19936.1	13336.9	11065.9	12043.8	11207.5	10802.9	12455.5	11012.5	15343.6	8072.2	14898.3
8672.3	5497.4	5582.4	6511.3	6207.5	5719.7	6422.4	5990.6	7015.2	5847.5	7479.7
1560.7	5094.4	5482.1	6341.4	5184.3	5292.9	5757.2	4994.5	2628.4	4694.3	5083.9
7677.8	6326.9	5860.8	5627.5	5379.8	5429.4	6423.4	5385.4	3885.4	3059.5	3321.6
139.3	3492.2	4462.0	5192.6	4423.8	3310.1	4641.0	3590.7	2094.1	1776.3	2334.0
12409.8	6001.8	5912.2	6368.1	5461.4	7228.4	7688.9	6089.2	6298.5	6053.1	7841.6
29398.5	9693.8	8831.7	9592.1	8550.4	9532.8	9966.6	8734.4	10263.1	10835.2	11270.0
53.7	2506.7	2748.1	2890.0	2840.2	3883.5	2691.5	2029.3	1147.2	9246.3	1371.5
1941.8	3479.9	3758.2	3687.2	4089.0	3507.1	4169.5	5054.2	2982.7	3031.1	3777.4
749.7	3158.4	3862.1	4430.9	4621.2	3250.3	5446.5	3319.5	1593.2	1541.8	2499.6
7753.4	6255.1	6188.4	7051.3	7362.2	6594.9	7415.0	7555.9	8787.7	7812.7	5063.4
9589.5	6089.9	5914.7	6648.2	6853.9	7538.3	8099.8	8208.7	6117.6	6230.3	9116.1
6339.1	6898.1	6766.1	7411.5	7933.7	7005.0	7994.3	7916.6	9384.4	9077.1	6298.0
3266.4	5282.6	5477.7	6313.2	7391.8	5369.9	7789.5	5722.3	4997.9	4467.7	5063.9
953.9	3583.1	3661.7	3626.4	3991.8	3826.0	4071.7	4863.3	2774.8	1917.9	5167.6
3086.5	3477.5	3510.7	4534.0	4700.0	3758.8	4953.6	4113.0	2365.3	1306.5	2278.1
4397.5	6131.7	6345.9	6383.9	5850.3	6929.6	6117.1	6855.1	8319.2	7147.6	6916.5
495.1	4339.0	4140.5	4460.8	4959.0	3316.4	5490.4	4547.2	1712.0	1238.2	4097.1
4988.2	4830.3	4595.7	5387.4	8299.7	5677.9	6966.0	5075.2	8882.8	6237.4	4958.1
3657.1	4130.1	4225.0	4695.8	5553.7	4203.9	5233.3	4675.1	4016.9	2307.1	7168.6
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6468.6	6908.3	6281.1
8413.1	7291.2	7615.4
3707.3	3535.6	3888.6
11232.9	10513.4	8962.9
219.1	309.3	249.7
1683.8	1231.0	723.9
2486.7	2827.6	2611.4
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1616.4	1966.7	1841.1
1751.0	1608.1	2331.0
5349.4	7957.7	5441.8
2843.1	4304.6	2499.8
7690.0	7852.0	6654.4
3007.5	4727.7	2712.2
1511.2	3315.4	1718.7
3421.6	4806.2	3454.9
3863.4	4596.4	3834.1
3625.4	4379.9	3222.3
11289.1	10613.5	7925.9
5459.0	6359.7	5948.9
4873.0	5579.4	3809.3
6122.6	6208.9	5344.8
4147.9	3288.9	3199.1
6805.6	7471.7	5359.2
9526.1	10243.5	8831.3
3109.2	2250.1	1014.6
3414.2	5218.9	3446.9
3775.5	3627.5	3436.1
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EU528191.1 gg_id:282600 Seasonal Dynamics Mudflat Mouth Major Kentucky Lake Reservoir Tributary sedime EU528
GQ500734.1 gg_id:593006 Surveys Biofilms and Sediments Mammoth Cave Karst Aquifers Charon's Cascade sa GQ500
AY963465.1 gg_id:150982 structures and correlated ecological factors soils two evergreen broad-leaved forests AY9634
AB198589.1 gg_id:135836 termite gut fluid and protists fraction clone RsC01-016 AB1985
EF061960.1 gg_id:182496 Xiamen China mangrove sediment clone XME35 EF0619
EU542478.1 gg_id:259999 Effects chemical structure concentration on pathways microbial during dechlorinatio EU5424
EF688386.1 gg_id:254180 soil clone F6-105 EF6883
GQ402680.1 gg_id:581215 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
EU202846.1 gg_id:326004 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo EU2028
DQ450180.1 gg_id:154435 (Uruguay) Atlantic coastal lagoon clone R7C24 DQ450
DQ984544.1 gg_id:235634 Mt. Nan-Jen soil clone IFD_90 DQ984
AB252886.1 gg_id:172615 Identification Shibayama lagoon Ishikawa Japan iron-oxidation biofilm clone 31 AB2528
EU669610.1 gg_id:320093 soil clone S11-50 EU669
EU150278.1 gg_id:277979 acidobacteria and soil Niwot Ridge LTER clone Ni_D05_SFDN EU150
AY963328.1 gg_id:156500 structures and correlated ecological factors soils two evergreen broad-leaved forests AY9633
AM935063.1 gg_id:544132 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM935
AY963375.1 gg_id:154604 structures and correlated ecological factors soils two evergreen broad-leaved forests AY9633
EU786122.1 gg_id:546319 cotton rhizosphere soil clone 3H-18 EU786
GQ094382.1 gg_id:422593 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ094
DQ451520.1 gg_id:156986 forest soil clone FAC81 DQ451
AM934850.1 gg_id:544494 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM934
EU150277.1 gg_id:277971 acidobacteria and soil Niwot Ridge LTER clone Ni_B09_SFDN EU150
DQ984567.1 gg_id:238284 Mt. Nan-Jen soil clone IFD_18 DQ984
FM200868.1 gg_id:556730 and distinct induced biofilm fouling operated under conditions laboratory-scale men FM200
EU542460.1 gg_id:258611 Effects chemical structure concentration on pathways microbial during dechlorinatio EU5424
GQ214101.1 gg_id:551472 China loess clone P830 GQ214
EU037949.1 gg_id:244526 Metabolic Profiles Microbial Chlorinated Pesticides Contaminated Sites Three Geogr EU037
EF520572.1 gg_id:232138 structure lakes: what controls ? acid-impacted lake clone ADK-MOe02-45 EF5205
FJ466238.1 gg_id:563462 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea FJ4662
EU150274.1 gg_id:278484 acidobacteria and soil Niwot Ridge LTER clone Ni_H9P1 EU150
EU193051.1 gg_id:364617 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo EU193
EU104062.1 gg_id:332574 Evidence Comamonadaceae determinants settling performance activated sludge clo EU104
EU409118.1 gg_id:274454 Impacted Mine Drainage Dabaoshan Mining Area mine drainage sediment clone DB EU409
FJ466231.1 gg_id:508976 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea FJ4662
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GU208300.1 gg_id:544822 Study on Sediment Dongping Lake sediment clone Ftd3-4 GU208
DQ659217.1 gg_id:225165 acid mine drainage clone DBS-Clone42 DQ659
EU134723.1 gg_id:255115 tallgrass prarie soil clone FFCH7151 EU134
AY221082.1 gg_id:85458 Mammoth Cave clone CCU5 AY221
EF516956.1 gg_id:222645 grassland soil clone FCPP404 EF5169

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3837.9	359.4	367.7	435.5	708.9	332.6	480.9	597.2	186.3	59.5	133.2
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3088.9	6049.3	5970.8	6341.8	8325.8	5728.8	8610.2	5152.3	4045.9	7836.4	4626.3
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EU104271.1 gg_id:332476 Evidence Comamonadaceae determinants settling performance activated sludge clo EU104
FJ612377.1 gg_id:533140 and Biogeochemistry Dongping Lake Ecosystems lake water clone DP10.3.23 FJ6123
FJ535074.1 gg_id:512616 microbial colonizing walls Karstic Slovenia cave wall biofilm clone 3PJM1 FJ5350
FJ672005.1 gg_id:516961 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6720
EU202845.1 gg_id:316643 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo EU2028
EU193057.1 gg_id:366851 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo EU1930
FJ478844.1 gg_id:560106 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4788
AM935088.1 gg_id:545602 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM935
DQ297982.1 gg_id:142342 Microbial hydrocarbon contaminated soil clone UE4 DQ297
AJ582039.1 gg_id:93780 soil near uranium mill tailings clone JG36-GS-61 AJ5820
AY963329.1 gg_id:153003 structures and correlated ecological factors soils two evergreen broad-leaved forests AY9633
EF019218.1 gg_id:209393 aspen rhizosphere clone Elev_16S_386 EF0192
EU403986.1 gg_id:346948 Microbial septic tank effluent and soil biozone infiltrative surface clean water clone (EU4039
AY963404.1 gg_id:156448 structures and correlated ecological factors soils two evergreen broad-leaved forests AY9634
FJ152814.1 gg_id:327382 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX5A_ FJ1528
EU528221.1 gg_id:282013 Seasonal Dynamics Mudflat Mouth Major Kentucky Lake Reservoir Tributary sedime EU5282
DQ984542.1 gg_id:252012 Mt. Nan-Jen soil clone IFD_16 DQ984
GU454892.1 gg_id:532025 Understanding short-chain fatty acids accumulation enhanced alkaline digestion: kir GU454
EU134725.1 gg_id:242587 tallgrass prarie soil clone FFCH10003 EU1347
EU150260.1 gg_id:278275 acidobacteria and soil Niwot Ridge LTER clone Ni_D7P1 EU1502
FJ535069.1 gg_id:542880 microbial colonizing walls Karstic Slovenia cave wall biofilm clone 3PJM137 FJ5350
AB179525.1 gg_id:105999 sedimentary rock clone MIZ34 AB1795
DQ279336.1 gg_id:142645 Dynamic during maturation Tuber magnatum Pico ascoma Xanthomonas clone TM1 DQ279
EF409868.1 gg_id:206356 acid mine drainage clone YSK40-06 EF4098
DQ451502.1 gg_id:156972 forest soil clone FAC63 DQ451
EF516354.1 gg_id:218090 grassland soil clone FCPS764 EF5163
FJ744832.1 gg_id:551627 Transporter genes expressed coastal response dissolved organic carbon surface wate FJ7448
GQ264209.1 gg_id:509396 Structure Simulated Level Waste Site simulated level waste site clone WW1_a84 GQ264
EU150279.1 gg_id:278427 acidobacteria and soil Niwot Ridge LTER clone Ni_D06_SFDN EU1502
EU193052.1 gg_id:369332 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo EU1930
AM176834.1 gg_id:159956 Recovery mangrove sediment clone SZB11 AM176
GU061304.1 gg_id:576363 Evaluation culturing methods cultivate previously Yel Sea intertidal beach seawater GU061
EU491633.1 gg_id:258366 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU4916
EU491862.1 gg_id:269926 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU4918
AY221036.1 gg_id:83068 Mammoth Cave sediment clone CCD24 AY2210
AM935258.1 gg_id:536028 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM935
EF999361.1 gg_id:252341 Vertical and Methanotrophs Estuarine Sediments Pearl River Estuary sediments 6cm EF9993
GQ264010.1 gg_id:589456 Structure Simulated Level Waste Site simulated level waste site clone WC3_08 GQ264
AY907782.1 gg_id:137174 identification picoplankton contrasting waters Arabian Sea water clone A712005 AY9077
FJ545453.1 gg_id:513570 Diveristy Seawater and Sediment Northern North Yel Sea sediment clone S1-23 FJ5454
EU491448.1 gg_id:261579 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X4 clone EU4914

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8310.5	7175.6	6871.7	8821.0	9930.5	5918.5	9547.2	6183.6	3894.3	3843.6	5345.4
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29841.9	10548.8	10080.9	11576.5	12715.9	10285.6	13410.8	10924.5	12505.7	10678.2	13328.5
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3691.4	3983.0	3992.5	4778.6	6368.0	3604.9	6418.7	4803.7	1938.7	1260.1	1863.7
10172.0	9475.9	8351.3	9622.9	8780.0	7374.0	10150.0	7682.7	7553.5	4567.2	8756.2
4538.7	3433.0	3440.9	3795.2	4938.6	4020.6	4191.3	4649.8	1456.1	1217.8	2056.1
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GQ246317.1 gg_id:511715 Temporal and spatial China North Yel Sea sediments clone Sd1-36 GQ246
EU491127.1 gg_id:276781 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak EU491
DQ351813.1 gg_id:146081 Microbial Adherent Sediment Particles Heavy Metal Contaminated North Sea Surfac DQ351
FJ202756.1 gg_id:338034 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2027
AJ567537.1 gg_id:90195 deep-sea sediment clone MBMPE11 AJ5675
DQ270631.1 gg_id:142048 hydrothermal carbonate chimney clone LC1446B-88 DQ270
EF125454.1 gg_id:175214 mangrove soil clone MSB-2F9 EF1254
EU617769.1 gg_id:336977 Seasonal variation microbial Yel Sea sediment clone C13S-11 EU617
EU491671.1 gg_id:269207 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU491
EU373852.1 gg_id:265200 southern Cretan margin (eastern Mediterranean Sea) canyon and slope sediment clc EU3738
EU617762.1 gg_id:339270 Seasonal variation microbial Yel Sea sediment clone D13S-135 EU617
AB015576.1 gg_id:7632 deep-sea sediment clone BD6-6 AB015
EU617760.1 gg_id:353103 Seasonal variation microbial Yel Sea sediment clone D13S-8 EU617
FM242213.1 gg_id:305299 sequences sediment clone 305 T0h-oil FM242
FJ203584.1 gg_id:324521 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h FJ2035
DQ351767.1 gg_id:145747 Microbial Adherent Sediment Particles Heavy Metal Contaminated North Sea Surfac DQ351
FJ416135.1 gg_id:366945 sediments sediment station NEC5 Northern Bering Sea clone 140J34 FJ4161
EU491722.1 gg_id:259776 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU491
EF174279.1 gg_id:181525 direct activated sludge compost maturation stage clone H49-814 EF1742
EF125451.1 gg_id:188380 mangrove soil clone MSB-2F4 EF1254
DQ334616.1 gg_id:175390 Impact metals on sediments heavy metal polluted marine sediment clone HB1-41-8 DQ334
EU287293.1 gg_id:239219 Pacific arctic surface sediment clone S11-110 EU287
FJ902650.1 gg_id:558486 phreatic limestone sinkholes northeastern Mexico biofilm 1m deep hydrothermal ver FJ9026
GQ259229.1 gg_id:512555 Microbial activities coastal marine sediments and column Svalbard deep water clone GQ259
EF061959.1 gg_id:194499 Xiamen China mangrove sediment clone XME27 EF0619
AY592131.1 gg_id:100439 marine ANAMMOX sediment clone AY592131 AY592
EF612422.1 gg_id:241321 historic semiarid lead-zinc mine tailings site soil clone OS-C47 EF6124
DQ395002.1 gg_id:155659 harbor sediment clone VHS-B4-54 DQ395
EU491622.1 gg_id:276755 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU491
FJ628326.1 gg_id:587067 transition and zone within near-shore basin: brackish water anoxic fjord Nitinat Lake FJ6283
GU369930.1 gg_id:522232 and mats vents Arc white microbial film on pebble aphotic zone shal hydrothermal v GU369
EU925888.1 gg_id:327055 sediments sediment station DBS1 northern Bering Sea clone 099G35 EU9258
FJ202726.1 gg_id:304768 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2027
FJ545563.1 gg_id:553394 Diveristy Seawater and Sediment Northern North Yel Sea sediment clone S2-30 FJ5455
FJ479452.1 gg_id:564382 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4794
EF208680.1 gg_id:201369 Vertical and horizontal structure microbial sandy carbonate sediment clone CI5cm.BC EF2086
EU290675.1 gg_id:243727 microbial structure biogeochemical contrasting shelf sediments Namibian upwelling EU290
GQ261760.1 gg_id:550306 shifts taxa and response localized organic loading deep sea sediment whale falls clo GQ261
AJ567539.1 gg_id:88336 deep-sea sediment clone MBMPE13 AJ5675
EU491447.1 gg_id:277437 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X4 clone EU491

11084.2	9594.5	10257.6	10925.8	11348.5	9646.1	11584.6	9577.4	9788.6	10879.0	11289.9
60.0	609.9	900.8	913.0	968.9	648.3	810.3	845.2	298.8	405.6	460.2
4897.3	5900.2	4756.1	5302.6	5175.0	5508.2	4904.9	5484.8	4570.3	4624.3	6044.1
53.1	24.5	25.0	21.4	22.3	25.5	39.7	17.4	22.8	17.1	18.9
74.5	2048.3	2690.6	3715.2	2730.2	1894.1	2186.1	2203.7	736.3	889.2	1164.9
2243.0	4281.4	4911.2	5889.5	5934.4	4453.7	6104.2	4911.5	4956.5	4435.6	5700.0
1073.9	1708.9	2025.2	2222.6	2257.7	2442.6	2215.7	2004.5	1888.2	2208.7	2020.1
72.5	1585.2	1904.9	2356.1	1984.1	1840.5	2531.8	1996.3	626.4	397.9	826.5
1052.7	2278.2	2290.5	2207.0	3296.7	2333.3	2401.0	2754.6	1637.3	544.6	1980.6
55.4	1110.7	1537.8	1535.8	1939.8	1734.8	2481.5	1831.9	640.3	764.1	496.8
7941.1	5297.5	4933.4	5562.3	6283.4	5017.3	6268.6	5301.9	7634.1	7216.5	6362.2
18843.2	6147.4	5732.5	6141.4	5774.7	6031.6	6501.1	5519.6	7561.2	5994.6	7220.1
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5421.8	6135.0	5637.4	7137.0	8935.9	6366.9	9787.0	6450.2	4275.3	5681.3	4809.8
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1375.7	4457.8	3246.3	3227.4	2672.3	2928.7	2568.1	2721.3	2935.8	2141.6	2529.9
6930.1	3914.9	3746.4	4843.9	4242.0	4130.4	3959.0	3336.9	4623.3	3588.3	5467.2
6734.9	5984.6	6127.4	6253.5	5204.3	5835.6	6278.5	5488.2	10125.8	8160.8	7592.7
9548.0	6082.4	6195.8	7242.3	9956.5	6206.9	9924.8	6987.6	4368.4	1776.3	4406.2
512.8	4333.7	4961.9	5566.6	5664.3	4945.0	6444.1	5935.3	3723.9	3023.3	3650.1
7215.9	7326.4	5500.3	6658.6	6862.8	6098.3	7023.7	5956.5	7827.8	6104.6	7782.6
3571.3	4890.2	5390.9	5760.6	6152.5	5436.4	6553.0	6460.0	5350.7	4149.1	4575.5
1529.0	7526.8	7854.1	8245.2	10806.5	6517.3	13009.5	7349.2	3858.9	4732.8	6054.4
6372.5	4263.1	4625.4	5646.3	5120.8	4558.8	6099.6	4945.5	3829.9	6917.1	4125.9
1943.5	3150.3	3337.5	4116.4	3366.9	3377.7	3509.3	4231.3	2554.6	2434.7	2869.6
12214.6	6567.5	6284.2	6781.3	6527.3	5907.0	6933.9	6398.4	7317.8	7352.1	9132.4
73.8	822.1	869.6	789.5	1248.7	638.4	1917.5	1172.3	168.8	200.6	307.6
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18389.6	5624.4	5391.2	5562.9	5880.8	5923.0	6585.3	4951.8	6485.6	5177.3	6683.2
287.0	3086.1	2888.9	2971.1	3964.0	2618.1	3691.3	3024.5	1761.2	2152.0	1688.1
3339.3	6682.3	6666.8	7229.8	6381.6	6386.9	7807.9	6023.3	11246.6	10536.7	6701.2
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4353.6	5304.4	3940.5
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2085.4	1908.3	1767.1
1881.7	1859.5	1124.1
4709.0	5060.7	5453.5
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6676.5	7862.8	6204.2
5230.1	6390.1	5390.4
6409.9	5991.0	7224.5
9059.7	8562.7	8300.7
2371.0	2991.5	2098.7
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5231.1	7244.0	5106.0
7184.4	5131.2	6170.7
4922.0	5477.4	4999.7
6006.5	6639.2	6491.0
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7034.0	5872.6	6190.5
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3935.2	3609.9	3309.3
6216.0	7487.9	6312.0
864.8	790.5	709.3
5043.8	6695.4	5591.5
3100.9	3112.2	2741.9
7335.0	7453.6	6748.4
4264.0	5172.9	5784.6
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4749.1	6115.2	4579.8
286.5	170.8	203.8
5068.0	5149.7	4108.0
2658.3	4061.1	2113.9
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346.9	344.5	236.6
1610.9	1881.4	1652.2

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AJ567568.1 gg_id:90324 deep-sea sediment clone MBMPE64 AJ5675
DQ070798.1 gg_id:146059 Prokaryotic Structures Seafloor Basalts Varying Age and Juan de Fuca Ridge basalt gl DQ070
AM176878.1 gg_id:160646 Recovery mangrove sediment clone SZB50 AM176
DQ395393.1 gg_id:154568 deep-sea octacoral clone ctg_BRRAA68 DQ395
FJ628300.1 gg_id:554137 transition and zone within near-shore basin: brackish water anoxic fjord Nitinat Lake (FJ6283
EU735012.1 gg_id:314085 assemblages sediment station DBSE Northern Bering Sea clone 108A48 EU735
GQ263482.1 gg_id:584461 Structure Simulated Level Waste Site simulated level waste site clone FW2_172B GQ263
AB015548.1 gg_id:7630 deep-sea sediment clone BD3-6 AB015
EU134721.1 gg_id:239488 tallgrass prarie soil clone FFCH6145 EU134
AY922078.1 gg_id:113125 farm soil clone AKYG940 AY922
GQ472813.1 gg_id:581306 Biodiversity planktonic Northern surface water northern Bering Sea clone b44 GQ472
AM997308.1 gg_id:575214 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A AM997
AY225636.1 gg_id:97007 Mid-Atlantic Ridge hydrothermal sediment clone AT-s2-59 AY2256
EU652512.1 gg_id:279257 Seasonal variation microbial Yel Sea sediment clone D8s-65 EU652
AJ633957.1 gg_id:114452 host's accessory nidamental gland clone 30ANG2 AJ6339
GQ259320.1 gg_id:557119 Microbial activities coastal marine sediments and water column Svalbard surface se GQ259
EU488042.1 gg_id:574507 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU488
GQ264525.1 gg_id:572359 Structure Simulated Level Waste Site simulated level waste site clone WW3_78 GQ264
DQ395047.1 gg_id:154352 harbor sediment clone VHS-B5-27 DQ395
FJ479498.1 gg_id:571867 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4794
AB252883.1 gg_id:166638 Identification Shibayama lagoon Ishikawa Japan iron-oxidation biofilm clone 496 AB2528
EU652513.1 gg_id:277629 Seasonal variation microbial Yel Sea sediment clone C8S-5 EU652
EU488031.1 gg_id:572374 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU488
GQ337138.1 gg_id:561386 Hydrography shapes biogeography deep Arctic Ocean water depth 1000m clone CB GQ337
DQ396093.1 gg_id:155768 deep-sea octacoral clone ctg_NISA258 DQ396
EU491461.1 gg_id:259137 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X4 clone EU491
EU287183.1 gg_id:239964 Pacific arctic surface sediment clone P13-90 EU287
GQ246393.1 gg_id:593413 Temporal and spatial China North Yel Sea sediments clone Cm1-56 GQ246
EF540428.1 gg_id:227143 oil-shale semi-coke solid waste clone MK6 EF5404
EF208690.1 gg_id:202816 Vertical and horizontal structure microbial sandy carbonate sediment clone CI5cm.FC EF2086
EF597713.1 gg_id:247624 Metagenomics deep mediterranean warm bathypelagic habitat 3010m depth Ionian EF5977
EU652527.1 gg_id:278838 Seasonal variation microbial Yel Sea sediment clone D8S-156 EU652
EU491388.1 gg_id:261546 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X3 clone EU491
AM040131.1 gg_id:145155 sandy sediments clone Sylt 35 AM040
GQ262923.1 gg_id:539093 Structure Simulated Level Waste Site simulated level waste site clone F1_71X GQ262
GQ262890.1 gg_id:567438 Structure Simulated Level Waste Site simulated level waste site clone F1_51X GQ262
AF129556.1 gg_id:7595 Achromatium sp. HK9 AF129
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L79966.1 gg_id:137055 Achromatium oxaliferum str. AP3 Eikelbloom type 021N L79966
AF129550.1 gg_id:7594 Achromatium sp. JD8 AF129

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139.9	783.9	921.5	1208.2	995.8	1084.7	887.7	1237.8	468.0	980.4	960.3
13678.5	6601.0	5911.8	6186.3	6442.4	6682.5	6835.4	6174.5	8331.4	6247.5	8065.6
849.3	839.5	989.1	1020.0	1172.6	714.2	1210.7	1495.8	539.8	217.2	490.2
254.6	1405.3	783.8	714.5	710.7	1031.5	840.9	868.5	962.8	541.9	512.5
8414.6	5560.3	7039.3	7282.6	7960.2	5796.8	7250.3	6130.1	6406.7	5260.7	5480.8
9388.9	7393.8	5798.4	5320.0	5680.4	7103.7	6668.9	6119.7	4971.0	3485.6	5761.6
8410.0	4280.3	3673.2	4120.1	6795.7	4225.2	5191.8	4402.9	4565.1	2152.0	3608.3
12203.1	6552.3	5177.2	5315.6	5210.4	5206.8	5616.8	6433.2	6849.5	6092.9	7698.6
508.6	4424.1	4562.9	5338.4	7083.0	4550.1	7501.5	5398.8	2854.4	972.3	2938.9
12368.3	5272.4	4787.7	5516.2	6176.9	6212.4	6141.5	5166.2	5181.4	3466.5	5911.1
233.3	1748.6	1746.0	2076.3	2305.6	2070.5	3322.4	1968.3	1043.4	1013.5	1249.2
9566.1	6849.8	5538.3	5858.5	5572.1	5476.4	5835.0	5615.1	5796.1	4816.4	6888.0
56.6	662.3	626.3	669.4	2023.5	674.2	2212.6	545.8	108.9	97.8	215.0
2215.3	4245.1	4060.1	3997.5	4375.1	4419.8	4712.6	4153.2	2765.6	5343.7	3396.9
18216.2	6558.3	5789.6	6441.0	6411.6	6304.0	6897.9	5679.7	9304.0	7542.8	6824.8
400.2	1931.3	2056.1	2249.5	2976.6	2356.0	4033.4	2712.5	1082.2	420.6	2325.9
23024.5	8947.6	8245.4	9199.5	9014.2	8454.6	9985.4	7964.1	13003.0	8621.9	11347.6
170.4	3531.1	3636.6	3591.8	5827.5	4478.3	5818.5	4080.0	1489.2	1245.6	1695.0
7707.5	3999.1	3278.7	3573.6	2857.3	3204.3	2957.8	2730.2	5491.9	4663.1	4225.5
1819.6	5351.1	5417.2	6496.6	8618.5	5456.2	9050.8	6542.4	2913.8	1725.0	5539.7
249.0	1311.2	1338.8	1555.6	7409.6	2126.5	7135.4	1058.7	717.0	769.7	579.9
17785.8	6471.5	6419.2	6574.2	6798.7	6416.1	7573.2	6674.2	8704.3	10817.1	8662.6
934.4	1348.7	1635.6	1947.8	1764.4	2083.1	1346.5	1666.0	795.2	1014.8	901.9
645.2	3843.7	4535.7	5479.3	5902.1	3970.7	6698.4	4329.6	2918.5	2099.3	3761.5
86.0	771.8	773.7	880.8	1483.5	745.7	1440.2	688.9	310.1	309.5	531.4
593.6	1840.3	2116.7	2489.1	2134.4	2071.8	2556.4	2663.8	2671.1	1607.7	1245.6
50.4	1354.1	548.8	905.8	1387.1	1404.9	1365.5	1631.9	284.8	259.3	1007.8
45.8	538.2	942.1	875.5	974.8	760.9	827.6	813.9	924.5	410.0	422.1
343.7	2022.1	2021.0	2579.6	3498.1	2338.3	3567.8	2459.2	1112.8	1850.6	1315.3
289.4	1588.6	1646.7	1289.5	1750.5	1858.1	1941.6	2352.1	834.5	458.1	842.8
12444.4	9959.9	9497.1	10680.4	10697.6	9391.7	11019.1	9438.2	9757.9	7839.2	10586.2
800.9	2278.4	2480.4	2502.2	3317.9	3016.3	2044.7	3850.2	1953.3	3048.1	1501.6
11613.4	4257.6	4396.6	4720.0	5632.6	3827.8	5177.0	4016.6	5162.7	4499.2	4763.1
1963.9	1812.2	884.6	338.9	290.9	1375.9	304.6	482.3	2174.5	1043.5	333.2
20230.0	9092.6	7575.2	8681.6	9446.6	8206.7	9145.7	8248.0	11591.9	7958.8	10494.5
16099.4	6730.5	5198.6	5345.7	7220.9	6130.6	6531.1	6611.5	7478.9	4461.5	4805.1
40.2	97.7	164.3	90.6	118.7	95.9	83.9	238.8	54.9	30.7	95.2
563.2	629.2	537.0	614.3	628.0	844.5	680.8	866.3	350.3	376.2	356.6
50.3	1150.7	1013.1	970.4	1569.4	955.4	1369.1	1037.7	1270.3	1066.7	820.7
117.1	505.7	570.9	579.4	637.3	453.8	745.5	751.0	309.1	129.2	331.4

5860.7	4966.7	5031.8
964.7	1709.1	1193.0
5575.6	6645.4	6676.2
1061.7	1206.0	1581.1
658.6	1358.4	948.9
6683.9	5745.1	6859.4
6688.1	7095.4	7394.3
4270.1	4578.2	3831.8
5480.9	5472.1	4541.4
4740.9	4977.7	5025.1
5534.1	4687.0	5018.1
1634.3	1887.4	2419.3
5627.9	5388.6	4412.2
347.4	585.6	355.4
4309.2	3869.4	3175.2
5458.1	6261.9	5330.7
2338.3	2668.1	2935.8
8033.1	9388.7	7788.0
3724.1	2798.9	3802.8
2549.2	4443.1	2819.1
5967.2	5592.5	7113.8
1119.7	1503.0	1392.8
6617.7	7919.4	5752.8
2039.2	2253.8	2371.1
3555.9	4393.1	4255.9
706.4	828.3	883.0
2813.9	2371.5	2171.9
1807.5	1606.2	1778.9
784.4	896.9	706.7
2308.7	2076.3	1924.3
1647.2	2019.4	1660.9
9875.2	9202.8	8369.9
4338.1	2636.6	2356.6
4103.9	5238.1	3645.7
97.6	606.1	424.3
7854.0	9434.9	7813.5
5686.8	6941.9	6794.1
151.4	140.4	67.8
728.0	903.4	598.8
852.8	1029.2	1033.2
496.6	661.1	601.9

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AF129551.1 gg_id:7610 Achromatium sp. JD13 AF1295
AF129554.1 gg_id:7602 Achromatium sp. HK3 AF1295
DQ066949.1 gg_id:133344 Lake Washington sediment clone pLW-25 DQ066
AY344377.1 gg_id:91521 Lake Kauhako 4 m clone K2-4-12 AY3443
AY265348.1 gg_id:82929 Dermacentor variabilis symbiont AY2653
U91786.1 gg_id:10204 Candidatus Arsenophonus triatominarum U9178
AY264674.1 gg_id:89402 Arsenophonus nasoniae str. ATCC 49151 AY2646
DQ158206.1 gg_id:140266 Averyella dalhousiensis str. 9501-97 1 DQ158
DQ158205.1 gg_id:139645 Averyella dalhousiensis str. 521-86 14 DQ158
DQ158204.1 gg_id:140650 Averyella dalhousiensis str. 2362-79 4 DQ158
FJ360760.1 gg_id:325971 Enterobacter aerogenes str. PSB28 FJ3607
DQ481464.1 gg_id:157163 Averyella dalhousiensis str. VTan-2 DQ481
DQ068917.1 gg_id:139129 microbiota antlions (Myrmeleon mobilis) whole animal laboratory starved antlion O DQ068
EU438866.1 gg_id:297157 Enterobacter amnigenus 2 EU438
EU741245.1 gg_id:335722 Enterobacter sp. str. KB3 EU741
AB291632.1 gg_id:241040 Insecticidal predatory antlion species (Neuroptera: Myrmeleontidae) larvae Myrmel AB291
EU879089.1 gg_id:305870 Pantoea agglomerans str. HDDMN03 EU879
AM184285.1 gg_id:161053 Enterobacter ludwigii str. WAB1946 AM184
AY676891.1 gg_id:136211 Baumannia cicadellinicola B6 AY6768
AY676878.1 gg_id:135960 Baumannia cicadellinicola B14 AY6768
AY676887.1 gg_id:136270 Baumannia cicadellinicola B34 AY6768
AF465797.1 gg_id:79588 Baumannia cicadellinicola AF4657
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AY676895.1 gg_id:137136 Baumannia cicadellinicola F02 AY6768
AF465795.1 gg_id:79106 Baumannia cicadellinicola AF4657
AY676877.1 gg_id:135411 Baumannia cicadellinicola B13 AY6768
U80203.1 gg_id:10307 Brenneria nigrifluens str. ATCC 13028 U80203
AJ233416.1 gg_id:10200 Brenneria quercina str. DSM 4561 AJ2334
FJ611885.1 gg_id:588495 Brenneria rubrifaciens str. LMG 2709 FJ6118
AJ233418.1 gg_id:51229 Brenneria rubrifaciens str. DSM 4483 AJ2334
U80207.1 gg_id:10197 Brenneria rubrifaciens str. ATCC 29291 U80207
AM237373.1 gg_id:156214 Sodalis glossinidius OS-75 AM237
Z96097.1 gg_id:10201 Brenneria salicis str. LMG 2698 Z96097
AB033772.1 gg_id:52753 Buchnera sp AB0337
AB033773.1 gg_id:20966 Buchnera sp AB0337
AJ296755.1 gg_id:50183 Buchnera aphidicola (Maculolachnus submacula) (Maculolachnus AJ2967
FJ655495.1 gg_id:579584 Buchnera aphidicola (Stomaphis aphananthae) FJ6554
M63251.1 gg_id:9645 Buchnera aphidicola M6325
M63252.1 gg_id:9648 Buchnera aphidicola M6325
FJ655509.1 gg_id:587576 Buchnera aphidicola (Lachnus tropicalis) FJ6555

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9949.8	9728.5	9416.4	10916.7	12112.6	10429.8	14438.2	10405.8	8777.0	13432.7	9297.7
12894.6	5459.4	5473.6	5234.6	7263.2	5281.7	6416.7	4706.8	4003.3	6317.1	5272.2
85.5	498.8	744.0	1198.1	650.2	932.9	1397.0	1143.5	721.8	1371.4	399.8
3079.6	1248.7	1177.5	1207.1	1192.9	1410.6	1656.4	1342.8	1054.3	1044.2	889.8
3409.1	4503.6	5298.4	6483.7	4655.6	6339.5	4721.3	6034.7	5313.0	12349.6	6955.8
33.3	30.4	19.2	80.1	13.0	43.2	11.5	15.7	14.4	19.8	14.4
448.3	4400.1	5194.9	5565.9	3655.9	5994.8	2699.4	7208.0	5891.4	9531.3	4131.3
106.8	4769.0	6627.6	7324.6	3726.1	9485.2	3401.6	7023.5	5337.6	16144.0	3922.3
104.4	3965.7	5684.7	6444.3	3196.5	8938.0	2630.6	5806.0	4082.7	16322.9	2986.9
7937.9	5216.6	7361.6	8253.1	4543.1	10400.1	4103.2	7160.4	5401.5	18345.5	4288.0
1000.1	4522.4	6124.2	7132.3	3984.2	10246.1	3566.5	6715.4	5499.1	18067.0	3473.6
318.3	4383.2	4932.2	4802.3	3860.4	5071.0	4389.5	4377.8	4709.8	7404.7	3458.8
7630.8	4981.3	6415.4	7115.5	4390.9	9879.3	4454.7	6540.0	6244.7	16588.0	5334.0
86.0	5087.5	6572.5	7111.9	4426.4	10553.4	3312.6	5760.0	3478.6	18559.0	3394.1
65.5	1931.4	3013.8	2826.1	1510.0	5652.5	1205.3	2455.7	1166.7	11317.9	1079.8
6928.8	5287.6	6314.6	7388.8	4129.6	9000.4	3629.6	5969.0	4044.9	17568.4	4582.1
38.0	872.9	1499.5	1608.5	923.9	3989.7	640.7	1308.0	363.9	10429.2	417.5
900.0	6518.6	7698.0	8421.1	6271.3	11354.1	5314.3	7159.9	4897.4	19298.5	4625.2
1928.4	2904.6	3967.5	3782.1	3391.3	3792.9	3281.1	3111.9	2744.5	2196.7	3007.8
74.3	133.0	256.4	377.5	357.7	217.0	416.0	309.9	193.5	484.0	211.6
97.3	1372.3	1190.0	1604.7	1097.6	1506.5	1408.1	1597.4	845.2	1899.1	981.9
605.5	650.5	656.3	843.6	673.8	880.8	637.1	828.0	426.6	1194.9	318.1
72.9	148.5	314.0	279.7	213.7	297.4	117.4	252.3	413.0	947.0	166.1
24.1	160.2	342.5	251.3	212.6	264.1	104.9	176.2	325.9	731.8	165.1
28.2	22.7	17.8	25.2	15.6	23.0	18.1	19.0	24.5	30.4	19.6
1147.9	4286.2	4454.2	4101.5	4352.4	4874.6	4062.8	4556.9	4669.8	3775.2	3231.7
4525.6	4429.8	5600.1	6462.3	4927.5	7803.2	4335.2	6122.3	4484.0	10714.9	5578.1
4305.9	5426.8	5641.3	6424.8	5691.4	7460.9	5341.3	5276.0	5131.6	8290.2	4966.2
91.3	2880.4	4153.1	4196.6	1688.7	5247.9	1087.6	4624.6	2965.1	9699.8	2538.3
4935.7	4341.8	4746.1	5050.7	3137.6	6031.5	2613.8	5069.3	5282.6	9615.3	4039.8
4347.4	7078.6	8648.8	8632.7	5820.7	9696.8	5975.3	10061.0	9519.9	14686.9	8523.2
102.9	3982.9	3843.3	4132.9	3580.4	5080.5	2553.7	3864.6	3090.9	7286.3	1711.8
1392.9	2506.3	2773.4	3255.5	2271.7	4150.6	1638.3	2659.1	2437.2	8037.0	1886.0
13928.3	4882.6	5170.3	5625.1	5843.1	5589.8	6943.1	5487.7	6137.0	7023.9	6059.1
1829.4	2283.5	2656.8	2773.5	2789.4	3286.6	3142.7	3412.3	3237.1	4053.2	2398.8
143.1	2178.7	3137.2	3092.5	2248.1	3626.1	3281.6	2925.3	3718.9	5682.9	1914.6
6994.3	7421.0	6680.7	7567.6	6561.0	7817.1	6694.1	7053.7	8832.8	8112.2	8839.2
3341.9	4651.9	4251.8	4283.2	4048.9	5034.2	4529.4	4568.8	6556.4	6206.0	4926.6
2515.7	2078.3	2910.4	3020.8	2778.2	4476.5	2302.7	3233.9	2944.2	7398.6	1734.4
3790.6	5370.4	4854.2	6440.6	4495.0	6079.2	5716.1	4824.5	7114.2	5973.7	6804.0

5831.4	6911.8	7309.5
11126.4	10357.2	11449.2
5611.3	4975.5	4899.2
1302.0	1267.5	284.9
1407.7	1518.1	1586.4
6236.4	7347.1	5210.2
21.1	33.3	51.6
6717.6	6581.1	4449.8
9831.6	7599.7	4370.0
9021.5	6589.1	3602.7
10354.4	7581.4	5021.6
10622.7	7909.6	4709.1
4614.6	6164.4	3688.2
8873.0	7786.9	4266.3
11210.0	7255.4	4218.9
5497.0	4486.2	1881.0
9041.2	6325.6	3908.1
2940.6	1702.8	403.1
12500.5	8998.4	6058.3
3817.9	4113.0	3300.1
171.1	443.6	638.3
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1046.4	1269.0	1917.4
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256.3	626.4	24.0
17.5	20.3	11.2
5346.9	4956.8	3598.9
7510.7	7021.1	4447.9
8475.6	6638.6	4279.7
5640.3	5184.4	2170.3
5344.2	5674.9	3113.4
10749.4	10037.2	7119.1
5809.7	4373.2	2055.9
5162.3	3737.2	2320.6
5650.4	6778.5	6006.1
3846.7	3791.7	2958.7
4572.6	4214.9	2086.5
7207.1	7605.2	5979.3
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s__unclassified	6579
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EU334768.1 gg_id:341117 Buchnera aphidicola (Cinara juniperi) str. BCju-1 EU334
AJ296752.1 gg_id:41602 Buchnera aphidicola (Baizongia pistaciae) AJ2967
EU334777.1 gg_id:308536 Buchnera aphidicola (Cinara cedri) str. BCce2-1 EU334
AJ296753.1 gg_id:36645 Buchnera aphidicola (Stomaphis quercus) AJ2967
AJ296747.1 gg_id:23181 Buchnera aphidicola (Pterocomma populeum) AJ2967
M63254.1 gg_id:9650 Buchnera aphidicola M6325
AJ296758.1 gg_id:23853 Buchnera aphidicola (Panaphis juglandis) AJ2967
M63250.1 gg_id:9642 Buchnera aphidicola M6325
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Z19056.1 gg_id:9651 Buchnera aphidicola Z19056
AJ296750.1 gg_id:53693 Buchnera aphidicola (Pemphigus populi) AJ2967
AB064508.1 gg_id:40406 Buchnera aphidicola (Yamatocallis tokyoensis) #317 (Yamatocallis AB064
DQ418492.1 gg_id:171684 Buchnera aphidicola (Eriosoma lanigerum) str. Zhaotong DQ418
EU334773.1 gg_id:308102 Buchnera aphidicola (Cinara tujafilina) str. BCtu-1 EU334
M63255.1 gg_id:9653 Buchnera aphidicola M6325
AJ296754.1 gg_id:24924 Buchnera aphidicola (Tuberolachnus salignus) (Tuberolachnus AJ2967
FJ655507.1 gg_id:577120 Buchnera aphidicola (Lachnus roboris) FJ6555
Y11972.1 gg_id:202061 Buchnera aphidicola Y11972
L81121.1 gg_id:111650 Buchnera aphidicola L81121
AE016826.1 gg_id:146724 Buchnera aphidicola str. Bp (Baizongia pistaciae) AE016
FJ655512.1 gg_id:510297 Buchnera aphidicola (Nippolachnus piri) FJ6555
Y11973.1 gg_id:9652 Buchnera aphidicola Y11973
AY518294.1 gg_id:105511 Buchnera aphidicola (Aphis fabae fabae) AY518
FJ655500.1 gg_id:560641 Buchnera aphidicola (Stomaphis takahashii) FJ6555
DQ223869.1 gg_id:165272 Buttiauxella agrestis str. RT1 DQ223
DQ223870.1 gg_id:172544 Buttiauxella noackiae str. RT7 DQ223
DQ440549.1 gg_id:153634 Buttiauxella agrestis str. HS-39 DQ440
AF227860.1 gg_id:73465 Pantoea sp. str. 57916 AF227
DQ223871.1 gg_id:167300 Buttiauxella agrestis str. P1 DQ223
AJ293684.1 gg_id:69815 Buttiauxella agrestis str. S3/3-203 AJ2936
AJ233402.1 gg_id:10052 Buttiauxella ferragutiae str. DSM 9390 AJ2334
FJ716025.1 gg_id:513551 Diet- gut microbiota Lumbricus rubellus fingerprinting technique and cloning intestina FJ7160
AJ233406.1 gg_id:10056 Buttiauxella warmboldiae str. DSM 9404 AJ2334
NR_025328.1 gg_id:575201 Buttiauxella brennerae str. S1/6-571; DSM 9396 NR_02
AJ293687.1 gg_id:69978 Buttiauxella noackiae str. BR 626 AJ2936
AJ233403.1 gg_id:10053 Buttiauxella gaviniae str. DSM 9393 AJ2334
AJ233400.1 gg_id:10050 Buttiauxella agrestis str. DSM 4586 AJ2334
X92552.1 gg_id:9961 "Candidatus camponotii" X92552
AY334368.1 gg_id:106321 Camponotus sansabeanus symbiont AY3343
AJ245598.1 gg_id:20928 USA clone 14/7 AJ2455
AJ245592.1 gg_id:17213 Peru clone 5-5 AJ2455

5719.6	3511.1	5169.0	3768.4	2975.3	3619.7	3088.9	3540.3	3014.6	2110.6	3713.6
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4446.4	3253.1	3752.8	4411.9	4081.5	3434.0	3504.1	4340.4	5089.0	2874.0	3414.8
1407.6	1100.8	783.1	1179.3	859.3	1089.6	2080.3	1502.3	1005.9	3049.8	832.1
14310.1	2606.6	2254.0	2589.9	1904.7	3149.0	2700.9	2133.5	4242.5	2804.9	4178.9
439.5	1799.6	1650.4	2072.6	1813.1	2052.0	1604.8	2442.1	1382.5	2200.1	797.1
185.6	92.6	105.6	120.9	103.6	160.7	107.0	237.2	88.5	137.3	97.2
130.1	401.8	467.9	391.1	592.8	549.1	375.8	405.6	443.4	385.0	237.8
53.2	75.1	132.5	149.9	123.6	92.7	131.9	165.7	126.6	94.5	87.3
2008.5	998.6	1348.5	1391.7	1133.2	1743.2	1422.2	1665.3	1151.3	2931.7	1585.2
165.9	2344.9	2117.5	2210.1	2409.8	2166.8	2508.8	2511.7	3185.4	2065.1	1297.7
127.2	639.4	788.3	772.1	1155.6	871.9	916.4	653.8	469.8	805.1	392.4
24749.8	6521.7	5934.8	6729.2	7108.7	7195.9	6865.8	6099.4	11987.6	4231.9	11224.7
81.3	167.3	195.2	272.2	300.6	199.6	329.3	203.0	88.5	76.2	104.5
672.7	3290.7	3188.9	3177.9	2802.5	3227.1	4305.7	3193.7	6516.4	2079.2	2776.4
1265.2	3367.0	3895.6	3936.8	2888.7	4462.3	3070.9	4483.3	3217.7	5267.3	2598.8
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7835.0	3823.8	3448.2	3304.1	2981.8	3710.7	4927.5	2956.6	5064.3	4394.1	3249.9
15695.6	4722.8	5588.7	5332.9	7542.1	4302.6	6678.5	5596.1	11341.2	4756.5	4969.7
1232.9	3444.8	4196.0	4330.5	3314.5	4862.4	3818.2	3919.5	4472.4	7036.7	3437.7
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284.7	1979.2	2216.4	2641.5	2801.3	2334.6	3145.9	2404.4	2585.7	1236.8	1604.7
1883.2	6383.9	5943.9	5034.1	4295.5	6346.0	4313.9	5173.0	6794.3	6138.3	6938.7
252.8	4657.9	5308.3	5711.7	3467.3	6912.6	2368.8	6346.6	5718.6	12078.5	3735.3
3869.3	5895.8	6820.1	7552.5	6029.0	9427.0	4573.5	7195.1	5768.9	16203.7	4829.3
1859.7	4003.4	5438.5	6229.3	3951.5	8700.9	3133.6	6234.1	4026.1	16713.9	3501.3
3509.7	2611.6	4204.6	4595.1	2910.7	6719.1	1786.7	4702.3	2174.2	12975.7	2456.6
520.6	2613.2	4057.6	4401.6	2626.7	6189.8	1399.0	4475.4	2272.6	11882.5	2172.7
6854.4	5779.2	7337.2	8258.4	6386.9	10046.8	4896.1	7098.3	4650.8	16020.0	4750.7
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111.3	3949.0	5808.6	5755.5	3794.0	8712.0	3285.5	4804.8	2779.5	12576.0	2497.3
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1773.2	5157.7	6368.2	6800.6	4763.0	8413.2	3396.1	6311.6	4654.6	15365.4	3258.8
852.7	3401.5	4250.0	4377.1	3275.9	6269.3	2126.6	4586.0	2668.1	11653.7	2087.1
1230.5	5734.9	5436.9	6587.3	3726.1	8631.1	3096.8	6682.0	3392.4	13705.5	3557.2
234.5	1473.8	2289.1	1962.1	1449.5	2508.2	1294.1	2182.1	1393.0	1928.8	1263.0
367.0	2977.1	2833.3	3212.5	2831.5	3473.2	2089.6	3680.5	3448.7	5598.1	2562.8
3730.7	2865.4	4181.2	4379.5	3138.8	4753.1	2539.5	4479.0	4198.9	7037.2	2710.4
15320.3	6401.0	6488.6	7173.3	6426.2	8285.4	6551.7	6511.5	7771.7	13122.4	8101.0

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1802.4	2534.0	585.0
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3266.3	4196.6	3288.1
1660.6	2546.2	1395.2
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2323.7	2865.7	1964.8
855.6	1223.3	1261.1
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4269.3	5553.6	4059.9
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5162.8	2760.9	1341.4
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7203.3	5465.8	2748.2
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g__Cedecea
g__Citrobacter
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s__unclassified	7029
s__Candidatus Hamiltonella defensa	7160
s__Candidatus Ishikawaella capsulata	7539
s__Candidatus Phlomobacter fragariae	6601
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AJ245596.1 gg_id:48707 Saint Kitts and Nevis clone 12/1 AJ2455
NC_012751.1 gg_id:431766 Candidatus Hamiltonella defensa 5AT (Acyrthosiphon pisum) str. T5A NC_01
AB067723.1 gg_id:28528 Megacopta punctatissima symbiont AB067
U91515.1 gg_id:10203 Candidatus Phlomobacter fragariae str. france fragariae U9151
AY136143.1 gg_id:86615 Brachycaudus cardui symbiont AY136
AY136152.1 gg_id:105167 Macrosiphum rosae symbiont AY136
AF293619.1 gg_id:25922 Macrosiphoniella ludovicianae symbiont AF293
FJ357496.1 gg_id:359629 symbionts clones English grain Sitobion avenae F. (Insecta: Homoptera) and host plan FJ3574
AF293627.1 gg_id:50997 Uroleucon solidaginis symbiont AF293
DQ228285.1 gg_id:150888 Acyrthosiphon pisum symbiont DQ228
AF493976.1 gg_id:82917 Cedecea davisae str. DSM 4568 AF493
DQ481466.1 gg_id:203232 Citrobacter freundii str. VTan-4 DQ481
DQ481470.1 gg_id:201655 Citrobacter freundii str. VTan-9 DQ481
EU468094.1 gg_id:299301 cheetah feces clone CE2_g02_2 EU468
GQ154806.1 gg_id:534457 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
GQ155543.1 gg_id:588290 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
DQ816142.1 gg_id:168998 mouse cecum clone aaa88f07 DQ816
GQ155506.1 gg_id:511336 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EU467996.1 gg_id:301223 cheetah feces clone CE2_g10 EU467
EU468053.1 gg_id:297805 cheetah feces clone CE2_a06_2 EU468
GQ155565.1 gg_id:556376 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EU540206.1 gg_id:283179 profile human microbiota antecubital fossa (inner elbow) skin clone nbt247b06 EU540
FJ658620.1 gg_id:509207 Metalworking Fluids and Aerosols Metallurgy Plant metalworking aerosol clone Sumn FJ6586
AY163805.1 gg_id:101294 Citrobacter freundii str. A1 AY163
AM184249.1 gg_id:160975 Citrobacter freundii str. WAB1908 AM184
DQ294286.1 gg_id:143708 Citrobacter freundii str. 8 DQ294
AY259630.1 gg_id:83212 Citrobacter freundii str. WA1 AY259
GQ154984.1 gg_id:532730 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
DQ817309.1 gg_id:173691 mouse cecum clone aaa72h09 DQ817
DQ816132.1 gg_id:167280 mouse cecum clone aaa88d04 DQ816
GQ155666.1 gg_id:589249 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
AB548827.1 gg_id:530232 Citrobacter freundii str. JCM 24062 AB548
GQ154694.1 gg_id:510488 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
FJ581026.1 gg_id:570627 Citrobacter freundii str. IITRL1 FJ5810
DQ192060.1 gg_id:166668 Citrobacter sp. I91-10 DQ192
EU528229.1 gg_id:280706 Seasonal Dynamics Mudflat Mouth Major Kentucky Lake Reservoir Tributary sedime EU528
DQ816596.1 gg_id:167950 mouse cecum clone aab20b03 DQ816
DQ816998.1 gg_id:169360 mouse cecum clone aaa94d12 DQ816
DQ294285.1 gg_id:141265 Citrobacter freundii str. 7 DQ294
EU365679.1 gg_id:258785 Citrobacter freundii str. M-8 EU365
FJ975807.1 gg_id:547342 Human gut microbiome adopts alternative state bowel transplantation ileum effluent FJ9758

242.7	1808.8	1114.5	940.1	1203.9	1886.0	960.0	2134.8	890.1	1524.6	1381.9
49.3	392.1	878.0	783.1	412.8	961.7	285.2	798.2	406.2	263.1	334.8
72.4	373.5	511.7	580.5	391.7	567.5	448.7	464.5	352.5	743.3	377.4
215.1	1776.5	1556.3	1905.6	1647.5	1365.4	1711.9	1470.8	1239.2	1762.5	1196.6
208.1	1741.9	3038.5	3023.1	1461.8	4631.3	916.7	2730.4	1309.9	8681.8	746.6
434.9	2218.1	2436.9	2418.1	2771.9	3201.5	2134.5	2830.2	2570.7	2389.7	1507.9
466.0	2760.7	3461.2	3628.4	3528.3	5455.7	2117.8	3681.7	1628.6	8568.0	1730.8
786.6	3599.8	5174.4	4790.1	3224.5	5621.3	3743.1	3927.4	2913.3	6817.2	2764.3
194.1	2113.5	2598.1	2585.9	2220.0	2939.4	1398.3	2817.9	2507.9	4517.1	1653.2
166.6	1532.4	1928.4	1638.6	1387.4	1834.7	1156.9	1912.5	1195.6	2298.9	822.3
43.8	2055.6	2796.5	3069.4	1668.4	4343.9	1491.2	3289.7	2345.0	10062.9	1656.6
502.6	6332.3	8159.9	8955.8	4810.8	10294.5	3481.2	9115.4	5581.9	17835.7	4830.4
42.7	3940.3	5492.8	5699.3	3429.5	8790.3	2013.3	5540.6	2578.7	15062.9	2759.6
2061.2	4843.7	6168.7	5462.7	5448.7	6561.4	5303.4	4540.9	4707.6	12431.4	4704.6
1972.0	7455.5	8919.9	9602.4	7301.8	11137.6	6770.2	9272.6	8081.8	17431.6	7197.4
134.7	4269.6	6102.9	6856.2	4674.0	8853.4	3670.1	5461.7	2379.7	17168.4	2764.1
102.7	4206.5	4882.4	5058.1	3686.2	7221.9	2635.2	5372.5	1773.6	14571.7	1644.9
212.7	7218.0	8588.9	8902.6	7569.6	11532.3	5760.3	8044.5	3890.8	21184.2	4300.8
389.6	5214.6	7154.8	7399.0	5747.1	8519.4	5778.4	6158.8	6013.7	15015.0	3914.7
126.2	4673.2	6184.9	6594.6	3448.0	8565.7	1664.4	6389.8	4377.0	15840.3	3516.6
109.6	6908.3	8594.6	9090.9	6218.2	11029.1	4359.9	8486.9	5727.8	19325.8	4781.1
1008.3	4337.3	5682.6	5994.6	4823.1	8396.1	3780.0	5191.3	3531.7	16867.0	3820.7
179.0	5590.8	7576.4	7499.8	5588.7	10502.3	4496.6	6440.8	3068.7	19574.9	3226.6
5841.0	5340.2	6920.2	6355.0	5824.1	9219.8	4957.6	5635.1	4504.5	16293.5	4961.4
169.3	5467.6	7446.3	7329.1	5944.7	9796.9	5195.1	6239.2	3696.1	18909.5	2874.4
1610.8	3794.5	4857.8	5091.6	3012.7	7173.7	1531.7	6283.1	3694.8	12176.3	2856.3
9271.5	7850.1	10025.4	9546.1	8018.3	10516.7	7331.4	9003.9	10066.3	17097.0	6920.6
169.5	6781.8	7837.6	8685.9	7306.7	10379.8	6844.1	7766.6	3573.4	19298.5	3946.7
33.0	15.4	11.5	16.4	14.7	9.4	8.7	7.4	13.4	8.3	7.2
982.7	1885.5	2307.6	2160.4	2316.6	4309.5	1042.5	2335.1	924.1	8618.5	726.0
8508.0	11184.6	12230.6	12887.2	11337.7	12508.5	11268.1	10776.6	15969.9	16531.0	12261.5
109.5	4367.2	6365.6	6375.9	3851.7	8674.3	1826.7	6180.2	4470.2	15823.8	3057.6
218.8	7323.9	9104.4	9220.5	5537.9	11018.9	3185.0	10002.7	7352.6	19289.0	5902.3
722.3	6975.7	9285.3	8937.0	7267.3	10300.6	6913.9	9004.6	6697.0	17765.2	5311.5
151.9	4727.2	6940.5	6700.9	5016.2	9456.1	4307.3	5707.2	3317.6	18093.9	2612.7
1427.8	5169.2	6258.8	6965.6	6363.9	6899.4	5514.4	6456.7	3381.7	10535.3	4019.9
53.9	1270.0	2370.8	1924.2	1377.4	3655.8	962.6	1673.1	993.0	7417.9	813.9
219.0	2759.0	3160.3	3307.3	3187.7	3953.6	2174.4	4858.1	3078.7	6006.5	2524.2
42.0	1550.5	2487.6	2559.0	1508.7	4185.3	579.4	2698.9	1577.1	8586.4	1138.6
622.3	6399.1	7022.6	7973.2	5863.0	9647.7	4470.9	7078.2	4438.1	17664.5	3594.1
564.8	6197.8	7353.6	7906.1	5564.7	10525.0	4422.3	7246.0	6393.8	19248.2	4687.0

1623.1	3294.1	2837.2
529.7	806.2	1255.8
488.4	791.5	721.1
1550.0	2288.2	2168.9
3473.2	2951.2	1145.1
3343.8	3725.0	2026.1
5985.3	5705.3	3004.0
5067.2	6427.1	3422.1
3243.0	4585.8	1512.8
1894.6	3101.4	1217.4
4502.7	3798.5	1239.2
11870.0	9584.5	6055.8
8183.6	5602.1	3436.9
6065.0	5162.3	3294.0
11372.9	10305.4	8836.9
9107.8	6168.8	3421.3
7203.9	4757.2	2148.8
11722.8	8017.5	6344.8
8293.2	6817.4	3622.5
7397.9	6901.4	3153.3
11828.0	8849.1	5894.4
7130.3	5221.0	3629.1
10886.2	7333.9	4619.1
9523.5	7084.5	4050.7
10710.1	7123.5	3878.9
6299.2	5818.9	2873.8
11037.0	10758.2	6596.0
10670.5	7561.0	6413.5
10.8	16.2	10.8
3573.0	3473.2	956.7
11777.7	12518.7	10954.0
7732.0	6743.8	3057.0
11360.8	9550.8	5817.6
10865.1	9301.6	6765.9
9955.0	6578.0	2999.9
7596.6	5815.6	3404.3
2923.6	2555.4	1030.8
5629.3	4478.0	3955.3
2021.3	2781.7	1342.0
10414.3	8110.2	4696.6
11273.3	8520.0	5378.5

k__Bacteria	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria
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s__Cronobacter muytjensii	4444
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EU545403.1 gg_id:534741 Citrobacter freundii str. XW722 EU545
EF593056.1 gg_id:251387 Identification cultivable and non-cultivable Nisargruna biogas plant predigester slurry EF593
DQ517285.1 gg_id:161301 Citrobacter freundii str. BRN1 DQ517
GU374110.1 gg_id:530539 soil East Calcutta wetland clone SRC_NBB9 GU374
GQ155532.1 gg_id:579108 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
DQ223880.1 gg_id:168759 Citrobacter sp. str. P11 DQ223
GQ155589.1 gg_id:552805 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ154756.1 gg_id:510480 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
EU468065.1 gg_id:295328 cheetah feces clone CE2_b11_3 EU468
EF371903.1 gg_id:213847 Citrobacter freundii str. TF13 EF371
DQ192058.1 gg_id:170521 Citrobacter sp. I91-5 DQ192
FJ658534.1 gg_id:511169 Metalworking Fluids and Aerosols Metallurgy Plant metalworking aerosol clone Sumn FJ6585
DQ816058.1 gg_id:169128 mouse cecum clone aaa86g12 DQ816
GQ155569.1 gg_id:510363 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ155471.1 gg_id:509639 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ154907.1 gg_id:567301 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
AB548831.1 gg_id:522347 Citrobacter freundii str. JCM 24066 AB548
GQ154858.1 gg_id:564251 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
DQ816447.1 gg_id:169742 mouse cecum clone aab18b07 DQ816
GQ155467.1 gg_id:544556 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
AF025373.1 gg_id:9852 Citrobacter werkmanii str. CDC 0876-58 AF025
EF059839.1 gg_id:226460 Cronobacter dublinensis str. E465 EF059
EF059874.1 gg_id:223014 Cronobacter dublinensis str. E791 EF059
EF059879.1 gg_id:224695 Cronobacter dublinensis str. E799; NCTC9846 EF059
EF059878.1 gg_id:224208 Cronobacter dublinensis str. E798 EF059
EF059887.1 gg_id:219603 Cronobacter muytjensii str. E888 EF059
FJ906909.1 gg_id:552376 Cronobacter muytjensii str. Jor112 FJ9069
EF059875.1 gg_id:224339 Cronobacter muytjensii str. E793 EF059
EF059849.1 gg_id:224182 Cronobacter muytjensii str. E616 EF059
GU227684.1 gg_id:587272 Cronobacter sakazakii str. KYU35 GU227
GU227677.1 gg_id:534869 Cronobacter sakazakii str. KYU8 GU227
GU122211.1 gg_id:579605 Cronobacter muytjensii str. 05CHPL61 GU122
EF059861.1 gg_id:222245 Cronobacter turicensis str. E680 EF059
GU122184.1 gg_id:573255 Cronobacter sakazakii str. CDC 20-83; 05CHPL02 GU122
EU458321.1 gg_id:297419 spotted hyena feces clone HY1_d03 EU458
GU227685.1 gg_id:593345 Cronobacter sakazakii str. KYU37 GU227
FJ906905.1 gg_id:584098 Cronobacter muytjensii str. Jor77 FJ9069
GU122215.1 gg_id:557422 Cronobacter sakazakii str. 05CHPL65 GU122
FN543093.2 gg_id:569973 Cronobacter turicensis z3032 FN543
EF059892.1 gg_id:217736 Cronobacter subsp. dublinensis str. DES187 EF059
FN539031.1 gg_id:559715 Cronobacter sp. str. 040407/32 FN539

69.7	5812.2	7659.1	7541.9	5723.2	10804.9	4177.1	6449.1	2966.0	21074.2	3180.9
8607.4	6630.3	6580.9	7308.5	7260.5	8092.3	7761.8	6730.7	8001.2	14015.1	5679.5
55.0	5903.2	7777.2	7437.3	6143.7	10410.3	4377.5	6581.6	2944.1	17668.1	3074.4
179.8	3251.3	5303.7	4906.7	4141.1	8083.1	2544.6	4261.6	1836.5	17327.7	1629.1
222.3	7720.7	8791.0	8952.0	8275.1	10795.6	8245.2	9509.7	7164.6	16756.0	5990.4
90.9	1714.9	2170.9	2308.8	1409.0	3433.5	1111.3	2210.9	1823.6	5492.0	1336.1
833.4	7763.3	8965.9	9457.4	8213.1	11830.7	6342.4	8572.4	5058.8	21738.4	5185.8
696.5	5446.3	6969.7	7090.3	5487.3	10212.4	3487.6	6675.7	3670.5	19685.5	3721.7
2901.4	4475.7	5708.1	5931.9	5520.9	6855.6	5174.3	5058.3	5130.2	11596.2	3877.4
8072.7	9206.9	9594.1	10439.9	10625.4	11200.4	11462.8	9643.2	13121.6	17455.0	9416.3
364.3	4851.9	5946.8	6287.2	4705.8	8623.6	4010.7	6288.5	5944.2	12849.9	3901.3
568.4	6818.5	8342.7	7559.2	6735.0	9376.0	5961.0	7661.1	6318.5	16814.0	5661.0
276.9	6307.5	7428.1	7714.5	6690.7	9912.3	6279.3	6971.1	5421.8	19863.6	4359.1
610.5	6254.0	7276.6	7915.4	5635.9	10608.1	4392.5	7280.0	6408.6	19135.3	4625.5
8334.7	8171.7	9684.5	9511.3	8718.8	12166.5	7262.0	8686.6	7586.8	20690.2	6765.4
6194.7	5734.5	7889.3	8689.7	5152.7	10589.8	4064.6	7637.9	7387.3	18760.8	5358.5
59.6	4884.2	6784.3	6836.3	4203.2	9250.8	2893.8	6293.2	3939.1	17504.2	3339.9
878.5	8037.4	8473.6	9936.8	9283.3	10379.2	8666.1	8615.8	4612.1	18381.7	4946.9
44.0	3944.1	4739.8	4746.1	3603.9	7086.9	2993.8	4169.6	1766.0	12816.2	1502.6
17968.8	7626.7	8849.3	9469.5	7159.6	11538.0	6828.6	7996.2	7917.3	19588.1	8135.5
85.7	4214.3	5829.8	5735.9	3583.3	8192.7	2092.2	5234.1	3161.8	17080.6	2609.0
125.7	2729.2	3284.4	3442.2	2971.6	4517.7	1554.6	3667.4	3446.6	6968.4	1751.7
199.6	3706.0	4219.8	4194.5	3442.8	5487.6	2359.8	4599.2	4727.5	7079.5	2487.7
145.6	2742.2	3555.7	3742.2	3079.9	5107.7	1534.6	3974.8	3605.9	8564.0	1923.5
732.3	2785.1	2919.1	3349.0	2959.6	4488.5	1634.9	3688.9	3080.6	8070.7	1872.1
140.4	3672.1	4951.6	5070.3	2552.9	5394.5	2502.2	4839.6	1784.2	10896.8	2271.9
144.1	3666.6	4892.4	5171.9	2724.4	5236.1	2557.4	4893.4	1895.1	11397.8	2355.4
167.9	4375.0	5355.1	5213.0	3386.7	6023.6	3106.5	5158.0	2813.3	10306.2	2539.4
1217.8	7261.4	7729.6	7703.5	7092.8	8712.1	5543.4	7737.9	7902.6	13974.2	5625.2
129.6	2128.1	3249.2	3219.1	2532.4	5454.0	926.7	3274.3	1704.2	12316.5	1278.9
201.5	4202.1	4343.6	4196.3	3760.1	6451.1	1860.3	4513.8	4025.9	15625.5	2663.2
1570.7	6880.4	7074.4	7174.9	6658.7	8593.3	5344.0	7267.9	6489.5	15712.2	5036.8
97.9	3814.8	4395.5	4359.4	3711.8	7000.7	2836.5	3700.8	2497.3	8067.0	2064.7
769.5	4090.3	5256.0	5654.4	4524.2	7256.7	3360.9	5714.4	7981.9	12545.7	4951.5
1144.2	4768.5	5836.0	6201.6	4048.7	5352.0	3620.0	5623.5	2877.3	12493.9	4324.1
154.3	2522.0	3535.3	3738.6	2507.5	5091.6	1345.9	4110.7	2948.7	9743.1	1873.6
787.7	5493.6	6355.9	6297.3	4548.8	7009.2	4251.0	6144.9	4274.4	11793.5	3592.0
1105.4	3672.1	4028.6	4085.6	4214.8	6420.6	1976.7	3953.7	3570.7	11380.9	2858.2
91.0	3045.3	3297.7	3626.4	3650.6	5767.3	1348.5	3469.4	2917.7	10157.7	1580.1
167.2	2345.1	3084.1	3180.7	2316.3	4279.3	1302.8	3496.6	2876.2	7425.2	1597.3
144.1	3623.3	3920.2	4197.0	4235.1	5501.1	2814.8	4075.3	2987.1	10602.5	2391.7

11061.9	7366.9	5390.3
7461.6	6888.1	6630.9
12088.2	8256.6	5375.3
7535.7	4245.8	2172.1
11657.8	8898.3	7238.3
3519.8	3785.3	1514.5
12242.8	8572.3	6925.2
10014.1	6903.4	5676.5
6709.8	5848.2	3840.1
10483.5	9673.2	9918.0
8327.5	7968.9	4120.7
9575.0	8650.7	5830.0
9119.6	7058.3	5807.2
11382.1	8595.3	5316.0
11672.8	9745.1	8648.7
10630.3	8552.4	5054.0
10163.3	7633.0	4250.8
10739.7	8337.3	6937.7
6927.3	5250.5	2351.6
11804.2	9636.2	7345.9
7576.3	6255.0	3242.7
5256.9	4958.9	2201.5
5671.2	5539.2	2898.6
5723.7	4899.7	2161.2
5035.0	4699.9	2122.1
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6685.0	4789.2	3004.7
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9503.0	9521.3	7139.1
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6536.3	5951.1	2062.5
9472.8	8424.2	6885.4
8825.5	6825.4	3567.1
7373.9	6880.9	4381.1
6405.9	5494.4	4069.3
5453.6	5012.9	1768.0
8721.7	6772.6	5154.3
5412.5	4977.6	1734.7
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4782.0	4419.7	1664.9
6432.8	4874.1	2556.2

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o__Enterobacteriales	f__Enterobacteriaceae
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s__Edwardsiella tarda	4124
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s__unclassified	5425
s__unclassified	5842
s__symbiont of Noeeta pupillata	5807
s__Enterobacter cowanii	4196
s__Enterobacter cowanii	4657

EU348325.1 gg_id:353216 symbiont
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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
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FJ405295.1 gg_id:358862 Edwardsiella tarda str. K6
FJ405305.1 gg_id:358984 Edwardsiella tarda str. K16
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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
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GU367394.1 gg_id:518647 Edwardsiella tarda str. Et4
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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
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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

EU348
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AB453
GU176
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GQ337
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DQ645
GQ264

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1059.2	3089.9	4289.2	3848.6	2975.1	6565.3	2638.8	3938.4	2764.8	11213.1	2462.2
1143.2	5075.2	7645.2	7674.9	4296.7	6484.5	2619.7	7592.9	5821.1	11222.2	4239.0
852.4	5011.3	7745.7	8071.3	3857.8	7032.2	2966.8	7956.5	5461.7	11790.6	4571.5
42.4	3380.9	5723.3	6066.1	1715.9	5825.0	2809.7	7552.7	4831.6	10241.8	3484.2
3063.7	6882.2	8371.9	9376.2	6439.5	9095.0	4846.6	9209.4	7224.3	14767.7	8304.7
1497.9	2198.2	2658.2	2723.6	2763.8	2765.1	2190.0	3341.5	1954.1	6058.1	2864.0
623.2	4570.3	7189.4	7725.0	2850.7	6778.3	2121.1	7425.6	4868.6	11981.3	3876.5
1079.5	5173.9	7117.0	7196.6	5023.2	5841.4	4416.3	8753.0	6188.1	10056.3	5171.4
1240.4	5846.9	7407.5	8017.2	4257.2	6674.0	3629.2	8490.1	5143.0	14067.2	4323.4
7355.1	2915.0	3822.5	4070.8	2512.4	5882.4	1736.7	3933.9	2575.0	9532.8	1568.8
14388.2	8123.6	8305.3	9467.0	7738.5	9222.6	7877.5	7987.7	11283.9	11315.0	13348.5
2813.7	7068.9	8109.9	8845.6	6048.8	10050.4	5427.0	8210.1	7493.8	16810.1	5676.9
124.4	3052.9	4115.1	4041.6	1991.2	5565.1	1369.7	3815.2	3028.2	8450.2	1915.0
2809.3	4186.1	4754.1	4985.0	3386.8	6118.6	3396.8	4911.2	4664.7	9223.5	3038.5
2808.7	5177.0	5912.3	6085.0	3895.7	7214.8	3668.7	6249.0	6350.0	11213.8	3836.7
5942.5	2588.1	3326.4	3359.0	1940.7	4686.4	1488.1	3408.4	2547.1	8706.1	1830.2
4329.1	5308.5	5751.6	5838.5	5088.5	6160.4	5464.5	5728.0	6538.3	10034.1	5340.1
1550.5	3941.9	3939.3	4189.4	3211.1	4609.4	2820.6	4527.8	4897.1	7080.5	3670.0
2600.5	4971.4	5645.3	5752.1	3701.4	6781.5	3501.1	5918.9	6171.2	10793.4	3958.6
21680.1	8385.0	8530.9	9946.1	7268.2	10266.0	7774.2	9042.3	9890.3	12884.5	8289.9
2600.5	4621.2	5266.2	5322.5	3367.7	6280.1	3187.1	5505.6	5676.7	9478.6	3556.3
429.7	1233.2	1686.7	1742.6	942.0	2293.4	764.9	1858.5	1235.1	3741.7	1069.5
166.2	3955.4	4667.8	4832.1	3079.0	5816.7	3578.2	4875.1	4848.2	8043.9	2733.2
168.3	3868.2	4581.4	4429.3	2498.1	5587.2	1988.6	4609.4	4569.1	9092.8	2852.6
419.7	1717.8	2392.1	2479.1	1623.8	3104.7	1674.1	2507.8	1794.3	4259.2	1519.9
7542.0	6802.9	7369.2	8336.3	7668.5	9220.9	8422.5	7593.4	5320.2	14270.8	4844.4
92.7	2730.5	3622.1	3828.5	1874.1	5156.9	1135.0	3807.8	3114.2	9850.4	1787.7
2390.7	4057.1	4662.3	4643.3	3234.1	5623.0	3078.6	5006.3	5531.6	8569.6	3206.7
748.0	1665.9	2267.7	2220.9	1234.2	2929.3	753.5	2102.6	2097.9	4268.9	1364.5
2056.4	4842.6	5622.4	5690.8	3606.1	6683.5	4132.1	5644.6	5422.0	8994.5	3811.2
2364.7	3636.1	4260.3	4427.6	3173.2	5719.6	3017.6	4286.0	3973.8	7940.1	2463.5
7252.1	6253.4	6853.5	7216.1	5329.6	8077.1	6184.0	7016.0	6956.9	11402.5	5201.2
487.9	2184.5	2834.4	3242.9	2094.4	3814.9	1428.7	3424.6	2029.9	5947.0	1757.4
118.3	1944.5	2611.9	2736.2	1670.8	3942.1	1121.4	2693.6	1564.0	7515.4	1234.1
4585.4	3684.1	4338.6	4494.7	2029.8	5023.9	2018.2	4513.5	3547.7	7629.4	2700.0
7136.3	8628.7	9468.8	10500.5	8353.4	11155.3	8957.8	9403.7	7932.3	16390.9	7523.6
2269.9	5592.6	6169.9	6501.5	5008.9	7465.9	5451.4	6191.0	5535.7	10650.3	4001.8
1921.1	4378.4	5392.4	5560.2	4551.1	6643.7	3476.2	5581.7	4486.8	10797.6	3615.8
1291.3	4568.9	5198.0	5435.5	3577.3	7467.8	3147.7	5784.5	2444.3	12494.9	2569.0
76.5	3295.3	3800.1	4047.4	2662.2	5568.5	2263.6	3846.7	1796.3	11662.8	1477.3

10743.0	9012.4	6365.0
5726.7	6322.4	3911.5
9010.0	8864.0	5059.7
9428.3	8975.0	5198.3
7986.0	7220.5	3578.2
10434.1	9760.6	6900.3
2810.7	4304.8	2652.9
9165.8	8733.0	5029.6
8983.8	7979.0	4785.4
9579.1	7567.6	5200.6
7409.3	5004.4	2413.7
8926.3	9994.6	7785.5
11605.5	8773.5	6041.9
7921.0	5800.4	2280.1
7774.0	5669.3	3795.5
8936.3	6906.7	4497.4
5863.9	4991.4	1938.4
7088.4	7568.1	5330.3
4651.0	5563.7	3206.2
8168.9	6445.7	4275.2
12123.8	10084.0	7407.4
8020.9	6353.6	3892.9
2621.7	2812.7	1046.0
6943.1	5879.8	3573.3
6982.6	5742.1	3053.3
3568.2	4419.2	2088.7
12040.9	6614.2	6510.0
6125.1	4990.9	1865.4
6674.6	5339.0	3610.7
3544.0	3465.6	1334.8
8293.6	6664.4	4448.7
7374.2	4729.3	3324.4
9609.5	7402.1	5796.6
3850.5	3970.9	4217.8
4465.3	4158.4	1603.7
5849.9	6162.1	3733.3
11775.6	9090.5	8176.1
8984.5	6392.4	5133.2
6921.8	6613.7	3763.5
8714.4	6226.7	3161.7
6684.7	4786.0	2836.5

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EF025326.1 gg_id:176468 Enterobacter cloacae str. SREPS1 EF0253
EU855207.1 gg_id:355066 Enterobacter sp. str. CTSP29 EU855
DQ855282.1 gg_id:216257 Enterobacter sp. str. FMB-1 DQ855
GQ260085.1 gg_id:561327 Enterobacter cloacae str. ICIRC107 GQ260
EU047701.1 gg_id:251565 Enterobacter aerogenes str. HC050612-1 EU047
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EU047556.1 gg_id:249130 Enterobacter hormaechei str. TMPSB-T10 EU047
GU071202.1 gg_id:587429 Enterobacter sp. str. DIT 14 GU071
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AY335554.1 gg_id:129942 Enterobacter aerogenes str. CBNU-20-1 AY335
DQ202394.1 gg_id:140607 Enterobacter cloacae str. B5 DQ202
GQ260081.1 gg_id:587124 Enterobacter cloacae str. ICIRC91 GQ260
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FJ868805.1 gg_id:541119 Enterobacter sp. str. BSRA1 FJ8688
EF446901.1 gg_id:214586 Enterobacter cloacae str. GW4 EF4469
AF130914.1 gg_id:10081 Pantoea endophytica str. A42 AF1309
GQ179978.1 gg_id:575168 Enterobacter hormaechei str. FS11 GQ179
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AJ854063.3 gg_id:108298 Enterobacter nickellidurans str. NiVas 114 AJ8540
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FJ976545.1 gg_id:556584 Enterobacter sp. str. LCR36 FJ9765
EU073021.1 gg_id:254448 Enterobacter cloacae HQ040619-1 EU073
CU915026.1 gg_id:448667 and dynamics adapted microbiota during degradation Tunisian zarzatine enriched se CU915
DQ837566.1 gg_id:172044 Enterobacter sp. XIV DQ837
AB244457.1 gg_id:257506 Enterobacter cloacae str. An20-1 AB244
FJ976587.1 gg_id:545162 Enterobacter aerogenes str. LCR78 FJ9765
FJ999766.1 gg_id:385869 Enterobacter hormaechei str. SP FJ9997
EF179825.1 gg_id:258793 sequences adult Anopheles darlingi (Diptera: Culicidae) mosquitoes clone 4.2 EF1798
Y17665.1 gg_id:10077 Enterobacter cloacae Nr. 3 Y17665
EF059890.1 gg_id:218876 Enterobacter hormaechei str. E904 EF0598
DQ273684.1 gg_id:144399 Evaluation two chromogenic media glucosidase and commercial oligonucleotide pro DQ273
AY217654.1 gg_id:84190 Escherichia senegalensis str. F1p AY217
EU302833.1 gg_id:240810 Salmonella sp. str. DAP8 EU3028
GQ478377.1 gg_id:551552 olive endosymbiont 'Candidatus Erwinia dacicola' switches intracellular extracellular GQ478
GQ131582.1 gg_id:460735 Erwinia rhapontici str. 1OP1 GQ131
Z96087.1 gg_id:9805 Erwinia rhapontici str. LMG 2688 Z96087
GQ131583.1 gg_id:451112 Erwinia rhapontici str. 1OP6 GQ131
GQ131584.1 gg_id:410468 Erwinia rhapontici str. 3OP1 GQ131
U80206.1 gg_id:9811 Erwinia rhapontici str. ATCC 29283 U8020

3370.2	6176.4	6872.7	7657.3	5675.0	8216.1	5611.2	7036.5	7331.5	12477.4	4486.6
793.3	4670.9	5090.3	5256.3	3769.4	5390.6	3934.8	4949.4	4338.7	8829.3	4182.0
3366.0	4204.2	4389.6	4525.5	3594.6	5286.1	3334.6	3736.2	1490.1	9537.8	1358.4
1284.0	6362.2	7160.2	7504.8	5799.6	9530.1	5216.3	6806.4	3475.4	15979.0	3468.7
14339.0	6640.9	5942.2	6891.2	6235.3	6681.6	6772.4	6364.4	7591.9	8646.4	10211.0
63.6	6010.0	7767.6	8211.1	4765.4	11515.0	3055.4	6953.8	4006.6	21701.9	3848.5
76.8	3515.4	4265.1	4287.9	2675.9	5424.6	2356.1	3986.2	2822.2	11474.2	3313.5
120.7	4720.5	6159.3	6460.9	3684.8	8115.7	2420.3	5298.5	2390.0	19481.4	3041.4
2252.4	6249.4	7920.7	8081.0	5134.7	8992.2	4430.0	8229.8	6385.6	16130.4	5531.7
12334.0	5718.2	5249.5	5592.2	4361.4	7326.5	5167.9	5077.6	5778.1	10637.0	4423.6
112.4	3162.6	5042.7	5460.7	3760.8	7100.7	2128.7	4258.0	2593.5	14888.5	3053.1
755.5	8027.4	9564.3	10016.1	7374.4	12980.9	6325.1	9079.0	6872.9	22859.2	6341.3
747.8	4985.8	6720.8	7005.0	5428.6	10342.3	3262.4	4906.3	2667.1	21454.9	2942.9
16488.4	11305.4	12280.9	12555.1	10409.2	12550.8	11994.8	10461.2	15846.3	19034.5	14765.6
256.3	4767.2	6647.3	6749.8	3456.1	8207.8	2771.3	6583.9	3546.0	15487.7	3512.8
159.6	3757.0	5206.0	5899.9	3097.0	7320.0	1851.4	4075.5	1504.5	18136.6	2335.7
268.0	4936.6	5709.7	6270.0	5034.4	8122.5	3986.1	5897.2	4090.6	15220.4	4450.3
1007.0	6077.8	7700.5	8400.4	5653.0	11439.5	4490.3	7660.6	4407.1	20330.8	5065.6
339.2	3103.9	3467.0	3713.3	2572.0	5549.6	1883.4	4147.2	2774.7	10124.0	2022.4
61.1	4333.0	5871.3	5896.3	2888.2	7753.2	1690.5	5042.9	2555.6	18871.1	2237.7
105.3	2620.8	3521.0	3197.4	1833.5	4501.8	1330.6	3574.4	2415.8	8840.8	1799.3
124.4	3665.3	5096.9	5368.9	2961.3	7722.9	866.6	3709.1	1591.5	18648.0	1908.9
61.7	4679.0	6367.6	6576.2	3388.7	9334.0	2213.7	5526.1	2726.6	19521.5	2539.6
3369.8	9474.3	10955.2	12049.1	9193.6	11833.0	9768.9	10327.2	9743.2	19165.6	8903.7
262.5	4834.0	6495.1	7002.2	2993.2	7604.1	2151.4	6544.0	3231.8	19299.3	3754.7
66.7	4531.0	7033.0	7800.8	3121.6	8646.4	3013.6	6204.9	1991.6	19464.9	4019.1
100.6	4819.1	6857.4	6790.6	3479.7	9324.8	2007.3	5703.8	2849.3	19970.6	2784.6
35.4	5338.8	7362.8	7173.6	4546.5	10136.4	3786.1	6917.7	3872.7	20476.2	3797.6
62.5	6236.0	8232.2	8198.5	4731.1	10836.2	3690.9	7823.4	3788.9	21439.1	4108.6
8288.1	3986.5	4361.7	4426.5	4385.5	6024.4	3705.3	3454.4	3122.5	13333.7	4124.5
137.7	4304.9	5674.4	5303.1	2798.7	5519.4	1391.3	4877.8	3140.5	12922.7	4064.1
64.0	6360.0	8986.0	9283.5	4379.7	10115.3	4216.3	8567.2	3510.9	21489.5	4978.4
96.7	2392.2	3039.5	3331.4	1949.6	4097.3	1499.6	2844.7	1788.5	5503.8	1597.7
66.1	2555.0	3220.9	3330.7	1815.4	4070.2	1499.0	3413.4	1062.0	8204.8	997.2
2280.8	5346.3	4871.6	5204.6	3596.2	6926.7	3441.5	5176.0	4870.3	7084.9	3687.8
53.5	2511.8	3589.0	3615.9	2006.8	6379.2	1787.5	2911.7	837.8	12308.9	1398.5
3928.5	7222.1	7433.1	7170.4	6122.0	8773.6	7824.0	6268.7	6630.9	16531.2	6385.7
93.1	2952.5	3799.4	3599.8	3157.9	5268.1	2269.0	2860.1	1405.4	7909.6	1240.6
82.3	2831.1	4020.6	3792.8	2197.3	6177.9	2183.1	3275.0	2371.8	9849.4	1376.3
82.7	3613.9	4920.8	4682.6	2790.1	6892.9	2637.6	4251.8	2861.3	11360.9	2017.9
241.3	8066.5	10221.7	9939.6	7317.0	12370.6	5565.0	8845.3	5757.4	21185.7	5070.9

8890.2	7654.0	4970.2
5510.2	5585.6	3600.0
7026.0	5704.3	3792.0
11552.8	7850.5	4982.5
6904.1	7897.5	6152.4
11699.2	7815.8	4395.0
5606.1	4598.9	2156.4
8984.0	4994.5	3078.6
9813.1	8971.8	4912.4
8410.7	7245.8	4647.0
7411.1	4802.9	2991.7
13675.3	10478.7	5991.9
10793.0	6257.2	3768.8
12119.5	11640.2	11160.1
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7439.4	3941.5	2484.3
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10122.3	6249.6	3886.5
12084.4	10747.9	8446.2
8787.0	6392.5	3253.5
9653.3	5696.8	3101.1
10571.0	6854.6	3764.1
10890.2	7885.8	3837.7
11967.5	8753.9	4376.9
6234.6	3887.0	2661.4
6585.3	4852.0	2304.6
11878.2	8567.7	4189.0
4437.7	3643.6	1915.2
5722.8	3741.0	1149.9
8080.0	7048.0	3571.7
4859.4	3404.9	2043.8
8016.4	8921.9	5546.2
6733.7	4822.2	1569.3
8005.8	5464.1	1613.2
8118.9	6200.4	2230.1
12430.6	11157.6	5841.2

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s__Erwinia soli	6224
s__Erwinia tasmaniensis	5031
s__Erwinia tasmaniensis	5591
s__Erwinia tasmaniensis	5597
s__Erwinia tasmaniensis	6222
s__Erwinia toletana	5774
s__Erwinia toletana	5791
s__Escherichia hermannii	4287
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s__Escherichia hermannii	5460
s__Pantoea dispersa	4369
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EF540891.1 gg_id:219853 Erwinia soli str. Ew02 EF5408
AM292080.1 gg_id:179624 Erwinia tasmaniensis str. Et2/99 AM292
AM055715.2 gg_id:149797 Erwinia pyrifoliae str. Ejp557 AM055
FJ594367.1 gg_id:569261 Erwinia amylovora str. EA312 FJ5943
FJ594360.1 gg_id:566379 Erwinia pyrifoliae str. WT19 FJ5943
AF130965.1 gg_id:9820 Erwinia toletana str. A89 AF1309
AF130964.1 gg_id:9814 Erwinia toletana str. A82 AF1309
GQ884173.1 gg_id:582459 Escherichia hermannii str. SH-2 GQ884
EF059889.1 gg_id:226692 Escherichia hermannii str. E895 EF0598
EF059869.1 gg_id:223949 Escherichia hermannii str. E757 EF0598
EU931561.1 gg_id:337373 Pantoea agglomerans str. ZFJ-6 EU9315
AB297966.1 gg_id:209376 Erwinia sp. str. AC81a (=SUPP41) AB2979
GQ024698.1 gg_id:484972 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ024
GU339282.1 gg_id:563485 Pantoea ananatis str. EH55 GU339
DQ273680.1 gg_id:141117 Evaluation two chromogenic media glucosidase and commercial oligonucleotide pro DQ273
U80201.1 gg_id:9861 Pectobacterium cypripedii str. ATCC 29267 U80201
EU289448.1 gg_id:253617 metagenomic approach biosynthesis ansamycin endophytes or symbionts enriched s EU2894
EU681952.1 gg_id:281980 Erwinia persicina str. WD1608 EU6819
FM163487.1 gg_id:289103 Achromobacter xylosoxidans str. RE1 FM163
AM055711.1 gg_id:149811 Erwinia billingiae str. Eb661 AM055
GQ024758.1 gg_id:484912 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ024
AF024607.1 gg_id:9823 Pantoea agglomerans str. TAC.I.94.1 AF0246
GQ043420.1 gg_id:423241 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw96 GQ043
GQ024848.1 gg_id:484822 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ024
AF141893.1 gg_id:71250 Erwinia amylovora str. BC202(=Ea491) AF1418
GQ024907.1 gg_id:484762 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ024
EU072495.1 gg_id:239362 pentatomid symbionts host gut clone Ah1 EU0724
EU362176.1 gg_id:351023 Erwinia sp. str. C3(2008) EU3621
FJ595863.1 gg_id:543943 Erwinia pyrifoliae str. WT36 FJ5958
AY373829.2 gg_id:101634 Salmonella subterranea str. FRC1 AY3738
GU124495.1 gg_id:582297 endosymbiotic (Stal) (rice brown planthopper) Enterobacteriales endosymbiont Nila GU124
GQ024853.1 gg_id:484817 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ024
GQ024769.1 gg_id:484901 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ024
AJ233417.1 gg_id:9810 Erwinia rhapontici str. DSM 4484 AJ2334
EF469631.1 gg_id:221786 Dioxyna bidentis ex Bidens tripartita symbiont EF4696
AB480771.1 gg_id:539151 Erwinia tasmaniensis str. Acj 205 AB4807
GQ024837.1 gg_id:484833 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ024
AM294946.1 gg_id:174382 Erwinia persicina str. LPPA 408 AM294
EU336938.2 gg_id:537651 Flavobacterium sp. str. AG13 EU3369
AF289542.1 gg_id:20321 Erwinia amylovora EA G-5 AF2895
AF024613.1 gg_id:9827 Pantoea agglomerans str. TAC.XII.93.2 AF0246

178.1	2138.1	3140.2	3392.1	1794.6	5637.9	1547.1	4139.3	1894.0	5180.0	2126.9
49.4	2893.3	4393.2	4252.3	2165.5	7809.1	2108.4	4180.0	1739.3	11335.5	1703.5
94.7	2176.0	2913.0	2641.6	2923.1	4721.6	1549.0	2619.4	1132.5	6289.3	988.9
187.4	4623.3	5586.5	5458.5	4047.7	7298.5	2374.3	5629.1	3434.5	11694.4	2989.9
619.1	4238.7	4666.0	5246.9	5891.2	7210.8	3986.2	4720.0	3341.6	9968.7	2787.3
1377.1	1809.7	2029.1	2388.7	1690.3	4093.2	1728.1	3067.1	2001.1	5142.5	838.2
359.0	2530.3	2249.1	3974.1	1861.3	4340.0	2801.4	4224.1	2215.5	3944.2	2001.2
70.3	4405.1	5413.4	5334.6	3697.8	8067.5	2726.7	4759.5	2022.2	14036.7	1982.3
58.4	3741.2	4674.3	4932.7	2918.1	8328.4	1981.4	3865.2	2101.7	13296.3	1482.6
77.2	3898.6	4499.3	4656.1	3677.9	6763.0	2681.7	4029.8	2821.6	12429.0	1687.4
6757.6	5951.4	6746.3	7015.0	6624.6	8280.8	5159.1	6112.2	4648.0	12890.4	4943.9
461.6	4148.8	5297.2	5291.1	3408.7	7365.3	3607.2	5809.3	4214.1	9032.3	3394.0
6944.9	6137.1	6117.3	6460.8	5692.3	6971.2	6065.0	6001.5	7190.7	8378.9	7588.0
1758.9	3017.0	3643.7	4059.3	4782.6	6498.7	2715.0	2933.6	1645.1	6318.0	1853.9
211.3	4020.0	4719.7	5864.5	4607.1	6895.0	3557.6	5694.2	3564.1	10904.1	3697.0
128.7	4301.1	6251.1	5841.8	4891.7	8735.9	5068.9	4831.9	2685.8	16170.1	1855.9
1556.3	3506.4	4881.5	5586.3	4056.8	7210.0	4071.5	4734.3	3801.0	12979.1	2395.6
57.6	1742.6	2612.4	2761.0	1369.2	5018.4	1448.9	2409.8	650.8	8480.0	870.9
78.0	1873.5	2667.9	2983.2	1292.4	4428.6	951.5	2429.6	875.5	7760.7	1094.5
90.7	3509.2	4353.8	4845.0	3012.9	8551.1	2858.8	4116.3	4178.3	12761.9	2097.9
251.1	2769.9	3460.1	3266.3	1966.1	3952.2	2091.7	3097.4	2529.9	5371.2	1583.3
1423.0	5218.3	5605.5	6304.7	6172.4	7239.3	4808.9	5868.4	4540.1	10959.1	4161.8
68.7	5064.3	7628.4	7931.4	4550.0	8276.3	4422.1	6359.5	3068.4	15476.0	3910.3
5275.0	3744.4	4188.5	4322.6	4532.9	4314.9	4783.5	5217.7	3701.7	11404.8	3230.8
1729.1	5100.5	6412.9	6886.0	4359.7	9636.3	3335.8	5830.1	4128.9	17380.3	3816.4
2950.0	4437.5	4867.7	5071.0	3551.6	6608.6	3574.9	4825.6	3827.2	7871.3	2880.4
5117.3	7591.2	8383.8	9629.5	7435.7	10577.0	6661.7	8552.2	9642.4	15319.1	7528.6
87.6	3119.7	3991.1	3965.2	3940.1	7095.6	2401.7	3639.4	2474.6	9097.2	1415.0
1084.3	2552.6	3443.0	3350.3	2227.6	5262.7	2104.2	4186.3	1998.5	9357.2	2564.0
1115.5	7831.4	9361.9	9730.5	6730.1	11941.8	5053.8	9032.0	6061.1	20803.9	5956.9
211.2	2866.2	3854.9	3889.4	2701.4	6265.0	2663.2	3934.6	4155.4	10568.1	2418.3
5065.8	5613.5	5716.3	5876.7	5049.3	7405.1	5066.2	5855.3	6492.0	10546.5	1374.3
9377.3	7663.2	7903.1	8567.5	7697.8	8571.7	7806.7	7590.3	9594.1	11447.4	11167.4
207.6	5998.2	6250.2	6257.5	4093.7	7662.2	2861.3	6235.5	4180.4	14367.6	3439.0
65.6	2486.5	3249.5	2940.3	1892.4	4641.5	1890.4	2345.3	1490.3	7746.1	1206.4
95.8	1925.0	3112.3	3551.4	1355.5	5348.5	1177.9	4052.6	3221.6	7469.8	1710.9
796.5	5197.5	5689.3	3550.0	2498.2	5942.7	2758.0	4174.2	5327.2	9486.9	2505.8
70.6	4973.5	6056.6	6046.9	6624.8	7969.3	4800.4	5510.8	3255.3	11588.7	3084.8
89.1	3106.2	4445.6	5030.9	2876.5	7328.6	2480.0	5011.8	2561.7	9612.5	2890.6
1270.7	7718.0	8414.8	9488.8	7918.1	9479.8	8150.0	9015.0	11328.7	11352.8	10004.9
377.8	3526.1	4064.7	4130.1	3609.9	5432.2	3859.4	3986.2	3236.8	8966.7	2498.6

6034.3	6271.4	2537.0
9525.0	6804.3	2739.9
5557.4	4580.1	2110.5
9285.7	7392.5	3393.4
7641.3	6522.6	4072.6
6074.2	4134.3	1400.2
5034.6	5032.8	2509.0
9704.3	6557.0	3405.2
9660.8	5599.2	2368.2
7787.0	5684.0	2479.4
9952.7	7687.7	4065.3
9092.8	7740.5	3770.5
8416.2	8171.5	5430.7
7093.9	5414.8	3571.6
7310.4	6399.9	3863.6
9733.5	6567.3	2750.8
7734.7	5740.5	2788.5
5738.0	4456.6	1540.7
4214.8	4682.8	1752.0
9831.7	6570.4	3015.0
5174.7	4750.6	2038.0
7889.6	7333.6	5062.1
10883.2	7312.1	3434.6
4939.3	5717.2	2713.4
11779.1	8661.4	5086.8
9219.3	6797.0	3568.9
10791.7	10673.8	7097.4
9000.3	5533.1	2781.2
6107.8	6214.1	2676.3
12528.8	9285.6	7941.1
6744.0	6298.1	2622.1
10509.6	7840.2	4276.5
9934.4	8917.1	7026.9
7190.7	8518.1	3744.6
6904.5	4619.4	2013.7
6341.1	4961.4	1780.1
7276.0	5650.9	3293.3
9770.7	6348.7	4709.3
7562.2	7212.9	3419.7
9512.5	9943.1	7541.4
6290.9	5292.2	3106.6

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GQ024930.1 gg_id:484741 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ024
AY702662.1 gg_id:169365 Margalefia venezuelensis str. MS12 AY7026
DQ532292.1 gg_id:171458 Geographical Variation Microbial Burden and Spacecraft Assembly Kennedy Space C DQ532
AB480775.1 gg_id:575074 Erwinia tasmaniensis str. Acj 211 AB480
FJ595871.1 gg_id:573072 Erwinia amylovora str. LMG2068 FJ5958
GQ097550.1 gg_id:395052 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw GQ097
EU926632.1 gg_id:350789 Escherichia albertii str. 1297-05-19 EU926
NC_010498.1 gg_id:263846 Escherichia coli str. SECEC SMS-3-5 NC_01
AE014073.1 gg_id:146636 Shigella flexneri 2a str. 2457T AE014
DQ411026.1 gg_id:151002 Escherichia coli str. FR-2 DQ411
CP000038.1 gg_id:138890 Shigella sonnei str. Ss046 CP000
CU928163.2 gg_id:544923 Escherichia coli str. UMN026 CU928
AP010953.1 gg_id:568499 Escherichia coli O26:H11 str. 11368 AP010
CP000800.1 gg_id:257376 Escherichia coli str. E24377A CP000
NC_010498.1 gg_id:263845 Escherichia coli str. SECEC SMS-3-5 NC_01
NC_010498.1 gg_id:263843 Escherichia coli str. SECEC SMS-3-5 NC_01
AAJV02000011.1 gg_id:314537 Escherichia coli str. E22 AAJV0
AAJV02000007.1 gg_id:340407 Escherichia coli str. E22 AAJV0
CP000819.1 gg_id:520568 Escherichia coli B str. REL606 CP000
CP000800.1 gg_id:257373 Escherichia coli str. E24377A CP000
FM180568.1 gg_id:369791 Escherichia coli 0127:H6 str. E2348/69 FM180
CP000948.1 gg_id:270792 Escherichia coli substr. DH10B str. K-12 CP000
CU928158.2 gg_id:554727 Escherichia fergusonii 35469 str. ATCC 35469T CU928
AAKB02000001.1 gg_id:281891 Escherichia coli str. 53638 AAKB0
CU928163.2 gg_id:544920 Escherichia coli str. UMN026 CU928
CU928161.2 gg_id:563144 Escherichia coli str. S88 CU928
EU009185.1 gg_id:238337 Shigella dysenteriae str. FBD014 EU009
AF233451.1 gg_id:17857 Escherichia coli AF2334
EF620924.1 gg_id:255332 Escherichia coli str. SYW003 EF6209
CU928161.2 gg_id:563145 Escherichia coli str. S88 CU928
CU928164.2 gg_id:536217 Escherichia coli str. IAI39 CU928
EU470924.1 gg_id:291766 red panda feces clone RP_2aaa03c06 EU470
EU470476.1 gg_id:301376 red panda feces clone RP_1aaa02h07 EU470
FJ950549.1 gg_id:428533 Escherichia coli str. c247 FJ9505
EU472923.1 gg_id:288465 red panda feces clone RPSD_1aaa04h11 EU472
GQ025583.1 gg_id:437123 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ025
EU472692.1 gg_id:303108 red panda feces clone RPSD_1aaa01c04 EU472
GQ008742.1 gg_id:500918 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ008
EU471177.1 gg_id:302439 red panda feces clone RP_3aaa04d05 EU471
EU472680.1 gg_id:288712 red panda feces clone RPSD_1aaa01d01 EU472
EU472729.1 gg_id:290328 red panda feces clone RPSD_1aaa02g10 EU472

135.6	3487.5	4008.9	4436.7	3041.8	5473.8	3167.1	4131.9	2788.0	6185.3	2273.3
55.9	1854.6	3285.6	3660.3	1854.1	6125.2	1230.4	3374.2	1126.1	9443.6	1476.8
5267.0	5239.9	6118.3	6922.8	5163.6	9136.4	6680.8	7373.0	6072.8	12720.6	5841.9
701.6	3051.2	2963.4	3506.0	2920.6	4378.5	1378.2	2912.1	2640.6	5841.7	1480.2
5381.0	4808.2	5460.4	5400.0	4540.1	7015.7	3699.8	5008.3	3916.5	10912.3	3268.2
81.1	4004.9	4797.7	4665.2	3913.4	7447.6	3294.9	3903.5	2051.3	11312.5	1888.1
60.6	2250.0	3370.3	3172.1	2389.3	3649.7	1629.2	3111.2	2090.5	7870.2	1451.9
1180.3	2727.7	3406.1	4013.3	2161.9	4648.9	1867.2	3094.5	1565.9	9025.2	2401.8
111.5	4003.6	5081.9	5448.1	2643.2	5461.1	2238.3	5169.7	4302.3	12207.0	3461.5
60.0	1630.7	3241.1	3376.5	798.5	2136.4	1440.7	2687.8	601.3	6596.7	1317.4
1789.8	5139.4	6029.0	6535.3	3858.3	7946.1	3078.6	5643.1	4262.7	15879.2	3728.3
459.0	6191.6	7216.0	8053.8	5286.7	9010.3	4683.9	6912.1	6624.6	16700.9	4959.8
857.6	4960.2	6357.9	6987.5	4183.5	6692.5	4542.4	6007.5	3536.0	13166.7	4564.8
963.0	6040.3	7619.7	8484.0	5171.9	8561.0	4739.2	7275.0	5232.8	17217.3	5385.5
181.0	3054.0	4346.4	4741.5	2161.5	4761.6	1852.7	4048.6	1498.7	10752.5	2321.9
136.5	2171.3	3315.3	3679.0	1403.7	2991.8	1322.0	2983.8	886.6	7568.1	1729.2
913.4	6156.5	7558.1	8222.3	5102.7	9007.5	4190.3	7304.0	5410.5	18054.6	4613.9
875.9	4510.5	5650.1	6208.0	3713.8	6348.1	2993.9	5683.4	4180.0	15939.8	3119.5
767.2	3937.1	4928.1	5453.6	2748.2	5572.5	2395.6	4531.7	3268.4	13235.3	3263.9
115.0	1885.0	2781.5	3122.5	1191.8	3464.3	1093.7	2594.9	545.8	7393.8	1092.9
2159.9	5136.1	6417.2	6729.0	4017.0	7537.3	3042.6	5922.2	4778.1	15109.9	4321.2
971.3	4818.6	6396.5	7072.9	3947.4	6485.6	4369.5	5922.1	3536.6	12955.8	4430.2
72.0	3245.8	5164.3	5741.7	1434.9	4445.6	1889.4	4442.9	885.3	13610.0	2673.7
1653.9	5550.9	7145.1	7859.9	4686.4	7724.4	3925.8	6957.3	5625.6	16592.9	5362.6
931.9	5614.6	6889.1	7309.4	4951.7	7483.5	4356.3	6642.7	5691.6	14577.7	4554.3
1946.0	3742.2	5338.0	6429.8	2471.1	4507.4	3060.5	4953.5	2389.0	11690.5	4801.4
145.4	3220.4	5445.4	5932.1	1204.3	3959.1	1424.5	5054.0	1909.6	12642.7	2514.1
896.9	4590.4	5796.3	6220.1	3856.0	6501.1	3968.5	5359.2	3377.9	12715.8	3573.9
4378.2	5150.9	6426.9	7128.9	4308.0	6795.8	3590.4	6204.3	6226.7	12957.3	5343.7
835.6	5268.9	6900.1	7615.6	4303.5	6851.8	4064.8	6518.6	4618.0	15184.5	4923.4
2216.9	5210.6	6409.7	7574.6	4133.5	7218.4	3949.6	6026.5	5018.4	14815.5	5299.6
1333.0	3023.1	4242.8	4879.6	2544.8	4836.7	2011.1	4834.3	2155.2	9307.2	3035.6
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634.0	3304.9	4948.6	5406.3	3265.8	4074.1	3254.7	4736.9	2284.4	9040.3	3699.6
210.9	4826.4	6122.7	6664.6	4175.0	7105.6	3484.6	6003.8	4201.5	14316.6	3797.3
147.8	3972.1	5490.7	5689.4	3031.4	5732.8	2855.1	4919.0	3111.3	12917.5	3232.5
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580.1	4067.5	5796.5	6241.9	3160.3	5510.4	3262.5	5557.1	2803.0	11991.1	3647.5
1150.7	1917.1	2544.3	2926.2	1912.3	3396.9	1521.9	2653.3	2985.8	8013.2	1419.3
692.4	3783.6	5677.2	6561.1	2675.8	5172.3	2720.9	5194.0	3219.2	12474.2	4372.8

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5767.7	3871.7	1708.2
10551.9	9819.4	6218.8
6297.4	3808.9	2021.7
9072.6	6988.1	3704.0
9326.4	5760.7	2726.3
4120.3	3620.8	1673.6
4409.3	4588.9	2079.2
6674.7	5489.6	2555.6
3240.8	2893.9	716.1
10075.3	6760.6	3972.0
10150.4	8094.1	5067.7
7712.1	6213.2	4301.7
9921.3	7491.4	4812.1
5157.4	4290.2	1755.6
3659.9	3318.1	1407.5
10521.9	7757.0	4906.0
8029.7	5953.5	3366.8
7526.1	5634.9	3001.4
4722.3	3921.1	983.1
9664.0	7153.1	4210.2
7473.6	6305.1	4148.5
6250.4	4050.8	1317.8
9739.0	7344.3	5088.7
9212.7	7696.4	5377.8
6202.2	4584.9	2840.3
5879.0	4209.7	1346.1
7501.0	6254.2	3947.0
7605.5	7112.5	5005.0
8544.8	6764.7	4243.1
8561.1	6685.5	3983.1
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5631.6	3853.2	1498.5
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6541.5	5768.9	2517.7
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6558.0	4664.7	1995.2
6722.6	5140.6	3077.6
3880.8	3162.8	1281.6
5862.8	4776.2	2327.0

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EU768736.1 gg_id:334493 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C5 EU768
EU464663.1 gg_id:287701 African elephant feces clone AFEL_aai32g02 EU464
EU472690.1 gg_id:290223 red panda feces clone RPSD_1aaa02d03 EU472
EU471064.1 gg_id:295395 red panda feces clone RP_3aaa04f12 EU471
EU472703.1 gg_id:298606 red panda feces clone RPSD_1aaa02d11 EU472
AY319393.1 gg_id:90202 Escherichia coli str. 5.2 AY319
EU472746.1 gg_id:301855 red panda feces clone RPSD_1aaa01e12 EU472
EU472863.1 gg_id:302968 red panda feces clone RPSD_1aaa01f04 EU472
GQ047684.1 gg_id:444206 Topographical and Temporal Human Skin Microbiome skin palm clone nbw137h05c GQ047
EU465326.1 gg_id:302392 lion feces clone LI3_aah75d02 EU465
EU470870.1 gg_id:289907 red panda feces clone RP_2aaa03c09 EU470
EU471112.1 gg_id:290411 red panda feces clone RP_3aaa03e02 EU471
EU470511.1 gg_id:297780 red panda feces clone RP_1aaa01c08 EU470
DQ456289.1 gg_id:157055 pre-adolescent turkey cecum clone CFT211E11 DQ456
EU472919.1 gg_id:299707 red panda feces clone RPSD_1aaa04f02 EU472
EU470601.1 gg_id:287806 red panda feces clone RP_1aaa02c12 EU470
EU466013.1 gg_id:299794 African elephant feces clone AFEL3_aao15g12 EU466
EU464642.1 gg_id:300980 African elephant feces clone AFEL_aai32d07 EU464
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AM184252.1 gg_id:160249 Escherichia coli str. WAB1911 AM184
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EU470756.1 gg_id:294273 red panda feces clone RP_2aaa02e05 EU470
GQ047713.1 gg_id:390942 Topographical and Temporal Human Skin Microbiome skin palm clone nbw138d02c GQ047
EU472878.1 gg_id:294985 red panda feces clone RPSD_1aaa03c02 EU472
EU778391.1 gg_id:314335 Red Panda feces clone RPSD_1aaa02b11 EU778
EU472908.1 gg_id:294073 red panda feces clone RPSD_1aaa03d09 EU472
EU472772.1 gg_id:300828 red panda feces clone RPSD_1aaa04a05 EU472
EU009180.1 gg_id:242457 Shigella boydii str. FBD009 EU009
EU471213.1 gg_id:295208 red panda feces clone RP_3aaa04f02 EU471
EU470490.1 gg_id:295383 red panda feces clone RP_1aaa02e01 EU470
EU470986.1 gg_id:301184 red panda feces clone RP_2aaa04d09 EU470
X96965.1 gg_id:9662 Shigella boydii X96965
GQ025582.1 gg_id:466050 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ025
FJ949576.1 gg_id:444646 Escherichia coli str. G4 FJ9495
EU472929.1 gg_id:297711 red panda feces clone RPSD_1aaa03f07 EU472
EU472728.1 gg_id:289118 red panda feces clone RPSD_1aaa03e05 EU472
EU462402.1 gg_id:287659 Sumatran orangutan feces clone orang1_aai53h05 EU462
GQ493756.1 gg_id:537192 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
EU470610.1 gg_id:300547 red panda feces clone RP_1aaa04e06 EU470
FJ673277.1 gg_id:516144 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6732

492.1	3641.7	5705.1	6079.7	2256.8	5112.9	2289.0	5215.0	2544.5	12585.7	3565.8
84.2	2545.0	3894.3	4189.4	1422.3	2931.9	2290.8	3775.8	1317.7	9344.1	2248.4
1695.2	1909.4	2845.1	3700.2	1574.1	2846.3	1960.5	3362.9	1046.4	7226.1	2808.7
4453.1	4102.1	5000.7	5407.5	3915.8	5673.7	3334.4	4976.2	3891.2	13067.5	4003.2
170.1	3092.1	4631.2	5213.4	2546.9	5142.3	2391.0	5118.5	3254.9	9617.7	2989.4
13866.9	5191.3	5534.8	5596.4	4970.0	5671.8	5903.6	5015.6	5249.2	9063.4	5793.4
2662.3	3794.7	4959.1	4715.7	3679.0	5534.9	2980.7	4551.5	4037.1	10247.9	3904.6
237.9	3206.1	4561.8	5104.7	2626.5	4185.8	2750.4	4298.3	2474.7	10782.7	3217.5
2645.8	4470.9	4570.0	5409.8	5241.8	5964.7	5392.1	5880.7	4941.8	10586.0	4432.4
1401.6	4110.1	5226.3	6121.1	4038.6	5021.5	4238.4	5516.1	4007.6	10896.0	4684.0
10374.5	4753.6	4901.5	5424.2	4433.6	4814.1	5304.4	4762.0	6098.2	7249.9	5890.8
722.9	5074.2	6084.0	6690.4	4787.0	6992.1	4347.6	6193.3	4842.9	14201.4	4365.9
8357.6	8286.6	10881.5	12544.6	8138.3	10006.8	9852.7	8722.1	12448.3	14204.0	10293.0
21008.6	6381.3	6795.3	7570.0	5497.3	5769.0	6332.6	6275.6	7956.0	8416.7	9770.9
268.2	4395.8	5951.5	6734.4	3596.9	5993.1	3202.4	5770.9	3842.2	13131.2	4294.3
174.3	2788.3	3595.7	3561.2	2629.2	4560.7	2060.0	3523.7	2848.9	11100.7	2342.0
597.9	4889.3	6011.1	6420.8	4578.6	6069.1	3904.0	5920.4	4227.6	13624.2	4054.1
998.6	2297.1	3378.2	3598.5	2562.2	3142.5	2653.4	3232.7	1308.8	9309.4	2214.6
147.3	3018.7	4254.2	4436.1	2155.5	4663.0	2044.6	3644.1	1525.8	12441.3	2262.1
110.0	4473.8	5304.8	5248.0	4182.0	5877.1	3084.0	4782.9	5630.2	13995.2	3269.3
887.3	4539.9	5860.4	6263.3	3855.9	6251.5	4155.5	5344.8	3503.0	12563.6	3840.2
340.2	4004.9	4395.1	4203.8	2877.4	3659.6	2933.3	3888.8	2366.7	5838.2	3966.2
14860.6	5838.1	6574.1	7012.5	4870.9	4923.9	5690.8	6146.4	7399.0	10251.7	7084.2
6277.4	3570.9	3929.1	3770.2	2858.2	3813.4	3045.9	3215.6	4585.1	7870.1	5527.1
281.7	3835.4	5479.7	6068.0	2590.9	5649.4	2072.6	6003.0	3123.6	11093.0	3400.0
2784.3	2921.1	3833.9	4075.8	2454.1	4207.2	2551.8	3715.3	2400.7	9628.5	2985.0
2526.3	3452.1	4657.6	4546.8	3203.2	5081.6	2330.8	4346.6	3824.2	11054.2	3277.1
254.3	4797.5	6261.8	6935.5	4712.0	6271.0	4387.2	6110.6	4053.0	13789.4	4175.8
1387.6	4797.1	6409.5	6549.8	4052.2	7496.0	3042.9	6049.1	4318.8	13991.9	4300.6
137.0	3760.2	5581.9	6115.3	3144.4	6488.6	2433.0	5363.5	3440.9	15759.8	3291.8
609.6	5417.2	6718.9	7217.0	4365.6	7512.2	3717.2	6666.1	4996.2	15102.6	4082.1
2539.1	3774.4	4644.5	5300.6	3755.6	4565.5	5186.7	4498.7	4217.6	3596.5	4095.9
525.2	4705.5	6105.3	6427.0	3491.0	6497.5	3274.2	5779.9	3861.2	14512.2	3615.1
204.4	3470.5	4678.9	4612.6	2789.8	5354.4	2576.8	3804.6	2699.5	12214.5	2812.0
1519.6	3706.6	5973.5	6541.8	3453.1	5148.8	3691.2	5566.4	3837.2	10910.3	5256.5
254.3	4776.4	6065.5	6555.1	4275.6	6718.2	3689.1	6051.8	4171.6	14251.7	3780.8
10669.4	6037.5	7555.4	9027.0	6958.2	7084.2	7694.8	7424.2	7129.9	12224.1	10324.0
240.6	3796.6	5367.1	5876.3	3115.6	5361.0	3022.3	5141.8	3052.4	12156.6	3686.4
1209.7	3425.3	4078.9	3828.7	2956.1	4220.5	4415.0	3655.0	3411.7	8353.4	4609.6
182.6	4069.0	5750.8	6334.3	3767.9	6994.8	2991.4	5688.7	4077.0	16050.1	3378.0
657.6	4748.2	6253.4	6797.4	3495.6	6622.9	2881.4	6020.3	3798.1	14306.2	4006.2

6474.4	5144.5	2530.8
3977.9	2213.1	859.5
3302.0	3009.2	1147.9
7796.4	5746.2	4525.7
5270.8	5670.6	1920.6
5446.8	6532.1	5259.1
5677.6	5393.9	3858.4
5661.8	4308.5	2457.0
6691.8	6838.1	4606.7
5314.3	4763.2	4192.5
5239.7	6577.4	5111.4
8077.2	6407.3	4287.3
9864.1	11273.4	7428.1
6656.8	8496.0	5503.6
7578.6	5896.0	3564.0
5229.2	4148.9	2418.9
6982.3	5663.9	3539.5
3714.9	2976.2	1264.0
5929.8	3857.7	1385.4
6773.7	5445.1	2891.3
7563.8	6018.9	4076.4
3355.1	3495.9	2192.0
5933.3	8617.0	5372.9
3814.1	3735.3	2399.5
6013.0	6294.3	2792.8
5013.4	4566.3	2412.4
5792.7	5603.9	2396.1
7490.2	5557.2	3497.5
7983.1	7276.5	4398.4
7968.2	5582.6	2658.0
8457.7	6796.0	4363.2
4021.4	4907.9	4239.7
7791.3	6095.0	3410.8
6115.4	5160.5	2610.8
6117.7	5239.4	3677.3
7855.5	6149.7	3912.1
7433.2	8171.0	6349.5
6270.8	5406.4	2913.1
4871.1	5197.3	3447.3
8444.5	6045.7	3239.3
8104.7	6164.2	3398.2

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EU471172.1 gg_id:290556 red panda feces clone RP_3aaa04a10 EU471
EU458135.1 gg_id:294276 North American black bear feces clone BB2_c08 EU458
EU470636.1 gg_id:300616 red panda feces clone RP_1aaa01d05 EU470
GQ031087.1 gg_id:414691 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ031
EU471061.1 gg_id:296334 red panda feces clone RP_3aaa01c11 EU471
EU472176.1 gg_id:297981 francois langur feces clone FL_2aaa04b02 EU472
GQ069091.1 gg_id:449962 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ069
EU472840.1 gg_id:298307 red panda feces clone RPSD_1aaa02b06 EU472
EU470804.1 gg_id:298326 red panda feces clone RP_2aaa03f10 EU470
EU472779.1 gg_id:294637 red panda feces clone RPSD_1aaa01b05 EU472
EU472793.1 gg_id:288476 red panda feces clone RPSD_1aaa03g10 EU472
EU470706.1 gg_id:293949 red panda feces clone RP_1aaa04g08 EU470
EU472879.1 gg_id:303261 red panda feces clone RPSD_1aaa01b03 EU472
EU470669.1 gg_id:289152 red panda feces clone RP_1aaa03e06 EU470
EU472824.1 gg_id:292653 red panda feces clone RPSD_1aaa02c07 EU472
EU472655.1 gg_id:290927 red panda feces clone RPSD_1aaa01f11 EU472
CP000036.1 gg_id:144321 Shigella boydii str. Sb227 CP000
EU471278.1 gg_id:292133 red panda feces clone RP_3aaa01c09 EU471
GQ047978.1 gg_id:419099 Topographical and Temporal Human Skin Microbiome skin palm clone nbw139g11c1 GQ047
EU776531.1 gg_id:329008 Lion feces clone LI3_aah76c06 EU776
EU468090.1 gg_id:288116 cheetah feces clone CE2_f03_3 EU468
EU472825.1 gg_id:291515 red panda feces clone RPSD_1aaa01c06 EU472
GQ021879.1 gg_id:487789 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ021
EU472913.1 gg_id:288396 red panda feces clone RPSD_1aaa04e12 EU472
EU472700.1 gg_id:288620 red panda feces clone RPSD_1aaa03d10 EU472
EU471279.1 gg_id:292445 red panda feces clone RP_3aaa02f07 EU471
EU471202.1 gg_id:298795 red panda feces clone RP_3aaa03c11 EU471
EU472777.1 gg_id:302310 red panda feces clone RPSD_1aaa01c05 EU472
FJ678202.1 gg_id:518667 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6782
EU470927.1 gg_id:288122 red panda feces clone RP_2aaa04b12 EU470
GQ047075.1 gg_id:391950 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw GQ047
EU470902.1 gg_id:291899 red panda feces clone RP_2aaa04g09 EU470
EU771755.1 gg_id:335863 African elephant feces clone AFEL_aai32a02 EU771
EU472815.1 gg_id:292496 red panda feces clone RPSD_1aaa04a06 EU472
EU470628.1 gg_id:295268 red panda feces clone RP_1aaa03c11 EU470
EU472092.1 gg_id:291590 francois langur feces clone FL_1aaa02e10 EU472
EU467743.1 gg_id:289022 North American black bear feces clone BB1_b07 EU467
GQ047710.1 gg_id:418353 Topographical and Temporal Human Skin Microbiome skin palm clone nbw138c06c1 GQ047
DQ819115.1 gg_id:167150 mouse cecal microbiota-colonized zebrafish digestive tract clone aab26a07 DQ819
EU472848.1 gg_id:303254 red panda feces clone RPSD_1aaa02g11 EU472
EU472786.1 gg_id:297825 red panda feces clone RPSD_1aaa02b09 EU472

2136.6	2205.0	3257.1	3302.9	1305.8	2288.1	1851.2	2493.0	1770.2	4547.1	3086.4
3200.7	3192.6	3613.9	4114.5	4030.5	4402.9	4751.8	3586.3	2447.5	7306.6	3675.7
223.4	5179.0	6609.0	6888.3	4361.9	7156.1	3656.3	6382.9	4793.8	14852.7	4097.7
2697.8	3673.6	4387.0	4371.0	3099.0	4738.8	3774.9	4590.7	5698.3	6999.3	4745.0
701.4	4931.5	6104.6	6637.2	4315.0	7262.4	4240.2	5955.8	4120.9	15149.8	3347.4
179.9	4138.4	5422.5	5971.4	3111.1	5993.4	2324.8	5038.2	4078.6	14770.2	3660.5
210.3	3617.5	4786.9	4708.3	3035.1	5388.2	3148.4	3932.9	2844.0	11881.1	3029.3
599.0	4209.0	4982.0	5093.5	3926.5	6161.5	3635.6	4921.8	4125.5	13661.6	2346.8
7740.6	4574.9	4914.4	5201.1	4651.4	5714.6	4279.9	4905.3	6547.4	11977.1	5360.2
14209.5	6193.6	6229.0	6695.8	5821.1	6739.8	6146.8	5499.4	7690.2	10308.8	7872.8
6785.4	2772.7	3771.3	3664.3	2472.1	4014.0	2911.3	2824.9	2926.4	9956.2	3308.7
1841.5	3517.7	4527.6	4560.3	3157.4	5075.0	1898.9	4069.5	3354.4	11318.5	2950.3
1282.1	4477.5	5927.2	6788.7	3963.9	6573.5	3081.0	6296.5	3796.4	12645.6	4615.2
32031.9	9867.5	10447.1	11629.1	9541.3	10401.4	8776.0	9671.3	12093.2	17157.9	13593.9
212.6	776.6	1070.4	1088.3	668.2	1744.2	382.3	962.1	701.8	6046.0	962.2
922.6	2663.1	3230.3	3329.7	2778.8	3627.0	2944.9	2893.4	3983.9	8030.6	2326.6
462.5	4276.9	5717.2	5599.2	3216.9	6937.5	1952.2	5307.5	3297.6	13200.6	2831.0
691.1	4757.7	6288.4	6902.8	3388.4	6589.2	2808.6	5995.8	4336.9	14039.6	4015.7
2958.3	5904.6	6521.4	7034.8	7046.8	7312.0	7404.5	7018.4	6882.6	11143.1	6109.6
370.7	2435.2	3414.9	3726.5	2476.4	2757.4	2134.3	3397.3	2364.0	5181.9	2870.2
2850.5	5580.9	4972.2	6262.6	5183.9	5873.0	5216.7	5250.9	5421.9	11376.1	5824.7
10311.7	3587.0	4183.4	4411.9	4007.1	4245.5	3936.0	4452.0	4469.6	7792.1	6636.9
968.8	3568.1	4222.8	4696.7	3865.4	5161.8	3417.7	4380.5	2913.7	9042.6	3201.2
6314.4	2921.5	2968.6	2890.0	2773.3	2973.2	2996.2	2186.0	3148.8	5102.5	6117.9
2067.4	3561.5	5122.6	5369.2	2920.6	4597.0	2641.0	4626.3	3297.9	9973.0	4646.6
646.7	4707.2	5840.5	6179.6	3969.4	6641.9	3329.7	5755.3	4009.1	13614.4	3388.3
3744.6	5757.6	6983.2	7800.2	5683.1	8045.8	5010.5	6865.6	5215.9	14876.1	5702.7
7820.1	3014.9	3909.2	3796.9	3080.7	4300.0	2924.2	3247.3	3749.7	8573.6	4244.4
47.2	2559.6	3679.3	3675.6	2117.6	4468.6	1108.3	2960.8	2434.3	12128.1	1227.2
1262.9	3862.1	4166.3	3922.2	2810.9	3278.7	2045.0	3589.5	3717.2	11103.1	2894.7
8464.5	6254.1	6919.6	7337.2	5783.1	7077.0	4970.2	6749.6	7853.8	10440.6	6963.2
651.3	4215.6	5428.5	5721.7	3792.6	6129.0	3495.2	5405.2	3260.0	13015.7	3103.1
10900.1	5540.5	7059.3	7385.5	4003.0	5583.6	4866.9	6445.1	5671.6	12041.2	5287.6
350.2	2961.9	4726.5	5139.2	2257.6	3816.5	2432.5	4606.0	1960.1	9981.4	3346.6
146.2	3236.8	4415.1	4762.2	2773.4	4937.3	2738.6	4045.1	2257.6	11157.7	2432.7
216.8	4261.8	5855.2	6315.9	3268.0	5876.2	3022.4	5476.5	3800.7	12914.8	3992.7
19521.8	7588.0	7601.0	8220.3	7686.3	7938.7	7086.3	7051.9	10102.5	14661.0	7287.0
736.0	3930.4	4634.4	5434.8	3167.3	6395.8	1910.6	5044.8	3127.8	12998.2	2591.8
5758.5	4409.4	4484.6	4782.9	3671.6	5309.7	3199.7	4564.0	4938.1	8715.9	5041.0
6785.8	2844.6	3681.6	3639.4	2497.3	3817.4	2989.9	2885.8	3616.4	9886.6	3600.7
1955.4	4021.7	5823.0	6842.3	2987.9	5338.9	3271.5	5419.9	3539.0	12861.2	5263.5

2726.4	3762.6	1438.7
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4292.3	5595.6	3459.5
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7265.5	5533.2	2849.6
6207.4	5309.3	2597.8
7389.9	5482.1	3280.2
6174.5	5819.9	3716.9
6392.9	6527.9	5155.2
4718.4	3321.4	1909.6
5917.6	4174.6	2853.2
6699.7	6554.6	3745.4
10431.1	10844.0	8893.0
1665.9	1362.4	392.3
3362.6	3345.4	1906.1
7084.9	6614.8	3550.4
7983.7	6251.2	3413.0
6895.5	8210.9	6171.7
3125.2	2757.9	1770.2
6263.4	5861.0	5116.1
4377.2	5418.2	3524.4
5738.5	5115.1	3569.6
2780.1	2895.5	2041.2
5159.6	4916.5	2649.5
7636.0	6058.8	3608.6
8729.2	7109.1	5292.0
4561.4	4064.6	2298.2
5388.9	3915.2	1434.4
5190.9	4368.2	2394.7
7474.1	7572.4	5109.5
7332.6	5534.0	3554.0
7134.2	6260.8	3025.8
5072.3	3772.7	1608.8
6205.8	4676.4	2577.2
6538.4	5868.7	3066.4
9152.6	8192.8	6418.0
7487.8	6840.6	3286.4
4833.9	5542.7	3492.0
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EF560788.1 gg_id:233865 Escherichia coli str. BEE3 EF5607
EU471295.1 gg_id:298340 red panda feces clone RP_3aaa03g05 EU471
EU470739.1 gg_id:289190 red panda feces clone RP_2aaa02e12 EU470
EU468348.1 gg_id:293649 lion feces clone LI2_aae47f10 EU468
GQ031673.1 gg_id:403434 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ031
EU471240.1 gg_id:289442 red panda feces clone RP_3aaa03h04 EU471
EU470710.1 gg_id:290311 red panda feces clone RP_1aaa04a05 EU470
EU470675.1 gg_id:301701 red panda feces clone RP_1aaa02e06 EU470
NC_011740.1 gg_id:471437 Escherichia fergusonii str. ATCC 35469 NC_01
EU471997.1 gg_id:292359 francois langur feces clone FL_1aaa02b11 EU471
EU472874.1 gg_id:298984 red panda feces clone RPSD_1aaa03c12 EU472
EU472807.1 gg_id:293337 red panda feces clone RPSD_1aaa03c08 EU472
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EU472693.1 gg_id:293094 red panda feces clone RPSD_1aaa04d06 EU472
EF620921.1 gg_id:238636 Escherichia coli str. SYW001 EF6209
EU471242.1 gg_id:293815 red panda feces clone RP_3aaa04h04 EU471
EU471056.1 gg_id:302667 red panda feces clone RP_3aaa04h09 EU471
GQ007327.1 gg_id:502336 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ007
AF527826.1 gg_id:71573 Escherichia coli str. RREC II AF5278
EU472637.1 gg_id:296080 red panda feces clone RPSD_1aaa03f03 EU472
EU470517.1 gg_id:297922 red panda feces clone RP_1aaa02g03 EU470
EU458385.1 gg_id:291249 spotted hyena feces clone HY1_a06_1 EU458
EU472805.1 gg_id:295661 red panda feces clone RPSD_1aaa01d08 EU472
EU472917.1 gg_id:288548 red panda feces clone RPSD_1aaa03c05 EU472
GQ047930.1 gg_id:391527 Topographical and Temporal Human Skin Microbiome skin palm clone nbw139b10c GQ047
EU472662.1 gg_id:294561 red panda feces clone RPSD_1aaa04b05 EU472
EU778485.1 gg_id:305760 Red Panda feces clone RP_1aaa01h12 EU778
EU470629.1 gg_id:290610 red panda feces clone RP_1aaa01b03 EU470
NC_009800.1 gg_id:245367 Escherichia coli str. HS NC_00
FJ950548.1 gg_id:401252 Escherichia coli str. c249 FJ9505
EU470620.1 gg_id:300756 red panda feces clone RP_1aaa02h01 EU470
EU472834.1 gg_id:288233 red panda feces clone RPSD_1aaa02g06 EU472
EU471158.1 gg_id:289812 red panda feces clone RP_3aaa02c10 EU471
GU065251.1 gg_id:535199 Escherichia coli str. BDS3 GU065
X80733.1 gg_id:9684 Escherichia X80733
EU472760.1 gg_id:298347 red panda feces clone RPSD_1aaa03e07 EU472
GQ008489.1 gg_id:501176 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ008
EU471035.1 gg_id:291503 red panda feces clone RP_3aaa04d07 EU471
EU471245.1 gg_id:288664 red panda feces clone RP_3aaa03f02 EU471

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416.0	4706.2	5434.7	6607.6	4353.4	6064.7	3897.4	6106.7	5006.2	14562.8	4130.5
624.3	5057.2	6125.5	6336.5	4457.6	7314.9	3884.4	5927.4	5204.4	14854.7	3308.8
5556.4	7805.9	8869.3	9945.0	7268.0	8406.2	7894.9	8052.8	11118.7	11484.8	10259.2
608.4	5363.8	6534.5	7030.6	4030.2	7705.4	3146.5	6342.2	4339.4	15640.2	3893.7
242.3	3187.4	4724.6	5178.4	2678.8	4380.4	2646.5	4541.1	2758.8	10353.8	3453.5
205.4	5255.5	6477.3	6726.3	4591.9	7535.6	4092.7	6025.2	5230.1	14738.9	3869.5
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23075.4	8212.1	8655.3	9800.3	7965.6	8157.9	8882.0	8114.4	11028.1	12284.6	11707.4
554.6	5104.7	6497.9	7675.2	5640.3	6529.5	5363.2	6633.4	4844.3	13621.0	5356.9
95.2	2555.7	4321.2	4729.4	1140.0	3490.0	1449.7	3748.2	844.2	12105.7	2256.5
588.7	5087.0	6206.9	6679.0	4352.5	7142.3	3824.5	6101.5	4680.9	14104.2	3988.2
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7158.9	5635.2	6514.3	6199.0	4662.1	6455.9	5693.2	5453.0	9025.7	11464.4	6457.4
160.2	3314.1	5253.7	5785.1	2678.6	4670.9	2807.0	5264.8	2735.8	10651.4	3474.4
222.9	2481.3	3704.2	3992.5	1739.6	3299.4	1653.0	3321.7	1206.0	9081.7	2180.7
6365.8	5128.0	6009.4	6989.2	5012.2	5012.3	4671.7	5249.8	4821.8	8547.7	7074.1
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2060.7	3250.9	4790.1	5717.8	2527.1	4300.8	3090.1	4593.1	2963.5	11572.3	4383.8
2375.5	4550.6	6491.3	6962.2	3604.3	5985.8	3504.4	6000.3	4018.7	13201.7	5656.6
9958.9	2910.6	3583.1	3603.8	3192.5	3220.0	3440.7	2790.1	3849.4	6544.1	5849.2
3775.1	4444.6	4865.4	5141.3	4339.6	5347.4	4568.2	4726.7	4451.2	7934.0	4750.0
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63.8	1870.8	2938.9	2885.2	1513.7	3490.6	1013.9	2377.0	1836.7	9547.0	1032.8
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7192.4	8718.0	6787.4
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8348.5	7424.0	4325.2
4635.3	4005.9	2467.4
8581.4	9256.1	7496.2
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5229.0	3498.1	922.1
7892.4	6437.9	4085.2
7974.2	8083.5	7706.0
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4991.3	5538.5	2253.1
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EU471044.1 gg_id:297206 red panda feces clone RP_3aaa04h10 EU471
NZ_AAKA01000007.1 gg_id:138896 Shigella boydii str. BS512 NZ_AA
GQ047653.1 gg_id:418972 Topographical and Temporal Human Skin Microbiome skin palm clone nbw137d03c GQ047
AF527827.1 gg_id:62512 Escherichia coli str. RREC I AF527
EU472717.1 gg_id:301245 red panda feces clone RPSD_1aaa04f12 EU472
GQ156189.1 gg_id:535325 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
EU470543.1 gg_id:293816 red panda feces clone RP_1aaa01a09 EU470
EU470705.1 gg_id:298055 red panda feces clone RP_1aaa03b10 EU470
AM184231.1 gg_id:161699 Shigella boydii str. WAB1890 AM184
EU470774.1 gg_id:289364 red panda feces clone RP_2aaa04f07 EU470
EU471270.1 gg_id:289897 red panda feces clone RP_3aaa04b12 EU471
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NC_011740.1 gg_id:471438 Escherichia fergusonii str. ATCC 35469 NC_01
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GQ047656.1 gg_id:430442 Topographical and Temporal Human Skin Microbiome skin palm clone nbw137d07c GQ047
AE014073.1 gg_id:146716 Shigella flexneri 2a str. 2457T AE014
EU471257.1 gg_id:298991 red panda feces clone RP_3aaa02h04 EU471
AP009240.1 gg_id:332176 Escherichia coli str. SE11 AP009
NC_009801.1 gg_id:241154 Escherichia coli str. E24377A NC_00
AF357563.1 gg_id:73454 mpn-isolate group 15 AF357
GQ025520.1 gg_id:413814 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ025
EU472812.1 gg_id:301009 red panda feces clone RPSD_1aaa03f05 EU472
EU472915.1 gg_id:291673 red panda feces clone RPSD_1aaa02f08 EU472
GQ069064.1 gg_id:438768 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ069
EU470553.1 gg_id:302025 red panda feces clone RP_1aaa04b03 EU470
EU708318.1 gg_id:348648 Ewingella americana str. CH6 EU708
EU678359.1 gg_id:284672 Ewingella americana str. CH5 EU678
U29438.1 gg_id:10324 Ewingella americana str. NCPPB 3905 U2943
AY581130.1 gg_id:101409 Ewingella americana B791 AY581
EU196321.1 gg_id:246905 Aranicola sp. NP34 EU196
AF010251.1 gg_id:10139 Klebsiella granulomatis str. KH 22 d peripheral blood monocytes AF010
AY369139.1 gg_id:94946 Klebsiella pneumoniae AY369
GQ098970.1 gg_id:467551 Topographical and Temporal Human Skin Microbiome skin palm clone nbw504e12c1 GQ098

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120.7	3528.5	4843.7	4875.4	2389.5	5467.9	1588.7	4282.6	2054.8	12907.1	2342.5
3454.9	6623.3	7210.9	7891.5	6599.2	6979.6	7344.9	7119.7	9881.6	9973.4	8333.0
7752.7	5122.4	5280.0	5777.1	4936.1	6099.9	5059.7	4995.2	8256.2	8220.3	6510.2
215.5	4846.3	6306.7	7021.2	4584.1	6714.0	4025.9	6058.9	4090.4	13883.1	4167.5
3200.7	5012.5	5398.4	6398.8	5794.9	6658.4	5436.8	6834.7	4843.2	12067.3	6567.1
13029.8	5053.8	5734.9	5955.9	4901.5	5673.1	4716.5	4914.2	7509.6	13149.1	5437.6
6408.5	4647.2	5875.0	6344.3	3633.2	5645.4	3692.9	5321.0	4605.7	11674.9	5379.3
551.5	6307.6	8274.6	9089.2	4359.3	8130.8	4301.1	8168.8	5377.2	17230.7	5660.4
715.9	3213.0	5151.9	5867.0	2667.0	4289.6	2851.1	5274.1	2261.3	10241.1	3880.9
4206.8	5211.9	5071.3	5784.0	3837.1	5017.8	3437.6	5264.3	5399.9	8315.2	7304.5
81.5	2563.0	3661.1	3715.4	2022.1	4239.6	1791.4	3422.5	1413.3	9301.3	1635.4
155.6	2991.5	4181.4	4492.2	2419.4	4370.0	2494.1	3733.1	1797.6	12198.6	2362.5
255.1	5546.4	6726.0	7423.0	3765.1	7005.8	2965.1	7469.8	5767.3	13053.6	5008.5
171.0	2826.1	3682.1	3990.5	2731.8	4024.6	2901.3	4884.0	3593.2	8393.3	3523.2
45.1	621.1	803.5	760.4	370.6	1521.7	176.7	572.6	238.6	2558.1	354.5
176.8	2975.2	4056.4	3984.3	2086.0	5033.1	1864.8	3171.3	1543.1	11872.4	1829.8
10262.9	5458.4	6287.3	6755.8	4305.0	7706.8	3793.9	5686.3	5888.9	15045.2	5723.3
196.5	4475.2	5685.4	6178.0	3636.9	6151.2	3176.9	5285.5	4317.4	14234.9	3646.0
645.7	2803.8	3783.6	3823.0	2173.0	4487.5	1616.9	3230.5	1941.0	9566.8	1822.4
5112.9	3996.2	4017.2	4061.8	3130.5	4362.2	3292.5	3855.0	5198.6	8099.1	5545.9
370.3	3577.6	4240.7	3975.0	2225.4	4720.4	2040.1	3263.6	3563.4	11249.3	3860.8
94.9	4128.7	5181.3	5004.5	3327.3	6467.1	2147.6	5279.4	4467.2	11439.5	3106.6
5883.5	5528.8	5959.9	6420.0	7283.1	7018.4	6619.5	6338.0	5370.3	11775.6	6199.7
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781.9	4107.4	5378.6	6083.2	3265.9	6364.0	2781.3	4985.5	3950.9	16437.1	2988.2
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701.4	5818.5	5612.5	5758.4	3247.1	6639.3	2382.1	5984.9	5613.3	9579.7	3689.7
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6873.4	8153.1	6447.7
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4500.9	4700.7	1893.4
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AY830396.1 gg_id:112865 Klebsiella pneumoniae Ml AY8303
EF633996.1 gg_id:244493 Klebsiella oxytoca str. M-2 EF6339
AF390083.1 gg_id:20393 Klebsiella oxytoca str. W-6 AF3900
AJ871859.1 gg_id:113127 Klebsiella oxytoca str. SB2908 AJ8718
AB353046.1 gg_id:257803 Klebsiella oxytoca str. No.6 AB3530
FJ816026.1 gg_id:577013 Klebsiella oxytoca str. GS-4-08 FJ8160
EF633998.1 gg_id:255739 Klebsiella pneumoniae str. M-4 EF6339
GU361112.1 gg_id:515224 Klebsiella oxytoca str. SHD-1 GU361
GQ075941.1 gg_id:461429 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ075
GU119910.1 gg_id:539869 Klebsiella oxytoca str. Bx-LA-0908 GU119
GQ098941.1 gg_id:392581 Topographical and Temporal Human Skin Microbiome skin palm clone nbw504b09c1 GQ098
AF543296.1 gg_id:58286 Klebsiella oxytoca str. ChDC OS46 AF5432
AF543283.1 gg_id:58294 Klebsiella oxytoca str. ChDC OS31 AF5432
AJ871861.1 gg_id:113052 Klebsiella oxytoca str. SB73 AJ8718
AB004754.1 gg_id:10108 Klebsiella oxytoca str. JCM1665 AB0047
AF319525.3 gg_id:71572 Klebsiella oxytoca AF3195
EU554427.1 gg_id:272485 Klebsiella oxytoca str. Ag01 EU5544
AJ871862.1 gg_id:113718 Klebsiella oxytoca str. SB3037 AJ8718
AJ871860.1 gg_id:113819 Klebsiella oxytoca str. SB2942 AJ8718
CP000964.1 gg_id:355056 Klebsiella pneumoniae str. 342 CP0009
EU048272.1 gg_id:254999 Klebsiella pneumoniae str. MG09 EU0482
GQ166862.1 gg_id:585007 Klebsiella pneumoniae str. EB6-THQ GQ166
NC_011283.1 gg_id:339581 Klebsiella pneumoniae str. 342 NC_011
EU078620.1 gg_id:240372 Klebsiella pneumoniae str. HR11 EU0786
NC_011283.1 gg_id:339576 Klebsiella pneumoniae str. 342 NC_011
AB368777.1 gg_id:284985 Klebsiella pneumoniae AB3687
EU240959.1 gg_id:273616 Klebsiella pneumoniae str. YC-A42 EU2409
FJ593858.1 gg_id:514856 Klebsiella sp. str. AL060225_04 FJ5938
GQ214541.1 gg_id:554914 Klebsiella pneumoniae str. HDMB-X GQ214
EU723828.1 gg_id:306451 Klebsiella pneumoniae str. HDDMM07 EU7238
AF394537.1 gg_id:64272 Klebsiella pneumoniae str. 342 AF3945
CP001891.1 gg_id:527918 Klebsiella variicola str. -22 CP0018
FJ593855.1 gg_id:516172 Klebsiella sp. str. MNS_801a FJ5938
CP001891.1 gg_id:527914 Klebsiella variicola str. -22 CP0018
EF608176.1 gg_id:552087 Klebsiella pneumoniae str. HT24 EF6081
GQ155813.1 gg_id:559700 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
DQ185604.1 gg_id:140302 Klebsiella pneumoniae str. Ac01 DQ185
GQ156091.1 gg_id:550532 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
DQ379507.1 gg_id:153149 Klebsiella pneumoniae str. TSL-4 DQ379
GQ156048.1 gg_id:578617 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
GU594298.1 gg_id:514480 Klebsiella pneumoniae str. B16 GU594

33.0	2231.3	3730.0	3418.7	3156.8	6873.1	1600.4	2500.2	1030.3	11199.2	882.3
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2577.6	5041.3	5882.8	6522.0	5589.4	7072.3	5616.7	5875.7	5684.5	11158.9	5803.6
828.3	7237.9	8699.1	9333.3	7636.8	12058.1	5468.3	7886.3	6227.2	21179.0	5463.1
133.1	4724.9	6410.0	6735.5	5897.5	9499.5	4490.5	5679.7	2873.9	17056.3	3103.9
521.1	6016.4	7775.5	8137.9	5725.7	11200.1	3938.0	6970.6	3908.7	20297.0	4058.0
334.4	6235.3	7839.2	8291.0	6317.9	11456.9	4488.6	7028.9	4869.6	20248.7	4347.8
311.0	5909.5	7540.1	8043.2	5906.5	11261.3	4269.8	6775.2	4853.2	20140.8	4159.2
15240.1	8009.3	9235.3	9654.1	9077.3	11295.9	9427.7	7733.5	8738.7	18445.6	9234.8
623.7	6488.9	7960.3	8547.7	6345.7	11651.0	4632.8	6829.8	4900.1	20299.9	4520.8
523.3	6656.8	8612.2	8993.1	6038.3	11676.1	4193.6	8196.6	5313.8	20808.2	4948.5
37.7	3031.1	4491.2	4174.0	3779.3	7362.1	2330.8	3357.3	1361.4	14555.4	1675.8
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840.3	6680.7	8440.9	9070.6	6815.1	11722.4	5217.9	7653.3	5480.2	20202.7	4826.0
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763.7	5912.6	7670.5	7884.8	5781.9	10735.2	4922.3	7067.8	3999.3	19301.4	3953.1
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788.9	5590.5	7448.2	7973.8	4357.0	9392.2	3806.7	7268.4	5299.6	17046.5	4636.1
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156.1	4352.8	6384.8	6789.1	3147.5	8589.9	2273.6	6340.9	4565.0	16328.6	3229.0
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159.9	3613.5	5425.2	5502.6	2815.8	7427.5	1870.9	5563.2	4360.8	15073.4	2910.8
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11896.9	8710.2	6092.8
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7345.0	5953.5	2924.7
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12352.5	9382.3	6125.1
11816.0	9271.7	7683.9
8462.1	7203.3	5525.9
6301.3	5044.5	3419.0
11368.5	8732.7	6248.7
9381.4	7427.3	4028.6
9306.5	7903.6	4804.3
10856.6	9010.5	3956.8
8653.5	6963.6	3619.0
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11317.4	9020.9	5378.2
6605.9	5177.7	3048.5
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9534.3	7823.7	4630.3
7606.2	8373.9	4491.8
11063.3	10146.6	7205.5
9652.3	7462.8	4266.8
10192.6	8160.6	3806.8
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10309.9	8731.0	6566.7
6906.9	8953.1	7392.1
8066.8	6588.3	3483.6
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EU086097.1 gg_id:241026 Klebsiella pneumoniae str. HR9 EU086
EU419756.1 gg_id:258442 Klebsiella pneumoniae str. L17 EU419
GQ154831.1 gg_id:582392 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
GQ154786.1 gg_id:554543 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
EU360116.1 gg_id:578618 Klebsiella pneumoniae str. PB24 EU360
AF228920.1 gg_id:72626 Klebsiella pneumoniae str. NLEP98-0472 AF228
GU594297.1 gg_id:525542 Klebsiella pneumoniae str. A38 GU594
GQ497246.1 gg_id:568000 Klebsiella sp. str. A4-1 GQ497
GQ154902.1 gg_id:587608 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
EU661374.1 gg_id:277703 Klebsiella pneumoniae str. K8 EU661
GQ155332.1 gg_id:557261 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
Y11488.1 gg_id:136340 Klebsiella pneumoniae str. AB2844 Y11488
EU771689.1 gg_id:307981 African elephant feces clone AFEL2_aao29h01 EU771
GQ154976.1 gg_id:565044 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
GQ156442.1 gg_id:591675 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
AY292865.1 gg_id:89119 Klebsiella pneumoniae 521 AY292
AM184253.1 gg_id:161438 Klebsiella pneumoniae str. WAB1912 AM184
EU881978.1 gg_id:350702 Klebsiella pneumoniae str. HDDMN06 EU881
GQ154733.1 gg_id:588616 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
NC_012731.1 gg_id:375667 Klebsiella pneumoniae str. NTUH-K2044 NC_01
EU776082.1 gg_id:319632 Spotted hyena feces clone HY1_f06_2 EU776
GQ154886.1 gg_id:584377 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
AY905691.1 gg_id:112401 Klebsiella pneumoniae str. CICC10072 AY905
GQ155971.1 gg_id:593698 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GU374001.1 gg_id:527950 dental caries clone SRC_DSA16 GU374
EU435386.1 gg_id:265566 Klebsiella variicola str. V2 EU435
GQ155807.1 gg_id:512044 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ155715.1 gg_id:567857 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EF031070.1 gg_id:215320 Klebsiella sp. CA17 EF031
Y11487.1 gg_id:136339 Klebsiella pneumoniae str. ATCC 13883 Y11487
GQ155784.1 gg_id:534117 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
DQ835530.1 gg_id:243623 Klebsiella oxytoca str. 20 DQ835
FJ975814.1 gg_id:593892 Human gut microbiome adopts alternative state bowel transplantation ileum effluent FJ9758
AF511429.1 gg_id:73274 Klebsiella pneumoniae CCCO2 AF511
GQ155370.1 gg_id:544564 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ154739.1 gg_id:568190 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
NC_012731.1 gg_id:375666 Klebsiella pneumoniae str. NTUH-K2044 NC_01
GQ155329.1 gg_id:570828 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ154908.1 gg_id:510655 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
DQ379506.1 gg_id:151643 Klebsiella pneumoniae str. TSL-2 DQ379
AY114159.1 gg_id:63980 Klebsiella pneumoniae str. 402-2 AY114

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131.2	5989.4	7659.3	8028.3	4529.3	10405.8	2750.4	7410.7	4236.3	20026.9	4218.0
7950.0	4287.6	5975.4	6887.1	4115.5	8521.2	3617.3	5795.3	4669.1	16776.4	3580.7
7675.9	7886.2	9546.8	9463.3	6274.3	9727.6	6368.8	8361.9	7725.0	17505.9	8802.0
109.4	4185.5	6053.8	5960.7	3682.9	8769.1	4372.4	6046.4	3885.5	13879.8	2943.0
1073.7	5819.5	6989.7	7794.5	5851.2	9039.7	4633.6	7379.1	5893.6	16993.4	4480.6
837.3	5814.0	7601.3	7949.1	4782.3	9352.5	3591.3	7967.5	6396.4	18337.4	4810.9
294.4	6989.3	7465.7	8495.6	5948.7	9005.5	5755.5	8071.2	6338.7	15038.0	6443.9
6864.2	7093.2	8706.1	8962.1	6750.6	10896.6	5543.4	8765.7	6616.3	18807.0	5304.4
197.0	4672.2	7001.0	7192.6	4394.9	9250.9	4119.0	6902.8	4619.3	18998.8	3342.9
7578.1	7428.9	7534.1	8691.5	5711.0	9758.4	4469.6	7847.4	7238.6	16239.7	7058.6
1156.1	6085.4	7101.4	7798.2	7614.2	9273.7	6649.0	7174.2	4535.2	16157.4	3958.6
62.9	1625.3	4714.7	2259.7	868.8	2133.0	981.9	4029.4	679.7	5176.8	2399.7
450.8	7329.0	8990.6	10096.7	6595.2	11198.4	5602.8	8690.0	6417.0	20219.2	5740.5
232.2	7996.3	8528.8	9553.1	6462.4	10581.0	5528.4	8669.4	7297.7	18772.8	6025.8
796.5	6304.3	7839.4	8568.2	5610.8	9832.4	4019.0	8259.1	6176.5	18612.1	5240.3
727.5	5090.9	6738.6	7247.6	4599.7	9558.5	3110.2	6647.8	4633.8	18362.6	3763.0
185.6	5470.7	6825.0	7444.6	4082.1	8706.5	3094.8	6477.1	4949.7	16721.2	3907.0
7750.5	7717.8	8451.9	8887.2	7575.5	10576.3	6639.1	9312.3	8410.7	19496.1	8357.2
232.6	6407.7	8862.1	9289.7	5424.0	11628.7	4154.8	8717.0	5020.5	22230.2	4503.6
1235.2	5160.0	5771.0	5874.3	4908.4	7231.7	5849.0	6350.4	6615.5	8188.0	5648.6
161.8	7039.7	8735.2	9166.8	6283.0	11500.6	4538.6	8215.4	7046.0	20145.5	4865.4
6105.5	5597.7	6586.5	6609.8	4933.5	8264.2	4167.8	6583.1	6279.6	13425.2	6308.9
173.5	6952.6	8885.8	9032.3	5014.2	10934.0	3882.4	8185.6	5463.1	19747.9	4959.3
109.4	4653.6	6704.3	7202.6	6616.9	8579.0	3271.8	5698.0	2777.2	15001.5	2747.2
17141.9	6920.1	8343.6	9625.5	7574.1	10548.1	6627.8	8564.8	5415.3	16726.5	6230.5
784.4	8282.8	9793.2	10142.0	6851.0	11597.8	5723.2	9764.3	7444.9	21033.5	6427.0
1601.0	7512.2	8078.5	9310.6	6722.2	10175.6	5589.6	8623.1	6857.1	18842.0	7160.4
45.5	116.7	167.6	160.9	96.9	230.4	146.3	164.0	62.2	268.9	86.2
5942.3	8507.8	9785.8	10740.5	8695.7	12861.2	6672.5	9265.6	6987.7	23865.2	6473.4
1856.0	5654.2	6739.9	7802.4	5147.4	8493.8	4192.8	7840.6	6828.8	16217.7	5043.4
99.2	5495.7	7026.7	7457.1	5126.3	9982.5	3950.5	6863.1	4350.2	17295.2	3739.0
5207.6	6810.9	7457.6	7539.8	6641.5	8369.3	6470.2	7128.0	10316.1	13829.7	7828.7
190.5	4480.9	6736.7	7094.6	3766.6	9065.4	3093.9	6943.3	4645.5	18202.8	3559.9
7899.5	7907.1	9947.5	11154.6	7502.6	11891.5	6283.3	10049.9	9516.2	21796.4	8904.9
563.2	8875.8	9006.0	4830.8	4079.1	9981.1	3391.0	4851.5	8061.3	11879.4	3403.5
231.6	5016.8	6652.1	7156.8	4372.9	8680.8	3597.6	6827.9	4522.0	16788.6	3698.7
3277.8	8649.1	10176.7	11031.0	6857.7	11915.0	6100.2	10307.0	9655.1	19727.4	9509.5
3407.0	7297.8	8367.8	8599.4	5874.4	9586.7	4720.7	8924.3	8476.5	17094.2	6239.7
903.7	6308.4	7383.4	8019.2	5401.2	9370.0	3703.1	7641.3	6028.9	17406.0	4995.3
205.6	4312.6	6584.5	6895.4	3836.8	8868.4	2465.9	6626.3	4948.5	16495.2	3928.7

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10925.6	8495.2	4263.5
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9190.3	7879.0	3802.7
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12432.9	9747.8	5700.3
9848.2	7517.1	4096.9
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9776.2	8024.9	5375.1
1948.3	1688.0	648.8
11305.1	8735.1	6356.4
12281.2	9981.9	6047.2
10275.0	8572.9	6179.0
9429.4	7423.0	4515.9
9084.6	7125.9	4477.7
10434.8	10786.6	7131.8
12413.1	9778.4	5057.8
6243.5	5645.3	5153.6
11716.4	9341.6	5858.1
8336.9	7947.7	4572.9
11558.3	9654.3	5098.4
7824.2	6066.4	3718.9
10869.9	9117.8	9229.6
12702.7	10560.5	6925.7
10717.2	9537.7	7282.6
309.4	489.3	121.5
13099.0	10480.7	7220.6
8584.7	9145.6	5516.1
10173.6	8018.8	5826.6
8324.6	8916.3	6424.8
9312.2	7073.8	4361.6
12176.0	10370.0	7623.0
6017.2	5573.5	2893.4
8804.8	7241.5	4624.3
11565.6	11448.3	8122.9
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EU036754.1 gg_id:327015 Klebsiella sp. str. SA07 EU036
GQ154799.1 gg_id:540518 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
NC_012731.1 gg_id:375670 Klebsiella pneumoniae str. NTUH-K2044 NC_01
GU227150.1 gg_id:584676 Klebsiella oxytoca str. A9-2 GU227
GU193983.1 gg_id:584760 Klebsiella pneumoniae str. IITRBL3 GU193
AB072699.1 gg_id:76366 Klebsiella pneumoniae F-5-2 AB072
GQ154948.1 gg_id:578178 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
GQ155672.1 gg_id:535765 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EU352755.1 gg_id:269092 Klebsiella pneumoniae str. NK 2.bp-1 EU352
NC_012731.1 gg_id:375669 Klebsiella pneumoniae str. NTUH-K2044 NC_01
AF390084.1 gg_id:37558 Klebsiella pneumoniae str. DM-5 AF390
FJ422735.1 gg_id:367184 Klebsiella pneumoniae str. 2N3 FJ4227
FJ222552.1 gg_id:354585 Klebsiella pneumoniae str. MR-M1 FJ2225
GQ154979.1 gg_id:513309 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
GQ154789.1 gg_id:590681 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
EU661373.1 gg_id:279251 Klebsiella pneumoniae str. K11 EU661
AF453251.1 gg_id:44635 Klebsiella pneumoniae str. ASR1 AF453
GQ156110.1 gg_id:539997 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
X93214.1 gg_id:10144 Klebsiella pneumoniae str. DSM 30102 X93214
GQ154895.1 gg_id:593574 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
EF154517.1 gg_id:189557 Klebsiella sp. str. CW-D EF1545
GQ156187.1 gg_id:560253 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
DQ226215.1 gg_id:142418 Klebsiella oxytoca DR.Y14 DQ226
GQ166865.1 gg_id:583479 Klebsiella pneumoniae str. EB55-THQ GQ166
AY598354.1 gg_id:109687 Klebsiella pneumoniae str. MCM B-325 AY598
GQ154945.1 gg_id:585107 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
GQ154754.1 gg_id:575147 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
AF130981.1 gg_id:32663 Klebsiella pneumoniae str. ATCC13883 AF130
DQ444287.1 gg_id:153811 Klebsiella pneumoniae str. 2 DQ444
GQ155333.1 gg_id:558921 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
AB004752.1 gg_id:10135 Serratia liquefaciens str. JCM1245 AB004
EU333881.1 gg_id:259427 Klebsiella granulomatis str. K22-14 EU333
GU339255.1 gg_id:532790 Klebsiella pneumoniae str. EH25 GU339
GQ155711.1 gg_id:589879 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
CP001891.1 gg_id:527920 Klebsiella variicola str. -22 CP001
FJ975784.1 gg_id:564752 Human gut microbiome adopts alternative state bowel transplantation ileum effluent FJ9757
Y17668.1 gg_id:10149 Klebsiella pneumoniae str. Klebs313 Y17668
EU661378.1 gg_id:278276 Klebsiella pneumoniae str. K42 EU661
GQ154950.1 gg_id:510291 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
GQ156083.1 gg_id:588769 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
EF551363.1 gg_id:222010 Raoultella planticola str. Rs-2 EF5513

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3385.0	7770.2	9187.0	10074.4	6389.3	11655.1	4998.6	9198.5	6814.7	21920.1	6012.5
123.0	3998.1	7247.6	6223.6	3438.6	8273.3	2796.8	5588.0	4187.9	17426.4	2620.4
12459.8	6828.7	7366.9	8212.8	6936.7	9568.8	6889.5	8178.7	8739.4	15885.5	7154.0
416.2	5409.6	7539.6	7642.1	4285.5	9428.8	3717.7	7201.4	4435.0	15716.4	4488.2
983.0	8394.8	9956.4	10822.3	7086.6	11153.3	6319.2	9315.4	10305.3	18213.2	7979.8
541.6	7197.9	8569.7	9548.2	6670.0	10416.5	5117.7	8889.1	7986.4	19665.1	6104.4
2581.8	9848.8	10922.4	11797.1	8758.6	12461.1	7665.5	10959.9	10187.8	21142.9	10116.1
9552.5	8967.8	10450.2	11369.5	9384.0	11753.9	9300.6	10056.9	10450.3	20395.4	10329.5
919.2	6351.5	8759.6	9185.1	5472.2	11539.2	3859.7	8674.6	5345.7	22289.4	4683.2
172.1	6080.5	8295.9	8692.3	5155.5	11393.3	3375.3	8094.5	4769.7	22365.0	4553.8
1550.7	4821.6	7183.2	7329.5	4052.8	9322.7	2942.3	6742.3	4463.0	18579.5	3395.3
93.9	2664.2	4681.6	4402.6	2380.3	6711.3	1700.8	4399.4	2130.7	14601.3	2053.9
177.8	3932.9	5975.6	6360.5	3555.6	7595.2	2520.6	6242.8	5203.1	12814.5	3277.8
369.5	7618.1	9217.5	10272.4	6809.5	11531.4	5838.5	8668.2	6213.3	20634.7	5781.3
890.2	5850.6	8120.4	8561.1	5030.8	10483.9	3473.8	8458.2	6341.1	20262.8	4822.0
18833.3	8823.5	8677.7	9122.8	7360.8	9825.0	7666.2	8747.6	8824.6	15365.9	10108.8
1318.3	6159.2	7903.3	8396.7	6369.4	10296.8	5587.8	7295.9	5832.8	19878.2	5417.1
924.3	5273.3	7001.1	7619.3	5028.0	9082.6	3654.1	7491.2	5792.9	17749.3	4258.4
6144.8	8725.4	9374.5	9213.4	6758.6	10023.4	6853.8	8860.0	9591.1	16558.0	8532.0
122.7	197.7	288.3	290.3	193.5	304.8	149.8	365.5	194.5	705.6	128.3
6617.2	10274.0	11431.0	12229.3	9213.7	11983.7	9105.5	11172.3	9725.0	20191.6	9638.8
1063.1	7748.3	9647.3	10118.1	7503.9	11287.7	6372.4	9986.4	9198.9	19341.8	8466.8
116.5	4278.0	6529.2	6529.3	3315.1	9177.6	2548.2	5970.9	3602.6	17664.6	2815.7
768.1	5358.7	6453.3	7058.3	4696.1	9070.1	3064.0	6338.4	4484.5	16809.1	3791.4
6177.4	6934.0	7861.3	9234.8	4939.4	9996.3	4034.3	9165.8	6877.2	16777.1	5321.8
148.1	5816.5	6747.4	6561.3	3594.2	7736.6	2465.1	7594.2	4643.3	12034.4	3971.1
307.7	5721.0	6798.0	7502.4	4657.9	9880.2	3302.7	7435.7	5075.9	17913.1	4814.5
179.5	4441.6	6493.4	6473.0	3786.3	8987.7	2474.8	6217.4	3785.6	18044.4	3158.5
1224.4	7473.2	9251.8	9342.2	6019.9	11075.8	4590.3	9154.8	8395.7	20224.6	6899.5
212.0	5810.4	7146.2	7439.7	5176.2	9375.7	3739.7	7991.1	5123.3	13826.8	4673.7
16929.9	7670.0	9975.7	10791.2	6498.6	12770.9	5787.8	9720.6	8334.5	22817.3	7640.3
80.7	3829.0	6020.0	6065.6	3340.5	8567.8	2499.7	5674.3	3776.1	18494.4	2575.3
795.7	8402.9	9762.1	10315.3	6855.8	11673.1	5738.5	9817.2	7483.2	20878.9	6506.6
3098.5	4514.8	6217.2	6613.4	3033.8	7826.7	2173.8	5744.4	4912.6	13909.2	3875.5
4051.3	5025.8	6121.3	6349.2	4506.8	7331.1	3745.3	5911.6	3992.3	10954.4	3696.1
143.2	3099.4	4784.3	4848.8	3141.6	7369.7	2088.9	4877.7	2997.2	15201.0	2328.7
972.2	5743.6	7794.0	8625.4	5566.9	10752.1	4119.5	7886.6	5454.9	20491.7	4425.5
1123.8	6785.5	7951.5	8003.9	6859.7	10437.1	5579.6	8415.2	6899.9	17658.3	5121.4
94.7	2188.2	3594.3	3137.1	1618.3	4782.1	995.9	3448.6	3023.7	10466.5	1895.6
219.7	5045.0	6669.9	7117.3	4555.2	8774.0	3772.8	6913.6	3969.4	17076.5	3698.8

12487.3	9589.9	6973.9
12415.1	9906.1	6261.3
8726.3	6535.3	3081.3
9257.5	9303.1	6631.2
9392.8	8048.0	4508.4
10981.6	10619.7	7105.7
10951.6	9543.5	6368.0
12579.2	10994.9	9628.4
11997.8	10104.2	9430.3
12233.1	9632.7	5307.5
12186.7	9313.2	4894.3
9201.2	7680.4	3690.2
7054.5	5716.3	2457.1
8109.3	7533.8	3329.6
11891.9	9158.5	6564.5
10508.9	8542.7	5236.1
9619.6	9669.2	7569.1
10351.5	8207.8	6375.0
9515.1	7899.2	5096.4
9797.0	9169.6	7814.5
330.1	558.3	155.4
12575.4	11272.2	9870.3
12478.3	11271.0	7883.9
9106.1	7539.2	3711.6
8860.9	6926.3	4512.7
10641.2	9691.4	5190.8
8500.5	7145.8	3814.9
9389.1	7462.9	5166.6
9627.9	7060.4	3544.5
11327.7	9550.1	6557.8
9979.2	7726.3	5823.4
13056.0	10675.2	6590.1
8752.4	6675.3	2959.2
12698.1	10704.8	7008.0
8038.2	6864.6	3476.9
7354.4	6458.0	4796.6
7108.9	5401.8	2707.8
10368.3	8337.5	5309.9
11680.0	9413.2	6230.4
4840.6	4274.6	1955.8
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s__unclassified	6192
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s__Leclercia adecarboxylata	5803

EU128493.1 gg_id:238762 Klebsiella pneumoniae str. SWU-27 EU1284
GQ156192.1 gg_id:575548 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
NC_012731.1 gg_id:375665 Klebsiella pneumoniae str. NTUH-K2044 NC_01
GQ154748.1 gg_id:556070 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
GQ155398.1 gg_id:579246 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
DQ837568.1 gg_id:168382 Klebsiella sp. III DQ837
EU734822.1 gg_id:349243 Pseudomonas aeruginosa str. NBRAJG90 EU7348
GQ155863.1 gg_id:539970 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ155396.1 gg_id:509168 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EF091148.1 gg_id:213635 Klebsiella pneumoniae str. 99 EF0911
EF566882.1 gg_id:273896 Klebsiella pneumoniae EF5668
FJ947063.1 gg_id:512541 Klebsiella pneumoniae str. fJ1 FJ9470
GQ155406.1 gg_id:572306 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
AY660026.2 gg_id:123487 Xenorhabdus poinarii AY660
NC_012731.1 gg_id:375668 Klebsiella pneumoniae str. NTUH-K2044 NC_01
CP001891.1 gg_id:527919 Klebsiella variicola str. -22 CP0018
GQ154942.1 gg_id:575251 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
GQ155346.1 gg_id:542868 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
FJ975804.1 gg_id:548574 Human gut microbiome adopts alternative state bowel transplantation ileum effluent FJ9758
EU078621.1 gg_id:251954 Klebsiella pneumoniae str. HR16 EU078
FJ593857.1 gg_id:532313 Klebsiella sp. str. AL060224_03 FJ5938
EU360793.1 gg_id:262483 Klebsiella pneumoniae str. ECU-21 EU360
GQ155955.1 gg_id:536479 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
FJ975797.1 gg_id:593596 Human gut microbiome adopts alternative state bowel transplantation ileum effluent FJ9757
GQ155996.1 gg_id:571066 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ155800.1 gg_id:537085 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ155680.1 gg_id:590210 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ155924.1 gg_id:590080 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
NC_012731.1 gg_id:375671 Klebsiella pneumoniae str. NTUH-K2044 NC_01
GQ154887.1 gg_id:511908 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
EF127829.1 gg_id:197404 Klebsiella oxytoca str. LF-1 EF1278
GQ155740.1 gg_id:512312 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
FJ436718.1 gg_id:358763 Klebsiella pneumoniae str. FIUMS1 FJ4367
GQ155340.1 gg_id:511148 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ155822.1 gg_id:513383 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
AJ233420.1 gg_id:27939 Klebsiella pneumoniae str. DSM 30104 AJ2334
DQ223868.1 gg_id:166493 Kluyvera intermedia str. P3 DQ223
NR_028802.1 gg_id:564215 Kluyvera intermedia str. 256; ATCC 33110 NR_02
NR_028803.1 gg_id:573005 Kluyvera cryocrescens str. 12993; ATCC 33435 NR_02
AJ277978.1 gg_id:22764 Leclercia adecarboxylata str. WG 162 AJ2779
AY451327.1 gg_id:99716 Leclercia adecarboxylata str. TERIPS4040 AY4513

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101.1	3669.2	4749.8	4581.7	2952.9	6693.0	2045.1	4730.7	3323.4	13098.2	2636.7
885.8	5465.2	7543.8	8189.1	5046.0	10024.3	3796.7	7983.5	5307.6	19620.5	4485.0
2243.7	4977.4	6362.8	7089.5	5029.1	8599.7	3925.7	6852.3	7469.8	15358.1	4534.7
1046.8	4316.2	4099.2	4356.8	2881.8	5244.7	2386.8	4357.7	4481.4	9500.7	3590.0
169.6	4128.8	4424.8	5259.8	3194.7	5447.3	2613.6	4454.7	3896.9	9118.5	5610.1
6335.8	6967.5	7868.8	8519.3	6530.0	8598.3	6268.8	7196.3	6366.8	13354.8	7494.2
238.1	6862.8	8177.8	8629.9	4660.0	9524.2	3274.3	8243.8	7382.2	17400.1	5446.8
246.1	5311.6	6315.0	6493.9	4136.5	8334.8	2932.3	6329.0	4253.8	12464.8	3779.5
222.6	5661.3	6957.3	7613.4	4166.3	8606.2	2897.5	6896.8	5821.3	16246.1	4361.9
893.3	6198.8	8486.7	9005.3	5211.2	11407.8	3626.1	8556.3	5338.3	21970.5	4711.8
258.9	5700.0	7207.9	7709.8	5131.1	9375.4	4179.8	7217.4	4506.9	17827.1	4218.8
293.0	4371.6	5769.1	5277.2	3413.8	6549.8	3916.7	5387.3	4968.1	11669.7	3590.6
11380.6	6411.2	7857.3	8729.1	5227.7	10336.8	4859.2	7993.1	7750.4	17217.8	6550.3
268.8	5609.8	7638.8	8165.6	4600.8	9644.6	3602.9	7972.2	5783.1	19004.9	4479.7
1308.2	3190.9	4507.7	4987.6	3189.9	5327.7	3022.7	4646.0	3551.6	10447.0	3094.2
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3397.2	7912.5	9433.1	10236.7	6354.7	11642.2	4821.5	9560.1	7039.4	21646.4	6225.4
8236.1	7630.2	7678.1	7640.2	6507.9	9177.2	6804.8	7629.2	9280.4	10812.0	7833.4
232.0	5030.6	7066.7	7429.7	4285.2	9567.9	2780.1	7004.1	4331.7	18888.3	3802.2
376.4	6703.3	7649.3	8640.5	5445.5	9766.3	5551.5	7886.6	6243.1	18760.7	5140.4
105.0	3988.9	5393.2	5114.5	3988.4	7692.1	2782.4	5006.2	2830.3	15975.3	2827.2
297.4	2718.3	3284.2	3621.6	1927.5	4645.1	1699.6	3953.9	2864.7	8596.4	2104.6
189.3	6796.8	7907.4	8776.1	4053.7	10113.8	3006.3	7864.7	5908.1	17244.3	5293.8
2936.1	8036.3	9127.3	9413.0	6918.3	10831.0	6314.2	8541.4	9420.1	16664.0	7633.4
16461.7	8871.6	9346.0	9898.2	6942.3	10864.3	6648.6	9707.9	11872.2	18438.2	10340.5
1557.3	6229.3	7263.8	7062.4	5362.2	7922.4	4477.2	6837.6	5823.0	14216.6	6213.1
184.3	6465.6	7736.6	8193.2	4320.1	9443.6	3238.1	7692.9	6503.2	17513.5	5041.2
170.4	5285.3	7240.9	7657.1	4869.4	10570.8	3184.9	7179.4	4836.0	21203.5	3991.2
1126.8	4295.9	4061.7	4297.8	3307.8	5363.7	2226.7	4335.5	2981.3	9190.9	2733.0
47.3	5582.6	7816.7	7904.0	5036.5	11065.0	3556.7	7252.7	3985.5	20460.6	3892.8
1328.1	6424.2	7861.5	8621.3	6421.6	9992.6	5222.9	7811.9	6566.4	19368.5	5848.4
833.9	6182.1	7963.9	8573.8	5113.4	10983.4	3483.9	7941.9	4956.2	21217.7	4516.2
1258.7	7227.5	8871.3	9430.8	6817.1	11199.2	5501.4	8635.9	6641.8	21475.5	6269.1
48.4	4578.9	5921.0	5655.3	3696.0	8124.1	2817.8	5384.6	3528.5	15774.9	2652.5
686.6	4134.5	6210.7	6526.4	3852.6	9236.2	2673.6	6000.9	3760.1	18088.8	2964.5
167.4	3400.4	5050.7	5307.3	3535.0	8782.6	2654.0	5059.5	4930.6	15231.1	2624.8
659.2	5498.9	7378.5	7772.3	6098.9	9799.7	5025.0	7594.7	5531.3	17986.1	5707.6
160.3	2425.2	3941.7	4903.7	1960.1	7238.4	1749.6	4216.7	3763.3	13768.5	2819.0
3874.0	6049.3	7718.5	8405.2	6296.3	11943.9	4546.7	6635.2	4468.0	21991.2	4685.5
185.9	6352.1	7432.8	8169.9	5744.9	11928.3	3853.0	6530.6	4406.5	21310.9	3876.5

9769.0	7908.4	4795.3
6806.0	5428.1	2995.6
10144.2	8203.2	5350.9
8942.8	7341.6	3980.6
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4698.5	4909.3	2747.4
8511.1	9542.3	6292.0
10179.3	8787.3	5376.6
8525.1	8980.7	4597.2
9035.6	7484.8	4687.9
11992.5	9515.9	5159.1
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10108.8	9313.4	7448.8
12730.2	10409.3	6150.4
8193.3	9661.9	7550.0
9647.7	7884.2	4187.6
10399.6	7910.8	6086.0
7720.6	6044.5	2996.6
4431.5	6038.9	2162.2
10536.4	8662.1	4966.7
10638.5	10828.5	7106.9
10036.8	10364.9	7160.0
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11475.8	9154.6	7022.6
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10031.3	8168.9	4479.7
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AJ853891.1 gg_id:108534 Enterobacter ludwigii str. EN-119 = DSMZ 16688 AJ8538
AF157695.1 gg_id:10087 Enterobacter cloacae str. drh3 AF1576
AY335552.1 gg_id:137221 Pantoea agglomerans str. CBNU-14-1 AY3355
AJ232240.1 gg_id:10085 isolate: SS-Unknown-1129 clone AJ2322
FJ592988.1 gg_id:432552 Pantoea agglomerans str. SB-2 FJ5929
EU302838.1 gg_id:247855 Pantoea sp. str. DAP13 EU3028
AJ276393.1 gg_id:71494 Leclercia adecarboxylata str. LBV 449 AJ2763
DQ011248.1 gg_id:136462 genes Da Qing Oil field microbial indicates presence variety sulfate-reducing fermen DQ011
AM184263.1 gg_id:161505 Pantoea agglomerans str. WAB1924 AM184
FJ587505.1 gg_id:586247 Pantoea sp. str. C-4-1 FJ5875
FJ593002.1 gg_id:447010 Pantoea agglomerans str. ST-1 FJ5930
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FN555402.1 gg_id:509744 Pantoea sp. I-Bh20-21 FN5554
FM210031.1 gg_id:334606 Enterobacter cancerogenus str. T2P18 FM210
EF428996.1 gg_id:208785 Pantoea agglomerans str. GIST-CPs1 EF4289
AY691545.1 gg_id:103577 Pantoea agglomerans str. ChDC YP3 AY6915
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EU590682.1 gg_id:258931 Pantoea agglomerans str. BH-18 EU5906
AM184264.1 gg_id:161559 Pantoea agglomerans str. WAB1925 AM184
AB004691.1 gg_id:10075 Pantoea agglomerans str. JCM1236 AB0046
AY488028.1 gg_id:99221 Enterobacter sp. str. BL-2 AY4880
EU557027.1 gg_id:266569 Enterobacter ludwigii str. KU201-3 EU5570
GQ070505.1 gg_id:376025 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw. GQ070
EF011164.1 gg_id:192215 Enterobacter hormaechei str. PT4 EF0111
DQ011253.1 gg_id:132962 stratum sewage clone 6 DQ011
EU302840.1 gg_id:257817 Pantoea sp. str. DAP15 EU3028
FM210030.1 gg_id:306906 Enterobacter cancerogenus str. R27c FM210
EF429005.1 gg_id:211593 Pantoea agglomerans str. GIST-Out2 EF4290
GQ374474.1 gg_id:533493 Pantoea agglomerans str. GS2 GQ374
AY792266.1 gg_id:123510 Humic Lake clone CrystalBog5A11 AY7922
AM184254.1 gg_id:160936 Pantoea agglomerans str. WAB1913 AM184
AM184266.1 gg_id:161444 Pantoea agglomerans str. WAB1927 AM184
EU884395.1 gg_id:368993 Enterobacter cloacae str. XA-2 EU8843
GQ478022.1 gg_id:570352 Enterobacter cloacae str. ham3 GQ478
EU164545.1 gg_id:239199 Enterobacter hormaechei 4 EU1645
AY900169.1 gg_id:142410 Pantoea agglomerans str. PCA0067 AY9001
AF199029.1 gg_id:27763 Pantoea agglomerans str. SP1 AF1990
GQ284566.1 gg_id:547400 Enterobacter ludwigii str. AR1.22 GQ284

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1077.6	5804.1	7126.5	7677.4	5945.6	11221.6	4026.9	6279.5	4223.8	21740.3	4213.5
178.6	4484.8	5755.5	5920.5	4652.9	8939.7	2905.5	4873.2	2870.2	18754.9	2599.5
217.0	4840.9	5576.0	5534.7	5121.1	6572.5	3358.2	5262.2	4953.7	11658.9	6933.7
6648.3	7772.3	8537.7	8379.9	6659.5	12683.8	5943.5	7685.5	7619.7	16823.1	6529.5
2516.3	5829.8	6929.5	7441.1	5627.8	10763.3	3513.9	5978.0	4173.2	20759.6	3716.5
220.3	5578.6	6753.0	7308.3	5224.4	10682.6	4802.8	5985.7	4857.8	20541.5	4559.8
10667.6	6924.2	8547.3	9307.5	7520.7	12304.6	5661.3	7336.1	5878.8	21930.2	5534.0
607.9	3692.4	4754.3	4345.2	3912.0	7144.4	3156.9	4607.2	2651.3	15117.1	2108.3
1154.2	6904.3	8541.5	9027.5	6897.3	11434.0	4925.3	7573.4	5375.3	21854.1	4648.2
186.7	4900.6	6529.7	6608.2	5068.1	9686.5	3401.9	5853.2	3239.9	19625.9	3142.6
808.4	5796.3	7245.7	7669.8	5884.9	11125.2	4013.7	5912.1	4006.7	21632.8	3482.5
4642.0	7143.7	8794.9	8873.4	7085.5	9734.5	7761.4	9120.8	8812.8	17469.6	6884.7
201.0	5518.6	7292.2	7329.9	5695.0	10807.1	4175.1	5954.2	3470.5	21498.4	3321.0
218.8	4385.8	5569.3	5958.3	4616.5	9272.0	2598.5	4498.3	2707.1	19557.5	2438.7
4490.3	6799.2	8116.1	8706.0	7336.7	11761.0	4972.6	7120.3	5926.7	22045.5	5298.1
416.5	4457.4	5565.8	5796.5	4762.5	7353.7	3123.9	6114.0	4767.1	12804.8	3714.7
1032.1	5088.2	6817.9	7068.8	5482.6	10820.1	3586.0	5493.5	3281.4	21277.4	3154.1
519.5	3206.3	4073.1	4090.2	4311.0	4622.7	3780.5	3538.2	3145.3	6806.3	2161.3
1006.4	5510.7	6825.5	7444.4	5835.8	11029.8	3891.6	5934.5	4129.4	21261.1	3997.3
6910.4	6033.5	7640.2	8453.2	5897.8	10976.2	3574.2	6392.6	5598.4	21045.1	4453.0
293.7	5616.0	7912.0	8069.5	5886.8	11475.1	3813.3	6140.3	3347.7	22125.0	3328.7
346.0	4795.4	6074.0	5931.4	5700.9	7668.2	3145.8	5052.3	3444.1	14325.0	4729.8
8959.5	7625.5	9370.4	9263.4	7587.1	11769.6	7150.3	9272.7	7055.9	21402.1	7974.6
450.6	3709.0	5096.0	5358.2	4099.8	7895.0	2045.3	4475.8	3634.2	13822.6	2682.6
3881.9	5460.4	7072.7	7688.9	5988.2	11173.3	4252.5	6130.3	4049.8	20927.6	4097.3
18097.2	6549.2	8278.7	9007.9	7289.7	9478.1	7413.9	8561.3	7717.8	14093.8	8578.8
776.6	6192.0	7852.1	8083.3	6374.1	11712.7	5027.8	6842.5	4202.4	22208.3	4191.7
113.9	3412.3	4461.2	4628.5	3195.0	7389.7	1886.9	4139.7	3146.4	14179.2	2301.3
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72.1	2403.1	3332.3	3216.5	2432.5	3935.6	2224.5	3659.2	1539.3	7691.4	1528.8
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3609.4	6056.2	8110.2	8141.5	6396.5	11379.3	5071.3	6972.7	4251.7	22065.7	4296.0
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7076.7	5616.8	2425.8
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s__Pantoea oleae	4993
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s__unclassified	4410
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AY691544.1 gg_id:103441 Pantoea agglomerans str. ChDC YP2 AY6915
DQ011254.1 gg_id:136479 genes Da Qing Oil field microbial indicates presence variety sulfate-reducing fermen DQ011
GQ374471.1 gg_id:570229 Pantoea agglomerans str. XJ1 GQ374
GQ856082.1 gg_id:556086 Leclercia adecarboxylata str. LMG 2803 GQ856
EF446899.1 gg_id:205646 Pantoea agglomerans str. AT2 EF4468
DQ392984.1 gg_id:156431 Pantoea agglomerans str. e DQ392
GU166185.1 gg_id:558052 intestinal tract larvae (Musca domestica) direct cloning and sequencing genes whea GU166
DQ358125.1 gg_id:163102 Morganella morganii str. AP28 DQ358
AB089243.1 gg_id:83678 Morganella morganii str. JCM1672 AB089
AY043168.1 gg_id:40697 Morganella morganii AY0431
DQ358138.1 gg_id:162198 Morganella psychrotolerans str. U2/6 DQ358
AB099401.1 gg_id:85614 Proteus vulgaris str. AU34 AB0994
AY792272.1 gg_id:121180 Humic Lake clone CrystalBog1F6 AY7922
AY616166.1 gg_id:104851 Pantoea agglomerans str. TJA 98.VII.6 AY6161
GU338400.1 gg_id:544871 Pantoea ananatis str. E-1-4 GU338
DQ068767.1 gg_id:168031 Pantoea sp. str. Co9945 DQ068
EF688011.1 gg_id:330341 Pantoea deleyii str. LMG 24200 EF6880
AY530796.1 gg_id:104588 Pantoea ananatis str. PA 4 AY5307
AY924374.1 gg_id:114198 Pantoea agglomerans str. Sc-1 AY9243
AY741162.1 gg_id:163464 Pantoea agglomerans str. S33 AY7411
EU072497.1 gg_id:239619 pentatomid symbionts host gut clone Cs1 EU0724
AY898642.1 gg_id:112237 Pantoea ananatis str. BD 435 AY8986
GQ332198.1 gg_id:534397 Pantoea ananatis str. M408 GQ332
AB033602.1 gg_id:9868 Pantoea agglomerans AB0336
GQ383918.1 gg_id:592050 Pantoea ananatis str. 4CBJ1 GQ383
FJ611846.1 gg_id:509337 Pantoea ananatis str. LMG 2676 FJ6118
GU324264.1 gg_id:591038 Pantoea ananatis str. M471 GU324
EF602556.1 gg_id:228308 Pantoea ananatis str. ESS29 EF6025
FJ611812.1 gg_id:585566 Pantoea ananatis str. ATCC 27995 FJ6118
FJ611861.1 gg_id:589121 Pantoea oleae str. CFBP 6632 FJ6118
DQ129257.1 gg_id:152527 microarray level air two cities Texas urban aerosol clone AKIW987 DQ129
AF130949.1 gg_id:9937 Pantoea agglomerans str. A87 AF1309
AF130918.1 gg_id:9921 Pantoea agglomerans str. new*47con AF1309
DQ365569.1 gg_id:148250 Pantoea ananatis str. JA04 DQ365
EU849107.1 gg_id:351329 Pantoea agglomerans str. PSB-UJ2-21 EU8491
AF130917.1 gg_id:9920 Pantoea agglomerans str. A46 AF1309
FJ611831.1 gg_id:537318 Pantoea agglomerans str. P9QLB FJ6118
AY941838.1 gg_id:114491 Pantoea agglomerans str. XW123 AY9418
EF516970.1 gg_id:218720 grassland soil clone FCPS402 EF5169
AF130932.1 gg_id:9887 Pantoea agglomerans str. A62 AF1309
GQ367483.1 gg_id:557905 Pantoea sp. str. A18/07 GQ367

806.2	3817.8	5161.0	5759.6	4192.1	7871.4	2592.7	4313.5	3145.7	14393.3	2862.5
6063.9	6107.8	6892.1	6997.7	5372.6	9085.2	4984.2	6677.7	6033.3	16365.5	5315.6
185.2	5013.8	6502.1	6588.5	4991.4	9475.8	3475.2	5395.2	3174.3	18906.4	2984.0
4168.3	6302.7	7892.3	8619.0	6633.6	12085.2	4974.0	6897.9	4615.6	22006.8	4794.5
792.4	7110.3	8900.7	9375.7	6758.3	11912.6	6226.3	8372.0	5534.7	21583.0	5231.0
963.9	5046.4	5949.8	6363.2	5655.9	6720.2	5431.6	5626.1	4551.1	11433.0	4404.1
3510.5	3408.9	3385.8	3598.0	1905.9	3601.6	2214.3	3944.3	4590.7	5660.1	3868.1
755.2	3195.7	3456.5	3453.3	2790.5	4449.3	2534.1	4259.2	3146.0	4465.0	2215.7
4531.6	5540.2	5353.0	5081.2	4740.8	5567.2	4781.0	5129.3	6156.2	6665.4	5160.1
24420.0	10308.4	8350.8	7079.2	8554.7	9360.8	8795.3	7641.0	11293.7	9247.0	9431.2
93.1	3538.9	4483.6	5250.9	1819.8	5645.1	1611.0	5101.4	4118.3	7884.2	3106.0
48.5	1035.7	843.8	653.4	273.1	1206.4	430.2	957.2	1081.8	1548.3	279.5
70.2	5265.8	6772.4	6915.4	4002.8	9991.7	3175.1	6258.4	3974.2	16976.5	3046.3
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6836.5	6287.0	7689.5	8966.7	6557.3	9007.1	6499.6	8023.6	6937.7	11479.7	5200.0
1468.5	4697.3	5513.6	5942.6	4345.2	9846.8	3562.7	4661.3	3445.3	11569.7	2777.4
4799.7	8256.2	8657.8	9694.8	9815.5	11523.5	8120.7	9898.8	11987.5	15902.1	8951.8
1185.1	5597.9	6538.7	6758.7	5516.1	10095.9	4798.3	6579.4	4742.5	13975.8	4527.2
2731.5	6243.5	7127.9	7862.9	8249.1	9877.6	6374.1	7286.1	4567.4	14164.1	4427.8
1119.1	3361.1	3510.2	3812.1	3077.0	6239.6	2645.8	3212.6	2380.5	6125.1	2120.0
25151.1	9900.8	9656.5	11233.3	11086.1	12437.6	12033.2	10177.6	11375.5	15138.9	12860.3
2509.5	4951.0	6062.6	6653.8	4683.0	9266.8	3522.4	5448.3	3798.0	12751.1	3676.1
1652.3	1401.2	1881.0	1913.3	1160.2	3150.1	1108.8	1737.7	1219.8	5006.9	910.1
6009.4	6528.1	7190.9	8466.3	7274.6	10652.8	7589.6	7890.4	6612.2	15015.2	6649.1
423.6	3391.0	4944.7	4700.0	2827.0	8879.5	2337.8	3496.8	1536.5	11024.7	1461.2
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37184.6	8639.0	9671.4	10443.8	11642.1	11840.6	12464.8	10974.4	11390.2	16806.1	11579.6
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211.3	3807.2	4061.9	4144.7	3356.8	4530.3	3514.7	4388.2	2851.2	6557.3	1847.1
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1208.4	5062.8	5838.3	6629.5	5416.7	7337.8	4715.0	7386.4	5688.3	11439.4	4162.0
3059.3	6286.9	7248.1	8269.5	5947.0	11614.0	5143.1	7439.1	5259.1	18998.1	4341.8
465.9	5741.5	6569.9	7297.3	5319.0	11223.4	4333.8	6725.6	5006.0	16717.1	4743.4
401.8	4044.0	5736.5	5705.6	3143.7	8841.9	2590.1	6413.8	3423.8	11270.2	2898.1
678.0	4694.9	5919.1	6400.3	4053.1	9339.8	2946.0	6273.5	3412.7	15280.8	3221.4
1031.5	4908.9	6269.1	6260.5	5140.5	9984.7	4619.2	5025.9	3517.4	13068.2	3025.3
8021.4	5027.2	5346.2	6424.0	5143.7	6884.9	5064.9	5877.7	5578.9	8356.5	5117.5
34.6	11.8	83.1	17.5	10.9	65.6	18.2	14.6	10.1	31.5	12.4
4313.7	5706.6	6657.1	7170.0	5799.7	10636.5	5167.0	7311.0	5705.1	14998.6	4844.0
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7613.4	5223.0	3508.8
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9436.8	6632.4	3522.8
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6997.3	6433.8	4751.4
4188.6	4745.8	3448.8
5179.4	5174.2	5042.9
5319.6	6314.0	5054.8
7686.8	8445.9	7227.3
6123.6	5913.0	3532.7
1457.9	1270.4	331.5
12904.5	9023.5	3791.3
11651.1	8922.1	6493.9
13590.7	7491.8	2753.9
10113.0	9677.8	6989.7
13218.2	8537.2	4238.7
12758.1	10081.0	7564.5
13031.2	8909.5	4644.5
14395.5	9547.6	6465.6
7593.9	5821.7	3106.6
14382.3	12501.3	10752.2
12389.1	8108.2	4719.8
3329.1	3333.8	1404.3
13902.9	10062.2	7377.2
13847.7	7575.6	2567.1
13323.0	7627.7	3867.6
14760.8	13151.6	10865.1
13271.8	7752.4	3928.3
4784.9	4516.6	2541.0
532.6	941.2	167.4
9510.8	7460.4	4432.2
13134.0	9219.4	5768.4
13548.4	9245.4	5117.0
12245.7	8644.5	3477.3
10943.0	7464.9	3504.8
12975.6	8017.9	3722.7
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13024.1	9203.2	5425.1
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g__Pantoea
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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	AF1309
AF130929.1 gg_id:9926 Pantoea agglomerans str. A59	AF1309
DQ065752.1 gg_id:132248 Pantoea agglomerans str. I10	DQ065
FJ999930.1 gg_id:560342 Pantoea agglomerans str. EQH1	FJ9999
AF130940.1 gg_id:9931 Pantoea agglomerans str. A72	AF1309
AF130931.1 gg_id:9927 Pantoea agglomerans str. A61	AF1309
AF130899.1 gg_id:9913 Pantoea agglomerans str. A21	AF1308
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AF130961.1 gg_id:9897 Pantoea agglomerans str. A9	AF1309
AY092079.1 gg_id:67501 Pantoea agglomerans str. 732	AY0920
AF130930.1 gg_id:9886 Pantoea agglomerans str. A60	AF1309
EF050809.1 gg_id:175147 Pantoea agglomerans str. PGHL10	EF0508
FJ611807.1 gg_id:563259 Pantoea agglomerans str. ACW 55802	FJ6118
AF130943.1 gg_id:9892 Pantoea agglomerans str. A77	AF1309
FJ592987.1 gg_id:433061 Pantoea agglomerans str. SB-1	FJ5929
AY679762.1 gg_id:102249 USA: Hawaii clone Nv5.2	AY6797
AJ251466.1 gg_id:73786 Pantoea agglomerans str. NCTC9381T	AJ2514
AM234150.1 gg_id:153891 Pantoea agglomerans str. IZSPGC	AM234
U80202.1 gg_id:9906 Pantoea agglomerans str. ATCC 33243	U80202
AF130905.1 gg_id:9914 Pantoea agglomerans str. A27	AF1309
AF130939.1 gg_id:9891 Pantoea agglomerans str. A71	AF1309
AM293681.1 gg_id:256894 Pantoea agglomerans str. PTA-AF2	AM293
FJ611835.1 gg_id:564421 Pantoea agglomerans str. LMG 2595	FJ6118
EU379306.1 gg_id:266034 Pantoea agglomerans str. 6R-J-7b	EU3793
AF130926.1 gg_id:9924 Pantoea agglomerans str. A56	AF1309
GQ169378.1 gg_id:537971 Pantoea eucalypti str. IEXa	GQ169
FJ999950.1 gg_id:561323 Pantoea agglomerans str. EQH21	FJ9999
AF130935.1 gg_id:9890 Pantoea agglomerans str. A67	AF1309
FM202484.1 gg_id:345858 Pantoea agglomerans str. EV2	FM202
AF130933.1 gg_id:9888 Pantoea agglomerans str. A63	AF1309
EU598802.1 gg_id:267618 Pantoea agglomerans	EU5988
GQ225111.1 gg_id:584259 Pantoea agglomerans str. NBRISRM	GQ225
AF130942.1 gg_id:9933 Pantoea agglomerans str. A74	AF1309
GQ130025.1 gg_id:463204 Genetic inventory 'JPL-SAF' during MSL mission spacecraft assembly clean room floc	GQ130
AM184091.1 gg_id:155126 Pantoea agglomerans str. 45	AM184
FM202485.1 gg_id:322033 Pantoea agglomerans str. EV3	FM202
NC_004547.2 gg_id:471486 Pectobacterium atrosepticum str. SCRI1043	NC_004
NC_004547.2 gg_id:471485 Pectobacterium atrosepticum str. SCRI1043	NC_004
EF530546.1 gg_id:221979 Pectobacterium wasabiae str. NZEC8974	EF5305
EF178667.1 gg_id:178973 Pectobacterium wasabiae str. NZEC12	EF1786
EF178665.1 gg_id:193423 Pectobacterium wasabiae str. NZEC9	EF1786

4323.8	5733.0	7097.1	7392.4	6477.3	10364.2	6512.7	6427.1	4887.9	13745.7	4665.0
3704.7	5374.7	6130.4	6738.1	5231.8	10630.4	4678.0	7029.9	5435.9	14440.2	4889.8
58.9	2781.7	4021.9	3682.8	2484.4	6758.2	1962.2	3011.6	1087.8	10491.0	1011.3
392.5	4162.5	5042.9	4980.2	3281.6	6849.5	3807.7	4007.0	3511.9	10813.1	3023.0
4266.1	5331.6	6076.6	6684.2	4898.3	9996.4	4624.1	6627.6	4954.7	14218.6	4324.9
24090.7	6997.5	6995.3	7949.0	8125.5	10064.1	8194.2	9740.2	8100.1	13058.5	8930.3
4690.8	6756.9	7571.7	8254.0	6816.9	11300.7	7042.8	7974.8	5824.4	14158.1	6251.1
157.0	4301.2	6185.2	6048.7	3248.9	6974.4	3270.5	6286.7	5124.5	11414.2	3747.7
2526.9	4310.2	5488.4	5720.2	3814.6	9281.0	4096.4	5425.5	3185.2	12137.8	3152.7
472.6	4965.4	5859.9	6195.2	4519.7	9675.6	3274.7	6003.0	4626.7	14800.1	3339.5
3326.9	5190.4	6328.8	6546.1	5508.9	9794.0	5420.3	6650.9	4653.9	13206.3	4584.1
83.0	11671.8	10653.1	10249.6	10565.8	14281.5	9947.4	10204.4	16154.7	17370.4	11535.7
47.1	3583.4	3736.7	4019.5	3157.6	5452.1	3439.1	4485.0	2650.7	6095.2	2286.5
1011.9	3998.5	5230.3	5320.6	3807.3	9218.2	2735.0	5135.1	2838.6	12928.1	2446.9
1095.8	4429.6	5988.9	5855.8	4617.7	9762.1	3789.8	4635.5	2914.0	12771.7	2424.2
33.6	1245.1	1897.8	2237.0	1172.5	2935.5	1047.7	1770.3	1155.5	4689.1	1086.7
3601.3	6638.4	7217.9	7933.3	8374.1	10672.1	6922.2	7478.2	5429.2	13539.1	5215.0
4189.0	3946.4	4349.1	4988.9	3652.7	7151.9	2762.8	6144.8	4825.8	11177.8	4215.5
5433.5	7449.8	8103.7	8514.0	7027.1	11674.5	6816.6	7902.0	7845.2	17210.7	7009.5
4081.4	4753.5	5416.5	5993.2	4839.7	9509.0	4806.4	5462.3	3987.1	10759.8	3923.5
3287.5	5590.7	6805.6	7063.0	5942.5	10372.3	5869.4	6229.7	4610.9	13600.0	4210.6
4684.7	6414.4	7057.5	7847.8	6384.8	10733.9	6364.5	7821.9	6032.1	13791.4	6032.5
1093.9	4693.2	6470.5	6159.6	4812.0	10060.1	3897.3	4837.9	3045.9	13568.1	2550.0
67.6	2989.2	4148.9	4010.9	3154.7	7206.0	2475.8	3983.7	2795.1	9208.4	1428.9
2086.7	4272.3	5194.9	5654.8	4016.7	9119.3	3018.8	5287.6	3978.8	13681.2	3158.2
79.3	4299.8	4705.7	4902.9	5390.6	8592.9	4899.2	4604.7	3717.7	8225.5	1945.3
22169.1	8277.9	7388.1	8425.9	7606.7	9715.2	8044.8	8273.3	11796.5	15436.9	7810.0
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1089.9	6162.2	6594.5	7201.5	5815.6	10412.8	5186.2	6095.8	5490.8	12791.8	3955.7
3990.0	4938.4	5974.1	6242.6	5096.5	9816.3	4619.6	6945.9	4905.8	13341.1	4589.8
3619.9	7134.3	7877.3	8809.1	6761.6	11856.6	6560.4	8411.2	7434.1	15636.2	6135.6
4436.2	5961.7	7202.9	7400.8	5973.5	9586.4	7333.3	8268.9	6287.4	14115.2	7383.7
15960.6	8984.7	9690.1	10657.8	9232.9	12471.5	8635.5	10440.3	11551.1	20428.5	10602.8
4850.1	3992.0	5428.9	4734.2	2711.9	8024.5	3282.0	3907.2	3033.2	12767.5	2457.5
9336.8	7554.6	8245.2	8934.6	8749.8	10298.5	8527.2	8309.0	8535.8	12143.8	10963.7
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96.3	2118.8	2629.3	2445.8	2456.5	3323.4	1770.5	3280.6	1679.6	4340.5	1393.7
981.2	3746.9	4753.3	5439.1	3846.6	6013.8	2711.7	4933.6	2902.4	8395.4	2763.2
167.3	3467.2	5632.3	5218.0	3582.5	6749.3	2182.4	5927.6	4455.5	11457.3	3091.1
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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
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EU136627.1 gg_id:238203 Photorhabdus sp. 3240
FJ006729.1 gg_id:356553 Photorhabdus luminescens str. SRK8
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Z76740.1 gg_id:10217 Photorhabdus luminescens str. Tn-5*2
FJ006727.1 gg_id:307512 Photorhabdus luminescens str. SRK6
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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
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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

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DQ885
DQ885

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2219.0	6107.4	8399.0	8870.6	4909.9	9770.5	4199.2	8694.1	5896.3	16489.8	5321.5
791.3	2884.1	4671.4	4909.6	1576.7	5142.9	1383.1	4465.2	3048.9	7497.7	2436.2
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996.5	4958.8	6338.2	6975.0	3068.2	8030.2	2367.2	6394.5	3529.0	10861.3	3626.3
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50.6	1807.3	1831.5	1780.3	935.9	2969.2	670.9	2187.9	1605.6	3908.1	1224.7
10730.9	4522.4	4220.9	2581.8	3198.9	4084.3	3783.7	3842.6	5150.7	5468.1	7014.5
9477.6	4267.4	4404.8	5793.7	4318.9	5226.8	5329.9	4912.3	4649.2	8351.4	4463.2
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580.5	1738.3	2268.8	2382.2	1291.6	2997.1	975.1	2756.5	2428.0	4232.1	1395.3
3013.7	4874.1	5271.1	5830.4	6944.2	6936.1	5546.6	5229.7	5236.1	5739.9	4957.3
13556.7	6875.5	7592.1	8530.1	6845.8	8036.0	7600.3	7761.1	11530.0	9577.7	10510.2
571.5	2214.4	2782.6	3164.7	1823.8	3906.5	1411.7	3605.4	2628.5	5385.4	1984.1
162.8	3243.6	3902.0	4227.4	3286.3	5332.3	2619.5	5351.8	3559.7	6188.1	2987.7
3492.9	3449.2	3746.5	4016.2	3177.8	4662.3	2029.5	3815.0	3459.8	6456.9	3915.2
111.5	1775.3	1950.1	2146.2	1229.5	2580.4	1587.6	1984.1	1717.5	4576.4	1368.3
53.4	3903.6	940.9	732.7	150.6	355.8	97.5	3956.7	1057.8	4349.4	1599.5
13382.6	6100.1	5664.8	6438.9	6351.2	6340.9	5944.6	6443.0	8404.0	7491.8	7310.5
68.6	1723.6	2168.2	2127.5	1773.5	2931.4	1001.5	2500.6	2736.1	3098.7	1331.4
12762.6	6579.3	5801.0	6167.9	7674.6	6736.5	6671.2	7273.9	6427.6	8700.5	8169.4
461.8	5043.6	6579.7	7154.2	5450.6	8370.6	4034.0	7270.3	6234.8	13528.5	4636.2
5149.7	6507.6	6581.0	7343.8	6763.9	7364.8	7345.6	7451.2	10926.2	13085.1	7812.4
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707.4	3059.8	3239.0	3699.1	2593.7	3812.0	2259.3	3687.9	5034.3	6455.6	2505.9
135.8	2437.5	3745.1	4028.9	2424.2	4276.5	1416.1	3494.7	3513.9	5951.4	2111.8
865.7	2236.9	3165.3	4133.1	2973.0	3240.7	2492.7	3861.6	2250.6	5023.3	2681.9
313.0	3169.1	4166.0	3701.3	2199.3	4540.6	1781.2	3735.2	3258.1	8859.9	3442.7
2390.7	3741.6	4178.3	4416.5	3068.0	5289.1	2406.9	4384.9	4059.0	7897.7	4112.5
129.7	2501.8	3470.0	3662.6	3274.8	4675.6	1812.3	3465.5	2883.9	5534.1	1867.4
7115.6	3645.1	3520.2	3728.4	3298.3	3924.6	3046.1	3761.1	3974.0	6022.7	3905.6
90.5	2747.4	3813.8	4052.0	2500.1	4094.4	1559.2	3499.5	2880.1	5035.8	2007.2
1814.9	2981.0	3158.9	3457.7	3580.8	4113.4	2975.1	4024.6	3310.3	6695.6	2367.3
144.4	3096.0	4076.5	4354.9	4028.1	5429.9	2696.5	4604.2	3293.3	9168.8	2532.0
7628.9	3937.9	4126.3	4485.0	3420.5	4940.8	3259.9	4596.8	6407.2	5773.1	3898.0
125.7	2310.2	3097.8	3315.1	2573.4	4488.3	1875.5	3839.9	2695.1	7135.6	1995.2
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6217.1	5095.5	3442.3
3623.6	3925.3	1409.5
6760.4	5879.6	5460.8
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2943.8	3040.0	1426.2
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3687.1	2881.1	1787.0
7875.2	7758.3	6479.4
10058.3	7311.5	4865.7
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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
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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
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DQ824750.1 gg_id:194664 human fecal clone RL185_aaj72f10
FJ811860.1 gg_id:591962 Rahnella aquatilis str. 3-WCH
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FJ222589.1 gg_id:315615 Rahnella sp. str. N2-2
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1447.7	3741.7	4889.7	5791.9	3253.9	6596.7	3000.1	5479.1	4270.4	13424.2	4129.2
40.5	1236.9	1294.6	1308.5	556.7	2342.2	414.2	1419.9	307.4	5477.3	403.9
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EF515374.1 gg_id:223756 Electricigen Enrichment MFC upf microbial fuel cell anode clone 23e09 EF5153
EF515458.1 gg_id:223163 Electricigen Enrichment MFC upf microbial fuel cell anode clone 24f06 EF5154
EF515419.1 gg_id:227289 Electricigen Enrichment MFC upf microbial fuel cell anode clone 24b11 EF5154
U78182.1 gg_id:49258 Raoultella ornithinolytica str. CIP 103 364 T U7818
Y17662.1 gg_id:10128 Raoultella ornithinolytica str. 590681 Y17662
EF515201.1 gg_id:222043 Electricigen Enrichment MFC upf microbial fuel cell anode clone 21c07 EF5152
EF515264.1 gg_id:225880 Electricigen Enrichment MFC upf microbial fuel cell anode clone 22b06 EF5152
EU294412.1 gg_id:257519 Raoultella ornithinolytica str. 38 sullage EU294
EF433545.1 gg_id:211783 Klebsiella sp. str. WW2 EF4335
AB099403.1 gg_id:86319 Raoultella planticola str. ATCC 43176 AB099
EF515440.1 gg_id:217863 Electricigen Enrichment MFC upf microbial fuel cell anode clone 24d09 EF5154
EF515404.1 gg_id:224329 Electricigen Enrichment MFC upf microbial fuel cell anode clone 24a05 EF5154
Y17666.1 gg_id:10130 Raoultella ornithinolytica str. FSK9555 Y17666
AY770415.1 gg_id:134449 insect gut clone AY770
FJ975874.1 gg_id:566870 Human gut microbiome adopts alternative state bowel transplantation ileum effluent FJ9758
DQ333356.1 gg_id:149677 Raoultella planticola str. 33-4ch DQ333
FJ975862.1 gg_id:511415 Human gut microbiome adopts alternative state bowel transplantation ileum effluent FJ9758
AY946284.1 gg_id:114650 Kluyvera cryocrescens 27 AY946
Y17663.1 gg_id:10129 Raoultella planticola str. 7444 Y17663
GQ154930.1 gg_id:511427 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
EU256396.1 gg_id:243243 Bacillus megaterium str. SZN4 EU256
FJ975841.1 gg_id:562152 Human gut microbiome adopts alternative state bowel transplantation ileum effluent FJ9758
AF129444.1 gg_id:42955 Raoultella planticola str. ATCC 33558T AF129
GQ154871.1 gg_id:583590 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
GQ154720.1 gg_id:509089 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
GQ154727.1 gg_id:533667 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
AF511435.1 gg_id:65398 Serratia fonticola CCCO11b AF511
GQ156035.1 gg_id:545206 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
X93215.1 gg_id:10127 Raoultella planticola str. DSM 3069 T X93215
FJ975867.1 gg_id:569459 Human gut microbiome adopts alternative state bowel transplantation ileum effluent FJ9758
GU374107.1 gg_id:525406 soil East Calcutta wetland clone SRC_NBB7 GU374
Y17659.1 gg_id:10126 Raoultella planticola str. ATCC33531T Y17659
GQ155652.1 gg_id:566917 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
FJ405282.1 gg_id:356864 Citrobacter sp. str. F41 FJ4052
GQ154876.1 gg_id:584525 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
GQ154760.1 gg_id:535915 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
EU704230.1 gg_id:296868 human biliary stents clone KLONE12 EU704
GQ156448.1 gg_id:593522 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
EU560831.1 gg_id:565501 Assessment genetic Apriona germari (Hope) larvae normalization techniques intestir EU5608
DQ223874.1 gg_id:170406 Obesumbacterium proteus str. RT6 DQ223
EU939439.1 gg_id:329096 Fecal wild pygmy loris feces clone WF16S_295 EU939

147.7	3180.0	5008.0	5945.6	3033.3	7953.2	2031.5	4974.4	2873.7	15727.6	2724.3
3891.7	5624.3	6766.0	7462.9	4771.1	7628.0	4367.7	6616.8	7300.9	12747.5	7790.9
153.3	1216.3	2185.7	2409.2	1165.2	3014.9	721.4	1846.0	1151.9	7282.8	945.9
161.7	3005.7	4657.3	5498.0	2922.9	7246.9	1876.4	4438.1	3090.2	14029.3	2601.6
124.3	2689.8	4630.8	5549.5	2660.6	7449.3	1742.9	4631.8	2764.6	14361.7	2341.8
66.1	340.2	750.6	698.9	400.1	1075.1	188.9	630.2	552.6	1892.1	330.1
557.4	5197.2	6787.6	7093.1	4522.9	9806.4	4135.0	6699.7	4987.1	16107.8	3763.7
108.5	2404.9	4174.5	5251.4	2253.3	7097.0	1237.1	4203.9	2032.8	13777.8	1942.2
101.2	4099.8	5759.9	6476.5	4150.0	9512.4	3038.7	5199.2	3427.6	17201.3	3264.5
3737.1	4032.0	4565.3	5553.2	4158.8	5717.5	4690.4	4792.7	3538.3	12151.2	4460.5
4404.6	5072.6	5463.9	6507.7	5302.1	7088.7	5438.6	5370.8	5183.6	10263.3	5775.6
5222.4	6607.8	8055.3	8321.2	5756.7	9664.9	5561.9	7236.8	7179.5	14722.8	6789.5
692.9	5302.2	6710.8	7149.8	4686.6	9804.9	4179.8	6533.1	4784.1	16391.1	3864.6
4889.5	6904.2	7864.5	8686.5	6575.6	10530.3	5817.7	7672.3	5773.8	18468.3	5442.2
6176.9	7162.0	8422.1	9447.1	6070.0	10954.2	4851.2	8634.7	8085.2	18007.4	6299.1
155.4	3858.9	4920.1	5555.0	4152.8	6875.7	3896.8	4873.5	3865.5	13220.8	2638.5
1724.5	4637.4	5341.7	5436.0	4286.7	6868.0	3742.4	5156.1	4261.3	8859.3	4694.3
3206.4	2353.4	3323.3	3556.9	2424.6	5750.6	1828.3	2969.8	3652.9	11091.1	2315.9
87.3	4397.7	5773.1	6044.9	3702.6	7348.6	2058.5	6455.5	6137.2	12503.9	4109.7
514.0	3993.5	3879.8	3692.3	2678.0	4483.5	1967.9	4302.0	4714.6	5855.1	2420.3
5146.8	5353.6	5964.9	6667.3	5428.9	8866.7	4053.6	5881.4	5420.8	13784.4	4256.3
9397.3	7242.8	7079.9	7874.4	5855.8	8311.2	6430.3	6913.7	7114.1	9885.0	7795.6
154.2	3847.8	5322.1	5746.3	4015.3	7577.2	3168.5	5364.1	3796.0	14332.4	2599.4
9679.5	3999.2	4239.6	4829.3	3164.8	5211.4	3236.5	4821.7	5448.9	8353.9	4195.4
549.4	4218.8	5536.4	5524.5	3660.2	7443.0	2556.7	5460.6	2684.0	11861.8	2911.3
1220.8	5239.1	6615.9	7458.5	4656.4	8001.7	4668.1	6911.8	5986.5	11198.0	5365.7
324.5	3838.1	4839.9	6024.7	3970.1	6780.3	1271.8	5242.0	3720.8	12461.4	3711.4
253.0	6025.3	7048.0	6812.7	3678.3	7580.2	2648.6	7786.5	7977.6	13252.6	5407.3
123.6	2359.8	3636.1	4567.4	2587.9	6032.4	1005.5	3100.4	1742.6	13083.1	1557.3
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453.9	4917.7	6836.5	7234.3	4416.8	9624.7	4036.9	6590.4	4740.0	14160.9	3974.2
108.5	3927.1	4973.9	5265.2	4310.9	7093.2	2739.6	5104.7	3722.1	12700.1	2590.4
1222.4	5943.1	5804.2	6346.4	6072.2	8557.5	3660.3	6243.4	5227.9	14081.1	4034.9
348.5	6082.1	7636.6	7668.9	6522.0	10248.1	4834.8	6288.3	3347.8	17794.0	3313.3
642.8	5213.8	6402.2	7040.3	5237.4	8001.4	4381.0	7182.0	7107.8	8848.9	4503.5
225.4	4859.7	6505.4	7134.3	4139.5	8295.0	2989.8	6920.5	4683.4	14790.8	3945.2
65.8	2943.9	3724.0	3539.0	2987.4	5595.6	2909.5	3392.2	1815.8	9354.0	2080.6
271.8	3823.0	4458.2	4923.3	3402.3	5843.7	3190.0	4762.5	4693.7	13413.5	2782.1
55.7	739.3	1165.9	1095.5	523.0	1622.4	325.9	807.6	346.1	5219.4	350.9
522.2	2991.8	4230.0	4508.8	2981.1	5463.2	2312.9	6071.9	4427.0	9510.7	2361.4
1652.9	4714.6	5968.7	5721.0	4552.4	7317.0	3292.4	6111.7	5395.9	12941.3	4949.6

8038.6	5818.2	3167.7
7966.5	6828.5	4724.5
2478.6	3282.5	1149.5
7170.1	5662.1	2841.3
7423.4	5414.7	2655.3
816.5	1140.5	326.4
11186.5	8250.4	5573.0
6765.2	4996.5	2327.4
11107.6	6872.1	3752.9
5590.3	4600.1	3517.4
7092.6	7185.6	5092.8
11183.1	9343.1	6468.0
11019.1	8278.9	5678.9
11128.2	9030.1	6408.9
12169.1	9375.8	5772.0
7126.9	5933.6	3567.1
7393.1	7455.0	4028.6
5941.6	4276.8	1308.8
9818.9	7192.9	3472.1
4371.7	5500.4	2357.9
10458.1	8013.0	5524.5
8498.2	8385.5	6648.2
8066.7	6448.2	3650.2
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7528.7	5489.0	3181.5
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7290.0	5955.4	3171.1
7965.9	8168.4	4544.4
5451.5	3465.1	1285.6
5636.5	4711.6	2339.5
10894.5	8589.0	5490.6
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9595.4	7578.8	4466.6
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1781.7	1669.8	454.5
7804.6	5523.8	2117.9
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s__Salmonella enterica	4435

AF181574.1 gg_id:73261 Raoultella planticola 7 AF1815
GQ154719.1 gg_id:542496 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
DQ133596.1 gg_id:138380 Pantoea agglomerans str. B1 DQ133
FJ823007.1 gg_id:533363 Raoultella ornithinolytica str. gx-49 FJ8230
GQ154944.1 gg_id:578463 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
EF608520.1 gg_id:234549 predatory Poecilus chalcites their response lab rearing and antibiotic treatment diges EF6085
EU560759.1 gg_id:538000 Assessment genetic intestinal flora Apriona germari (Hope) larvae -RFLP techniques EU560
DQ113752.1 gg_id:132380 dog duodenum clone D1-50 DQ113
GQ154965.1 gg_id:550873 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
GQ156483.1 gg_id:540487 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
GQ156476.1 gg_id:579281 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
GQ154749.1 gg_id:536503 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
GQ154730.1 gg_id:575117 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
X93216.1 gg_id:10131 Raoultella planticola str. DR3 X93216
GQ156507.1 gg_id:535104 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
AF129443.1 gg_id:25616 Raoultella planticola str. ATCC 33531T AF1294
AB364958.1 gg_id:235818 Raoultella ornithinolytica str. R1 AB3649
GQ154797.1 gg_id:540793 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
AJ508301.1 gg_id:80910 Enterobacter kobei str. CIP 105566 AJ5083
EU870376.1 gg_id:315511 Enterobacter sp. str. SZDA EU8703
AF029226.1 gg_id:9779 Salmonella bongori str. JEO 4162 AF0292
EU014682.1 gg_id:241394 Salmonella bongori str. DSM 13772 EU0146
EF604050.1 gg_id:231538 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040
EF604013.1 gg_id:233727 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040
EF604026.1 gg_id:233581 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040
EF604059.1 gg_id:233315 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040
EF604025.1 gg_id:232625 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040
DQ344533.1 gg_id:147628 Salmonella serovar Typhimurium subsp. enterica DQ344
EF604459.1 gg_id:228090 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6044
EF604061.1 gg_id:230866 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040
EF604251.1 gg_id:228632 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6042
EF604271.1 gg_id:230532 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6042
EF604068.1 gg_id:232240 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040
EF604369.1 gg_id:229101 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6043
EF604430.1 gg_id:230474 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6044
DQ344536.1 gg_id:148570 Salmonella paratyphi DQ344
EF604057.1 gg_id:229934 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040
Z49264.1 gg_id:9760 Salmonella typhimurium str. E10 NCTC 8391 Z49264
EF604005.1 gg_id:229722 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040
EF604076.1 gg_id:234402 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040
EF604396.1 gg_id:229998 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6043

61.5	3668.5	5033.7	5981.8	2955.3	7398.3	1258.2	5716.5	3724.9	12873.2	3184.9
140.1	2993.7	4115.9	3950.2	1530.9	4911.5	1513.5	3957.4	2025.6	7596.7	1570.0
965.0	4684.0	5844.2	6133.7	5203.8	7953.5	4074.6	5910.7	4924.5	14278.1	3958.6
131.0	5724.7	7029.6	6925.5	5770.3	10360.1	5417.8	5904.7	3241.4	15430.1	3561.7
187.9	3848.5	4723.2	5216.8	4062.0	6592.4	2964.3	5619.9	3943.3	11453.8	3242.5
37.9	38.0	50.4	54.4	27.9	46.1	23.9	37.1	39.4	47.9	21.2
151.1	2608.5	3201.1	3161.3	2997.1	5235.1	3622.7	3074.4	2432.1	8307.4	1426.4
59.4	2571.6	3133.0	3584.4	3090.7	5183.9	1171.2	3230.1	2326.6	10447.5	1797.2
1081.1	6475.6	7944.8	9037.3	5705.6	9133.5	5342.6	8265.1	8288.1	14873.8	5844.2
225.4	5351.9	5997.7	6699.2	4643.4	7465.9	4045.8	6113.4	4312.7	13969.8	3716.1
149.2	2726.1	3578.8	3674.2	2184.8	4374.3	1348.4	3319.9	3331.4	9571.9	2014.6
1275.6	5611.3	7244.0	8100.2	4716.3	9816.6	3795.7	7247.2	6964.8	15804.8	5025.4
644.4	5497.4	5936.2	5475.2	4176.3	6253.7	3126.4	6508.1	7527.5	9653.8	4187.9
115.0	2035.1	2714.6	2990.5	1856.9	5040.0	1730.1	2249.8	1953.3	10717.6	1488.6
964.8	3666.2	4416.8	4442.8	3430.6	6441.4	3324.0	4481.5	3847.2	12059.4	3269.0
98.6	4045.6	5251.2	5553.3	4417.5	7704.6	2846.5	5142.6	3632.1	13562.8	2632.7
9548.0	6426.0	7839.7	8966.1	5588.9	10967.1	5156.8	9057.6	8372.3	17417.1	7753.9
990.0	7731.0	8104.2	8189.5	7280.3	9901.6	6464.7	7525.1	4823.2	16438.4	5168.2
2221.8	5825.5	7217.5	7866.1	5777.9	9304.7	5532.0	7066.3	5293.1	16527.8	4999.6
378.7	6144.1	7232.2	7595.9	5825.9	10285.9	4215.0	6421.6	3365.6	19216.4	3513.7
72.4	2797.3	3879.3	3705.3	3014.7	5131.7	2186.5	3858.6	1924.2	9019.6	1357.8
87.7	5126.5	6190.9	6516.4	4868.5	7912.0	3607.1	6447.7	3578.9	11999.9	2939.0
71.9	3313.4	4815.4	4967.6	2602.8	6523.3	1845.6	4816.8	1798.2	12951.5	2343.0
308.9	2221.8	2505.6	2988.0	2526.5	3454.3	1741.4	3244.0	2865.8	7386.0	1937.5
2428.2	5061.4	6050.0	6659.8	4302.3	5548.2	4768.6	6273.7	7443.5	11331.2	6249.1
11541.0	5984.7	6326.0	6212.4	6168.5	6025.6	5961.9	5439.3	6581.3	11520.9	7338.4
13869.4	6588.5	7178.6	7961.9	6023.0	6787.7	6753.7	6967.9	6487.1	13281.7	5517.5
144.0	4716.4	6213.0	6554.2	4183.7	7943.3	3092.6	6144.9	4642.8	15224.3	4166.3
8111.9	2768.4	2745.3	2765.9	2132.5	2885.6	2402.6	2260.7	2997.2	5907.5	3970.6
51.2	1662.5	2048.4	2025.4	1338.6	3045.4	918.4	1984.9	865.3	8455.1	1183.4
2203.3	1984.4	2578.8	2301.3	1449.0	3046.9	1386.4	2270.2	2504.7	6026.4	2522.8
98.1	3387.8	4896.8	5105.7	3322.2	6689.2	2682.8	5223.6	3296.6	12852.2	3241.2
86.3	2716.4	3807.2	3729.1	2056.4	5411.9	1350.4	3760.3	2361.0	10181.3	1876.5
1011.2	5440.7	7973.5	7160.2	3597.3	5033.0	4280.9	6496.7	4958.8	11355.4	7376.8
100.3	1487.9	2437.3	2237.4	1958.8	4634.2	557.7	2262.8	776.4	12992.3	926.2
47.3	2594.4	4154.9	4317.0	1546.1	4172.2	1601.9	3916.1	1249.0	10402.7	2199.4
8819.5	3317.4	3833.8	3920.7	2873.7	4825.6	2646.4	3649.9	3396.8	11265.0	4132.5
52.6	4477.0	6699.2	7588.9	2643.5	6647.7	3077.5	6012.4	2445.6	16329.3	3593.4
5960.5	4292.9	5579.4	6035.3	2896.5	4442.5	3671.0	5646.2	4162.4	9817.2	6172.7
46.2	1991.0	2837.0	2925.4	1554.3	3825.8	937.7	3023.0	1342.9	5704.2	1286.9
1826.9	4286.1	5248.9	5318.2	4453.5	5672.1	4732.0	5301.2	4843.0	9210.6	5716.8

7733.8	6003.2	2190.6
5182.0	3671.0	1700.0
8179.5	6537.2	4209.9
12186.5	9000.1	6226.1
7552.5	5615.5	3784.4
213.8	76.5	20.9
5385.8	4482.8	1918.5
5768.0	4138.9	1341.9
10068.1	9007.1	5977.3
7800.7	6462.4	4647.9
4383.3	4396.6	2169.0
11057.7	8262.3	4890.7
6739.9	7690.5	3930.9
5290.4	4544.9	1727.4
5925.1	4552.9	2972.1
8368.2	6439.5	4031.4
10765.8	9017.2	6434.2
10652.1	7980.6	5287.5
9618.0	8753.1	5967.9
10123.8	7836.7	4954.0
6013.5	5090.6	2155.7
10083.1	7266.7	3959.2
8272.0	5049.0	2150.8
4121.5	3938.0	1866.2
6345.0	5350.7	4067.3
6516.9	7057.3	5499.2
7475.6	7072.6	5257.3
8703.6	6716.0	3752.2
3183.3	3537.0	2008.7
4174.9	2554.7	991.7
2674.5	2962.2	1294.2
7292.9	5612.7	2867.7
5589.3	4332.8	1873.7
6287.7	6234.4	4150.5
4155.5	1659.5	951.5
5873.4	3318.0	1365.0
5642.1	4963.7	2477.1
8714.6	5099.1	2230.0
5759.5	6075.0	3309.8
3670.1	4716.1	1551.1
6402.0	5926.6	4156.0

k__Bacteria	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria
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k__Bacteria	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria
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o__Enterobacteriales	f__Enterobacteriaceae
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EF604073.1 gg_id:227660 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040
EF604267.1 gg_id:231474 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6042
EF604034.1 gg_id:231667 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040
EF604355.1 gg_id:231430 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6043
EF605237.1 gg_id:232727 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6052
EF604242.1 gg_id:230860 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6042
EF604458.1 gg_id:230835 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6044
EF604038.1 gg_id:231547 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040
EF604070.1 gg_id:234703 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040
EF604265.1 gg_id:232599 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6042
EU073022.1 gg_id:253204 Salmonella sp. 'group B' HQ010915-1 EU073
EF604087.1 gg_id:235257 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040
EF604376.1 gg_id:227666 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6043
EF604048.1 gg_id:233068 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040
EU118102.1 gg_id:249888 Salmonella enteritidis str. E3 EU118
EF604237.1 gg_id:227737 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6042
DQ683179.1 gg_id:165358 Salmonella paratyphi str. 50973 DQ683
EF604419.1 gg_id:228264 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6044
DQ153191.1 gg_id:138268 Salmonella typhimurium str. S1.I DQ153
EF604015.1 gg_id:230265 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040
EF604056.1 gg_id:229595 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040
EF605231.1 gg_id:228781 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6052
EU118104.1 gg_id:247090 Salmonella enteritidis str. E4 EU118
EF604039.1 gg_id:228911 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040
AB273733.1 gg_id:256256 Salmonella enterica subsp. houtenae str. GTC 1734 AB273
AF130890.2 gg_id:9770 Pantoea agglomerans str. A11 AF1308
EF604075.1 gg_id:230988 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040
EF604427.1 gg_id:231487 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6044
FJ609417.1 gg_id:572114 Salmonella enterica str. PRSC-1 FJ6094
EF604238.1 gg_id:233123 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6042
AF227869.1 gg_id:40959 Salmonella subsp. enterica serovar Typhimurium str. 65946 subsp. AF2278
NC_003197.1 gg_id:128871 Salmonella typhimurium LT2 str. LT2; SGSC 1412; ATCC 700720 NC_00
FJ377885.1 gg_id:363910 Salmonella typhi str. MR9 FJ3778
EF604017.1 gg_id:235063 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040
EF604089.1 gg_id:227942 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040
EF605240.1 gg_id:230644 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6052
EF604062.1 gg_id:230359 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040
EF604030.1 gg_id:232928 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040
EF604003.1 gg_id:233622 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040
EF604016.1 gg_id:227916 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040
EF604423.1 gg_id:234837 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6044

11724.4	4196.2	4449.6	4637.8	3433.0	4848.3	3538.2	4397.5	5089.2	9846.2	5255.6
1705.9	4017.3	4198.5	4320.1	3230.1	5074.8	2882.8	4654.6	3915.0	10744.9	3927.2
110.1	3099.1	4582.7	4464.9	2236.5	6043.3	1649.3	4209.2	2222.2	12072.9	2252.2
96.8	2598.8	3826.2	3869.6	1830.2	4850.0	1357.9	3694.0	1766.8	10475.5	1956.0
63.2	2987.9	4450.1	4216.2	2136.8	5997.5	1481.1	3896.5	1843.0	11842.0	1964.2
62.7	1546.2	2666.6	2791.1	794.5	2928.3	939.0	2938.5	830.8	6625.1	1798.6
502.4	3284.9	3988.3	4725.8	2787.4	5871.7	1870.5	4111.6	3054.2	9991.5	2656.8
3458.6	3125.0	3722.4	3424.7	2550.2	3916.9	2443.3	3913.9	4361.3	5179.6	4088.5
3410.0	7069.0	7618.4	8020.9	6219.1	7146.8	6826.8	6514.9	10111.8	10617.5	7481.7
22427.1	5619.0	5652.8	6023.5	5716.2	7161.1	5394.5	5527.6	7452.1	11216.7	8458.1
188.3	2072.0	2580.2	2908.7	2504.7	3263.3	2093.1	3373.5	2301.1	6903.4	2051.8
166.4	3364.5	5545.0	5721.9	2322.2	5825.7	2680.3	5037.8	1855.2	12360.4	2949.6
133.0	4502.0	6096.0	6363.0	3826.7	8009.1	2891.4	5816.1	4223.6	13075.6	3936.4
497.9	2288.8	3404.0	2487.1	1667.9	2903.7	1660.4	2042.8	1678.1	6436.8	2612.2
72.1	2773.9	3503.1	3582.1	2306.5	5365.9	1395.9	3460.7	2456.3	11624.8	1491.6
8309.0	9390.3	9054.1	10223.3	11056.2	9449.1	10069.5	8867.4	12256.0	11172.0	13142.0
81.4	2472.6	3636.2	4004.8	1442.4	3965.4	1614.0	3467.8	1305.6	9540.6	1913.8
115.9	4449.3	4877.1	5589.4	4763.3	5648.8	3685.1	4908.3	3798.5	11033.2	3265.9
44.9	2563.3	3254.1	3100.0	2287.0	4531.3	1383.6	2981.2	2695.3	12917.3	1136.6
260.9	3853.3	6522.7	6891.8	3393.9	6785.7	3806.5	5862.8	2500.0	13615.8	4180.8
95.1	3168.2	4602.5	4381.4	2593.6	6415.6	1879.2	4474.6	2432.5	12763.9	2401.0
6061.0	3775.0	4262.2	4548.6	2358.5	3277.3	3097.3	3253.0	3409.9	5363.2	6049.6
47.1	938.1	1314.8	1162.0	667.4	1872.2	478.8	1105.6	720.2	4679.2	419.4
9308.6	6096.9	5828.1	6285.9	5708.7	6359.0	5708.2	6020.8	8566.3	7905.0	9070.8
1670.8	5170.9	6132.9	6467.2	6278.4	8021.3	4579.9	6096.6	3926.8	15790.7	3816.4
205.6	3382.6	4870.7	4974.2	3358.5	6985.8	1651.4	4228.1	2489.4	13982.9	2066.6
97.0	2909.0	4235.2	4221.6	2112.7	5765.9	1497.0	3937.3	1661.0	11280.4	1897.6
4123.4	2558.1	3001.5	3316.4	2632.9	3994.5	2605.0	3500.5	3504.5	7489.0	3008.3
12598.4	9660.4	10032.7	10193.9	9686.9	10075.9	9862.9	9427.1	17159.4	14325.3	12786.1
284.5	3510.8	5721.3	5846.1	3473.6	6740.0	3373.1	5279.5	2831.6	12479.0	3364.6
74.0	3172.5	4348.5	4548.7	3052.0	6636.6	998.5	3506.1	2509.4	14137.3	1633.9
35.6	2332.7	3135.2	2846.7	1828.0	3989.8	984.0	3104.2	2791.6	11434.6	1352.5
11301.9	6377.2	6313.3	7171.0	5846.9	8174.1	5025.2	7006.6	8117.5	12705.6	6726.1
89.9	2509.8	4782.4	4792.5	2498.5	5973.2	2192.5	4477.7	2104.7	11826.1	2686.3
71.2	2451.1	2997.5	3227.4	1833.1	4634.4	1219.8	3333.1	2204.7	9973.7	1621.6
53.5	1515.4	1988.2	2098.6	1319.3	2638.0	961.5	1829.8	945.8	7085.0	1231.5
109.0	2821.8	4211.2	4205.2	1921.3	5716.2	1403.9	4034.8	2040.7	12052.7	2340.2
2723.5	4257.4	4589.6	5477.0	3934.4	5505.2	4143.2	4628.8	5472.1	7770.0	7199.0
6877.4	6866.1	6697.7	7397.3	6259.0	7019.4	7391.3	6154.4	8815.6	10490.1	9827.0
275.0	2287.2	3601.8	3968.0	1733.9	3444.4	2091.0	3705.9	941.2	9293.2	2239.6
159.6	3641.3	4833.2	5240.7	2620.0	6516.6	2127.8	5567.5	3392.8	14215.5	3359.4

5566.1	5351.1	3400.7
5836.2	5208.1	3477.7
6788.3	5085.3	1890.8
5390.8	4001.7	1584.3
6667.6	4644.5	1820.1
3877.1	2671.7	952.2
5894.8	4566.7	2842.7
4132.4	4702.6	2808.6
7153.8	7991.0	6217.2
6421.5	6901.5	5182.0
4255.4	3132.8	2038.1
6502.5	4547.2	2030.2
8338.0	6556.7	3629.6
3162.8	2665.0	1509.8
5632.2	4073.2	1777.6
8995.4	10980.9	8743.4
5082.9	3447.0	1515.0
6107.3	4894.5	3985.3
5041.7	3332.6	1245.3
7526.4	5303.1	2892.9
6691.8	4564.7	2251.6
3436.6	3593.2	1738.9
1922.1	1282.9	541.3
6306.0	6748.5	4609.0
8941.9	5846.9	4488.8
7793.3	5294.7	2198.3
6470.2	4680.9	1773.3
4080.4	5147.1	3327.6
9080.4	10282.4	9096.9
6983.0	5400.3	2904.1
6660.2	4054.3	2033.5
4298.2	3403.0	1070.6
7969.2	8602.5	4874.2
5992.4	4378.2	2192.8
5313.6	3742.9	1658.2
3512.8	2612.4	958.4
6294.0	4234.3	1816.8
4642.8	5467.9	3699.9
5888.5	6924.8	6056.0
4050.5	2973.8	1319.4
7431.5	5486.8	2501.4

k__Bacteria	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria
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s__Salmonella enterica	5947

EF604371.1 gg_id:231981 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6043
EF604394.1 gg_id:229717 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6043
EF604064.1 gg_id:232978 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040
Z47544.1 gg_id:9756 Salmonella typhi str. Ty2 ATCC 19430 Z47544
EF604385.1 gg_id:233497 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6043
EF604103.1 gg_id:232094 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6041
EF604429.1 gg_id:229314 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6044
EF604416.1 gg_id:231885 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6044
AB273736.1 gg_id:248512 Salmonella enterica subsp. arizonae str. GTC 1732 AB2737
AE008820.1 gg_id:34689 Salmonella typhimurium LT2 str. LT2; SGSC 1412; ATCC 700720 LT2 AE0088
EF604012.1 gg_id:228028 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040
EF605229.1 gg_id:234498 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6052
EF605238.1 gg_id:232278 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6052
EF604380.1 gg_id:227822 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6043
EF604124.1 gg_id:232989 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6041
EF604049.1 gg_id:229879 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040
EU118106.1 gg_id:241765 Salmonella enteritidis str. E6 EU1181
EF604278.1 gg_id:229337 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6042
EF604417.1 gg_id:234591 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6044
EF604046.1 gg_id:228201 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040
EF604418.1 gg_id:228980 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6044
EF604007.1 gg_id:231467 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040
EF604266.1 gg_id:232902 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6042
EF604004.1 gg_id:230964 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040
EF604058.1 gg_id:229270 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040
EF604250.1 gg_id:231095 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6042
EF604370.1 gg_id:232705 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6043
EF604258.1 gg_id:229218 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6042
EF604382.1 gg_id:227996 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6043
EF604042.1 gg_id:234592 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040
EF605236.1 gg_id:231367 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6052
EF604252.1 gg_id:228883 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6042
AF008580.1 gg_id:52635 Salmonella enterica arizonae subsp. IIIa str. ATCC 13314T AF0085
EU118080.1 gg_id:247476 Salmonella paratyphi str. A5 EU1180
EU118113.1 gg_id:249809 Salmonella typhi str. T6 EU1181
EU118101.1 gg_id:251997 Salmonella enteritidis str. E2 EU1181
EF604366.1 gg_id:233919 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6043
AB273735.1 gg_id:255286 Salmonella enterica subsp. diarizonae str. GTC 1733 AB2737
EF604389.1 gg_id:228797 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6043
EF604006.1 gg_id:230459 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040
EF604041.1 gg_id:234900 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040

82.5	3061.3	5714.4	5993.6	2380.5	5893.7	2741.9	5245.5	2133.8	12644.6	3632.1
11499.3	6267.5	6174.9	6572.1	5906.0	7030.4	6342.3	6638.4	8763.9	12030.7	7009.0
13983.3	6666.0	8285.5	9378.7	6203.7	8357.6	8396.2	5869.8	9341.1	13158.6	10343.6
88.0	6599.4	9175.4	9706.6	4626.3	9505.0	4183.8	8761.4	6412.4	16864.0	6279.9
4144.1	6529.3	6221.7	5956.0	5691.1	6700.8	5577.3	5849.6	9058.6	10811.4	7172.9
202.0	2500.2	3986.1	2778.2	2121.9	2745.1	1748.4	2548.4	1941.2	6634.1	2779.8
70.6	3080.6	4996.3	4976.0	3016.1	7091.1	2341.8	4568.3	2374.3	12883.7	2653.0
135.8	3166.2	4774.2	4847.0	2100.6	6466.1	1531.5	4713.0	2653.5	13566.9	2719.6
203.1	1882.7	2355.9	2329.5	1024.3	3601.0	1334.4	3333.7	1915.2	8826.4	1322.5
69.9	3401.5	5210.5	5551.5	2048.9	5475.0	1905.0	5588.2	3070.6	12834.4	2906.2
6356.6	5401.8	6278.2	7296.2	4443.5	5956.0	5155.1	6745.3	5742.2	9956.7	8634.9
55.9	2424.0	3944.8	3544.9	1090.8	4766.1	935.4	3845.5	2696.3	7937.8	2232.4
2652.9	4755.0	4801.3	5010.1	5002.1	6275.2	4543.6	5863.5	6560.4	11015.1	5438.7
7229.9	3146.7	3394.5	3600.5	2590.5	3779.2	2387.3	3259.9	3868.4	7836.9	4007.3
76.0	2193.1	2677.5	2786.9	1824.5	3867.2	1304.1	2728.1	1870.4	9991.1	1765.4
283.3	3066.3	3455.2	3764.7	3104.9	4716.3	2415.2	3621.3	2603.9	7965.6	2144.3
104.1	2628.6	3152.6	3178.4	2019.7	4491.8	1347.7	2786.1	1494.4	11370.8	1623.2
93.6	3351.2	4579.6	4789.9	2482.2	6065.4	1763.8	4560.8	2323.2	12594.4	2350.1
3446.4	6008.7	6867.0	7690.8	5650.7	7695.5	4892.0	7244.4	8287.8	11414.9	7680.5
6535.4	5197.4	5398.3	5787.0	4829.4	5836.6	4203.1	5627.6	6984.8	7506.1	8090.0
25580.6	5795.5	5901.4	6368.5	5544.7	6836.8	5514.9	6098.0	8405.4	11595.5	8951.3
148.0	4527.7	6404.9	6202.5	3510.6	8286.6	2576.3	5708.0	3333.5	15675.7	3561.4
4408.3	7004.7	7082.9	7904.2	5474.9	9108.8	5305.6	6366.4	5799.3	15411.5	6228.6
76.1	3307.9	5146.4	4957.9	2593.7	6978.1	1835.5	4496.2	1792.2	12887.0	2339.2
269.2	5234.2	6970.6	7071.9	4733.5	9160.0	3446.2	6440.1	4489.2	14900.0	4056.2
6429.3	3313.7	3727.0	3734.8	2828.0	4626.6	2653.3	3451.8	3794.1	10058.3	3961.5
82.1	2713.4	5106.8	5020.7	2614.5	6232.0	2253.2	4732.5	2326.8	12335.9	2858.8
3960.2	3676.2	3927.6	4232.2	3236.1	4928.0	3136.3	3872.1	4133.4	9934.2	3526.3
3877.5	6761.2	7733.2	8551.5	8038.1	8012.3	7825.6	7627.1	8346.9	14879.0	10667.7
314.2	2637.9	3194.7	3020.2	1526.7	3278.4	1459.5	3017.5	3244.2	7276.6	3623.4
185.2	3797.7	6322.0	6641.3	2550.7	6308.9	2976.2	5828.6	1978.2	14085.5	3589.1
138.0	3724.9	3674.3	3979.0	2962.3	4583.5	2761.1	3748.1	1015.5	5998.9	3489.5
47.0	58.7	82.4	73.9	58.6	115.9	48.5	58.6	55.6	510.4	40.0
132.4	3229.6	4967.1	5045.0	1979.3	4657.8	2210.2	4868.3	2149.7	10767.3	2525.1
107.0	4277.4	6080.9	6532.6	3287.0	7330.3	3019.8	5387.9	3155.1	14528.4	2909.3
43.9	1179.5	1847.1	1613.9	895.3	2453.2	735.7	1666.1	1229.6	4580.1	743.3
2763.8	6523.4	8151.3	8717.5	6380.2	7058.5	7107.1	7453.7	6196.8	13576.7	7981.4
41.0	2505.5	3098.2	2929.0	1992.5	4626.7	987.7	2168.7	1079.7	9308.1	726.0
177.5	5329.1	7341.9	7327.7	4647.7	9205.9	3315.9	6839.7	5383.4	15671.2	4831.5
11975.7	4823.3	5322.4	7278.9	4866.6	5939.1	5392.2	5338.8	6242.0	8455.8	12480.7
776.5	2973.2	3766.1	4065.5	2888.1	4209.2	2536.1	4202.0	2908.7	7569.1	3713.6

6565.0	4733.6	2255.5
7579.8	7442.8	6036.6
8210.4	9126.9	6181.6
9841.5	9308.9	5293.0
6476.2	6940.9	5474.0
3346.1	3506.7	1805.9
7567.7	5177.2	2667.0
6942.0	4660.3	2100.6
4106.9	3644.1	1476.3
6460.1	4857.3	1849.7
6668.3	5828.5	3892.5
5083.3	4009.0	1885.3
6853.1	5429.2	4112.2
4262.7	4561.3	2274.0
5075.3	3355.7	991.7
5150.7	5163.9	2864.1
4998.5	3491.3	1549.2
7212.2	5376.2	2109.1
7223.0	8584.4	5555.4
4923.8	6706.6	3907.5
7185.1	7306.1	5083.7
8879.8	6419.6	3040.8
10461.2	8077.4	4813.8
7682.4	5031.9	2125.1
8869.2	7018.7	4210.4
5425.0	4670.1	2369.5
6164.4	4548.7	2303.0
5823.2	4613.6	3211.6
8903.8	8404.5	7708.0
3341.7	3818.2	1993.6
7506.3	4958.9	2099.2
3735.0	3055.4	2942.4
121.1	136.9	39.4
6281.4	4289.2	2127.4
8960.2	5630.0	2933.4
2288.0	1903.0	873.2
7995.8	6901.0	6158.6
3951.7	2439.6	1387.9
9349.0	7102.3	4253.4
6253.5	6373.8	4563.5
3919.5	4510.1	3044.6

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s__Serratia fonticola	5980

EF604259.1 gg_id:233544 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6042
EF604264.1 gg_id:230650 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6042
EF604071.1 gg_id:234981 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040
EF604053.1 gg_id:232636 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040
EF604065.1 gg_id:233811 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040
EF604269.1 gg_id:228519 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6042
EF604055.1 gg_id:228129 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040
EF604029.1 gg_id:232688 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040
EF604368.1 gg_id:229317 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6043
EF604047.1 gg_id:228301 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040
EF604229.1 gg_id:230785 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6042
EF604290.1 gg_id:228932 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6042
EF604350.1 gg_id:230452 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6043
EF604231.1 gg_id:228528 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6042
EF605222.1 gg_id:228682 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6052
X80676.1 gg_id:9753 Salmonella sp str. ATCC 9712 X80676
EF603996.1 gg_id:230075 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6039
EF603990.1 gg_id:229961 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6039
FN555100.1 gg_id:557204 Salmonella enterica str. 22/M185/01/98 FN555
EF603999.1 gg_id:230399 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6039
EF603993.1 gg_id:240102 Salmonella enterica serovar typhimurium exploits inflammation compete intestinal n EF6039
EF605223.1 gg_id:228777 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6052
EF603997.1 gg_id:233210 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6039
EF604009.1 gg_id:231236 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6040
EF604439.1 gg_id:229380 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6044
EF604378.1 gg_id:257266 Salmonella enterica serovar typhimurium exploits inflammation compete intestinal n EF6043
EF604233.1 gg_id:229474 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6042
EF605227.1 gg_id:230960 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6052
EF605226.1 gg_id:230722 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6052
EF604352.1 gg_id:233030 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6043
AF170176.1 gg_id:9773 Salmonella typhimurium LT2 str. SGSC1412 AF170
GU370899.1 gg_id:560434 Serratia entomophila str. AB2 GU370
AM696814.1 gg_id:222538 sequencing libraries indoor dust clone BF0001A101 AM696
AM696771.1 gg_id:221173 sequencing libraries indoor dust clone BF0001A058 AM696
AM696796.1 gg_id:219190 sequencing libraries indoor dust clone BF0001A083 AM696
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AM696767.1 gg_id:222647 sequencing libraries indoor dust clone BF0001A054 AM696

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89.6	3099.1	4582.7	4464.9	2236.5	6043.3	1561.8	4105.0	1897.8	11824.2	2081.6
731.6	1534.4	1771.1	1947.5	1463.7	2489.4	1602.1	2188.1	910.2	5832.8	1103.2
4013.7	5088.3	5955.8	5671.0	5716.5	5788.9	5758.4	5904.9	5356.9	8001.4	6221.1
446.7	2674.7	3144.5	3317.5	2597.7	4268.3	1949.8	3328.4	2151.5	8473.6	2413.1
1230.9	1806.8	1759.3	2020.2	1903.0	2426.3	2183.9	1411.7	798.5	7495.4	1440.9
181.1	5063.0	6942.7	6674.5	4521.5	9580.5	3111.7	6220.9	3871.5	15535.2	3537.9
167.1	1917.7	2202.6	2351.8	1929.5	3028.3	1903.9	2391.9	1820.1	8558.4	2020.6
505.9	3733.2	5510.7	5324.5	2318.2	4049.2	2827.7	4346.3	2022.6	10220.3	4538.6
17486.1	5918.7	5385.3	5908.6	5289.5	6304.4	5870.9	6137.0	8316.3	11575.8	7089.6
85.2	3279.6	4968.1	4786.3	2479.8	6746.5	1740.8	4261.0	1788.7	12720.1	2158.6
5952.1	3036.1	2677.5	3658.1	2729.7	4494.0	2272.4	3459.6	2931.4	9675.4	2782.9
482.9	4891.9	5353.0	5592.3	4183.9	7009.3	4056.8	5173.0	4449.2	14974.2	3116.3
5466.2	8949.2	9657.7	10530.7	7907.5	10908.8	8289.6	8654.3	12339.8	15492.3	11196.6
189.8	3968.8	4895.3	5138.7	3125.8	7026.5	2559.0	4659.8	3213.7	14935.6	2168.1
4254.1	4470.3	6467.0	6809.2	4485.2	5502.8	5086.9	5718.3	5098.5	10046.7	8596.6
8804.1	6023.0	6674.4	6878.2	5013.8	7658.0	4441.2	5884.6	6047.6	13625.1	6466.7
198.5	4217.1	5288.3	5554.6	3399.3	7452.0	2769.7	5150.6	3710.0	14773.8	2506.6
108.1	3327.7	5104.4	5316.0	2173.2	5297.7	1563.4	4708.9	2800.1	13803.0	2446.8
197.6	3721.2	4682.1	4818.1	3054.5	6472.8	2510.0	4491.3	3696.6	14097.2	2083.4
2523.7	4900.8	5068.2	4963.2	3526.6	5926.4	3207.3	4932.2	5662.4	11055.1	3438.5
165.8	4486.5	5206.3	5555.8	3654.3	7429.8	2949.4	4867.6	3118.2	15676.3	2576.4
2832.9	4007.0	4975.1	5269.2	3227.7	6122.7	3080.6	4934.9	4732.8	11618.9	3599.3
146.3	4336.4	6286.2	6207.2	3976.9	7996.2	2942.6	5772.8	4258.3	14103.9	4012.9
2794.6	2600.2	2952.0	3018.1	1894.2	3543.8	1847.7	2800.3	3656.3	9396.0	1931.8
1033.1	2754.1	3221.3	3551.6	2349.8	3975.2	2650.1	3435.0	1937.9	6818.3	2665.9
1928.4	4191.0	4829.4	4951.4	3321.1	6629.4	2705.6	4661.7	4114.6	13669.7	2609.7
1402.1	3130.9	3365.8	3556.8	2051.1	4137.8	1439.2	3921.7	3092.2	7057.1	2455.4
14969.8	7924.7	8113.7	9062.5	7399.8	10180.3	7563.3	7781.4	8858.5	18049.6	8876.0
166.7	3869.5	4772.3	4986.6	3260.9	6921.3	2658.2	4528.7	3411.3	14841.8	1988.2
56.7	2956.9	4297.1	4253.5	1792.2	5203.3	1188.8	4727.3	3624.4	11755.3	2239.6
86.9	4216.8	5696.9	5698.3	3211.8	7128.6	2802.0	7352.6	6520.3	12743.2	4008.0
406.4	7008.7	7833.5	8464.8	6912.3	9627.5	5979.6	8029.2	9136.0	13886.8	5968.2
415.6	7298.1	7557.7	8216.8	7292.8	9575.6	7150.2	7614.9	8323.8	12351.8	5627.2
385.8	6996.2	7432.6	7965.7	7135.1	9052.6	6881.5	7313.0	8243.9	12236.8	5509.6
5257.0	6599.3	6233.7	6654.6	6911.6	6647.2	8216.3	5626.6	7160.4	6390.9	7182.0
369.1	6752.0	6928.3	7374.0	7276.2	8853.0	7377.0	7023.6	8015.8	11289.7	5045.8
388.7	5135.5	5670.8	6087.1	5375.9	6932.3	5880.7	5708.5	6761.5	9435.9	4168.7
386.4	6645.3	7086.0	7408.2	6596.1	8741.0	6282.1	6854.2	8058.9	12530.3	5076.3
168.4	5490.3	6218.5	6405.0	6591.1	8404.1	6473.5	6514.8	7502.0	9479.4	3907.0
342.7	5914.6	6312.6	6564.5	6451.5	8073.4	6694.0	6343.2	7343.3	10322.6	4308.8

4726.3	3402.5	1556.6
6688.6	4852.6	1890.8
3336.6	3382.1	1653.0
5554.3	6539.1	6031.4
5372.4	4415.6	2178.9
3141.8	2205.0	1410.1
9606.6	7165.1	3504.0
3632.2	4311.2	1659.3
4839.5	4336.5	2254.2
6650.3	7769.0	5617.3
7212.0	4896.6	2015.4
5634.9	4209.8	2470.1
6878.8	6525.6	3489.8
9088.6	10362.6	7736.8
7005.9	5725.9	2519.5
6067.3	6969.2	3937.3
7105.4	7632.2	4548.8
7382.1	6190.2	2785.3
6316.4	4920.7	1737.3
6360.0	5415.5	2311.8
5356.2	7118.2	3439.1
7864.4	6164.8	2679.1
5885.5	6883.4	3119.7
8280.1	6204.7	3577.4
4128.0	4807.7	1629.3
4459.7	4015.6	3013.9
6280.3	5844.5	2682.0
3944.3	5174.6	2267.7
9031.7	9891.9	6331.1
7156.7	5413.7	2426.5
6276.7	5702.6	1812.8
7823.9	7436.1	3548.2
9600.7	9223.6	5509.9
9825.0	8633.1	5543.2
9027.2	8390.4	5219.0
6637.8	6652.0	5368.8
8979.4	8140.5	5614.0
7364.1	6975.1	4115.4
8716.0	8353.6	4906.0
8120.6	7586.2	5133.6
7958.4	7651.3	4916.2

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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
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FM163485.2 gg_id:290724 Serratia marcescens str. BC16
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GQ906774.1 gg_id:586809 Serratia marcescens str. MR-4
DQ182325.1 gg_id:140269 Serratia marcescens str. RS-10
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EU558695.1 gg_id:269858 Serratia marcescens str. ITA-4
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FM213393.2 gg_id:314820 Serratia marcescens str. MN51
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FJ655524.1 gg_id:583608 symbiont
FJ655485.1 gg_id:566162 symbiont

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FJ6555
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97.1	3472.7	3833.4	4218.4	2204.1	4217.0	1800.3	4267.8	3996.3	7347.5	2926.7
261.1	5187.4	5825.9	6541.2	4059.4	7236.3	3321.4	6346.7	5040.6	12116.5	4231.7
120.1	3075.6	3343.9	3015.0	2220.2	4205.1	1500.8	3706.6	2837.7	5564.6	1845.8
932.8	6322.4	7121.5	8081.4	5240.2	8830.9	4333.0	7907.1	6664.0	14525.9	5412.4
525.8	8281.7	9684.9	10870.3	7479.9	11136.4	4523.8	11079.1	11022.3	20216.2	7777.8
2117.1	3777.3	4949.2	5100.6	3251.4	5561.5	2708.7	5589.2	4115.5	8364.2	3471.3
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116.6	5260.7	6558.0	6525.3	3734.9	7852.7	2973.5	7287.2	5494.2	15161.6	4276.1
4951.3	2905.5	3937.3	3760.9	2210.4	4968.5	2307.8	3005.5	3433.3	9696.0	3576.5
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204.6	5777.8	6601.5	6528.6	3609.1	7331.2	2110.3	7204.1	7940.5	13458.9	5071.0
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233.2	2823.7	3937.4	3855.7	2474.9	4273.4	2375.3	3778.2	2824.6	7717.6	2480.4
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513.8	3889.2	4316.8	3945.4	2920.7	4680.9	3060.5	4560.0	3310.5	6921.0	3155.3
83.2	3871.4	4171.0	4430.9	2457.7	5448.4	1676.1	4419.0	4145.2	8109.7	2538.9
795.8	3442.9	3855.7	4034.4	2270.4	4829.5	1703.0	4340.3	4679.8	7652.9	2269.0
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1479.4	6729.9	7362.6	7819.8	5179.4	9035.4	3656.1	7889.4	7102.6	15186.0	5478.5
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AJ233430.1 gg_id:10170 Serratia grimesii str. DSM 30063	AJ2334
AB334771.1 gg_id:247431 Serratia proteamaculans str. MPU8	AB3347
EU024331.1 gg_id:240135 intestinal microflora Hepialus gonggaensis larvae RFLP larval gut clone Hg03	EU0243
EU554429.1 gg_id:275241 Pseudomonas fluorescens str. Ag03	EU5544
FJ527460.1 gg_id:563283 Pectobacterium subsp. carotovorum str. Ecc4-4	FJ5274
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FJ469981.1 gg_id:544455 Serratia grimesii str. N10-1	FJ4699
U93263.1 gg_id:10181 Aranicola proteolyticus	U93263
AJ279002.1 gg_id:33276 Serratia fonticola str. IB4	AJ2790
DQ321559.1 gg_id:146025 gut- microorganisms larvae and adults southern pine beetle Dendroctonus frontalis	DQ321
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FJ811865.1 gg_id:546427 Serratia liquefaciens str. 1-BCH	FJ8118
EU266583.1 gg_id:256972 Serratia plymuthica str. RG 6	EU2665
FJ527469.1 gg_id:569600 Pectobacterium subsp. carotovorum str. Ecc7-1	FJ5274
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DQ103512.1 gg_id:131626 Serratia sp. F2	DQ103
GU292825.1 gg_id:541724 Serratia sp. str. L5	GU292
AM696720.1 gg_id:217962 sequencing libraries indoor dust clone BF0001A007	AM696
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EU236755.1 gg_id:250856 Serratia plymuthica str. R1	EU2367
EU031768.1 gg_id:249473 Serratia sp. str. BS18	EU0317
AM696754.1 gg_id:218671 sequencing libraries indoor dust clone BF0001A041	AM696
AB004751.1 gg_id:10186 Serratia rubidaea str. JCM1240	AB0047
AJ233429.1 gg_id:10169 Serratia fonticola str. DSM 4576	AJ2334
AJ279044.1 gg_id:27304 Serratia quinivorans subsp. quinovora str. CP6	AJ2790
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DQ991163.1 gg_id:189593 Serratia grimesii	DQ991
EU075114.1 gg_id:239779 Serratia sp. str. Lac5	EU0751
AM696779.1 gg_id:224560 sequencing libraries indoor dust clone BF0001A066	AM696
FJ790328.1 gg_id:387955 Serratia sp. C1(2009) str. C1	FJ7903
AM157437.1 gg_id:142918 Serratia proteamaculans mother C4	AM157

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916.0	5470.0	6198.5	7208.3	4397.8	8096.8	4210.6	7367.9	6133.1	12755.4	4966.8
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161.0	3405.8	3466.1	3488.3	2879.4	4546.8	2438.1	3910.5	3738.1	6490.5	2420.4
170.7	4085.6	5051.0	5104.9	2122.4	5608.9	1287.7	6789.3	4725.1	8650.5	3549.4
75.8	2848.1	3464.7	3455.7	1390.0	3976.7	1012.4	4103.6	2819.3	6407.8	1724.9
7229.0	4652.4	5278.0	5807.8	4977.1	6605.0	4057.2	5667.8	4829.1	9171.2	5206.7
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AJ279054.1 gg_id:30929 Serratia ficaria str. NCTC 12148 AJ2790
DQ833334.1 gg_id:166089 Title: Anaerobic Reductive Dechlorination Vinyl Chloride ly Enriched AuSable River S DQ833
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AJ306725.1 gg_id:27899 Serratia liquefaciens str. CIP 103238T AJ3067
AY573038.1 gg_id:101976 Yersinia sp. str. ARCTIC-P11 AY573
AJ233436.1 gg_id:10189 Serratia rubidaea str. DSM 4480 AJ2334
EU196322.1 gg_id:247118 Hafnia sp. NP33 EU196
AF286870.1 gg_id:43863 Serratia odorifera str. DSM 4582 AF2868
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AM992015.1 gg_id:293839 Serratia sp. str. 5.3R AM992
AM696774.1 gg_id:226256 sequencing libraries indoor dust clone BF0001A061 AM696
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AY308053.1 gg_id:88177 Serratia sp. str. AZ22R6 AY308
FJ527455.1 gg_id:512247 Pectobacterium subsp. carotovorum str. Ecc7-2 FJ5274
AB009954.1 gg_id:10175 unclassified proteobacteria str. L101 AB009
AJ288154.1 gg_id:71258 Serratia sp. SK-3-30-2 AJ2881
AM696805.1 gg_id:225126 sequencing libraries indoor dust clone BF0001A092 AM696
DQ321632.1 gg_id:149012 spb29A1-1 DQ321
AF286869.1 gg_id:34707 Serratia fonticola str. LMG 7882 AF2868
FJ527459.1 gg_id:556535 Pectobacterium subsp. carotovorum str. Ecc1-7 FJ5274
EF428994.1 gg_id:216947 Serratia sp. str. GIST-WP4w1 EF4289
AY243097.1 gg_id:85224 Serratia liquefaciens str. Hf1 AY243
AM696787.1 gg_id:219390 sequencing libraries indoor dust clone BF0001A074 AM696
AM992014.1 gg_id:290849 Serratia sp. str. 5.1R AM992
EU024350.1 gg_id:253194 intestinal microflora Hepialus gonggaensis larvae RFLP larval gut clone Hg28 EU024
FJ811861.1 gg_id:557977 Serratia proteamaculans str. 2A-CDF FJ8118
AM696769.1 gg_id:225884 sequencing libraries indoor dust clone BF0001A056 AM696
AY902209.1 gg_id:113392 Serratia proteamaculans str. BR5 AY902
DQ530081.1 gg_id:160086 Serratia sp. CI20 DQ530
FJ655531.1 gg_id:586383 symbiont FJ6555
FJ655517.1 gg_id:554574 symbiont FJ6555
AY620432.1 gg_id:99056 Cinara cedri symbiont AY620
EU348314.1 gg_id:316943 symbiont EU348
EU348315.1 gg_id:352486 symbiont EU348
FJ655518.1 gg_id:576533 symbiont FJ6555
EU348318.1 gg_id:355736 symbiont EU348
NC_007606.1 gg_id:145027 Shigella dysenteriae str. Sd197 NC_00
FJ405353.1 gg_id:365131 Escherichia coli str. 4097 FJ4053
NC_004337.1 gg_id:140570 Shigella flexneri 2a str. 301 NC_00

350.9	4956.0	5814.2	6254.5	4700.4	7660.4	4720.4	6252.0	7337.9	11564.8	4046.0
431.8	3772.0	4562.3	4739.6	3258.6	6540.6	2109.1	6465.0	4381.9	12107.0	3318.5
2203.9	5959.8	6729.4	7277.8	5485.8	8666.3	5630.3	7096.5	8230.4	13354.9	5082.5
6395.3	3226.0	3412.6	3205.6	3496.7	3995.9	4077.0	3846.3	4331.0	4802.4	2739.8
81.9	3008.1	3340.5	3665.3	2088.4	4659.7	1650.2	3903.7	3430.9	7963.5	2290.0
93.5	2931.8	3814.7	3628.2	1718.1	5599.8	1582.3	4250.1	3229.6	8317.8	1786.7
92.3	1340.5	3747.6	3492.0	1116.2	4405.0	1231.2	2933.6	3194.6	7396.2	1502.1
6137.4	7087.4	7094.5	7400.4	6271.9	8399.0	5940.9	7138.3	8847.4	12406.4	7551.3
1032.7	4721.4	4720.7	5571.6	4413.9	7989.5	3070.9	5908.2	5365.0	11681.6	3308.9
2675.7	5600.6	5322.5	5702.0	5234.3	6346.7	5107.3	5577.6	6549.6	9029.8	6694.7
113.5	3538.2	5043.2	4831.0	1899.5	5294.4	1079.0	6301.0	4691.4	9651.8	3355.8
141.4	4685.4	4721.7	4820.1	5715.7	6193.8	6327.7	5025.1	5902.7	6086.3	2974.6
97.8	3336.4	3821.7	3825.5	3050.5	5385.2	1859.3	4270.4	3616.4	11273.9	2627.5
150.2	1519.5	2059.8	2213.2	1205.7	2744.6	607.9	1823.0	718.1	3358.7	942.2
274.2	4929.1	5789.7	6574.6	4183.5	7190.0	3557.3	6305.3	5406.4	12432.6	4319.0
95.2	3379.7	4346.5	4381.2	1926.4	4943.5	1485.7	4910.2	3778.5	8611.9	2434.5
421.5	2062.4	2344.2	2480.8	1733.5	2794.2	2125.3	2878.3	4200.3	6539.8	2152.8
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119.7	4094.6	4687.9	4735.0	5068.1	6606.2	5424.7	5087.8	6297.6	7216.6	2709.6
749.0	2276.4	2485.8	2444.8	2349.7	3055.2	2878.8	3424.8	3171.6	3771.8	2217.7
194.1	6100.2	6013.6	6134.6	5009.9	6116.9	4625.5	6169.6	6466.9	9198.7	4181.0
246.0	3988.1	4683.2	5335.1	2757.3	5609.6	2421.2	5154.8	3697.2	8839.1	3479.4
2943.9	6642.1	7117.6	7761.7	9441.7	7398.6	7998.2	7166.7	6356.8	7191.6	6931.9
250.5	4318.5	5012.1	5788.6	3488.7	6404.7	2740.7	5600.6	3833.6	10576.6	3528.7
2655.6	5651.3	5987.2	6594.7	6443.2	6976.1	7334.3	6323.9	6834.7	6393.0	5526.8
4364.2	3626.0	4522.1	4101.3	2208.0	4965.7	2639.7	6003.8	3642.0	7448.7	3949.9
1121.8	2557.4	3378.0	3568.3	1793.3	5711.5	1810.7	4022.6	3419.2	8422.0	1588.2
101.4	2706.1	3266.5	3153.6	2218.0	3618.6	1652.3	3781.8	2749.2	5250.0	2087.3
1919.8	3870.2	4441.5	4706.2	3565.6	5604.9	4193.0	6067.1	4064.1	10071.6	4605.6
67.6	1509.6	1924.0	1823.4	908.2	1740.1	498.0	2307.4	1310.3	3649.7	998.8
29355.6	8229.1	9079.0	10361.1	9651.7	10898.7	8859.0	11393.3	10055.0	16868.5	9054.5
76.5	1390.5	2342.3	2058.3	775.4	1866.6	714.7	1756.4	1630.0	2814.6	1121.8
4139.5	6681.5	4984.2	4970.4	4455.6	6718.7	4752.9	5656.1	3905.1	12265.1	5295.4
65.4	218.5	247.4	215.5	180.7	360.3	126.9	228.8	275.2	217.1	104.5
336.2	4333.8	5997.3	5403.3	3989.7	6076.2	3919.4	5442.8	4353.7	9974.0	4058.7
234.3	3774.6	4804.8	5188.0	2714.1	6012.3	1917.7	5871.1	4908.4	9244.2	3999.4
5638.5	8502.8	7786.6	9076.5	6878.9	9247.0	6337.9	9123.4	9172.3	13230.6	7395.0
1977.8	3852.6	5097.1	4502.3	4070.9	4893.9	5304.4	5491.1	6517.6	7373.6	4272.4
319.1	4803.6	6517.4	9117.5	2627.1	4461.6	4252.6	6587.2	4167.3	11742.7	7595.8
180.9	3671.8	5413.4	6198.7	2640.7	4912.7	3980.6	5502.4	3571.9	11125.3	3469.0
142.8	5317.8	6633.9	7057.4	3753.7	7446.4	3683.0	6905.0	5968.4	14724.8	4424.6

8415.3	7544.0	4014.3
7766.3	6505.7	3280.7
9411.4	8439.7	4891.1
4545.9	4421.4	3122.6
4957.4	4606.7	2187.9
6384.0	6028.9	1989.4
5015.0	4072.6	1785.5
8771.3	9050.3	6197.6
9406.3	8102.3	3883.4
5640.2	6659.4	3928.9
6528.9	6633.7	2542.4
6397.2	5586.9	4402.0
4759.6	5203.8	1645.6
2711.7	1875.5	1085.9
7624.8	7473.3	4167.5
5824.3	6465.5	2436.3
2466.1	3677.1	2158.4
5831.3	7343.6	5195.9
6786.2	6154.2	4270.7
3737.8	3895.2	2314.4
7008.5	6308.7	4265.3
6089.2	5615.9	2994.6
7978.6	7179.2	6472.5
6802.1	6547.6	3493.1
6905.5	7716.8	5812.1
5747.3	6314.4	4946.3
6176.1	5968.0	1912.5
4287.8	3999.3	2181.8
6267.4	6829.9	5044.3
2632.4	2510.8	916.0
11804.3	12131.9	8646.8
2475.2	2389.5	1152.6
6639.3	7162.8	7479.5
281.0	584.8	172.8
5579.0	5961.3	3764.7
6620.8	7066.9	3043.8
9009.2	9085.1	7521.7
4321.9	5851.3	3923.0
6047.8	3499.8	1998.2
6160.0	5180.1	2957.4
8399.9	7708.7	4500.0

k__Bacteria	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria
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g__Shigella
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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
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s__unclassified	4525
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s__unclassified	5749
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 NC_00
AE014073.1 gg_id:146756 Shigella flexneri 2a str. 2457T AE014
EF643608.1 gg_id:249718 Shigella flexneri str. FBD001shig EF6436
NC_008258.1 gg_id:168833 Shigella flexneri 5 str. 8401 NC_00
NC_004741.1 gg_id:129308 Shigella flexneri 2a str. 2457T NC_00
EU467921.1 gg_id:293331 cheetah feces clone CE2_b06 EU467
GQ048030.1 gg_id:421118 Topographical and Temporal Human Skin Microbiome skin palm clone nbw140e08c1 GQ048
GQ141872.1 gg_id:410166 Escherichia coli str. petra-05 GQ141
EU766807.1 gg_id:342976 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU766
EF528266.1 gg_id:222400 Escherichia coli str. CICCHLJ Q41 EF5282
GQ155203.1 gg_id:543477 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EU458164.1 gg_id:296929 North American black bear feces clone BB2_g06 EU458
GQ007663.1 gg_id:502000 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ007
GU594305.1 gg_id:521179 Escherichia coli str. B50 GU594
GQ155258.1 gg_id:588262 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EU470621.1 gg_id:293683 red panda feces clone RP_1aaa03d04 EU470
X96966.1 gg_id:9686 Shigella dysenteriae X96966
GQ155109.1 gg_id:543251 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ155303.1 gg_id:577035 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ155087.1 gg_id:586921 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ155248.1 gg_id:548241 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
AY098487.1 gg_id:66579 Escherichia coli AK108 AY098
DQ819201.1 gg_id:162903 mouse cecal microbiota-colonized zebrafish digestive tract clone aab27a07 DQ819
GQ155047.1 gg_id:513655 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ155132.1 gg_id:551754 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EU472747.1 gg_id:293399 red panda feces clone RPSD_1aaa03h08 EU472
EU778502.1 gg_id:304899 Red Panda feces clone RPSD_1aaa03a11 EU778
GQ155304.1 gg_id:563327 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ047990.1 gg_id:441018 Topographical and Temporal Human Skin Microbiome skin palm clone nbw140a03c1 GQ047
GQ155143.1 gg_id:593967 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
AM184304.1 gg_id:159905 Shigella flexneri str. WAB1966 AM184
GQ155305.1 gg_id:578663 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ155234.1 gg_id:590391 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
AB303383.1 gg_id:246629 slender pigeon louse Columbicola columbae symbiont AB303
AY861702.1 gg_id:112007 Sodalis glossinidius str. GA-SG AY861
AF005235.1 gg_id:9987 primary endosymbiont Sitophilus oryzae str. SFr of AF005
AF548137.1 gg_id:96697 symbiont AF548
AM774412.1 gg_id:237905 Biostraticola tofi str. BF36 AM774
AF548139.1 gg_id:95263 symbiont AF548
AF548142.1 gg_id:95903 symbiont AF548
DQ133565.1 gg_id:148901 Preliminary survey insects (Hemiptera: Coccoidea) scale insect clone DQ133

640.7	2510.4	3555.4	3808.6	1756.8	3838.7	2910.7	3153.5	3102.5	8951.1	2424.5
105.6	4302.1	5164.8	5395.7	3022.9	6283.0	3214.2	5361.5	5408.5	11737.0	2994.1
136.2	3555.9	4893.3	5325.8	2263.4	5343.9	2972.2	4629.2	3292.9	12536.1	2777.1
141.2	4762.1	5811.5	6471.0	3251.7	7015.7	3088.1	6076.8	4869.6	15492.0	3684.7
171.4	4812.9	6141.4	6809.0	3251.0	7040.9	3127.5	6221.5	5094.0	14635.8	3730.1
978.0	6858.4	8514.7	9564.2	5825.4	9714.8	5371.8	8098.6	5968.9	18773.1	6102.3
3346.8	4783.2	5743.1	6919.2	5089.2	5618.8	6250.8	6433.7	3383.3	8801.1	4497.4
758.8	6071.1	8207.1	9229.0	4419.9	7556.2	4488.5	7924.0	4931.5	17585.3	5947.8
755.3	6231.1	7707.8	8629.9	5145.2	8301.1	4868.0	7452.4	5307.5	16957.2	5739.8
783.9	4170.8	5265.8	5705.3	3228.6	5920.7	2422.7	5129.9	3630.5	15122.1	2872.4
122.3	5227.7	6202.8	5907.5	4304.6	7642.6	3414.4	5763.0	5160.3	15169.9	3576.5
3879.3	5117.9	5912.2	6122.6	5887.9	6843.5	5606.5	6113.0	5906.9	14501.9	4827.1
2160.2	5282.6	6613.1	6789.0	4077.8	7630.3	3204.0	6070.4	4853.4	14806.3	4426.2
815.7	5703.1	6759.6	7202.4	5156.3	7653.2	4489.1	6660.3	5657.5	14788.7	4650.7
13262.3	7147.3	7901.7	8272.8	7333.5	8583.9	9012.5	7332.7	8723.1	14750.5	8887.0
1567.8	5956.2	7085.8	7499.8	5910.0	5871.9	5980.8	6569.3	6508.8	11440.8	7344.5
3678.1	9023.3	9042.9	10586.9	8341.4	9498.9	7803.8	8787.1	12008.1	13303.9	11429.5
774.4	5713.2	6399.4	6933.8	5043.8	8311.0	4813.2	6052.6	5069.5	16178.7	4067.6
2660.9	6117.3	6556.6	7039.4	6080.5	7344.3	6085.1	6314.9	7940.0	12687.0	4677.1
9279.4	6427.1	6708.4	7608.0	6361.3	8637.0	7417.1	7896.6	7358.3	13433.9	6188.3
29448.3	9505.4	9848.3	10412.7	8893.2	11027.7	7618.8	8819.7	11807.0	17365.5	11454.9
162.4	3282.7	4154.7	4169.7	3070.8	3968.0	3207.4	5045.7	3778.6	7784.4	3714.4
3203.8	4165.6	5765.4	6604.3	3582.9	4822.6	3815.6	5093.3	5330.3	9720.3	7210.9
11717.2	6778.5	7367.9	7498.0	6553.7	8369.6	5715.3	7080.5	8963.5	15516.4	5475.7
933.9	7117.5	8384.0	8949.1	6723.8	10075.6	5809.7	7992.9	7670.8	19148.8	5607.2
170.8	3251.2	4655.6	5382.0	3137.8	5787.5	2947.8	4388.7	3136.2	14252.2	2977.1
817.8	4913.9	6048.4	6511.7	3571.6	6635.3	3386.0	5612.4	3968.4	14448.8	3552.5
781.2	5213.9	6131.9	6626.4	4646.6	7586.3	4265.1	5923.2	4528.7	14160.4	3935.1
2352.6	3705.0	4839.4	5666.9	3496.3	3981.1	4479.8	4885.4	2779.2	7539.9	4033.3
862.2	6872.9	8214.3	8795.6	6258.6	9994.2	4902.7	7813.5	7525.1	19861.7	5873.5
877.5	6266.4	7845.2	8547.3	4890.6	8648.1	3616.5	7451.6	6156.2	18321.0	5544.2
978.8	5181.8	5366.1	5918.2	4537.6	6495.5	4412.3	5784.0	4780.7	11439.9	4568.3
844.1	6676.1	7800.7	8441.5	5991.3	9559.6	5061.9	7746.7	6573.8	17466.8	5418.9
6427.6	6353.9	6368.0	6745.7	4630.9	7864.8	5147.7	6372.2	8544.3	12699.1	5694.2
2547.8	2632.0	3461.6	3435.6	1591.0	4046.9	2524.4	4183.9	2582.1	6474.3	2305.7
117.1	2908.5	3815.4	4051.5	2845.0	4857.2	2102.7	5049.9	2751.6	8489.8	2214.8
57.1	1504.7	2262.0	2264.7	1232.4	2897.4	898.9	2087.4	1508.8	4854.1	984.6
95.2	2204.6	2906.0	3235.3	1760.7	3815.1	1030.1	3318.3	2059.9	7607.9	1339.3
928.7	2829.5	3235.8	2872.9	3297.5	3655.6	2946.3	3260.8	2602.6	5491.7	2746.2
3323.5	3979.5	4403.1	4586.7	4686.2	4411.9	4464.6	4444.9	3928.1	2984.7	2354.8
12171.7	5224.0	5873.1	5890.0	4741.9	5677.9	6365.7	5457.7	6901.6	5692.9	6924.9

4739.6	4911.5	2708.4
7060.9	7089.1	3878.8
7148.2	5956.2	3173.6
8159.4	6712.8	3330.3
8176.7	7634.0	3539.4
11198.9	8384.6	5465.7
6838.1	6494.3	6321.5
9793.6	6942.8	4633.7
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7387.7	5696.8	2979.1
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9379.6	7510.5	5495.3
9546.0	8708.4	8255.8
5961.3	6907.1	4662.4
9574.9	9054.1	6582.2
9078.8	6917.2	4506.6
7943.8	7572.6	6463.0
9332.3	10018.4	8437.1
10561.0	10933.1	8339.4
3867.5	4766.3	1941.0
5139.7	6184.5	3153.9
8494.5	8439.3	5365.7
10866.3	8684.7	6292.4
7494.4	5419.1	2602.4
8378.6	6776.2	3853.9
8883.4	6727.2	4922.2
5031.3	4761.9	4477.7
10848.2	8531.4	5894.1
9819.2	8286.7	5138.8
7310.1	7071.2	5454.5
10874.8	8171.6	6109.1
8173.0	8048.0	5150.8
4777.1	5232.5	2525.1
5682.7	6070.3	2556.9
4440.0	3867.6	1152.0
3735.7	5382.7	1517.4
3749.5	6128.6	3913.4
4445.1	6161.9	4774.0
5449.7	7226.8	5196.2

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s__Tatumella ptyseos	5764
s__unclassified	4475
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s__Citrobacter farmeri	4447
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s__Citrobacter farmeri	5790
s__Citrobacter farmeri	5875
s__Citrobacter farmeri	5990
s__Citrobacter rodentium	4772
s__Enterobacter radicincitans	6229
s__Kluyvera ascorbata	4413
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s__unclassified	4159

EF688008.1 gg_id:341714 Pantoea citrea str. LMG 22049 EF688
FJ617235.1 gg_id:570566 Tatumella morbirosei str. LMG 23359 FJ6172
AJ233437.1 gg_id:10066 Tatumella ptyseos str. DSM 5000 AJ2334
EU877956.1 gg_id:565203 Tatumella ptyseos str. UAPS07005 EU877
EU215774.1 gg_id:257750 Tatumella saanichensis str. 06-3099 EU215
FJ611886.1 gg_id:552042 Pantoea punctata str. LMG 22097 FJ6118
EF688007.1 gg_id:330933 Pantoea terrea str. LMG 22051 EF688
AY837748.1 gg_id:142906 Thorsellia anophelis str. CCUG 49520 H2.1 AY8377
GU185859.1 gg_id:535185 Citrobacter amalonaticus str. SA01 GU185
AB088049.1 gg_id:77675 Citrobacter sp. str. VA53 AB088
AB504755.1 gg_id:386435 Citrobacter farmeri AB504
EU030438.1 gg_id:350440 Citrobacter farmeri EU030
FN433041.1 gg_id:573221 Citrobacter farmeri CCM30B FN433
DQ187379.1 gg_id:140670 Citrobacter amalonaticus DQ187
AY379978.1 gg_id:98643 Salmonella sp. str. AHL 6 AY379
FN433046.1 gg_id:561185 Citrobacter farmeri CCM35B FN433
NR_028686.1 gg_id:586695 Citrobacter sedlakii str. I-75; CDC 4696-86 NR_02
EU931550.1 gg_id:335500 Klebsiella oxytoca str. ZFJ-11 EU931
AF176567.1 gg_id:71543 Kluyvera ascorbata str. CDC 2064/78 AF176
AM933758.1 gg_id:332628 Kluyvera ascorbata 4105 AM933
AJ627203.1 gg_id:106098 Kluyvera ascorbata 276 AJ6272
AF025370.1 gg_id:9766 Citrobacter amalonaticus str. CDC 9020-77 AF0253
GQ205104.1 gg_id:558666 Enterobacter sp. str. RF-100 GQ205
DQ923474.1 gg_id:235571 Enterobacter sp. str. g1 DQ923
FJ593851.1 gg_id:527723 Enterobacter sp. str. MTP_050512_17 FJ5938
AY683044.1 gg_id:137822 Enterobacter sp. str. CBMB30 AY683
EU753977.1 gg_id:315576 Enterobacter sp. str. FR7 EU753
NR_024861.1 gg_id:559750 Citrobacter farmeri str. CDC 2991-81; CIP 104553 NR_02
EF025329.1 gg_id:178177 Enterobacter cloacae subsp. dissolvens str. SREPS 3 EF0253
AB475140.1 gg_id:518801 Cimex lectularius endosymbiont str. SYDL AB475
GQ492450.1 gg_id:590760 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
AAJU02000050.1 gg_id:311814 Escherichia coli str. F11 AAJU0
EU773756.1 gg_id:323418 Cheetah feces clone CE2_h04_1 EU773
AB244469.1 gg_id:253351 Enterobacter cloacae str. NC1111 AB244
AM980865.1 gg_id:369200 Escherichia coli str. ATCC 35218 AM980
EU460669.1 gg_id:289561 polar bear feces clone PB2_aai24b09 EU460
AB244459.1 gg_id:248864 Citrobacter freundii str. C3-1 AB244
FJ811872.1 gg_id:586506 Enterobacter aerogenes str. 11-WCH FJ8118
GQ047957.1 gg_id:440793 Topographical and Temporal Human Skin Microbiome skin palm clone nbw139e11c1 GQ047
AY253921.1 gg_id:85035 Rahnella aquatilis m 46 AY253
GQ155272.1 gg_id:575075 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155

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70.5	1336.8	2367.9	2467.7	1545.2	4846.1	1510.5	2388.1	1448.9	9920.1	943.4
400.6	3558.2	4684.2	4588.1	3310.2	5757.6	2847.9	4240.9	3741.7	10209.8	2466.2
349.2	3430.4	4485.6	4199.6	2648.2	5521.8	2627.4	3852.7	3123.5	8530.3	2784.6
49.0	2285.8	3860.9	4173.1	1718.2	7924.7	2092.3	3860.8	3927.2	12349.2	1733.5
166.5	4162.7	4930.8	5083.8	3207.0	8118.0	2283.8	4486.1	3518.8	15007.8	2833.6
115.0	4620.3	5507.1	5751.9	3345.7	8060.8	3167.5	6843.8	6833.3	12122.4	4435.8
48.9	565.9	335.8	224.8	129.9	480.6	65.3	393.6	302.9	257.5	211.2
92.1	4388.4	5087.9	5374.4	3366.4	5893.7	2123.5	6023.1	4125.0	10420.0	2733.3
181.1	3951.5	4755.5	5184.8	3160.5	6941.6	1728.0	4155.1	2764.7	12548.9	2212.6
53.2	1798.4	2334.8	1934.5	1238.2	2893.6	575.2	2541.8	1480.6	8121.9	1183.7
65.1	4087.6	5725.6	6287.1	2834.0	6799.2	1269.5	6846.7	3964.3	13432.6	3413.6
4625.5	8034.5	8812.4	10349.5	9477.9	9914.0	9058.2	8560.2	7964.1	14157.5	8949.1
182.0	3271.5	3835.9	3872.1	2099.4	4147.0	1742.9	4301.4	2240.2	9039.4	2110.6
71.2	3286.6	3488.4	3642.9	2488.8	4701.9	2043.5	3775.5	3651.1	11231.7	1788.5
113.3	4035.7	4953.9	5002.5	3355.7	6238.7	3179.5	5041.1	4412.7	11195.2	2295.9
85.2	2223.8	3949.8	3335.3	1167.1	4724.1	706.3	3458.9	1758.6	9882.8	1427.3
5457.4	5804.1	7585.5	7291.6	6154.8	9620.8	5302.0	6228.3	4347.2	14678.8	5035.8
87.9	2279.8	3023.1	3260.0	1606.3	5408.5	1119.1	3811.9	1599.1	7681.8	1662.9
79.1	2072.7	3706.2	3586.1	2353.1	5107.2	1490.2	3026.8	1434.1	13076.8	1255.1
149.7	5772.4	6621.7	7062.7	5190.7	9700.9	5161.4	6810.0	3898.6	15766.0	4179.2
187.0	4283.7	5337.3	5605.7	3133.3	5481.3	2175.6	6030.0	4281.5	10774.1	3126.2
170.9	6590.9	7672.2	7813.6	5492.7	9942.2	4106.3	7350.3	5382.4	19000.3	4477.5
384.1	5240.4	7693.1	7246.1	5216.5	9770.5	3146.3	5591.6	3107.4	18240.9	3188.4
6152.2	8324.8	9895.8	9949.7	7953.5	10904.4	6632.7	9015.2	7974.4	17784.8	8466.2
4361.5	6456.4	8555.9	8484.7	6543.7	8632.0	6106.8	7448.7	5842.3	13334.5	5505.8
1526.2	5547.5	6577.6	6726.3	5407.0	7638.4	3838.2	6061.5	4735.6	13851.8	4206.2
123.2	3374.6	4005.5	3970.3	2209.8	4458.5	1447.9	5106.9	3384.6	7351.1	2468.2
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1424.4	4702.8	6082.2	6550.7	3895.0	7480.2	2633.3	7379.0	5879.1	11943.5	4528.0
110.3	4114.8	6340.1	7298.4	2824.7	5552.6	3397.2	6225.1	3674.5	16147.4	4410.1
329.1	5506.7	6820.3	7407.5	4508.4	7658.2	3944.9	6605.7	5809.3	14568.6	4300.3
21994.6	6927.0	6291.7	7028.8	7106.2	6916.4	7782.1	6529.8	9341.9	9465.3	9096.0
772.8	8063.5	9634.1	10227.6	7362.8	12406.9	6532.3	9180.8	6740.3	22590.3	5947.9
127.9	897.4	1141.9	1464.4	877.9	2643.8	1303.6	1028.4	1274.0	6992.1	1057.5
2481.9	5327.3	6540.0	7225.2	4433.4	7781.2	3728.4	5963.2	6027.1	15664.6	4635.7
155.3	4251.3	5415.5	6005.7	4594.2	6908.7	3524.5	4040.2	1674.6	12413.3	2067.6
1770.6	4609.9	6089.5	6581.7	3833.9	8568.4	2796.3	6292.1	5013.0	14288.9	4260.2
8423.8	7282.9	8255.3	9496.3	7249.7	7843.7	7768.3	8425.0	9846.1	12499.4	9363.8
2526.7	7148.8	8421.8	9349.2	9357.0	10121.8	8454.5	10163.0	9653.0	15013.6	7595.2
12185.9	6354.5	6054.6	6701.2	6326.0	6672.5	6678.9	6283.9	8365.9	10583.1	7447.3

12383.0	9229.4	6612.1
4687.9	3018.9	1121.9
5398.9	6598.8	2280.9
5666.6	6002.8	2029.9
8237.9	6776.2	2747.5
7854.5	6501.7	3149.8
8426.9	7332.5	3495.4
599.2	603.1	169.3
6770.7	6084.7	2621.1
6862.6	5912.8	2926.9
3250.8	2481.9	796.5
8031.1	6924.1	2822.6
10426.8	10843.7	9889.5
4992.1	4339.9	1901.0
5953.1	4099.3	2055.8
8066.7	6019.7	2654.1
5529.2	4774.4	2186.6
10264.8	7625.2	5803.6
5203.4	3615.2	1805.4
4941.2	3404.8	1232.9
10222.9	6811.5	5179.6
6126.9	6325.3	2644.5
11318.6	8888.1	6080.7
9751.6	7289.9	4197.4
11146.8	9854.9	7052.5
10204.2	8687.3	5501.1
7955.1	6564.3	4961.4
4680.4	4889.1	2140.6
4796.0	4869.7	1630.8
9009.8	8156.8	4315.0
7635.9	5002.9	2202.4
9491.1	7953.8	4912.9
7426.4	8486.4	7007.0
12536.1	8968.9	6673.3
3112.8	2669.2	820.3
8607.1	7109.7	4264.3
6657.5	4711.7	2069.2
8294.9	7556.7	4230.2
8597.8	9071.0	7320.8
11162.6	9767.8	7233.1
7031.7	8525.7	6965.3

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AF373174.1 gg_id:72751 Erwinia chrysanthemi str. GSPB 413 AF373
GQ167172.1 gg_id:592775 Effects Hydraulic Retention Time on Anaerobic Hydrogenation Performance Microbi GQ167
EU472695.1 gg_id:288236 red panda feces clone RPSD_1aaa02d08 EU472
GQ047715.1 gg_id:441491 Topographical and Temporal Human Skin Microbiome skin palm clone nbw138d06c GQ047
GQ155218.1 gg_id:561972 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EU723822.1 gg_id:345487 Shigella sonnei str. HDDMG06 EU723
AB479110.1 gg_id:561984 Escherichia hermannii str. YS-11 AB479
GQ155226.1 gg_id:513466 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ155033.1 gg_id:572044 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EU472730.1 gg_id:290622 red panda feces clone RPSD_1aaa01a11 EU472
EU470818.1 gg_id:288035 red panda feces clone RP_2aaa01b05 EU470
ABHR01000009.1 gg_id:292182 Escherichia coli O157:H7 str. EC4401 ABHR0
EU472797.1 gg_id:295950 red panda feces clone RPSD_1aaa03d01 EU472
DQ441386.1 gg_id:184632 human intestinal biopsy clone CD135 DQ441
EF179843.1 gg_id:271664 sequences adult Anopheles darlingi (Diptera: Culicidae) mosquitoes clone 1.1 EF1798
GQ047641.1 gg_id:385282 Topographical and Temporal Human Skin Microbiome skin palm clone nbw137b10c GQ047
GQ491694.1 gg_id:593660 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
AY689045.1 gg_id:105300 Enterobacter sp. str. 6B_5 AY689
EF189919.1 gg_id:365055 Pantoea stewartii 40G RT2A EF1899
EU466029.1 gg_id:295053 African elephant feces clone AFEL3_aao16b08 EU466
FN433049.1 gg_id:547245 Citrobacter braakii CCM33B FN433
EU460308.1 gg_id:299829 polar bear feces clone PB1_aai26c12 EU460
GQ155101.1 gg_id:565925 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ047977.1 gg_id:445372 Topographical and Temporal Human Skin Microbiome skin palm clone nbw139g10c GQ047
EU472889.1 gg_id:293518 red panda feces clone RPSD_1aaa03f04 EU472
EU471175.1 gg_id:293468 red panda feces clone RP_3aaa01g02 EU471
AY792270.1 gg_id:122049 Humic Lake clone CrystalBog1E3 AY792
FJ364672.1 gg_id:370240 feces adult twins and mothers; TS19 clone TS19_a01f10 FJ3646
EU460405.1 gg_id:294051 polar bear feces clone PB1_aai28b07 EU460
DQ818978.1 gg_id:168683 mouse cecal microbiota-colonized zebrafish digestive tract clone aab40d10 DQ818
DQ133536.1 gg_id:138463 Citrobacter freundii str. GM1 DQ133
EU470874.1 gg_id:300686 red panda feces clone RP_2aaa01h11 EU470
AJ223409.1 gg_id:9789 Pectobacterium cacticida AJ2234
EF608524.1 gg_id:228556 predatory Poecilus chalcites their response lab rearing and antibiotic treatment diges EF6085
AY227805.1 gg_id:100736 Pantoea dispersa UQ68J AY2278
GQ155135.1 gg_id:578405 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EF551364.1 gg_id:223793 Enterobacter cloacae str. Rs-35 EF5513
GQ156545.1 gg_id:510870 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
GQ025567.1 gg_id:419206 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ025
GQ031700.1 gg_id:436114 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ031
EF643377.1 gg_id:236811 Mangroveibacter plantisponsor str. MSSRF40 EF6433

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1999.6	5654.3	6609.5	6693.7	4751.3	8811.0	4044.4	7079.3	4058.6	15626.1	4192.8
7757.9	4654.5	5134.0	5675.7	4864.1	5091.1	5390.4	5286.6	6025.4	8486.4	7098.7
289.4	2068.6	3437.9	3872.8	1734.7	3099.1	2061.6	3616.7	1423.3	6760.9	2311.2
812.8	6389.1	7278.1	8088.2	5579.5	9239.3	4811.1	7264.3	6631.6	17015.6	5274.6
2817.6	4005.7	4815.1	5510.3	3479.5	6081.8	2695.5	4933.5	3581.6	10667.9	3936.5
925.0	8367.9	9655.9	10575.3	6868.4	12232.4	5155.5	9405.3	9262.7	22758.2	6636.4
755.2	5138.8	5743.9	6283.2	4887.5	7918.2	4432.2	5754.4	3924.0	15437.4	3224.6
692.0	4350.5	5138.8	5564.6	4587.8	6184.3	3671.3	5190.8	3577.6	11526.6	3103.6
1715.1	6185.7	7684.1	8273.9	5267.4	8073.3	4858.4	7425.4	6182.1	15389.4	5949.2
1878.0	5746.5	6998.3	7954.4	5256.2	7427.4	4504.6	7226.0	6309.0	15192.5	5418.4
627.5	3775.9	5748.7	6785.4	2698.3	4813.3	3120.5	5602.5	3071.2	9959.5	4545.4
901.3	6302.1	7787.6	8734.9	5528.7	8820.9	5259.9	7411.0	5171.5	17881.1	5603.7
971.3	6913.5	8426.6	9289.3	6052.2	9988.6	5120.0	8104.8	6542.5	19239.2	5843.0
357.7	1893.4	2771.2	2705.5	2170.0	3250.6	1666.9	2396.8	2658.9	5039.4	1587.9
796.9	2579.8	3705.2	4092.4	2095.2	3325.4	3134.0	3345.7	1127.4	6881.1	2508.3
399.8	3208.9	3563.1	4458.5	2570.7	4611.1	3405.8	4055.9	3641.7	7524.3	3598.3
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2044.9	4124.0	5007.6	5058.8	3872.6	5036.0	4060.4	4070.4	7328.5	8645.3	3854.0
736.6	5241.8	6217.1	6411.0	5087.5	7607.4	4673.4	6198.0	6836.2	14968.1	3760.0
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63.2	2751.0	3979.0	3392.3	2189.4	5918.2	2016.0	2768.2	1590.8	9919.7	1248.2
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476.4	5334.9	6972.2	7240.8	6068.4	9927.2	3045.7	5461.0	4323.0	20389.5	3025.5
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7988.2	8138.3	8540.5	8986.2	6819.5	9954.5	5821.1	8737.0	8158.2	16771.2	6122.8
21672.7	7722.8	8095.7	8872.0	8427.5	7754.1	8523.5	6909.4	10199.9	12666.2	10311.2
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GQ099252.1 gg_id:408166 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ099
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EU472888.1 gg_id:287425 red panda feces clone RPSD_1aaa01a08 EU472
GQ280089.1 gg_id:564812 Enterobacter sp. str. JS-19 GQ280
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EU472787.1 gg_id:292501 red panda feces clone RPSD_1aaa04h10 EU472
AF273037.1 gg_id:25611 Samsonia erythrinae AF273
EU459221.1 gg_id:292667 hedgehog feces clone HH_aai34c03 EU459
DQ418491.1 gg_id:167165 Pectobacterium sp. str. Zhaotong DQ418
EU766876.1 gg_id:338288 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU766
GQ155237.1 gg_id:576536 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EU471097.1 gg_id:288710 red panda feces clone RP_3aaa04h05 EU471
GQ492914.1 gg_id:574632 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
GQ032083.1 gg_id:402097 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ032
EU471321.1 gg_id:301319 red panda feces clone RP_3aaa04c11 EU471
GQ047644.1 gg_id:442743 Topographical and Temporal Human Skin Microbiome skin palm clone nbw137c01c1 GQ047
GQ102003.1 gg_id:443904 Topographical and Temporal Human Skin Microbiome skin palm clone nbw502d01c1 GQ102
EU468008.1 gg_id:294204 cheetah feces clone CE2_b02_1 EU468
EU762556.1 gg_id:321515 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A> EU762
GQ493642.1 gg_id:551110 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
GQ155290.1 gg_id:561147 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ155055.1 gg_id:509758 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ492249.1 gg_id:536894 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
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EU596536.1 gg_id:273327 Pantoea agglomerans str. SZ009 EU596
EU289465.1 gg_id:240399 metagenomic approach biosynthesis ansamycin endophytes or symbionts enriched s EU289
AB548574.1 gg_id:531505 Escherichia coli str. JCM 24001 AB548
EU466771.1 gg_id:289838 African elephant feces clone AFEL2_aao29c08 EU466
EU472860.1 gg_id:295962 red panda feces clone RPSD_1aaa02g08 EU472
GQ155181.1 gg_id:512375 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ114745.1 gg_id:385051 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ114
EU472794.1 gg_id:294989 red panda feces clone RPSD_1aaa03a08 EU472
FJ683754.1 gg_id:530543 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6837
DQ248277.1 gg_id:142545 carbon tetrachloride contaminated soil clone TA2 DQ248
EU772604.1 gg_id:322410 North American Black Bear feces clone BB1_h09 EU772
GU166291.1 gg_id:588020 Pantoea sp. str. Y1 GU166
E05133.1 gg_id:28107 Escherichia coli E05133

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4135.2	4430.9	5660.9	6030.1	3858.9	5659.6	3246.3	5278.1	4740.1	11136.1	5165.6
946.7	2597.3	3071.2	2840.9	2882.2	4390.2	2862.8	4100.5	1759.7	12897.8	2262.2
69.2	3795.5	5024.6	4963.8	3935.7	8244.1	2186.3	3831.5	1560.2	15630.4	1782.2
872.5	6117.1	7622.8	8634.7	5095.0	9098.2	4555.4	7214.6	4688.0	17052.5	5436.1
626.8	3352.4	4775.6	5582.7	2594.6	4688.0	2508.2	4735.2	2935.8	9831.5	3819.7
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6606.7	7081.2	8320.8	8940.3	6217.5	8210.0	6731.9	8074.8	7116.1	15181.3	8133.0
9505.4	7322.4	6565.7	7251.2	6700.3	7539.4	6867.1	6831.7	8988.1	10265.5	6310.7
2357.5	3573.6	4817.8	4582.5	2485.4	4978.5	2040.4	4696.2	4359.3	9652.7	3379.8
1920.5	6551.7	7739.0	9010.2	5229.2	7860.5	5869.4	6843.9	7752.5	12842.5	8482.0
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3782.7	4319.4	5134.0	5643.3	3694.2	4171.4	4609.7	5074.1	4731.9	7001.4	7230.0
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173.9	4390.8	5935.9	6525.6	3274.1	6222.0	3011.1	5327.5	3143.1	12756.1	3458.6
2179.3	4298.7	6039.1	6839.4	2938.2	5078.8	3811.8	5881.0	2731.9	14094.4	4847.5
6820.1	7022.2	7849.8	9427.8	6683.3	8729.4	6768.9	7398.3	9117.1	15770.2	8426.3
23478.3	7234.6	8272.2	8595.6	7292.6	9245.2	8095.9	7877.7	10815.5	14617.4	6963.2
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914.7	2172.2	3309.5	3590.4	1786.0	3713.7	2484.9	3283.8	1672.2	9055.5	2425.1
88.9	2464.0	3644.6	3621.7	2012.3	4654.6	1101.7	3984.7	2774.2	9323.8	1820.1
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9865.9	7815.8	8968.0	9384.5	8123.8	10008.6	6428.2	9587.3	8785.5	17608.9	8439.1
16544.5	8994.1	9932.5	9964.1	8659.0	11648.4	8118.6	9127.5	10055.0	18909.9	9435.4
5697.4	6591.3	7530.9	8635.2	5865.5	8010.4	6080.4	7976.6	7164.2	12522.5	7277.3
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65.8	2383.6	3649.7	3912.9	2531.0	6727.2	1521.3	3431.4	1137.6	9631.5	1633.3
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7350.9	4981.1	2965.8
10564.9	7857.1	4833.7
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8045.7	8405.9	5678.6
8140.2	7497.7	6071.5
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9202.7	8323.8	6515.4
9695.8	9532.6	6797.1
9381.9	7272.2	4697.0
6413.8	5520.5	4145.3
4574.6	3986.9	1397.7
4207.7	4686.2	2258.0
6092.6	6814.9	5293.9
10745.8	7618.0	3550.5
7398.8	6788.1	3079.1
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9223.0	7493.8	5122.8
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10444.9	9357.2	7489.9
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GQ025616.1 gg_id:409079 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ025
AB548828.1 gg_id:514244 Citrobacter freundii str. JCM 24063 AB5488
GQ304782.1 gg_id:585624 Shigella flexneri str. A6 GQ304
NC_008253.1 gg_id:162759 Escherichia coli str. 536 NC_008
GQ101929.1 gg_id:465791 Topographical and Temporal Human Skin Microbiome skin palm clone nbw501a07c1 GQ101
AJ010486.1 gg_id:9947 Enterobacter pyrinus str. KCTC2520 AJ0104
DQ785510.1 gg_id:171754 Pectobacterium carotovorum str. ZJR1 DQ785
EU472892.1 gg_id:289762 red panda feces clone RPSD_1aaa01f07 EU4728
GQ031973.1 gg_id:484652 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw: GQ031
AM419020.1 gg_id:196793 Rahnella sp. str. NJ-8 AM419
EU470589.1 gg_id:290393 red panda feces clone RP_1aaa03e10 EU4705
EU530394.1 gg_id:261413 mucosa adherent and invasive microbes adenoma colorectal cancer profile non-ader EU5303
AB004744.1 gg_id:10064 Enterobacter asburiae str. JCM6051 AB0047
EU887834.1 gg_id:349857 and RFLP slurry Nisargruna biogas plant aerobic predigester clone 11A EU8878
GU594302.1 gg_id:519860 Escherichia coli str. A23 GU594
GQ155206.1 gg_id:569366 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EF515196.1 gg_id:226252 Electricigen Enrichment MFC upf microbial fuel cell anode clone 21b10 EF5151
EF560793.1 gg_id:238066 Escherichia coli str. BEG21 EF5607
DQ818882.1 gg_id:166890 mouse cecal microbiota-colonized zebrafish digestive tract clone aab39b10 DQ818
GQ155211.1 gg_id:546826 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EU470583.1 gg_id:302277 red panda feces clone RP_1aaa04a10 EU4705
FJ906906.1 gg_id:571278 Cronobacter muytjensii str. Jor93 FJ9069
DQ068925.1 gg_id:139022 microbiota antlions (Myrmeleon mobilis) whole animal laboratory starved antlion O DQ068
AM184307.1 gg_id:160426 Pantoea agglomerans str. WAB1969 AM184
GQ009455.1 gg_id:500210 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw77 GQ009
GQ102029.1 gg_id:442720 Topographical and Temporal Human Skin Microbiome skin palm clone nbw502f06c1 GQ102
GQ155009.1 gg_id:566225 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
AP010960.1 gg_id:546416 Escherichia coli O111:H- str. 11128 AP0109
X80729.1 gg_id:9692 Escherichia coli str. PK3 X80729
GQ155095.1 gg_id:510292 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GU223214.1 gg_id:581700 Enterobacter cloacae str. SK_C-2 GU223
U92195.1 gg_id:9714 Salmonella enterica subsp. houtenae serovar Houten str. Sh1 subsp. U92195
GQ102010.1 gg_id:386695 Topographical and Temporal Human Skin Microbiome skin palm clone nbw502d08c1 GQ102
GQ491972.1 gg_id:550764 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
GQ031668.1 gg_id:440795 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ031
FJ009375.1 gg_id:338379 Enterobacter cancerogenus str. H3 FJ0093
AJ605115.1 gg_id:112171 Escherichia coli str. BL21 AJ6051
AB548825.1 gg_id:514639 Citrobacter freundii str. JCM 24060 AB5488
DQ392983.1 gg_id:156485 Pantoea agglomerans str. d DQ392
GQ154854.1 gg_id:511626 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154

79.7	4500.0	5390.8	6076.3	3459.3	8237.1	3194.5	4932.1	4425.3	11865.3	2674.1
3108.7	6178.0	6652.6	7276.3	6646.8	7911.6	6307.4	6952.1	6524.0	14997.9	7028.3
277.5	7714.8	9159.3	9399.0	8096.6	12087.3	7661.4	8371.4	5064.8	20616.8	4691.9
1349.0	4892.5	6214.8	6564.8	3320.8	6038.2	2814.7	5884.4	3261.4	14309.3	4178.2
2022.5	4836.9	5659.0	6723.8	3955.5	6704.0	3877.3	5550.9	4688.1	12394.9	5032.1
231.3	5759.3	5824.6	6233.5	5061.3	6793.3	4070.8	6569.1	5809.1	10120.1	4495.8
274.0	4821.7	5548.1	5432.4	4660.1	7332.4	4523.6	5036.6	4355.7	11580.4	3710.3
3339.5	7914.5	8136.0	8796.4	7307.5	9496.5	7659.4	8361.9	6931.0	15177.8	6236.5
166.9	1665.4	2520.3	2279.0	1138.4	3242.4	1165.2	2971.3	1829.8	6290.8	1297.4
287.2	3412.2	4643.6	5237.9	2764.4	5183.3	2485.0	4522.4	3037.8	11883.2	2509.9
72.1	1682.6	1532.6	1570.1	1546.3	2109.6	990.4	1815.4	1059.7	3169.7	688.4
5034.0	7083.5	6941.8	7284.6	6262.6	6992.8	6638.0	6252.5	11391.2	10352.1	10414.5
30756.7	10792.3	10470.7	11571.6	9484.6	10457.4	10103.2	10444.3	14781.6	15235.2	13879.7
642.5	7312.8	9562.5	9624.8	6004.3	12549.1	4865.5	9476.8	5033.9	22993.0	5262.2
3249.9	7184.7	7989.6	8911.2	6572.1	11294.8	5806.0	8672.9	7650.5	15730.3	5432.5
465.4	5476.6	7292.0	8130.7	4640.2	7725.3	4733.9	6691.5	4705.4	15299.2	5070.3
824.8	7196.9	8322.7	9062.5	6481.8	9828.5	5546.5	8292.5	7745.6	18013.9	5941.0
257.1	3356.0	4722.7	4574.2	3671.8	6085.6	2601.5	4467.4	3544.2	11338.2	2895.0
916.0	5267.8	6649.5	7162.6	3899.9	7330.9	3087.5	6442.2	5054.1	14146.0	3735.7
28805.2	10310.7	10422.2	11847.4	11696.6	10992.3	11866.0	10746.5	15160.8	14511.3	16977.0
8950.0	5905.1	5726.6	6294.6	5603.2	6876.7	5829.5	5780.7	7216.8	11397.0	6393.3
796.5	3873.0	4895.1	5281.8	2754.2	5270.4	2721.7	4544.2	2624.0	12090.6	2797.7
2682.5	3651.0	4414.0	4461.4	3395.4	5308.4	2023.2	3743.6	2530.1	8436.1	2724.5
6132.4	5217.2	6029.2	6062.7	4715.2	9496.2	4070.0	5629.9	5692.3	14005.3	4230.0
1072.9	4731.0	5730.1	5736.2	4231.7	8246.9	2749.8	6589.5	3956.6	16125.4	4336.6
113.6	4752.5	6160.6	6616.4	7904.7	9256.5	6327.3	5982.2	4458.8	12167.8	3860.6
494.7	5222.9	5426.9	5973.2	4979.0	5738.7	4990.0	5785.3	5958.5	8201.4	4364.4
6181.2	5546.1	6586.2	6796.8	6681.4	7300.7	7278.9	6502.8	5793.5	10506.1	4448.4
466.6	5427.1	6522.4	7222.7	4728.5	7859.0	4368.0	6052.1	5827.8	15473.8	4307.1
2076.2	4337.6	5375.9	5545.5	3908.7	6173.2	3220.7	5029.9	3072.5	11806.5	3164.1
147.7	3660.3	4944.3	5184.0	3481.6	5630.5	2560.4	5303.5	3024.0	10974.3	2557.9
8839.1	7223.4	7832.3	8857.9	7781.4	7927.5	8296.8	7220.0	10577.3	13615.0	9014.2
95.2	4137.1	5636.9	6258.2	3700.1	5504.7	2837.8	5772.1	1958.6	9345.9	3075.4
259.4	5663.1	5806.4	6299.7	4988.7	6810.5	3835.2	6644.5	5844.6	9559.4	4494.7
1092.1	6615.6	8192.5	8787.0	5780.3	9781.0	4458.2	7704.2	7070.4	18622.4	5671.4
734.0	4857.2	5163.0	5576.6	4635.0	5676.6	4541.3	4658.8	5579.3	11665.9	3530.8
695.2	7056.9	8226.2	9196.5	6136.0	12074.9	4950.3	7717.8	5714.0	22324.8	5657.4
2320.5	7860.9	8582.2	10472.6	7743.9	8567.7	8058.3	6874.5	11797.7	12728.0	8072.5
167.8	7455.1	9225.8	8830.6	7390.0	11269.1	7109.5	8917.9	5138.0	20569.1	5242.7
122.9	5126.6	6562.7	6649.5	4866.9	10345.4	3200.0	5652.4	2712.2	20596.7	2990.7
152.7	5781.5	6302.8	6729.7	4906.4	8148.9	4931.8	6413.1	5041.8	14483.4	3827.9

9138.9	7732.8	3904.4
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8188.6	5712.5	4132.2
7846.8	6449.6	4208.1
6899.1	6898.1	4621.0
8050.4	7380.3	5952.2
9544.9	8271.3	6444.4
3848.9	4518.0	1370.9
5802.7	4944.8	2186.3
1886.3	2211.5	1268.3
6812.1	8404.5	5852.1
11949.8	11409.2	9551.5
13672.2	10457.6	5307.3
13877.1	10793.9	6648.2
8767.9	7318.9	4438.6
11322.2	8787.9	6618.8
5927.4	5108.0	2773.0
8731.1	7555.8	4713.9
10794.2	12635.3	10411.3
7564.6	7971.5	6050.5
7432.4	5599.6	3041.8
5029.0	5054.7	2346.9
8742.1	8593.6	4197.9
8799.2	5885.0	3338.8
9392.6	8039.9	6622.9
6098.4	7642.2	4831.8
8593.2	7398.9	4999.8
8600.5	7339.0	4343.0
8007.2	6244.1	3602.7
6297.0	5528.3	2706.1
7718.8	9302.6	7949.3
6989.1	4729.6	2787.3
6831.7	6930.6	4611.0
11114.8	8822.5	5794.5
5895.0	6304.3	4096.6
12438.3	8636.2	6064.1
9598.4	9292.6	8681.3
12236.0	8764.2	5817.6
9609.4	5972.7	3977.7
9033.3	7243.4	5617.4

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Z96085.1 gg_id:9839 Erwinia psidii str. LMG 7034 Z96085
GQ031716.1 gg_id:435217 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ031
EU464991.1 gg_id:302227 African elephant feces clone AFYEL_aaj66d03 EU4649
CP001790.1 gg_id:523633 Pectobacterium wasabiae str. WPP163 CP0017
GQ025498.1 gg_id:405896 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ025
GQ155325.1 gg_id:582831 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
FJ611867.1 gg_id:538150 Enterobacter cancerogenus str. LMG 2693 FJ6118
EF418614.1 gg_id:216720 Escherichia coli str. WR EF4186
GQ156571.1 gg_id:566976 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
EU466945.1 gg_id:296544 African elephant feces clone AFEL2_aao31f11 EU4669
GQ155259.1 gg_id:553265 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
CP000247.1 gg_id:169669 Escherichia coli str. 536 CP0002
EU464454.1 gg_id:293609 African elephant feces clone AFEL_aai29d08 EU4644
GU171376.1 gg_id:580156 Rahnella aquatilis str. 5YN04-01 GU171
AM157447.1 gg_id:141508 Escherichia coli mother V4 AM157
FJ906795.1 gg_id:568033 Erwinia chrysanthemi str. Lichuan2 FJ9067
FJ997269.1 gg_id:430317 Escherichia coli str. DSPV 247T FJ9972
GQ155006.1 gg_id:568846 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ155014.1 gg_id:538134 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EU472748.1 gg_id:290732 red panda feces clone RPSD_1aaa04e08 EU4727
EU780667.1 gg_id:307587 Pantoea sp. str. CWB304 EU7806
GQ031664.1 gg_id:465153 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ031
GQ155195.1 gg_id:582588 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EF446900.1 gg_id:210269 Enterobacter cloacae str. AW3 EF4469
GQ101953.1 gg_id:441943 Topographical and Temporal Human Skin Microbiome skin palm clone nbw501f08c1 GQ101
EF560774.1 gg_id:233520 Escherichia coli str. 228 EF5607
AM184220.1 gg_id:159834 Enterobacter cloacae str. WAB1878 AM184
EU937744.1 gg_id:329159 Enterobacter sakazakii str. JG 09 Iti 7 EU9377
DQ444288.1 gg_id:154803 Klebsiella oxytoca str. 17 DQ444
GQ047998.1 gg_id:430834 Topographical and Temporal Human Skin Microbiome skin palm clone nbw140a11c1 GQ047
GQ156028.1 gg_id:566205 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
EF102835.1 gg_id:257820 Pectobacterium carotovorum str. G-1-7 EF1028
EU470480.1 gg_id:291647 red panda feces clone RP_1aaa02b02 EU4704
DQ068852.1 gg_id:139468 microbiota antlions (Myrmeleon mobilis) GI tract freshly caught antlion OTU9 clone DQ068
EU470518.1 gg_id:288607 red panda feces clone RP_1aaa01b06 EU4705
CU915024.1 gg_id:449170 and dynamics adapted microbiota during degradation Tunisian zarzatine enriched se CU9150
CP001637.1 gg_id:524975 Escherichia coli str. DH1 CP0016
EU472906.1 gg_id:298938 red panda feces clone RPSD_1aaa02d07 EU4729
GQ155318.1 gg_id:509391 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
AY690711.1 gg_id:101221 Erwinia sp. str. MK01 AY6907
GQ048037.1 gg_id:462729 Topographical and Temporal Human Skin Microbiome skin palm clone nbw140f06c1 GQ048

6436.9	6139.3	6753.5	7000.7	5372.6	7560.2	4042.8	6726.8	6024.1	11796.5	5088.9
3653.5	6339.3	7150.1	7797.0	6033.5	7983.9	5157.8	6698.7	8145.8	15990.9	6290.3
4292.5	4298.4	4392.6	4407.1	4842.8	4965.6	5115.0	4890.5	9590.2	11287.3	4414.9
196.4	5714.4	7992.4	8236.6	4161.3	9179.6	2473.1	8377.6	5132.0	16608.9	4075.8
8138.8	7345.7	8127.3	7638.6	6978.7	8363.0	7581.4	6987.3	9729.9	13711.1	8108.0
682.3	6644.8	7773.9	8193.8	6049.3	9506.7	5321.7	7458.6	7003.4	18198.5	4971.8
66.4	6590.6	8741.0	8966.2	5339.8	12183.7	3796.7	7826.3	3831.5	22914.4	4178.2
790.9	4394.8	5277.9	5567.3	3679.4	6447.5	2998.1	4992.5	3659.9	15636.5	2933.8
784.6	4726.5	5512.9	5922.4	5681.7	6279.6	4823.9	5701.4	3861.4	11368.8	3427.3
11576.6	4875.1	5150.9	5244.9	4856.8	5340.4	4924.6	4320.3	6844.6	9891.7	6016.3
705.0	4460.7	5285.8	5581.7	5127.9	5998.3	4082.0	5312.0	3360.6	10599.2	3175.3
238.4	4278.0	5466.7	5803.4	4435.2	6246.0	3244.5	5629.2	4061.8	12185.0	2862.2
2086.7	5904.1	7741.0	8504.1	5306.5	8306.9	4124.3	7817.2	6462.6	17372.5	5452.4
122.9	6115.3	6762.9	6380.5	4887.4	8432.0	4987.2	5990.3	5326.4	13150.6	3703.4
3367.8	5986.1	6425.4	7444.0	5845.1	8085.2	6047.4	5823.3	6277.7	10039.0	5813.4
1225.4	4248.1	5906.7	6410.9	4114.4	6162.0	3860.9	6816.1	5107.2	9850.6	4280.8
198.4	2576.0	3724.9	3493.5	3014.8	4206.6	1943.1	3395.5	3703.8	9437.5	1519.0
4545.6	6816.5	7677.8	9038.9	6687.0	8753.2	6738.5	8678.3	6930.7	14160.4	9698.7
5191.0	5543.8	5836.8	6596.7	5236.4	8137.9	4608.3	6509.8	5068.0	13440.9	5423.5
1861.3	5925.2	6893.4	7025.2	6290.0	7973.2	6981.8	6457.9	5049.1	14579.5	5730.9
112.4	4109.9	4063.8	4318.4	5295.0	6699.3	2982.9	5084.3	4839.4	10844.5	2592.2
2423.3	6266.7	7680.5	8214.3	5688.3	8793.4	5021.0	7332.0	6103.5	17022.8	5247.8
6823.2	6769.4	7168.6	7377.3	6134.6	7651.2	5788.3	6727.9	9129.1	12573.2	7045.5
53.7	338.6	471.0	492.6	328.2	692.3	166.0	336.0	161.5	2107.8	235.4
811.5	5130.2	5744.2	6327.1	4681.7	6416.0	4936.2	6029.2	5818.3	8482.8	5454.3
842.7	4375.2	5290.0	5648.2	3795.9	6346.3	2899.8	5238.2	4224.4	15323.5	2749.9
97.4	5660.2	7086.8	7389.0	5146.8	10400.7	3327.9	5815.0	2872.6	21589.4	3342.2
465.0	2941.9	4500.7	4174.8	3159.2	5397.4	2354.6	5089.9	3642.9	7633.4	2828.5
103.6	3257.7	4523.5	4385.8	2772.4	6451.7	2184.6	3268.0	1984.9	12683.7	1827.9
1605.9	5680.3	6880.1	7673.0	5358.1	7221.4	6205.3	8909.9	4685.5	12260.9	9245.4
21557.5	5814.4	6106.0	6695.4	6491.9	7850.3	5282.9	6852.7	5673.3	12685.0	5231.8
866.0	4353.5	6031.8	6596.7	3180.0	8756.3	2379.1	6078.9	4461.4	14547.6	3676.6
1654.1	5649.0	8205.0	9441.0	5011.1	7078.4	6267.0	8320.6	3562.8	12756.3	7426.4
90.5	4139.5	5812.8	6579.5	2340.3	8443.6	2166.4	5829.7	4007.9	16093.2	3186.0
133.3	2962.8	3748.9	4002.4	2189.5	4158.2	1780.3	4041.5	2772.4	9790.7	2000.8
77.3	4832.8	6208.0	6833.3	4139.0	10388.4	1707.7	4760.6	2284.1	20737.6	2503.6
80.0	3733.1	4411.6	5074.2	2756.9	6841.5	1795.5	3858.2	1865.5	13547.0	1994.1
904.1	6984.6	8325.3	9159.0	6036.4	10065.4	5426.0	7891.7	6060.2	19293.3	5724.5
2049.7	6272.1	7120.1	6637.6	5434.6	6907.9	5144.3	5876.7	7449.8	16307.4	6691.0
2710.5	3027.5	3096.8	3381.6	4275.6	3584.6	3518.0	4190.2	3524.2	4142.3	4475.1
12499.1	7594.6	6354.2	6913.5	6650.5	6951.2	7221.9	6516.2	11358.5	10415.9	8139.2

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10351.6	9431.9	4757.2
6981.9	7915.4	7720.3
10324.2	8332.0	5606.3
13093.4	9441.4	4913.5
8038.7	5922.0	3508.9
7810.5	5718.2	4430.7
5681.4	6261.4	3525.3
7076.4	5544.3	4012.0
7976.7	5719.9	3482.0
9623.1	8090.1	5217.4
9919.6	7347.0	3231.0
8194.7	6168.0	5211.0
7648.1	7975.9	4510.1
5105.4	5361.4	1688.9
9914.0	9267.9	8043.8
10052.8	8144.0	5813.5
8132.6	7754.1	6232.9
8369.8	5811.6	3002.0
9973.3	8248.3	5494.3
7864.6	7802.1	5007.2
666.0	1000.9	324.4
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7805.7	5959.4	3511.2
10732.4	6008.0	4239.5
5919.7	6660.5	3090.4
6693.7	5318.3	2806.5
9588.2	8410.4	5791.2
9075.5	8113.8	5397.9
9532.6	7661.1	3955.3
8087.2	6793.9	5235.1
8362.6	6305.2	3469.7
4843.2	4286.2	1727.8
10583.8	5410.2	3518.3
7687.0	4324.5	2662.1
11566.8	8623.0	5662.9
7159.6	7168.9	4587.4
4310.0	4038.5	3514.6
8585.3	8260.1	7405.1

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FJ370038.1 gg_id:359179 feces adult twins and mothers; TS55 clone TS55_a03g03 FJ3700
FJ976607.1 gg_id:540908 Enterobacter sp. str. LCR98 FJ9766
CU928161.2 gg_id:563140 Escherichia coli str. S88 CU928
AY834756.1 gg_id:110694 Rhodopseudomonas palustris str. 2c AY8347
GQ099129.1 gg_id:380807 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ099
DQ223872.1 gg_id:164430 Buttiauxella sp. str. P5 DQ223
NZ_AAJU01000010.1 gg_id:139105 Escherichia coli str. F11 NZ_AA
EU471308.1 gg_id:294785 red panda feces clone RP_3aaa03b08 EU4713
GQ155251.1 gg_id:594208 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ155172.1 gg_id:544931 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EU472722.1 gg_id:295041 red panda feces clone RPSD_1aaa03b06 EU4727
GQ416532.1 gg_id:565456 Temporal succession biological degreasing systems clone F7jun.10 GQ416
EU216734.1 gg_id:329496 Pantoea sp. str. LMG 5345 EU2167
Z96077.1 gg_id:10042 Enterobacter nimipressuralis str. LMG 10245-T Z96077
GQ025526.1 gg_id:446114 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ025
GQ095671.1 gg_id:410941 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw4 GQ095
AF130892.2 gg_id:10079 Pantoea endophytica str. A13 AF1308
GQ155872.1 gg_id:581530 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
AY253920.1 gg_id:86492 Rahnella aquatilis k 62 AY2539
GQ025170.1 gg_id:405718 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1 GQ025
AJ583836.1 gg_id:95192 Pantoea agglomerans str. Pa4842 AJ5838
GQ102051.1 gg_id:394557 Topographical and Temporal Human Skin Microbiome skin palm clone nbw502h07c1 GQ102
GQ155846.1 gg_id:510610 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
FJ969376.1 gg_id:394960 Pectobacterium carotovorum str. KKH3 FJ9693
CP000948.1 gg_id:270797 Escherichia coli substr. DH10B str. K-12 CP0009
EU468003.1 gg_id:290774 cheetah feces clone CE2_a06_1 EU4680
AE005174.2 gg_id:128878 Escherichia coli O157:H7 str. EDL933 AE0051
GQ155038.1 gg_id:554226 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ492044.1 gg_id:572998 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
EU472657.1 gg_id:297746 red panda feces clone RPSD_1aaa04c10 EU4726
DQ278909.1 gg_id:144626 Enterobacter sp. str. Eg8 DQ278
EF560790.1 gg_id:228008 Escherichia coli str. BEE13 EF5607
EU430750.1 gg_id:260369 Enterobacter sp. str. ZJUPD6 EU4307
NZ_ACGN01000123.1 gg_id:470367 Escherichia coli str. 83972 NZ_AC
DQ068760.1 gg_id:172586 Salmonella sp. str. Co9936 DQ068
AF395913.1 gg_id:38659 Enterobacter aerogenes AF3959
GQ492576.1 gg_id:535166 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
GQ101935.1 gg_id:375951 Topographical and Temporal Human Skin Microbiome skin palm clone nbw501b03c1 GQ101
GQ047665.1 gg_id:449134 Topographical and Temporal Human Skin Microbiome skin palm clone nbw137e10c1 GQ047
EU471071.1 gg_id:297139 red panda feces clone RP_3aaa03f12 EU4710
AB286558.1 gg_id:217008 Reducing production and domination comamonadaceae reducing oxygen supply was AB2865

800.1	4546.8	5721.4	6207.0	3068.0	6291.4	2453.1	5330.5	3712.8	14483.1	3346.3
272.4	5766.5	6185.7	6802.6	5346.2	9054.8	4301.6	5657.7	3541.4	18559.2	3942.4
109.9	3986.9	6151.2	6745.9	1889.9	5321.6	2275.6	5854.1	2113.5	14972.4	3417.0
644.9	4034.3	5525.5	5693.5	2889.2	7510.2	1593.4	5732.6	4023.0	15307.8	2124.0
15866.7	7199.7	6466.1	7126.7	6516.6	7388.8	6485.0	6583.5	10542.8	9367.8	11428.1
264.2	2838.7	3832.3	3732.0	2927.1	4691.1	1845.2	3769.9	3425.4	7964.0	2523.6
5510.8	2628.8	3953.5	4249.8	1351.0	2848.4	2938.0	3142.3	1809.1	8820.7	4253.5
3409.9	3738.6	4841.6	5824.5	3484.9	4897.8	3424.0	5411.8	3114.3	9527.0	4213.3
10425.9	5284.1	4228.2	6002.6	4958.2	7398.2	3930.8	5853.7	5959.8	14253.9	4937.8
4705.6	5121.0	5357.4	5695.1	6068.9	6215.0	5666.4	5475.3	4690.7	10353.3	4505.1
6406.9	5574.2	6278.8	7112.8	5811.4	6655.0	5385.2	6634.1	6907.4	10879.3	9131.8
241.9	4070.1	5382.4	6167.0	3697.4	8172.6	2839.7	4607.3	3258.2	12445.1	2626.2
75.1	1634.5	2182.0	2248.2	1113.1	5291.8	1377.4	2222.2	1448.0	7960.5	897.4
162.1	4050.4	7075.5	7322.6	3102.5	9614.6	2217.3	6850.7	3533.6	18252.9	3431.2
23424.7	7837.5	7873.7	8580.0	8700.1	7380.5	8223.4	7076.5	11235.1	11252.3	9728.2
3882.9	5759.8	6478.0	8102.0	6113.1	7222.5	5793.5	7280.5	5528.5	13566.4	6401.9
2083.5	9789.4	10029.6	10753.0	9553.9	11181.6	9208.3	9356.4	13683.2	16724.2	10951.3
327.4	6568.2	7705.8	8539.6	5548.0	9755.1	4650.5	7709.7	6691.5	17551.4	5164.9
432.5	2415.8	3240.6	3409.9	3171.9	3883.1	1980.9	4165.4	3874.6	5207.0	1945.2
5233.2	2729.6	2858.5	3925.2	2790.0	4114.9	2937.8	3873.1	2456.0	5816.3	3664.0
67.1	4543.8	5747.2	6081.7	4042.7	8507.8	3698.0	5452.6	3425.1	13013.2	2674.3
1217.6	5187.5	4949.4	5780.0	5330.0	6410.4	5265.8	6035.1	6045.7	8975.3	5035.7
110.6	2378.7	2803.7	2768.5	2827.1	3574.4	2433.3	3000.3	1241.9	7237.2	1155.3
62.4	2820.2	4535.8	4312.2	1959.0	4944.3	1695.1	5672.4	4300.4	9178.7	2948.5
6308.5	3405.1	4271.6	4670.1	2723.5	5204.8	3273.0	3357.5	2962.8	11027.0	4264.3
1138.7	6710.5	7729.4	8173.3	7115.2	7954.4	7316.9	7719.5	6518.2	13277.2	7937.6
2532.4	2365.6	3062.5	3351.5	2860.3	3788.5	2238.4	3719.9	2807.7	6966.1	2156.9
18373.4	8029.1	7957.7	8462.7	7422.3	9087.4	7647.7	7683.1	9887.8	13816.8	8800.4
719.2	5217.3	5080.6	6177.4	3323.8	5880.9	3986.8	4800.3	4929.7	9462.0	5841.3
887.7	6470.9	8010.0	8922.4	5275.6	9109.0	4730.2	7540.4	5336.4	17614.9	5720.1
9611.0	7828.4	9031.7	9629.9	7427.4	11885.8	6793.3	9619.5	7779.6	20033.4	6625.9
736.4	4297.3	5531.8	5740.2	2891.9	6444.3	1922.4	5040.8	3443.8	12845.4	2656.8
249.0	4627.0	5476.9	5518.3	3368.2	6745.4	3814.9	6055.7	4808.2	12944.7	4318.3
309.8	5231.5	6700.6	7354.7	3932.0	7150.6	3482.3	6418.7	5116.3	14414.4	4325.9
715.6	5823.5	7010.3	7632.5	7034.1	8813.0	5254.3	8146.3	5199.4	13783.6	4344.5
127.0	5453.2	8198.1	8299.4	4480.2	11238.9	2763.8	6885.0	3444.6	22362.5	3418.8
8739.0	7107.3	7507.4	9182.7	6520.9	7810.3	8049.2	6849.4	9206.3	10720.5	12498.3
213.1	3780.6	3808.6	3690.1	3182.7	4397.9	2721.0	4244.3	3152.8	5528.7	2620.0
1255.7	4418.0	5955.1	6262.3	3484.5	5415.4	4157.3	4607.6	6403.2	9213.5	5602.0
10483.2	5360.4	5804.3	6701.4	4580.2	4407.7	5088.4	4920.3	5206.1	8614.6	5598.2
205.3	3793.3	4820.2	4578.0	2332.2	5864.0	1942.1	4884.1	4702.6	8300.7	2715.5

8509.8	6318.4	3510.1
9036.9	5598.9	5117.8
7872.2	4923.2	2232.0
8184.9	6661.0	3084.1
6178.4	8036.8	5248.5
5104.3	5763.0	2233.2
4490.3	2943.8	1623.3
6148.8	5752.2	3165.9
7306.7	6275.5	3590.5
7615.6	6291.3	4864.5
7067.2	7940.9	4600.9
7926.2	6695.0	4145.2
6626.9	4731.7	1031.0
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9667.3	7291.9	5735.3
10639.2	11373.9	8702.9
11153.3	8436.7	5644.2
4201.9	5549.1	2323.0
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9060.4	7023.7	4197.3
6036.9	7462.5	4458.1
4953.3	3446.9	1691.1
5869.4	5240.1	2448.7
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7836.1	8751.8	6908.4
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8395.4	10705.7	7609.7
6549.6	6634.3	4707.1
10480.9	8043.2	4978.1
13587.3	9692.2	6371.1
7267.6	6604.5	3482.6
7580.0	6499.4	3847.1
8932.9	7566.5	4251.9
10872.2	8416.0	4811.3
11391.3	7857.8	4292.4
7542.6	8687.8	7936.3
4180.9	4482.3	3069.8
4520.5	5935.7	3334.0
5986.4	6082.3	3973.1
6071.5	6342.7	3045.5

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GQ155099.1 gg_id:540372 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ099217.1 gg_id:375279 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ099
GQ114706.1 gg_id:453826 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ114
EU472653.1 gg_id:297848 red panda feces clone RPSD_1aaa01e06 EU472
AM184226.1 gg_id:160051 Enterobacter sp. str. WAB1884 AM184
AF520708.1 gg_id:61203 Dickeya dianthicola str. CFBP 1200 AF5207
EF489443.1 gg_id:219392 Pantoea agglomerans str. GIST-NKst1 EF4894
EF153300.1 gg_id:186788 identification gut fourth-instar red imported fire ant (Solenopsis Buren) larvae GI trac EF1533
EF560782.1 gg_id:233200 Escherichia coli str. BE33 EF5607
U90758.1 gg_id:10315 Rahnella genosp. 3 str. DSM 30078 U90758
AJ233409.1 gg_id:10306 Brenneria alni str. DSM 11811 AJ2334
EU761873.1 gg_id:346129 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1 EU7618
GQ155273.1 gg_id:591917 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EU464932.1 gg_id:290119 African elephant feces clone AFYEL_aaj65d02 EU4649
GQ025120.1 gg_id:438223 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1 GQ025
GQ025542.1 gg_id:460697 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ025
EU430755.1 gg_id:259306 Enterobacter sp. str. ZJUPD1 EU4307
EU430752.1 gg_id:267416 Enterobacter sp. str. ZJUPD4 EU4307
EU430753.1 gg_id:270355 Enterobacter sp. str. ZJUPD3 EU4307
DQ223881.1 gg_id:168597 Citrobacter gillenii str. P9 DQ223
NC_004431.1 gg_id:128802 Escherichia coli str. CFT073 NC_004
EU471669.1 gg_id:297637 Asiatic elephant feces clone AE1_aaa03f11 EU4716
DQ112330.1 gg_id:136199 Pantoea agglomerans str. RS-18 DQ112
EU470656.1 gg_id:287789 red panda feces clone RP_1aaa03g09 EU4706
DQ068872.1 gg_id:139038 microbiota antlions (Myrmeleon mobilis) whole animal freshly caught antlion OTU1(DQ068
GQ048022.1 gg_id:442026 Topographical and Temporal Human Skin Microbiome skin palm clone nbw140d07c GQ048
AM062693.1 gg_id:249744 Enterobacter amnigenus p412 AM062
EU471187.1 gg_id:291079 red panda feces clone RP_3aaa04e11 EU4711
GU185862.1 gg_id:587224 Enterobacter ludwigii str. HSBN1 GU185
GQ155216.1 gg_id:583212 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
AM491468.1 gg_id:213014 Aranicola sp. str. Nj-67 AM491
GQ101988.1 gg_id:430225 Topographical and Temporal Human Skin Microbiome skin palm clone nbw502b08c GQ101
GQ155035.1 gg_id:587112 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EU471045.1 gg_id:293597 red panda feces clone RP_3aaa02e12 EU4710
EU458408.1 gg_id:295685 spotted hyena feces clone HY1_f04 EU4584
GU374094.1 gg_id:526760 soil East Calcutta wetland clone SRC_NBB2 GU374
GQ047705.1 gg_id:399615 Topographical and Temporal Human Skin Microbiome skin palm clone nbw138b11c GQ047
DQ298156.1 gg_id:142765 Escherichia sp. SWM_Isolation_4 DQ298
EU472916.1 gg_id:287896 red panda feces clone RPSD_1aaa04b06 EU4729
U88545.1 gg_id:9669 Salmonella typhi str. St111 U88545
EU472820.1 gg_id:294893 red panda feces clone RPSD_1aaa03c03 EU4728

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18111.2	8825.7	7971.0	7929.7	8388.4	8084.5	8422.5	7268.2	12537.7	10499.9	9658.1
10789.7	7691.5	8166.0	8410.3	6661.4	10196.8	5986.6	7430.8	8219.7	16175.8	7779.9
1789.4	5379.3	6899.6	7564.7	5164.2	7671.5	4350.2	7168.4	5799.3	17580.5	4933.7
119.2	4537.5	5044.3	4959.6	2753.6	6541.9	2362.7	5597.5	5229.9	10936.2	3232.9
2918.9	7799.1	8310.4	9329.9	7899.8	9151.1	6975.6	9403.5	8301.5	15666.4	9273.6
217.3	4371.9	5602.8	5980.0	4629.5	7673.8	4291.8	5662.1	3280.0	16351.3	4241.3
203.8	3330.1	4813.7	4728.0	2758.9	5562.6	2246.7	5642.5	3036.1	10574.6	3571.7
4214.6	6068.4	7723.5	9186.0	5381.5	6736.5	5726.7	7723.5	5960.8	12332.4	8493.8
158.0	4804.8	5172.2	5232.2	4640.2	6328.3	3680.7	5844.8	4328.7	8402.4	3191.6
2693.7	2898.6	3758.1	4179.1	2933.7	4790.7	2920.6	5003.7	3700.4	8115.5	4009.1
833.3	4723.1	5971.7	6509.3	4027.8	6267.8	3730.7	5654.5	4561.5	13175.1	4562.9
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1301.1	2873.1	3978.1	4317.0	2478.5	2854.1	2811.4	3709.0	3887.9	6772.5	3442.2
7536.3	5021.8	5518.2	6493.3	4335.7	5331.3	4510.9	6045.2	5531.2	7465.6	6914.9
2455.4	5129.5	6180.6	6859.4	4600.3	6960.8	4499.6	5670.3	6037.5	13770.6	4572.7
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2002.2	5304.8	6720.8	8090.0	4103.4	7424.0	3740.9	6592.9	5234.4	14423.0	6282.6
10648.8	5193.2	5915.5	6505.0	5403.2	5678.0	5333.4	5026.8	6165.0	10721.2	7015.5
88.1	6093.7	7220.9	7512.4	5287.9	10666.1	4509.4	7983.5	6247.3	21276.8	5553.5
12157.4	5450.3	5967.9	6048.2	4925.5	6173.9	4607.5	6468.8	5687.2	8877.9	5241.5
10342.2	6111.0	6964.8	7975.8	5633.8	10615.8	6075.8	7054.9	7792.1	17682.5	5496.0
4841.9	7616.7	8124.3	9306.5	7013.3	8976.4	7230.6	8280.9	9896.8	14034.1	8119.7
973.6	4669.6	5543.3	6179.8	5236.6	8086.1	4093.5	5961.0	4808.7	14706.7	3960.8
842.7	4237.8	5427.5	6018.9	3142.3	6174.8	2361.4	5145.6	3583.7	15054.0	3324.3
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829.3	7047.9	8011.1	8759.8	6026.2	10861.5	4786.6	8200.7	5644.6	16622.9	6009.3
125.4	12240.6	12392.4	11234.1	10116.1	13411.5	8892.2	11475.5	18702.7	19388.0	12222.8
772.8	5617.5	6562.7	6839.8	5044.8	7925.5	4588.4	6419.9	5277.1	14769.3	4445.3
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9420.2	5102.3	5695.9	6624.4	4526.3	4987.3	4847.8	5890.9	6036.5	7666.7	9163.9
853.3	6875.3	8234.6	9035.2	5952.2	9879.1	5346.3	7784.2	5500.5	19126.4	5543.6
148.1	3628.1	4665.4	4914.6	3055.2	6584.0	1648.0	3934.3	2652.4	13355.2	1667.8
241.4	4776.0	6578.5	7078.9	4263.4	7305.4	3664.0	6334.9	4539.2	15148.7	4878.5

9527.3	6807.4	4645.0
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9412.7	6893.1	4716.2
6306.4	6650.8	2661.2
10078.8	9834.8	7730.6
7833.0	5514.6	4205.3
6100.3	6060.5	2785.5
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7692.7	7565.4	5474.0
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5732.3	7032.6	4512.6
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9743.9	8946.7	5926.8
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9464.3	8549.7	5036.0
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EU472736.1 gg_id:294375 red panda feces clone RPSD_1aaa01e05 EU472
EU855221.1 gg_id:347116 Enterobacter aerogenes str. CTSP48 EU855
GQ070404.1 gg_id:392752 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ070
FJ267520.2 gg_id:343017 Escherichia blattae str. DSM 4481 FJ2675
FJ683659.1 gg_id:523290 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6836
X80680.1 gg_id:9721 Shigella dysenteriae X80680
GU272220.1 gg_id:592196 Escherichia coli str. wz_1977 GU272
DQ223879.1 gg_id:168024 Enterobacter amnigenus str. P4 DQ223
EU472796.1 gg_id:292881 red panda feces clone RPSD_1aaa04e04 EU472
EU464977.1 gg_id:302241 African elephant feces clone AFYEL_aaj66b03 EU464
GQ101931.1 gg_id:441169 Topographical and Temporal Human Skin Microbiome skin palm clone nbw501a10c GQ101
EU471959.1 gg_id:298277 francois langur feces clone FL_1aaa03d06 EU471
CU915010.1 gg_id:456734 and dynamics adapted microbiota during degradation Tunisian zarzatine enriched se CU915
EU554444.1 gg_id:273128 Enterobacter asburiae str. Ag18 EU554
GQ099291.1 gg_id:395047 Topographical and Temporal Human Skin Microbiome skin interdigital web space cl GQ099
EF446895.1 gg_id:210966 Acinetobacter radioresistens str. Philippines-11 EF4468
ABHO01000021.1 gg_id:285987 Escherichia coli O157:H7 str. EC4196 ABHO
GQ155878.1 gg_id:549556 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ155057.1 gg_id:568864 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
FJ975887.1 gg_id:534463 Human gut microbiome adopts alternative state bowel transplantation ileum effluent FJ9758
FJ593037.1 gg_id:572846 Pectobacterium wasabiae str. JU-1 FJ5930
GQ155094.1 gg_id:593339 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
CU928162.2 gg_id:547290 Escherichia coli str. ED1a CU928
EF620926.1 gg_id:254200 Escherichia coli str. WD02 EF6209
EF620923.1 gg_id:254591 Escherichia coli str. SYW004 EF6209
GQ047692.1 gg_id:449355 Topographical and Temporal Human Skin Microbiome skin palm clone nbw138a03c GQ047
FJ906925.1 gg_id:562225 Cronobacter sakazakii str. Jor204 FJ9069
NR_024706.1 gg_id:562424 Pseudomonas flectens str. ATCC 12775 NR_02
FJ581031.1 gg_id:568374 Cronobacter sakazakii str. IITRM16 FJ5810
GQ165811.1 gg_id:548859 Enterobacter aerogenes str. IEY GQ165
FJ949577.1 gg_id:373419 Escherichia coli str. H1 FJ9495
EU778499.1 gg_id:325455 Red Panda feces clone RPSD_1aaa03f09 EU778
GQ099209.1 gg_id:452629 Topographical and Temporal Human Skin Microbiome skin interdigital web space cl GQ099
EU472713.1 gg_id:289582 red panda feces clone RPSD_1aaa03f02 EU472
EU537173.1 gg_id:285808 profile human microbiota antecubital fossa (inner elbow) skin clone nbt67h04 EU537
EU470953.1 gg_id:293383 red panda feces clone RP_2aaa01e06 EU470
EF604173.1 gg_id:233448 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6041
EF102834.1 gg_id:242926 Pantoea agglomerans str. G-4-13-2 EF1028
GU374071.1 gg_id:516475 soil East Calcutta wetland clone SRC_NBB14 GU374
EF515452.1 gg_id:224577 Electricigen Enrichment MFC upf microbial fuel cell anode clone 24e12 EF5154

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193.5	3763.2	5011.6	5414.7	3959.3	7728.4	1632.8	4121.6	2829.0	15840.0	2288.1
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785.1	5362.5	6021.2	6652.7	4806.3	7749.2	4598.8	5819.2	4197.2	14336.6	4008.1
1411.4	2532.7	3746.6	3172.0	2244.9	3761.0	1925.2	3267.2	4868.9	6828.5	2103.8
347.1	1944.8	3606.7	3904.3	1429.9	4475.5	1294.6	3420.5	1668.7	7513.2	1505.7
5109.6	8197.2	9106.6	9468.6	7617.7	9893.3	7041.5	8065.0	11520.9	15927.9	8182.2
2022.1	5275.6	6191.9	7387.4	4576.2	7417.4	4399.6	6102.8	5458.9	12882.8	5876.0
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2910.2	5418.6	6638.1	8225.4	5826.0	6149.6	6701.1	7602.4	5143.3	10271.1	7542.2
592.3	2820.0	4275.0	3720.3	2548.5	5508.0	2430.5	4220.7	2698.4	6382.6	2138.9
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7350.4	7515.7	4159.0
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6999.7	6197.1	3245.9
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AY501386.1 gg_id:99525 Pantoea sp. str. PPE7 AY501
GQ155204.1 gg_id:509434 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ155021.1 gg_id:544405 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
AM184290.1 gg_id:160595 Pantoea agglomerans str. WAB1951 AM184
AF015258.1 gg_id:10180 Aquamonas haywardensis str. CDC 2404-94 EG121 AF015
EU471256.1 gg_id:291269 red panda feces clone RP_3aaa02b01 EU471
AM157425.1 gg_id:141026 Escherichia coli mother C3 AM157
EU078564.1 gg_id:236821 Enterobacter sp. str. R11-2 EU078
AJ871857.1 gg_id:113218 Klebsiella oxytoca str. SB136=ATCC 49131 AJ8718
AF130958.2 gg_id:10082 Pantoea endophytica str. A6 AF130
GQ155121.1 gg_id:575470 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EU471089.1 gg_id:292812 red panda feces clone RP_3aaa04g10 EU471
EU472826.1 gg_id:300494 red panda feces clone RPSD_1aaa02e07 EU472
AY831405.1 gg_id:112441 Escherichia coli str. AB1157 AY8314
GQ099170.1 gg_id:396992 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ099
CP000819.1 gg_id:520569 Escherichia coli B str. REL606 CP000
EU555536.1 gg_id:266023 Escherichia coli str. CNM 477-02 EU555
EU239468.1 gg_id:255707 Enterobacter asburiae str. XJUHX-5 EU239
FN433037.1 gg_id:543947 Escherichia fergusonii CCM27B FN433
EU778487.1 gg_id:305294 Red Panda feces clone RPSD_1aaa03c07 EU778
AF373173.1 gg_id:66748 Erwinia chrysanthemi str. 340 AF373
EU471241.1 gg_id:297916 red panda feces clone RP_3aaa01a04 EU471
AM933759.1 gg_id:330563 Kluyvera ascorbata 1919 AM933
FJ811870.1 gg_id:578058 Pantoea sp. str. 1-CDF FJ8118
AJ971890.1 gg_id:136113 Erwinia sp. Ob 05 AJ9718
EU470487.1 gg_id:302808 red panda feces clone RP_1aaa04c12 EU470
EF560781.1 gg_id:230035 Escherichia coli str. BE30 EF5607
AM184235.1 gg_id:160492 Enterobacter ludwigii str. WAB1894 AM184
EU535068.1 gg_id:283165 profile human skin microbiota ear punch biopsy female C57BL/6J mouse clone nbt18 EU535
GQ479959.1 gg_id:561718 Enterobacter aerogenes str. MZQ-HZ01 GQ479
DQ086778.1 gg_id:136046 Enterobacter cloacae str. I5 DQ086
AE005674.2 gg_id:128438 Shigella flexneri 2a str. 301 AE005
FJ405334.1 gg_id:366426 Escherichia coli str. 4061 FJ4053
EU470595.1 gg_id:289857 red panda feces clone RP_1aaa04h08 EU470
AJ233414.1 gg_id:9838 Erwinia mallotivora str. DSM 4565 AJ2334
GQ048031.1 gg_id:436643 Topographical and Temporal Human Skin Microbiome skin palm clone nbw140e09c1 GQ048
AJ308467.1 gg_id:34327 Enterobacter sp. 22 AJ3084
AJ309974.1 gg_id:45848 enterobacterium str. dtb112 AJ3099
AY825036.1 gg_id:109467 Enterobacter aerogenes str. NTG-01 AY825
GQ493841.1 gg_id:580139 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493

154.8	2705.7	3187.8	3564.8	2847.9	4963.8	2850.6	3933.9	3602.4	7085.1	1926.3
171.9	2348.4	2915.3	3179.4	1796.6	4677.5	1832.9	2993.3	4173.8	7246.6	1427.0
4706.2	5687.4	6009.1	6338.0	7412.5	6821.2	6677.7	6152.9	4946.9	10866.9	4771.4
4967.4	7159.1	7285.9	8807.8	7476.4	7625.6	7580.9	7376.9	11416.7	11788.3	8678.1
3167.4	4710.3	5770.3	6194.7	4965.6	9952.6	1830.3	4662.5	3114.7	18628.0	3576.9
26.6	46.4	52.8	51.2	33.9	50.4	32.8	65.6	41.3	106.1	32.0
1314.7	6363.6	7579.6	8354.0	5685.3	6748.6	6483.5	7014.7	9426.2	8355.8	7608.2
841.4	4960.0	6174.8	6688.4	4297.4	6547.9	3889.3	5834.9	4659.3	13413.0	4448.9
227.8	4102.9	5395.1	5626.3	3606.2	8405.9	3421.7	4389.8	2377.1	16258.5	2903.3
93.8	4088.2	4895.5	4805.1	3757.1	6713.3	2958.7	4406.7	3633.8	11621.4	2694.6
224.0	5545.8	6548.8	7396.0	4580.5	9262.0	3182.7	5710.5	3780.2	17365.0	4272.7
7350.3	5124.6	5261.6	5537.7	5901.9	6295.2	6758.9	5913.3	7193.5	9170.1	5917.1
4000.1	3339.8	4425.4	4647.8	2897.3	3765.2	3519.7	4409.6	3008.6	6346.6	4079.6
981.0	5959.3	7398.7	7886.3	5446.0	8865.7	4266.0	6885.8	6247.3	17923.5	5094.0
6867.9	4521.9	6309.9	7196.6	2841.5	4934.4	3917.2	5935.9	3271.2	14143.7	5670.4
2092.8	4107.2	4449.6	4803.6	3274.1	4804.2	3239.6	4384.4	5174.6	6168.9	3299.8
4369.2	5091.3	6420.7	6716.6	3982.0	7273.9	3197.6	5839.3	5084.3	14397.8	4644.2
4497.4	2865.6	3755.8	3760.3	2289.2	4236.0	2390.8	2921.5	2457.6	9555.0	2773.7
56.5	4233.8	5857.2	5471.5	3454.5	7134.5	3060.4	5650.7	3051.4	14689.3	3141.9
925.8	5599.1	6820.8	7381.3	4946.9	8435.0	4028.7	6271.8	5558.9	17416.0	4266.8
899.8	4659.0	5946.7	6689.9	4063.0	5963.6	4174.2	6503.1	4464.4	11158.6	5034.2
270.0	2904.2	4263.2	4426.9	1947.9	4783.7	1490.3	4815.8	3720.1	9981.1	2095.8
2147.2	4599.9	6511.5	7537.9	4221.5	5668.5	4816.2	6731.7	3867.4	12761.4	5604.2
530.5	1770.4	2222.3	2524.2	2066.8	4012.8	1438.0	3689.1	3106.2	7667.4	1893.8
75.9	2136.4	2516.9	2741.8	2114.5	3916.8	2131.4	3335.3	2104.4	4291.0	1443.8
105.7	3048.7	3826.0	3554.6	3930.7	4616.0	2717.4	4744.1	2387.2	7606.9	1928.1
868.3	5460.4	6920.8	7790.6	4436.0	7930.0	4099.2	6506.8	4008.8	15757.8	5287.8
1555.8	5901.3	6694.4	7793.4	10599.6	6709.2	8329.3	7098.6	3658.0	8751.7	4314.0
655.8	8035.5	9335.0	10399.1	7016.3	13271.7	5600.9	8913.1	6368.2	23970.0	6244.8
98.1	3628.9	4870.8	4819.4	2524.6	5870.1	2066.2	4404.6	2619.5	12014.2	2003.1
9221.4	9097.0	9787.6	10649.1	8876.2	11045.2	10032.5	8615.6	9284.2	17191.1	11594.3
175.8	4667.4	6094.9	6166.7	4676.9	9541.0	2808.8	5537.0	3429.3	19552.2	2984.4
866.2	5332.7	6765.1	7262.7	4347.6	6986.8	3788.2	6453.3	5005.9	14422.9	4564.1
34737.2	11472.1	9617.9	12530.8	10280.8	10708.2	11366.0	10050.0	12800.4	14417.7	14312.9
179.5	4129.5	6173.3	6768.0	2737.3	7351.1	2173.8	5523.2	2477.3	15533.8	3321.1
5181.3	8047.4	8427.3	9232.0	9088.0	9861.8	5355.8	9292.2	8761.2	15086.8	6228.3
2369.8	4949.6	6385.0	6338.2	4513.3	5231.2	5468.6	4878.3	3805.9	8102.2	6017.6
270.3	3463.8	4700.4	4589.8	3852.6	6354.2	2652.1	4398.1	3545.3	11881.8	2755.0
39.5	756.6	1052.9	903.9	579.1	1837.1	308.8	908.4	440.0	3375.0	346.3
161.3	5813.6	7127.6	7558.9	4312.9	9739.1	3106.8	6659.9	6167.7	18614.9	4258.5
5769.7	3537.2	4401.8	4953.4	3438.0	4817.3	4202.2	4002.3	3243.0	9640.1	4441.2

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8448.4	5946.4	3419.0
60.8	119.3	29.3
6533.7	8542.4	6150.4
8017.2	6940.4	4370.5
9070.3	5728.7	5540.4
6607.4	6019.5	3811.0
9536.6	5706.4	4003.9
6951.4	6676.3	4832.0
3620.8	5106.9	3083.4
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6909.0	5862.2	2996.9
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9396.3	6836.9	4235.3
4831.8	4008.1	1931.9
7988.8	6648.8	3763.8
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6433.8	6673.2	3885.7
6751.8	6682.0	2535.3
7303.0	5509.1	3899.8
4475.5	4692.3	1527.8
3523.1	4484.8	1824.5
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9319.6	7038.9	4252.3
8740.8	6506.1	5303.6
13993.5	9293.2	6829.3
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9411.7	5988.4	3257.3
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7177.6	5734.6	2710.7
10766.7	9840.8	6090.7
5525.6	6262.5	4142.8
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EU464476.1 gg_id:301303 African elephant feces clone AFEL_aai29g04 EU464
GQ047964.1 gg_id:468430 Topographical and Temporal Human Skin Microbiome skin palm clone nbw139f07c1 GQ047
GQ155178.1 gg_id:539032 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ156080.1 gg_id:588129 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
EU472802.1 gg_id:290812 red panda feces clone RPSD_1aaa04f09 EU472
AB273732.1 gg_id:243322 Shigella sonnei str. GTC 781 AB273
FJ906921.1 gg_id:542455 Cronobacter sakazakii str. Jor176 FJ9069
EU472837.1 gg_id:295363 red panda feces clone RPSD_1aaa02h08 EU472
GQ155060.1 gg_id:509438 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ031670.1 gg_id:381600 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ031
AB273742.1 gg_id:245432 Cedecea lapagei str. GTC 346 AB273
FJ405361.1 gg_id:358229 Rahnella aquatilis str. SPb FJ4053
EU471082.1 gg_id:295799 red panda feces clone RP_3aaa04g04 EU471
FJ366024.1 gg_id:361492 feces adult twins and mothers; TS25 clone TS25_a01g12 FJ3660
EU472850.1 gg_id:301348 red panda feces clone RPSD_1aaa03d12 EU472
FJ975869.1 gg_id:513372 Human gut microbiome adopts alternative state bowel transplantation ileum effluent FJ9758
ABHO01000013.1 gg_id:286158 Escherichia coli O157:H7 str. EC4196 ABHO
DQ347522.1 gg_id:147724 Paracoccus sp. B-1012 DQ347
DQ124676.1 gg_id:136582 Enterobacter aerogenes str. S2-1 DQ124
U90314.1 gg_id:9706 Salmonella subsp. enterica serovar Blockley str. Sb1 subsp. U90314
X80725.1 gg_id:9741 Escherichia coli str. ATCC 11775T X80725
FM180568.1 gg_id:369788 Escherichia coli 0127:H6 str. E2348/69 FM180
DQ068864.1 gg_id:139117 microbiota antlions (Myrmeleon mobilis) whole animal freshly caught antlion OTU1 DQ068
GQ493963.1 gg_id:583626 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
EU834264.1 gg_id:332053 Raoultella ornithinolytica str. DS44 EU834
EF178670.1 gg_id:180411 Erwinia chrysanthemi str. NZEC135 EF1786
EU857633.1 gg_id:366089 Shigella flexneri EU857
AM933754.1 gg_id:340632 Kluyvera cryocrescens 169 AM933
EU472757.1 gg_id:301762 red panda feces clone RPSD_1aaa02d04 EU472
EF560786.1 gg_id:231669 Escherichia coli str. BE45 EF5607
GQ025603.1 gg_id:416339 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ025
FJ811871.1 gg_id:552136 Enterobacter aerogenes str. 7-WCH FJ8118
EU773798.1 gg_id:346813 Cheetah feces clone CE2_e03 EU773
GQ047918.1 gg_id:402513 Topographical and Temporal Human Skin Microbiome skin palm clone nbw139a08c1 GQ047
EU778388.1 gg_id:354647 Red Panda feces clone RP_1aaa02f05 EU778
EU471154.1 gg_id:297213 red panda feces clone RP_3aaa03f09 EU471
AF024608.1 gg_id:9727 Pantoea agglomerans str. TAC.III.94.1 AF0246
GQ155244.1 gg_id:571288 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ025550.1 gg_id:382453 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ025
GU186121.1 gg_id:584341 Pantoea agglomerans str. IHB B 1383 GU186
EU460458.1 gg_id:293981 polar bear feces clone PB2_aai21b06 EU460

1901.9	5051.5	6748.4	7274.9	4597.7	7244.5	3740.0	6661.4	5292.6	16128.0	4618.1
833.0	6319.0	7701.9	8306.0	5286.4	8716.1	4540.1	7543.4	5892.9	15636.9	5538.6
10035.2	5502.0	6794.8	7307.9	5383.2	8275.1	5699.9	6813.2	7344.1	12315.2	5154.4
290.6	5509.5	6467.7	6938.0	4601.4	8120.9	4177.1	6383.0	5394.8	14854.0	4191.3
5324.7	5312.6	6653.7	7271.4	4932.1	6916.5	4697.9	6254.6	7415.3	12943.7	6161.2
4961.5	3429.0	4296.5	4448.4	2892.7	4846.2	2921.3	3554.9	2908.3	10101.1	3976.9
8186.5	6553.7	7548.5	8228.4	6941.9	8997.8	7214.1	7314.5	5382.8	13193.7	8839.9
27670.9	9476.6	10651.7	11469.6	9533.3	10442.0	9673.5	10513.1	12817.8	16546.7	13774.7
11050.4	8898.7	10477.8	10670.4	8346.1	11884.7	7708.8	9519.5	11062.6	21739.3	9057.8
4065.1	6595.8	7289.6	8401.9	6271.0	8636.4	4903.0	7348.5	8965.3	16136.5	6398.1
1828.9	6993.2	8624.4	8815.2	9322.9	9950.8	8948.4	7620.0	4420.4	16875.5	4383.6
766.0	5615.1	5636.6	6085.0	4481.7	6855.6	4415.8	6436.5	5874.3	11142.1	3891.4
2660.2	7560.9	9415.7	10147.9	6686.8	7947.3	8102.4	7931.0	11762.9	10431.4	9930.1
2572.4	4711.4	6322.8	6563.6	4145.2	5246.0	5442.9	5578.6	4866.9	8593.5	6053.2
11686.4	6501.6	7484.5	7734.3	6335.0	6154.4	6554.3	6612.0	6787.5	10492.6	7660.4
1337.1	6464.6	7265.3	7483.3	6394.8	9445.5	4671.6	8107.8	5459.0	15634.6	4878.9
656.6	3359.7	4834.2	5595.5	2666.3	4658.3	2590.8	4841.8	3577.5	9935.5	3760.9
850.1	4747.8	5796.8	5965.0	4242.8	6296.8	3938.5	5451.1	4439.7	12951.8	3661.4
249.5	3552.3	3690.3	4089.7	2096.3	5218.9	1360.4	4587.9	3747.6	9758.3	2649.4
21662.1	6427.5	6423.6	6542.7	6335.5	7922.7	6330.2	5629.8	8172.4	14160.1	6486.7
792.7	5037.0	6401.3	7304.1	3915.5	6733.8	4048.6	6007.0	3464.2	14664.3	4334.0
1122.5	5280.0	7286.4	7794.7	3679.2	7432.8	3319.2	7162.7	4888.8	16089.1	4413.4
1102.7	4051.8	6200.3	6062.9	3125.3	8176.5	2839.2	5926.8	3100.1	13565.6	2536.5
3809.6	4907.5	6450.7	7971.5	4386.6	6191.9	4933.4	6655.5	5171.0	14012.7	6729.3
70.0	4575.7	6439.0	7578.3	4110.1	9901.0	3006.4	5413.9	2386.4	18813.8	3200.7
285.4	4670.5	5090.8	5724.3	3651.9	7140.6	2635.5	6827.7	4887.2	10752.5	4462.1
720.6	3464.5	4391.3	4639.1	3328.9	4357.0	3241.7	4207.9	1939.3	10608.3	2329.6
750.9	5768.2	6656.1	7426.1	5350.4	11056.2	5619.7	7408.1	6786.4	18493.6	5297.9
22776.7	8499.3	7721.3	8674.9	7723.5	8087.4	8734.0	7563.9	10804.8	13826.0	11307.8
406.5	5875.4	7552.1	8491.5	4828.3	8577.2	4327.9	7198.3	5257.4	17208.2	5097.8
190.8	5035.0	6294.4	6372.8	3789.5	8147.9	2978.5	5823.9	4043.0	15361.4	3222.6
14253.9	7879.2	8921.0	9201.8	7628.3	9435.8	7318.2	7540.6	8482.0	15917.7	9559.6
501.1	4943.1	5747.9	6387.3	3903.9	5794.2	3954.9	5930.1	6345.4	13637.5	4194.7
956.8	4438.4	6107.9	6767.4	3440.2	6151.4	3634.1	5637.5	3300.0	13057.7	4235.4
891.9	5219.9	6820.2	7437.7	4047.9	6898.3	4177.3	6208.0	4254.6	13664.0	4690.0
109.3	2743.8	3199.0	3705.9	2567.6	3494.0	2000.1	3623.6	2129.1	6574.1	2494.3
342.3	2453.5	3008.4	3738.1	2411.9	3848.8	2092.4	3482.9	2617.8	6698.6	2128.9
6564.4	9772.5	10410.3	11141.9	9762.2	11124.3	9474.6	9636.2	13683.6	14777.3	11398.4
1677.5	4255.7	5026.5	4985.7	4704.7	5425.8	6010.3	4265.1	2497.8	11346.3	3701.4
9087.5	7509.0	8209.1	8883.3	8196.7	9723.5	7545.2	6990.2	8046.2	16037.7	7464.7
4319.2	10488.9	11578.4	12163.9	9648.3	10164.9	9518.8	10127.3	11001.1	15098.4	11529.3

8616.9	7159.1	4382.4
9435.5	8062.4	5557.3
8936.9	8643.8	5419.2
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7708.8	8240.5	4668.2
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10879.1	11054.6	9259.5
12225.9	10306.1	8305.8
9233.4	8972.6	5485.3
10745.2	8035.9	5433.8
7224.4	7303.2	4290.4
7422.2	9124.2	6501.0
5069.8	6994.4	4912.8
6743.2	8343.9	6008.2
9961.2	7337.5	6490.3
5620.3	5174.6	2679.5
8000.8	6657.3	4412.3
4715.0	6001.0	2459.3
7372.1	5759.8	5885.5
8575.2	6463.7	3878.2
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8028.4	7810.6	3441.6
7667.3	5822.5	4715.2
9566.6	5856.9	4132.6
7487.3	6943.7	4619.9
6378.6	4667.3	2665.6
11633.4	8109.0	5674.0
7999.2	10308.1	7450.4
10011.3	7665.5	4378.2
8377.2	6282.0	3769.1
9705.6	9224.6	7749.1
6489.7	6017.9	3364.2
7077.4	5893.4	3837.7
7666.1	6711.2	4229.7
3356.1	4396.1	1460.9
4423.9	4377.2	1860.6
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GQ048476.1 gg_id:467365 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbu51 GQ048
GQ024535.1 gg_id:485135 Topographical and Temporal Human Skin Microbiome skin palm clone nbw123e03c1 GQ024
Z96089.1 gg_id:9989 Pectobacterium carotovorum str. LMG 2404-T Z96089
GQ154883.1 gg_id:547125 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
GQ025585.1 gg_id:403646 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ025
EU684953.1 gg_id:295125 Erwinia chrysanthemi str. E353 EU684
AB244472.1 gg_id:248467 Enterobacter aerogenes str. NC4211 AB244
GU594308.1 gg_id:531073 Escherichia coli str. AC3 GU594
EU470599.1 gg_id:303181 red panda feces clone RP_1aaa01f04 EU470
GQ101940.1 gg_id:429707 Topographical and Temporal Human Skin Microbiome skin palm clone nbw501b10c1 GQ101
FJ906923.1 gg_id:548205 Cronobacter sakazakii str. Jor183 FJ9069
GQ416891.1 gg_id:572750 Temporal succession biological degreasing systems clone F1jun.25 GQ416
FJ192752.1 gg_id:308904 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior FJ1927
EF515391.1 gg_id:220037 Electricigen Enrichment MFC upf microbial fuel cell anode clone 23g08 EF5153
GQ492620.1 gg_id:561719 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
GQ155307.1 gg_id:553345 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ493735.1 gg_id:590258 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
AM184247.1 gg_id:161342 Enterobacter aerogenes str. WAB1906 AM184
FJ405332.1 gg_id:367948 Escherichia coli str. 4059 FJ4053
EF560785.1 gg_id:232471 Escherichia coli str. BE42 EF5607
GQ155160.1 gg_id:585374 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ114876.1 gg_id:466445 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ114
AB273737.1 gg_id:236285 Trabulsiella guamensis str. GTC 1379 AB273
EU240950.1 gg_id:272583 Enterobacter hormaechei str. YO-B EU240
GQ085256.1 gg_id:409792 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw273b02c GQ085
AB548824.1 gg_id:529730 Citrobacter freundii str. JCM 24059 AB548
GQ031696.1 gg_id:454885 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ031
GQ155185.1 gg_id:582498 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
AJ233421.1 gg_id:9796 Leminorella grimontii str. DSM 5078 AJ2334
FJ364615.1 gg_id:362183 feces adult twins and mothers; TS19 clone TS19_a01a10 FJ3646
EU471104.1 gg_id:297764 red panda feces clone RP_3aaa03f01 EU471
FJ611877.1 gg_id:582578 Enterobacter sp. str. ATCC 27981 FJ6118
FJ404760.1 gg_id:368274 Mangroveibacter sp. str. WG-1 FJ4047
NZ_ABHL02000001.1 gg_id:316857 Escherichia coli O157:H7 str. EC4045 NZ_AB
NC_002655.2 gg_id:150516 Escherichia coli O157:H7 str. EDL933 NC_00
GQ155256.1 gg_id:545159 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
FJ608656.1 gg_id:566084 Klebsiella pneumoniae str. EP4 FJ6086
EU468018.1 gg_id:301955 cheetah feces clone CE2_c10_2 EU468
FJ178002.1 gg_id:333293 Escherichia coli str. AC 521 FJ1780
EU430751.1 gg_id:272055 Enterobacter sp. str. ZJUPD5 EU430
GQ492150.1 gg_id:537226 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492

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945.5	5371.0	6401.1	6963.6	4345.0	8341.1	3420.4	5961.0	4710.5	15752.7	4460.8
113.8	3984.0	5973.0	5960.2	2462.9	7712.6	1152.3	7083.8	5661.8	12380.8	3878.6
6028.8	5396.6	6831.3	7447.4	4749.8	9990.2	3701.5	6178.7	4552.7	18804.8	4522.9
589.5	4387.7	5877.9	6146.9	3815.0	7011.8	3628.2	5407.9	5559.3	13746.6	4085.4
1140.7	4829.9	6965.3	7577.4	3305.4	7431.1	3073.8	6836.2	5538.7	12216.3	4316.0
126.6	4375.2	5566.5	6271.7	3802.5	8130.3	2169.1	5391.7	3959.2	15768.2	3268.7
36295.4	8443.6	9673.0	10548.5	8905.5	9603.5	8408.0	10202.3	9957.9	18588.4	9699.5
4328.2	7602.2	8574.2	9917.6	8171.1	8771.5	8245.8	8572.5	10685.9	11986.5	9210.7
4668.9	4362.0	4495.0	5440.2	4504.8	6443.0	3958.6	6024.3	4733.2	8979.6	4627.1
1410.2	5987.7	6545.3	7290.3	9317.5	7709.5	9004.5	6049.4	5384.5	7058.6	5890.1
867.7	5682.3	7548.8	8766.4	5189.5	8041.0	4046.1	6940.8	6385.2	13685.9	6407.1
53.4	1308.3	2109.1	1882.4	1150.0	3682.5	642.9	1282.5	560.6	8568.2	658.4
39.3	1193.8	1606.6	1764.0	992.6	3323.9	932.4	1477.8	492.6	6842.4	832.2
8168.7	5032.4	5499.3	5852.7	5368.0	5371.9	5238.7	5252.6	5600.9	10656.0	6628.9
1228.9	6134.6	7386.9	7231.5	6393.7	7258.6	6509.2	6571.4	6431.8	12749.2	5926.3
804.3	6283.5	8123.5	9147.8	4691.8	8687.0	4271.6	7867.6	6069.2	18417.0	5453.8
593.9	7296.7	8971.3	9347.8	6520.8	12316.1	5720.0	8450.3	4621.1	23239.2	4968.2
2239.0	5091.9	7312.5	8758.2	4241.2	7231.6	4093.9	7549.3	6583.9	12140.3	6337.9
79.5	2628.9	2726.5	2783.6	2571.5	3545.8	2439.9	3180.3	2157.2	8244.4	1910.4
3229.1	7912.1	8391.0	8945.8	7978.0	9243.7	8097.6	8050.3	10480.2	14697.6	7861.0
427.7	3975.2	3939.0	4270.5	2593.4	6310.8	1760.8	4307.4	3587.1	11790.9	2370.5
193.5	5687.0	7228.0	7574.2	4560.2	9457.9	3813.8	7798.2	6102.5	16811.6	4251.6
71.0	5376.4	5969.9	6415.0	5475.7	7903.3	4564.0	5833.2	3585.2	16881.0	4016.0
462.9	4227.6	5560.2	6548.9	4286.0	5748.9	4834.2	5640.8	3677.1	10913.7	4080.5
141.7	6537.0	8135.5	8245.4	7153.2	10388.6	5921.7	7288.1	3464.2	17667.0	3336.9
492.3	2124.3	2909.0	2791.8	1206.2	3611.5	1252.4	2523.0	854.3	9377.0	1591.8
840.9	5302.1	6231.2	6930.0	5136.7	8375.9	4712.9	5928.8	4874.7	16060.4	3984.1
1100.1	6460.6	8384.4	8769.2	5466.6	10338.4	4839.5	8221.6	8193.7	15120.9	6290.4
371.0	6316.4	7946.6	8929.5	4953.5	9250.5	4422.1	7468.5	5359.5	17644.6	5450.3
2148.1	5030.3	6989.2	8257.7	4452.4	6611.5	4967.9	7130.5	4374.7	13484.0	5961.0
116.4	5934.0	8094.2	7797.0	5716.4	10656.5	4915.5	6654.8	4649.4	17365.4	3498.5
324.6	1609.6	2470.7	2704.5	1080.6	2671.3	1139.1	2583.1	1448.8	3322.6	1545.2
930.5	4369.9	5144.4	5976.4	4144.3	5699.2	3805.3	5297.3	4042.2	11411.5	4188.2
198.5	2898.1	4311.9	4929.4	2284.1	3962.7	2136.1	4113.2	2848.5	8981.6	2933.4
741.3	6649.6	7637.9	8374.8	5575.9	9640.0	4810.1	7253.1	5948.3	17411.1	5027.5
9996.0	7206.9	8018.1	8302.2	6247.6	9558.1	5936.1	7339.3	7983.6	16022.5	6460.9
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6565.6	5679.5	5585.6	6315.0	4415.3	5751.4	4435.8	5865.9	6162.6	10286.8	8260.0
835.8	6083.3	7478.4	7929.5	6559.7	10020.4	4645.0	8022.2	5850.0	19435.4	5073.9
1822.1	4424.3	6931.6	7844.3	3239.7	5937.6	3928.6	6714.6	3536.5	16265.7	5312.5

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7544.0	7030.3	2613.1
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8080.3	7639.4	3462.3
9379.0	8636.5	4739.8
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3296.9	2390.3	1215.0
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8660.0	7171.3	6044.7
10515.5	7687.0	4605.1
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9530.5	9361.0	7435.3
7424.3	6087.3	2636.8
9899.0	9049.3	6047.3
9023.1	6153.9	4123.1
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11289.7	10322.0	5902.5
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EU275356.1 gg_id:256517 Enterobacter amnigenus str. CONC4 EU275
GQ493157.1 gg_id:592185 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
NC_007946.1 gg_id:156719 Escherichia coli str. UTI89 NC_00
GQ069665.1 gg_id:467129 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ069
EU460420.1 gg_id:292398 polar bear feces clone PB1_aai28d07 EU460
U88546.1 gg_id:9709 Salmonella paratyphi U8854
EF059884.1 gg_id:226386 Enterobacter pyrinus str. E872 EF0598
U90318.1 gg_id:9667 Salmonella enteritidis str. SE22 U9031
EF604220.1 gg_id:231694 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6042
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FJ997270.1 gg_id:422465 Escherichia coli str. DSPV 284T FJ9972
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FM180568.1 gg_id:369789 Escherichia coli 0127:H6 str. E2348/69 FM180
CP001790.1 gg_id:523634 Pectobacterium wasabiae str. WPP163 CP001
NC_002655.2 gg_id:150515 Escherichia coli O157:H7 str. EDL933 NC_00
FJ976591.1 gg_id:586643 Enterobacter cloacae str. LCR82 FJ9765
EU471123.1 gg_id:297308 red panda feces clone RP_3aaa04c06 EU471
EU470963.1 gg_id:291712 red panda feces clone RP_2aaa01f10 EU470
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EU470754.1 gg_id:298335 red panda feces clone RP_2aaa03f01 EU470
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GQ048034.1 gg_id:414459 Topographical and Temporal Human Skin Microbiome skin palm clone nbw140f03c1 GQ048

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656.1	5064.8	7270.3	8051.3	3436.6	6538.7	3807.3	6908.1	4293.8	16419.0	5455.7
66.1	2654.1	3948.2	3953.6	2620.7	4442.3	1943.4	3782.4	3086.6	8372.4	2207.1
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78.1	1482.8	2141.1	2266.5	1244.3	3787.6	563.9	1972.1	819.0	9346.5	591.4
39.7	4705.5	6176.1	6041.8	3556.3	8544.2	3119.4	5775.9	4635.7	13922.0	3133.3
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EU470945.1 gg_id:294418 red panda feces clone RP_2aaa03f03 EU470
GQ025521.1 gg_id:442426 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ025
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AY941834.1 gg_id:114469 Pantoea agglomerans str. XW112 AY941
AB269763.1 gg_id:167919 Escherichia coli str. AE1-2 AB269
GQ155076.1 gg_id:587663 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EU471300.1 gg_id:297539 red panda feces clone RP_3aaa02b11 EU471
GQ099117.1 gg_id:373130 Topographical and Temporal Human Skin Microbiome skin interdigital web space cl GQ099
DQ836638.1 gg_id:165472 gut- microorganisms pupa and adults pine engraver gut Ips pini larva clone ips8e3 DQ836
GQ095896.1 gg_id:412687 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ095
NZ_AAJU02000034.1 gg_id:351276 Escherichia coli str. F11 NZ_AA
AB428447.1 gg_id:331682 Ewingella americana str. GLD AB428
FJ605379.1 gg_id:449339 Enterobacter cloacae str. AceL-1 FJ6053
AJ884896.1 gg_id:191235 Rahnella sp. N1EH1 AJ8848
GQ155165.1 gg_id:589437 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
Z14096.1 gg_id:9994 Parasite BEV of E.variegatus Z14096
GQ493261.1 gg_id:592641 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
GQ155053.1 gg_id:511492 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EU470684.1 gg_id:292570 red panda feces clone RP_1aaa03a02 EU470
DQ356903.1 gg_id:153848 Pantoea agglomerans str. P29 DQ356
GQ025092.1 gg_id:386644 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1 GQ025
EU470757.1 gg_id:292134 red panda feces clone RP_2aaa02d12 EU470
DQ347838.1 gg_id:145311 Enterobacter cloacae Ecl_IIT-BT08 DQ347
EF059824.1 gg_id:222822 Enterobacter sakazakii str. E283 EF0598
GU594312.1 gg_id:531208 Escherichia coli str. E36 GU594
FJ368408.1 gg_id:361452 feces adult twins and mothers; TS3 clone TS3_a04a06 FJ3684
GQ155271.1 gg_id:586018 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EU816587.1 gg_id:305982 Enterobacter sp. str. MB-2-2-4 EU816
EF604008.1 gg_id:228026 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6040
GQ047651.1 gg_id:462723 Topographical and Temporal Human Skin Microbiome skin palm clone nbw137c11c1 GQ047
EU472845.1 gg_id:300896 red panda feces clone RPSD_1aaa03f06 EU472
EU472732.1 gg_id:293451 red panda feces clone RPSD_1aaa02f03 EU472
EU420928.1 gg_id:274149 Citrobacter freundii str. SA-A5-98 EU420
GQ155187.1 gg_id:592787 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
FM180568.1 gg_id:369793 Escherichia coli 0127:H6 str. E2348/69 FM180
FJ823386.1 gg_id:592076 Escherichia coli str. TCP-1 FJ8233
FJ975788.1 gg_id:589157 Human gut microbiome adopts alternative state bowel transplantation ileum effluent FJ9757
EU471298.1 gg_id:293377 red panda feces clone RP_3aaa01g05 EU471
EU560861.1 gg_id:547859 Assessment genetic Apriona germari (Hope) larvae normalization techniques intestir EU5608
EF515421.1 gg_id:217233 Electricigen Enrichment MFC upf microbial fuel cell anode clone 24c02 EF5154
NZ_ABHT01000152.1 gg_id:260777 Escherichia coli O157:H7 str. EC4501 NZ_AB

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381.8	6052.0	7087.5	7617.5	5553.2	6945.2	5302.7	6532.4	5985.3	12329.4	5892.8
4048.2	7901.6	9220.9	9979.1	7236.0	8114.4	7926.8	8317.0	11486.2	11612.1	8151.8
127.8	5885.7	7621.0	8368.9	5489.5	11282.4	4751.7	6788.4	4865.7	20452.9	4023.5
711.8	2749.8	4363.0	5204.1	1516.6	3686.3	2364.8	3966.1	2003.9	9777.4	3271.4
259.3	3783.8	4783.0	4617.4	3323.6	6496.0	2575.0	5192.8	3876.9	13527.7	2212.3
873.2	4599.4	5649.2	6215.7	3134.8	6369.4	2425.1	5362.4	3726.7	14377.2	3288.7
7062.5	4318.7	4575.2	4176.1	4593.3	4922.9	4205.2	4845.5	4561.5	7390.8	4658.0
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116.4	1644.0	2214.3	2097.8	1397.8	2246.1	1282.8	2615.1	1771.8	3894.2	1166.7
1776.8	7640.0	9125.3	9486.8	6998.5	11182.9	5541.6	8295.8	7980.8	21255.0	5552.7
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235.5	3712.8	4571.8	4724.7	3751.9	5744.1	2642.2	4387.7	3931.3	7474.4	2872.0
253.0	5514.2	6746.8	7330.8	4476.5	7814.7	3766.6	6632.1	5188.9	15152.2	3975.6
597.1	3866.6	4360.5	4605.3	3055.0	4992.1	3172.2	4064.6	5157.1	7011.5	3687.7
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24369.3	8752.7	8757.1	9022.9	7007.9	8042.5	7739.5	7645.0	11394.9	13670.8	11441.4
1463.0	6998.0	8684.9	10033.4	6006.3	8703.5	5322.2	8556.7	7881.4	15600.0	8319.1
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120.0	4093.2	6109.9	7024.2	2351.5	5619.1	2945.6	5762.8	3022.0	15701.1	4113.7
399.4	5646.9	6829.8	8012.2	6044.7	8581.4	5690.4	6072.5	4212.4	15152.0	4418.2
199.6	4129.7	5297.8	5569.9	5206.8	5850.3	4425.5	5416.2	3779.2	11197.9	3178.3
1009.7	6400.4	8197.6	8963.7	5671.0	8969.5	4976.5	7889.1	5921.2	17724.9	6157.6
667.8	2729.2	3311.4	3367.1	2262.9	3705.2	1398.2	4769.0	2296.7	6924.4	1703.3
10870.3	8252.1	9964.2	10561.6	9429.6	12256.3	9771.5	9918.8	9591.8	21619.9	7997.0
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7931.3	5446.7	2669.1
8618.7	6388.9	3451.5
5264.2	6700.4	4389.0
4402.1	2790.0	1748.1
7063.0	6262.7	4108.2
6421.9	4326.1	2831.8
8787.3	8904.8	5659.8
9105.0	7894.9	4670.8
2203.0	3676.6	1417.8
11748.0	8838.0	6386.4
3226.8	3633.6	1815.7
10617.5	7757.6	4546.4
8599.5	9173.4	7742.0
5404.1	4549.4	2862.4
12983.2	7591.5	5498.5
5113.3	4214.6	2736.1
4939.5	5511.6	3212.9
12258.4	8396.9	4885.3
6147.4	5590.8	3613.4
9427.1	7502.9	4775.2
6974.1	5776.4	3465.0
7632.8	9776.8	6328.1
7804.7	6663.8	4897.7
9012.5	6748.9	3591.2
8052.3	8814.3	7119.7
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4042.6	3540.1	2036.9
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7354.0	5413.2	3858.7
10445.7	8047.0	5317.1
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FJ369784.1 gg_id:366939 feces adult twins and mothers; TS51 clone TS51_a04g06 FJ3697
GQ048041.1 gg_id:388811 Topographical and Temporal Human Skin Microbiome skin palm clone nbw140f10c1 GQ048
GQ155197.1 gg_id:585037 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EU472785.1 gg_id:299402 red panda feces clone RPSD_1aaa01c08 EU472
Z83204.1 gg_id:9679 Escherichia coli Z83204
FJ364841.1 gg_id:365623 feces adult twins and mothers; TS19 clone TS19_a03g09 FJ3648
AF373200.1 gg_id:66725 Erwinia chrysanthemi str. 572 AF3732
EU130557.1 gg_id:244222 Escherichia coli str. LR09 EU1305
Z96093.1 gg_id:9800 Erwinia chrysanthemi str. LMG 2804 Z96093
EU472665.1 gg_id:299098 red panda feces clone RPSD_1aaa04f11 EU4726
EU470631.1 gg_id:287354 red panda feces clone RP_1aaa02h10 EU4706
GQ023992.1 gg_id:485677 Topographical and Temporal Human Skin Microbiome skin palm clone nbw124h03c1 GQ023
GQ259886.1 gg_id:582624 Shigella sonnei str. 136 GQ259
EU554428.1 gg_id:273485 Enterobacter cloacae str. Ag02 EU5544
GQ155046.1 gg_id:538073 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EU535123.1 gg_id:280193 profile human microbiota antecubital fossa (inner elbow) skin clone nbt171c02 EU5351
EU464506.1 gg_id:297762 African elephant feces clone AFEL_aai30c11 EU4645
GQ048005.1 gg_id:385167 Topographical and Temporal Human Skin Microbiome skin palm clone nbw140b08c1 GQ048
AB273744.1 gg_id:236091 Erwinia aphidicola str. GTC 1688 AB2737
GQ154843.1 gg_id:553840 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
EU470615.1 gg_id:291008 red panda feces clone RP_1aaa04d04 EU4706
GQ025492.1 gg_id:441988 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ025
GQ026798.1 gg_id:457125 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ026
EU778387.1 gg_id:356210 Red Panda feces clone RPSD_1aaa04a08 EU7783
EU470573.1 gg_id:301959 red panda feces clone RP_1aaa03e03 EU4705
GQ154857.1 gg_id:580141 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
GQ047689.1 gg_id:449074 Topographical and Temporal Human Skin Microbiome skin palm clone nbw137h10c1 GQ047
CU928161.2 gg_id:563141 Escherichia coli str. S88 CU928
EF059842.1 gg_id:224891 Enterobacter asburiae str. E531 EF0598
EU467838.1 gg_id:297319 North American black bear feces clone BB1_b07_2 EU4678
GQ492166.1 gg_id:590121 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
GQ492874.1 gg_id:535252 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
FJ405333.1 gg_id:369236 Escherichia coli str. 4060 FJ4053
AY373830.1 gg_id:105259 Trabulsiella guamensis AY3738
AB198445.1 gg_id:135844 termite gut wall fraction clone RsW01-004 AB1984
GQ025599.1 gg_id:389061 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ025
GQ114854.1 gg_id:415761 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ114
U90316.1 gg_id:9661 Salmonella typhimurium str. Stm1 U90316
DQ068855.1 gg_id:138975 microbiota antlions (Myrmeleon mobilis) GI tract freshly caught antlion OTU6 clone DQ068
EU470655.1 gg_id:297290 red panda feces clone RP_1aaa04h06 EU4706
GQ031692.1 gg_id:383643 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ031

1817.0	3777.7	4580.7	4815.1	2782.3	5637.8	2094.4	5014.3	2774.4	9376.4	2727.2
36036.0	9612.8	9754.2	11458.9	9092.9	9354.8	10645.6	9959.6	14592.1	12300.9	15509.7
778.5	6961.3	8136.7	8720.7	5964.0	9780.2	4826.4	7918.6	7102.0	17893.1	5616.9
3694.7	5618.7	7565.2	8202.7	5301.0	6382.5	5854.1	7314.7	5832.7	12029.6	7734.5
6803.0	3552.5	5103.6	5727.6	2399.4	3965.1	3742.9	4301.5	2946.1	11158.5	5489.1
782.6	3724.4	4366.5	4738.9	4153.6	5347.9	4487.1	4537.5	3660.7	11100.8	2862.1
6122.4	5706.3	6025.2	5983.4	4463.1	5549.1	4259.4	4976.3	4281.9	7693.7	5270.4
201.5	4324.3	6256.9	6998.9	2357.6	5576.7	2916.3	5777.4	3273.7	13366.7	3560.9
714.1	8069.2	8574.1	8503.3	5620.9	9715.1	5747.7	9424.8	9142.9	14195.4	7105.9
3837.4	7583.8	7836.8	8987.4	7005.1	8836.7	7358.0	8314.6	7578.1	13098.1	8197.8
1646.0	3072.9	3833.9	4017.5	2636.7	4490.2	2106.5	3413.4	3266.3	11409.6	2080.5
154.5	2386.0	3966.7	4686.8	1825.6	2291.3	2707.9	3948.2	963.0	6324.9	2885.5
4782.7	5689.0	6349.9	7394.6	5888.5	7110.8	6174.4	7532.1	6321.9	11724.4	11241.0
127.1	3676.1	4264.4	4517.6	2251.2	7170.2	689.2	4525.4	2029.2	18483.6	2110.0
773.3	6132.7	6827.6	7429.9	5420.1	9275.8	5097.8	6454.1	5306.0	17447.0	3987.4
205.3	3591.8	4987.4	4846.0	2527.0	5626.2	2160.1	4315.4	2313.1	12092.2	2532.1
1290.2	2336.6	2904.4	3426.0	2334.4	2789.7	2365.8	2462.5	1985.9	6680.5	2925.6
1212.6	3067.9	3603.3	4553.7	3576.4	5181.2	3644.6	4450.6	2390.8	10030.6	2941.1
253.1	4660.2	6315.7	6186.7	5390.4	7788.6	5023.0	4533.1	1992.9	15028.1	2155.2
486.9	6571.3	7942.1	8312.2	6163.4	11219.0	4858.2	7708.8	5474.0	20505.7	4267.5
10742.3	4402.3	5115.7	5556.7	4240.5	4450.4	4594.4	5021.6	5817.2	8696.3	5561.6
2276.5	5023.0	6128.4	6655.3	4173.4	7091.9	3924.7	5460.3	5500.7	13915.0	4334.1
2242.2	3125.6	3537.6	4383.2	2388.4	3067.2	2637.3	3726.7	2862.2	5675.2	3725.6
2889.9	6061.5	6557.8	7435.9	6211.8	7558.3	5942.7	7833.9	7590.3	12134.9	6841.5
946.6	5662.8	7206.7	8177.1	4979.3	8549.5	4552.8	6927.5	4541.2	16617.5	5082.6
304.4	8335.5	9964.1	11028.6	7540.7	11969.5	6229.5	9647.0	8135.1	21084.9	6536.5
903.0	5092.0	6805.4	7206.2	4409.8	6659.9	4429.4	6063.1	4070.2	13378.7	4989.6
1162.9	4526.7	6928.7	7860.3	3109.1	6126.2	3323.4	6832.9	3710.5	15086.7	5061.9
121.0	7351.0	9005.0	9312.1	6275.1	12402.7	5633.2	8752.9	5589.6	23221.2	5363.6
9510.8	5997.4	7516.4	7685.1	6131.0	6733.8	6629.2	7056.9	7118.6	14313.3	6905.4
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1381.4	5361.9	5758.0	6986.6	6289.5	6813.2	6386.0	6786.9	5222.9	12374.5	6745.4
261.5	1631.6	2446.5	2873.5	1185.2	1699.5	2290.2	2372.2	1029.7	4534.4	1944.0
16708.5	6679.7	8693.2	8426.6	7802.7	9516.9	6969.2	8318.5	7790.3	14976.2	6319.1
432.1	7478.1	9852.6	10387.9	7291.6	12478.8	6022.9	9484.1	7061.6	22444.7	6037.9
2704.0	5411.1	6688.6	7332.9	4510.4	7935.4	3800.6	6128.0	6196.9	16053.2	4650.0
4325.1	7716.6	9096.1	8969.1	7528.7	10171.1	7352.7	8338.8	9021.8	18502.1	6186.6
47.7	3203.2	3713.2	3896.5	2837.0	5719.4	2116.6	3449.1	1027.8	7710.8	1330.8
194.9	5032.0	5743.5	6121.9	3411.1	7937.6	3234.4	5909.8	3431.9	17753.7	3575.9
3286.8	5657.0	6783.8	8021.5	5703.6	6912.1	5857.1	7653.3	5664.8	13223.6	6771.4
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5757.4	3641.5	2641.5
6050.4	5528.5	3691.6
7074.9	6164.6	4727.7
7540.5	5959.8	2697.3
10579.0	10236.6	5996.2
8482.8	7519.4	7969.8
5788.5	4780.7	2893.9
3709.1	2838.1	1464.3
8759.0	8035.9	6956.4
5854.0	4548.0	1844.3
10012.3	7509.8	4857.8
5724.0	4459.0	2266.2
3063.4	2691.9	2863.2
5864.1	4181.6	3620.8
7906.0	5195.4	2786.0
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4978.5	6160.4	3623.1
7718.7	6746.7	3919.7
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10010.9	7292.9	4658.2
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7564.8	6806.9	4301.0
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12671.7	8558.9	5626.7
7849.9	6573.9	3848.0
8689.8	9670.8	5107.6
7785.7	8393.6	7865.4
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12663.2	9682.8	6785.9
8800.0	7230.5	4307.9
10407.9	9960.1	5817.4
6499.2	5887.4	3238.8
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10194.8	7154.9	5909.5
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EF191171.1 gg_id:189337 Escherichia coli dcm EF1911
EF515376.1 gg_id:225183 Electricigen Enrichment MFC upf microbial fuel cell anode clone 23e11 EF5153
GQ155116.1 gg_id:511824 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ155122.1 gg_id:569621 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EF428236.2 gg_id:218527 Enterobacter hormaechei str. HDYM-06 EF4282
GQ155942.1 gg_id:574837 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
DQ818881.1 gg_id:164892 mouse cecal microbiota-colonized zebrafish digestive tract clone aab39b09 DQ818
EF515182.1 gg_id:226172 Electricigen Enrichment MFC upf microbial fuel cell anode clone 21a07 EF5151
GQ047658.1 gg_id:400299 Topographical and Temporal Human Skin Microbiome skin palm clone nbw137d10c1 GQ047
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GQ493947.1 gg_id:532961 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
AP010953.1 gg_id:568503 Escherichia coli O26:H11 str. 11368 AP010
GQ102038.1 gg_id:456984 Topographical and Temporal Human Skin Microbiome skin palm clone nbw502g05c1 GQ102
CU928161.2 gg_id:563143 Escherichia coli str. S88 CU928
GQ069819.1 gg_id:465176 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw1 GQ069
FJ975865.1 gg_id:554433 Human gut microbiome adopts alternative state bowel transplantation ileum effluent FJ9758
FJ368169.1 gg_id:362886 feces adult twins and mothers; TS3 clone TS3_a01a10 FJ3681
EU472720.1 gg_id:289568 red panda feces clone RPSD_1aaa03g08 EU472
GQ155176.1 gg_id:512507 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
AM933757.1 gg_id:353249 Kluyvera cryocrescens 4701 AM933
CU928162.2 gg_id:547289 Escherichia coli str. ED1a CU928
NZ_ABHK01000009.1 gg_id:260250 Escherichia coli O157:H7 str. EC4206 NZ_AB
EU472859.1 gg_id:302247 red panda feces clone RPSD_1aaa03f11 EU472
GQ155100.1 gg_id:539752 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ047953.1 gg_id:434609 Topographical and Temporal Human Skin Microbiome skin palm clone nbw139e07c1 GQ047
EU472801.1 gg_id:295032 red panda feces clone RPSD_1aaa04g01 EU472
AF373203.1 gg_id:66723 Erwinia chrysanthemi str. GSPB 1406 AF3732
EU723875.1 gg_id:349834 Shigella sp. str. 121405 EU7238
GQ033388.1 gg_id:388657 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw1 GQ033
AY360397.1 gg_id:93777 Erwinia chrysanthemi str. S3-1 AY3603
EU275357.1 gg_id:250107 Pantoea agglomerans str. CONC7 EU2753
EU560857.1 gg_id:562063 Assessment genetic Apriona germari (Hope) larvae normalization techniques intestir EU5608
EU471032.1 gg_id:295686 red panda feces clone RP_2aaa01c11 EU4710
AB288903.1 gg_id:201514 termite gut homogenate clone BOf5-16 AB2889
GU594301.1 gg_id:516250 Escherichia coli str. A5 GU594
EF515211.1 gg_id:217868 Electricigen Enrichment MFC upf microbial fuel cell anode clone 21d06 EF5152
GQ155921.1 gg_id:548341 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EU009178.1 gg_id:250393 Shigella boydii str. FBD007 EU0091
GQ491471.1 gg_id:588423 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
EF608546.1 gg_id:230213 predatory Poecilus chalcites their response lab rearing and antibiotic treatment diges EF6085

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1453.0	3179.0	3988.8	4384.7	2795.5	4634.9	1951.6	3765.6	3214.9	11113.8	2644.6
348.9	2452.7	4539.1	4763.9	3554.4	7073.0	1898.8	5350.3	3264.6	14617.4	2588.9
2024.7	9554.0	9603.9	10732.2	10246.8	10030.6	11235.1	9665.8	8801.9	14921.1	9906.0
9678.1	4957.1	5594.4	5910.3	4951.9	6627.5	5278.6	5463.8	6245.6	13760.9	3887.7
2110.8	5979.4	6523.8	7520.0	6176.5	9597.7	5388.7	7048.2	5214.5	17106.7	4516.1
7245.7	3941.8	4236.9	4378.3	3366.1	5710.9	3530.8	4027.7	3347.0	11588.7	3974.6
1447.8	3298.7	4327.2	4801.2	2456.4	4331.7	2451.3	4722.6	2649.6	7872.9	3582.6
2089.6	5715.3	6457.9	7068.4	6233.6	7764.1	6488.5	6671.9	7629.5	13123.5	6954.9
3232.8	7939.6	9379.4	11116.2	7754.5	10883.2	5952.6	10704.5	9083.1	17407.8	9133.7
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1274.3	6190.7	6653.7	6391.7	4813.2	5316.4	4664.1	6310.1	6883.0	10418.4	5367.1
758.2	5909.1	6181.7	6781.6	6310.3	7724.8	5256.1	7136.2	5250.4	11050.2	4249.9
654.5	5589.9	7804.5	8697.0	3820.2	7562.2	4073.6	7407.7	4559.7	18109.1	5641.2
25961.0	7550.2	8336.6	8952.8	7530.0	10138.0	7557.1	7875.0	12187.2	15447.7	10472.1
938.7	9360.2	10125.5	10775.8	9073.9	11599.5	9195.3	9900.8	6227.4	18582.7	8153.8
2340.1	2948.3	3222.1	3607.0	2243.5	4544.7	2188.8	3626.0	2509.0	8646.7	2675.5
1131.2	3448.8	5383.4	6375.3	2031.5	4812.7	2558.4	5704.7	2026.2	12706.7	3509.8
650.1	5526.6	6359.3	6726.5	5046.1	7978.8	4738.0	6017.7	5707.1	16347.1	4155.8
166.2	2489.4	3416.2	3266.2	1950.5	4773.7	1565.1	3031.9	2019.0	9299.4	2336.7
657.8	3205.5	4831.8	5709.7	1758.7	4284.3	2389.8	4601.0	2318.7	10944.2	3506.3
663.9	2400.7	3474.1	3788.2	2054.2	3060.0	2101.4	3314.0	2672.2	6194.7	3616.4
1422.7	5006.0	7447.4	8400.2	4234.0	6983.9	4142.1	6778.4	4027.8	14803.5	5573.7
828.1	6316.9	7520.3	8221.1	5430.4	9391.3	4102.3	7482.8	6319.1	18037.8	5561.1
22780.6	8517.1	9152.5	10497.1	8104.3	9267.1	8431.7	9185.2	9782.1	13489.2	12084.3
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117.0	4958.6	6850.5	7285.3	4331.4	9479.6	2376.7	6648.1	3504.7	15478.3	3524.6
744.7	2945.6	3851.6	3929.6	3743.6	3691.4	3237.6	3643.5	2071.2	7987.7	1958.5
214.1	2679.1	3701.7	4226.9	2180.8	3973.2	2370.9	3819.0	2304.5	10073.2	2524.1
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156.1	4022.2	5531.6	5880.6	4057.9	9197.4	1506.2	4178.3	1936.9	19305.9	2107.9
2201.9	3941.6	4604.6	4845.2	4411.4	5587.8	3919.2	5043.0	4189.4	6502.4	3013.0
849.1	4127.2	5054.1	5628.7	3656.5	5933.5	3109.6	5014.8	3812.9	15161.0	2999.6
639.3	4649.2	5374.7	5558.9	4490.1	6531.1	3818.6	6081.1	2547.5	10648.7	2889.3
841.3	4781.1	5922.5	6307.3	3948.0	6355.6	3688.0	5507.5	4264.6	12841.3	4133.3
772.4	4463.8	4833.4	5661.9	4166.3	8285.7	3602.6	5962.9	3468.0	14765.0	4416.5
175.3	4185.7	5071.2	5597.3	4226.2	6222.6	3260.0	5114.0	3603.9	11517.5	2849.6
232.7	5012.5	6372.8	6870.1	3749.2	6616.9	3369.7	6001.2	4690.2	14214.9	3880.0
2089.4	4739.8	5055.3	7019.7	5199.9	6477.9	6018.4	5737.4	4346.8	11462.2	6782.9
90.9	1990.3	2828.2	2501.2	1862.7	3056.2	1528.0	2844.1	1614.5	3925.6	1610.8

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6819.8	4518.4	2674.8
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7525.9	6140.0	3809.3
10591.8	8579.1	3850.1
7416.0	5580.3	2915.0
5078.7	5585.8	2995.7
7752.8	8389.7	6260.8
11324.9	11225.6	7905.4
11649.4	9116.2	6617.0
4794.0	6648.7	3817.6
6403.5	7499.4	4162.1
8470.8	7742.4	4954.0
9549.2	6916.7	3845.5
7727.3	7495.1	7267.1
11810.5	9690.7	9660.1
4935.8	4336.0	2195.5
6158.0	5604.3	1561.2
8926.8	6866.4	4474.7
5433.4	4233.0	2254.2
5849.8	4384.2	2094.8
3451.8	4224.0	1448.0
7933.8	5907.7	3808.2
10701.9	7867.0	5630.0
9441.8	10232.2	9064.6
5588.8	4547.2	1316.9
10206.1	7715.7	4164.7
4995.5	4416.7	2616.5
4625.3	4200.3	1679.5
6859.3	6040.0	4144.0
8484.6	4570.1	2950.8
6296.1	6642.4	4112.7
7431.6	5565.3	3051.5
7593.5	6268.1	4301.8
8295.6	6848.5	4036.1
8331.2	6055.6	3957.4
7234.4	5854.6	3658.9
8225.9	6972.8	3853.0
6529.7	6017.1	6133.5
2993.2	3537.5	1361.1

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AB368994.1 gg_id:569024 and microbial oils produced Asia petroleum crude oil (Arabian Extra light) clone PT-A AB368
CP001637.1 gg_id:524976 Escherichia coli str. DH1 CP001
AM184214.1 gg_id:161150 Pantoea agglomerans str. WAB1872 AM184
EU472148.1 gg_id:288731 francois langur feces clone FL_2aaa02a09 EU472
EF515321.1 gg_id:219651 Electricigen Enrichment MFC upf microbial fuel cell anode clone 22h03 EF5153
EF011116.1 gg_id:199506 Enterobacter cancerogenus str. EBD EF0111
EF471230.1 gg_id:226404 Enterobacter sp. str. BBTR105 EF4712
CP001790.1 gg_id:523631 Pectobacterium wasabiae str. WPP163 CP001
AM157436.1 gg_id:141413 Escherichia coli mother C4 AM157
CP000247.1 gg_id:169667 Escherichia coli str. 536 CP000
EU470717.1 gg_id:302020 red panda feces clone RP_1aaa02h08 EU470
FJ368186.1 gg_id:366961 feces adult twins and mothers; TS3 clone TS3_a01c05 FJ3681
EU778424.1 gg_id:326151 Red Panda feces clone RPSD_1aaa01b11 EU778
AY804014.1 gg_id:112448 Escherichia coli str. T10 AY804
EU471322.1 gg_id:303145 red panda feces clone RP_3aaa04b03 EU471
GQ029738.1 gg_id:413180 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw926f08 GQ029
EU554433.1 gg_id:273281 Shigella boydii str. Ag07 EU554
EU472761.1 gg_id:301142 red panda feces clone RPSD_1aaa02f12 EU472
L10328.1 gg_id:9702 Escherichia coli L10328
EF560776.1 gg_id:232981 Escherichia coli str. BE14 EF5607
EF676101.1 gg_id:257345 Klebsiella oxytoca str. XJU-1 EF6761
GQ102000.1 gg_id:409168 Topographical and Temporal Human Skin Microbiome skin palm clone nbw502c09c1 GQ102
AJ854062.1 gg_id:108296 Serratia ureolytica str. NiVa 51 AJ854
GQ099091.1 gg_id:389986 Topographical and Temporal Human Skin Microbiome skin interdigital web space cl GQ099
GQ031106.1 gg_id:395646 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ031
FJ368221.1 gg_id:369163 feces adult twins and mothers; TS3 clone TS3_a01f08 FJ3682
CP000247.1 gg_id:169665 Escherichia coli str. 536 CP000
EU470534.1 gg_id:296475 red panda feces clone RP_1aaa04e05 EU470
EU471185.1 gg_id:290380 red panda feces clone RP_3aaa03b07 EU471
GQ927306.1 gg_id:540402 Enterobacter sp. str. M6 GQ927
EU761952.1 gg_id:316329 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1 EU761
FJ364654.1 gg_id:368156 feces adult twins and mothers; TS19 clone TS19_a01e03 FJ3646
GU186117.1 gg_id:593155 Enterobacter cloacae str. IHB B 1374 GU186
GU594309.1 gg_id:521580 Escherichia coli str. AB6 GU594
U88435.1 gg_id:10311 Rahnella sp. 'CDC 21234' str. CDC 21234 U88435
EU470575.1 gg_id:302778 red panda feces clone RP_1aaa03a07 EU470
EU999992.2 gg_id:343920 Enterobacter ludwigii str. T4384 EU999
EU240200.1 gg_id:236031 interfering detection phytoplasma universal phytoplasmic primers Mexico EU240
EU460602.1 gg_id:298145 polar bear feces clone PB2_aai23c03 EU460
EU472738.1 gg_id:302314 red panda feces clone RPSD_1aaa03d08 EU472
NZ_AAJU02000035.1 gg_id:318422 Escherichia coli str. F11 NZ_AA

3724.9	6316.6	6538.1	5313.6	4235.8	5962.5	3921.0	5092.9	7951.7	13354.8	7767.0
164.5	3220.6	4568.1	4509.9	2126.1	5355.6	1830.9	3901.3	1651.1	11358.3	2011.2
162.2	3178.4	5742.6	6189.5	3156.2	8849.5	1123.7	4650.1	2057.4	20548.2	2122.3
4006.8	7252.2	7757.2	9837.7	8330.5	8138.3	8879.1	7722.3	8948.2	10471.2	10919.8
41.1	2974.9	3950.1	4072.4	2809.7	6584.2	2037.9	3956.7	1920.0	12353.5	2272.5
6079.9	7143.3	8659.2	9258.3	6667.9	10780.7	6443.0	7961.1	5234.2	19624.3	5400.9
46.8	166.8	248.3	251.4	195.8	573.1	259.9	215.4	135.4	1180.1	79.7
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54.9	1889.1	2651.2	2958.0	1018.7	3654.4	1021.6	2346.0	1084.9	7858.5	1092.2
574.2	4946.7	6252.9	6959.1	4556.0	7231.4	4336.5	6127.7	6050.0	12726.1	5194.7
1019.5	5207.1	6627.5	7430.2	4741.6	7384.8	4973.1	6351.9	3962.4	14523.5	4697.1
4042.4	5289.7	6264.3	6730.9	5521.5	7187.7	5298.1	6136.3	5599.4	11697.9	5678.8
745.9	2454.0	3640.4	4575.7	2323.9	3410.7	2741.9	4219.3	1579.7	6809.3	2964.4
114.2	2960.1	4565.2	5411.0	2219.2	3512.0	2861.6	4397.6	1148.2	10126.7	2929.6
1741.9	3886.8	4702.0	5415.6	2842.3	7969.6	2126.9	5360.8	3934.1	16155.9	2659.8
4568.8	4392.2	5692.3	5971.5	3582.6	6031.0	3186.1	5067.5	4344.7	13051.0	4676.7
1354.6	5238.1	6450.9	7068.0	4429.1	7992.1	3278.9	6353.9	5484.1	16831.7	4793.7
868.4	5639.3	7173.1	8148.0	4785.3	8122.4	4300.4	6834.1	4403.4	16329.5	5624.4
3966.7	2966.9	3604.1	4135.8	2776.7	4392.8	2356.5	3887.8	2385.7	8921.6	2818.4
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101.4	5472.9	6492.1	6862.0	4410.4	9252.3	3704.1	7089.7	7221.7	15272.2	4806.0
5936.7	7499.9	6955.2	7692.2	6592.5	7913.5	6086.1	7896.9	7038.3	10772.1	8591.6
62.0	3023.8	4290.6	4312.1	2837.0	6214.7	1646.1	3799.0	1900.8	12685.4	1592.8
146.5	4197.1	3955.5	3888.3	4475.1	4129.5	6190.2	4450.5	2239.9	4608.0	3172.2
8436.4	3145.0	3867.1	3977.0	2395.8	4132.7	3781.3	3486.3	4320.5	9249.9	4820.7
145.0	2240.5	3717.2	4559.0	1321.4	2928.7	1812.0	3452.1	1134.5	7793.9	2502.9
957.8	4082.4	5385.6	5957.0	3445.4	5444.1	4019.5	4907.4	2468.9	11452.0	3766.9
153.3	4298.6	5863.7	6329.6	3738.3	6818.1	3246.9	5533.3	3517.3	14488.0	3556.7
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7215.1	4268.7	5254.9	5485.7	3881.8	5432.1	4203.0	4262.0	5550.3	10495.8	6516.0
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21537.2	6568.9	7590.5	8550.5	7102.7	9875.4	6346.0	6226.3	7999.4	15882.5	9170.9
1449.1	4058.2	5476.5	6667.0	3468.2	4890.2	4947.2	5556.0	2886.0	9993.2	4754.8
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1448.7	5624.3	7764.7	8318.9	5212.1	8696.2	4379.0	7475.9	5707.5	16092.4	5402.1
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11677.7	8991.3	6288.8
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11092.8	9622.2	4979.8
4282.3	3935.5	1098.3
7781.3	7948.1	3866.0
8700.7	6573.4	4436.3
7210.3	8159.4	6445.3
3932.2	4157.7	2911.9
5432.2	3430.6	1673.0
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8808.4	7678.6	5029.5
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11452.5	8024.5	4916.7
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AJ233424.1 gg_id:10115 Pragia fontium str. DSM 5563 AJ2334
GQ101959.1 gg_id:464725 Topographical and Temporal Human Skin Microbiome skin palm clone nbw501g08c1 GQ101
GQ099081.1 gg_id:403628 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ099
GQ155052.1 gg_id:574054 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
AF511430.1 gg_id:65406 Escherichia coli CCCO4 AF5114
AY344368.2 gg_id:91670 Lake Kauhako 30 m clone K2-30-35 AY3443
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FJ976582.1 gg_id:592530 Enterobacter cancerogenus str. LCR73 FJ9765
CP000247.1 gg_id:169666 Escherichia coli str. 536 CP000
EF102825.1 gg_id:257388 Enterobacter sp. str. G-226-1 EF1028
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EF219421.2 gg_id:441069 Enterobacter cloacae str. ATCC 43560 EF2194
U92197.1 gg_id:9711 Salmonella subsp. enterica serovar Agona str. Sa1 subsp. U9219
GQ154820.1 gg_id:535230 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
GQ031713.1 gg_id:452836 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ031
NZ_ABHM02000001.1 gg_id:317271 Escherichia coli O157:H7 str. EC4042 NZ_AB
GQ155096.1 gg_id:594320 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
FJ859683.1 gg_id:573410 Enterobacter ludwigii str. BIHB 336 FJ8596
GQ155198.1 gg_id:586724 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
CP000468.1 gg_id:175186 Escherichia coli str. APEC O1 CP000
NC_008563.1 gg_id:176527 Escherichia coli str. APEC O1 NC_00
GQ155253.1 gg_id:582117 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
FJ976590.1 gg_id:581741 Enterobacter sp. str. LCR81 FJ9765
FJ811874.1 gg_id:593519 Enterobacter aerogenes str. 5-WCH FJ8118
ABHS01000007.1 gg_id:302893 Escherichia coli O157:H7 str. EC4486 ABHS0
X80726.1 gg_id:9698 Shigella sonnei X80726
FJ364922.1 gg_id:363434 feces adult twins and mothers; TS19 clone TS19_a04g07 FJ3649
FM180568.1 gg_id:369792 Escherichia coli 0127:H6 str. E2348/69 FM180
AAMJ02000006.1 gg_id:342676 Shigella dysenteriae str. 1012 AAMJ0
EU778390.1 gg_id:333367 Red Panda feces clone RPSD_1aaa01b09 EU778
EU554431.1 gg_id:273912 Shigella flexneri str. Ag05 EU554
AF400480.1 gg_id:18267 Secondary endosymbiont Bemisia tabaci clone TANZ3-2 of AF4004
DQ837613.1 gg_id:164437 structures honeybee intestines and their response insecticidal proteins gut clone HB DQ837
DQ026512.1 gg_id:134671 Xenorhabdus sp. str. PDBC SCX7 DQ026
GU480985.1 gg_id:521599 Xenorhabdus hominickii GU480
AB030020.1 gg_id:32418 Antonina crawii (Insecta Homoptera Pseudooccidae) symbiont AB030
AF286129.1 gg_id:21132 eubacterium Aleurodicus dugesii AF286
AF476107.1 gg_id:63935 Planococcus citri symbiont AF476
AY676889.1 gg_id:136328 Baumannia cicadellinicola B37 AY6768
AF400474.1 gg_id:50143 Secondary endosymbiont Bemisia tabaci clone IND34 AF4004

407.4	4668.0	4213.0	5316.7	3653.4	7076.9	3292.9	5174.5	3891.1	9020.0	3405.0
3999.4	8984.0	8756.8	8954.9	8445.4	8023.4	10119.5	8110.8	11507.2	11244.5	9381.6
11642.1	9084.5	8813.1	9425.5	8109.3	8896.8	7907.1	8424.0	11794.9	11700.6	9258.2
725.3	5629.4	6250.8	6826.2	4972.0	8156.9	4741.1	5887.8	4899.8	15790.2	4052.2
696.4	4995.9	7032.3	8125.7	3217.0	6265.4	3813.7	6722.7	2965.8	16304.3	4812.2
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145.2	4832.7	4766.5	4224.9	3844.4	5330.8	2767.2	4410.2	3710.1	6667.0	3273.0
462.6	4408.8	4539.0	4517.6	2821.1	6706.5	3253.7	4888.7	3479.5	11675.1	3516.9
336.9	5698.5	6966.0	7664.7	4746.0	8105.7	4000.5	6740.9	5854.2	15640.2	4380.9
4041.7	5634.6	7266.2	8019.5	5153.2	10459.3	3732.9	6448.7	4354.8	19702.3	3995.8
6060.1	8239.1	9062.6	10258.7	8180.5	11056.9	7378.0	8808.8	5672.8	19499.4	6243.1
217.9	3953.2	6234.8	6536.5	2888.8	5853.3	2380.5	6712.0	5795.4	10859.0	4577.8
659.7	5651.9	7135.9	7406.1	5453.3	10266.1	3471.0	6269.8	3490.9	21967.1	3725.0
11523.0	4663.4	4109.1	5375.2	5094.0	5305.4	5206.8	4787.4	4943.9	6645.8	5215.0
3070.3	6706.1	8245.5	8408.4	5766.6	10932.7	5571.8	7593.1	7715.1	18054.3	6761.4
17153.0	9641.8	9886.3	10031.2	8928.2	10706.4	9148.9	9705.2	12735.0	17449.6	9541.0
1018.4	4520.1	5589.4	6644.7	4227.4	5633.3	4107.7	5795.7	4200.8	11596.8	4683.9
82.1	3465.3	3897.5	3860.6	3449.2	5850.8	3964.7	3863.1	2670.9	10741.5	1583.5
183.7	3344.3	5617.3	6126.3	3508.1	9319.2	1087.1	5000.9	2165.7	20065.6	1982.2
756.2	5881.7	6654.9	7297.6	4916.8	9141.4	4163.2	6298.5	5091.6	17740.3	4064.8
495.4	5028.2	6348.4	6827.1	3542.0	7724.6	2736.7	5885.2	4888.5	15100.1	4083.0
265.9	5834.2	7308.0	8004.5	4856.6	9282.7	3618.7	6751.0	6257.9	17750.4	4770.0
715.6	4389.1	5345.9	5387.0	4440.3	6613.8	4189.3	5368.2	5674.3	13504.8	3244.4
352.4	2757.0	3794.6	3827.5	2119.0	5464.8	1636.5	3476.0	1678.2	13426.8	2153.9
24666.0	9756.3	9797.8	10085.4	9341.9	11259.9	9795.5	9032.2	9648.3	19351.4	10342.9
604.1	2565.5	3837.6	4466.4	1956.0	3627.5	2154.9	3788.3	2407.0	8420.1	2885.4
2074.9	4804.4	5840.8	6195.8	4320.1	7268.8	3416.7	5482.5	3276.4	14041.7	3280.3
323.4	5851.3	7329.8	7984.4	5002.7	9040.4	3854.7	6848.9	6365.0	17914.4	4821.9
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6695.2	4555.8	5916.5	6446.4	3438.4	7932.0	2484.0	6197.3	4919.7	14780.8	3749.4
20334.4	7690.4	7940.8	8627.1	8540.1	8323.9	8574.0	8204.9	11866.9	11800.5	10016.4
14264.7	5664.1	5750.8	6425.6	4891.4	6635.2	4808.6	6936.2	6507.7	9209.1	8231.7
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78.6	936.5	1072.3	1133.4	864.4	1648.1	490.0	1765.3	1702.5	3531.5	832.2
55.0	82.5	80.8	134.9	84.4	83.0	56.4	136.5	48.3	35.4	66.4
56.0	131.6	250.7	198.4	52.9	112.8	44.9	170.8	64.1	190.6	60.9
1005.4	2699.8	3177.3	3440.0	3424.6	3824.9	2388.1	3369.0	2979.3	5687.9	2072.7
145.1	1601.1	1401.5	1821.7	843.4	1951.3	363.3	1925.3	1746.4	2370.7	1173.8

7830.8	6837.0	3917.0
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6909.4	5794.3	3051.9
4546.9	6009.9	3325.1
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9963.9	7410.5	3803.4
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6054.1	6629.1	4950.1
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99.3	71.0	69.2
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4063.2	4570.3	2866.5
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EU348311.1 gg_id:338822 symbiont	EU3483
DQ837612.1 gg_id:170811 structures honeybee intestines and their response insecticidal proteins gut clone HB	DQ837
AY660027.2 gg_id:119010 Xenorhabdus bovienii str. PDBC SCX6	AY660
AB064513.1 gg_id:49541 Buchnera aphidicola (Yamatocallis tokyoensis) #207 (Yamatocallis	AB0645
DQ068832.1 gg_id:139463 microbiota antlions (Myrmeleon mobilis) GI tract freshly caught antlion OTU7 clone	DQ068
AF476104.1 gg_id:63945 Dysmicoccus neobrevipes symbiont	AF4761
GU374099.1 gg_id:531978 soil East Calcutta wetland clone SRC_NBB4	GU374
AY676885.1 gg_id:136092 Baumannia cicadellinicola B30	AY6768
FJ655533.1 gg_id:592467 symbiont	FJ6555
DQ133564.1 gg_id:146333 Preliminary survey insects (Hemiptera: Coccoidea) scale insect clone	DQ133
AB013087.1 gg_id:9649 symbiont	AB013
FJ655532.1 gg_id:542044 symbiont	FJ6555
EU348312.1 gg_id:348059 symbiont	EU3483
GQ154740.1 gg_id:534965 Human gut microbiome adopts alternative state bowel transplantation ileum intesti	GQ154
AF286125.1 gg_id:52069 symbiont	AF2861
AB083058.1 gg_id:60304 Placobdelloides siamensis symbiont	AB083
AF263559.1 gg_id:54656 Cacopsylla myrthi symbiont	AF2635
AF077608.1 gg_id:9978 symbiont	AF0776
AF286128.1 gg_id:27576 symbiont	AF2861
AF400478.1 gg_id:52003 Secondary endosymbiont Bemisia tabaci clone TANZ15 of	AF4004
AY167945.1 gg_id:76905 Isolation and identification hyper-ammonia producing swine storage pits manure	AY1679
AY676882.1 gg_id:136397 Baumannia cicadellinicola B23	AY6768
AF476110.1 gg_id:63934 Vryburgia amaryllidis symbiont	AF4761
AY999971.1 gg_id:200690 Placobdelloides jaegerskioeldi symbiont	AY9999
AF476101.1 gg_id:63942 Antonina pretiosa symbiont	AF4761
AF286127.1 gg_id:20298 symbiont	AF2861
NC_004344.2 gg_id:141977 Wigglesworthia glossinidia endosymbiont Glossina brevipalpis	NC_004
EF153305.1 gg_id:192342 identification gut red imported fire ant (Solenopsis Buren) GI tract Solenopsis invicta	EF1533
AB083059.1 gg_id:55799 Parabdella sp. symbiont	AB083
DQ211709.1 gg_id:164016 Xenorhabdus sp. str. FRM16	DQ211
D78008.1 gg_id:10301 Xenorhabdus japonica str. SK-1T (=IAM14265T)	D78008
GU480979.1 gg_id:529286 Xenorhabdus griffiniae str. T87	GU480
GQ923884.1 gg_id:589696 Xenorhabdus sp. str. KB-3	GQ923
DQ205450.1 gg_id:173648 Xenorhabdus sp. str. USNJ01	DQ205
GU480982.1 gg_id:526425 Xenorhabdus sp. str. R00I-293	GU480
GQ373385.2 gg_id:526191 Xenorhabdus sp. str. SGas1	GQ373
AY286478.1 gg_id:87839 Xenorhabdus nematophila	AY2864
FN667741.1 gg_id:524496 Xenorhabdus bovienii str. SS-2004	FN6677
AB243427.1 gg_id:160641 Xenorhabdus sp. str. MY8 IkWj136	AB2434
GU480989.1 gg_id:517099 Xenorhabdus szentirmaii	GU480

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4990.4	3396.0	3483.3	4268.3	3133.7	3613.0	3048.7	3931.3	5155.3	6222.9	4423.2
40.8	1944.5	2231.6	2527.2	1401.7	3576.1	1011.8	2547.2	1344.2	3261.6	1457.1
12287.9	4244.4	4177.7	4445.6	3664.9	5347.3	4404.6	5239.3	5475.8	11442.8	4269.0
90.1	211.9	284.5	265.6	198.3	238.0	197.4	330.2	248.6	250.0	141.8
48.2	401.7	684.3	783.8	269.5	823.3	207.0	759.9	562.4	817.9	370.5
230.2	2120.4	2528.7	2626.9	2368.6	2652.6	1840.0	3318.9	2856.6	3688.2	1838.7
3411.8	2269.6	3216.7	4184.6	1819.4	4496.7	1703.7	3709.4	2992.7	8747.4	1686.0
40.1	286.2	314.5	372.7	294.2	391.0	258.4	493.9	288.1	451.8	172.6
6787.2	6649.6	6603.6	7102.7	7500.0	8367.3	5786.6	6871.9	8194.1	7029.1	6466.9
45359.9	12069.8	10890.1	11551.9	12506.9	11196.9	12402.0	10656.1	15424.4	13123.0	19439.6
74.8	322.8	369.3	204.8	176.5	278.1	278.8	308.3	804.7	634.3	376.3
870.5	3742.5	3650.0	3442.6	2996.8	4077.3	2728.8	3660.8	3105.0	4216.7	2702.5
1884.8	4442.6	4304.8	5553.2	4389.2	5132.1	4179.7	4707.9	4271.0	7589.2	4137.4
250.5	2875.8	3287.1	3141.1	2298.7	3908.6	1576.0	3524.9	3487.0	6374.6	2376.3
78.5	362.0	383.2	319.7	255.4	175.8	442.3	317.8	311.8	150.9	390.9
1575.2	325.5	422.8	387.5	243.1	491.2	407.8	529.0	390.5	1421.5	329.3
5422.5	3758.5	4073.1	4641.3	4882.4	4214.7	4922.1	4428.6	3780.7	5811.6	3850.3
74.8	932.5	1422.1	1400.4	807.0	1382.2	541.7	1495.2	957.2	2117.7	1146.1
29.8	942.3	1515.8	1178.2	777.1	1230.2	893.2	717.8	179.2	1138.3	245.6
6949.3	2679.6	2864.0	3430.1	2496.0	3533.4	2517.0	3447.3	3271.4	6640.1	2451.2
195.9	1802.0	1949.8	2073.3	1467.5	2595.9	1587.7	2555.8	2689.5	3260.9	1297.5
386.8	3530.7	4537.9	4349.0	2646.5	4231.1	2992.2	4103.1	2887.8	4578.4	3322.3
88.6	1704.2	2220.1	2487.1	1920.6	3180.2	1012.2	2779.6	2168.2	6343.6	1286.6
630.7	3197.8	3486.8	3214.4	2807.6	4614.3	2413.2	3373.3	3015.4	5781.2	2032.7
1890.2	3701.3	4194.6	3870.1	4111.3	5456.8	2697.3	4904.6	3527.4	8611.7	3525.3
53.7	48.5	87.1	71.9	43.8	227.3	51.4	90.6	83.7	381.2	45.8
541.3	3688.6	4856.4	4471.0	3135.6	4440.0	2686.3	3971.8	4954.1	6488.8	2984.6
2199.0	2323.1	3613.6	3212.0	3167.9	4032.2	2319.9	3503.8	2674.1	6346.8	1819.9
3966.0	2057.3	2423.3	2954.0	2166.5	3212.7	1836.6	3034.4	2417.3	6655.2	2059.9
1237.9	3165.0	4153.3	4495.5	3037.9	3653.2	3834.5	5166.0	2450.8	5360.8	2587.8
1030.6	5342.0	6644.0	6967.6	3768.9	7556.5	2925.4	6625.8	6661.2	10749.3	4679.3
68.4	1925.7	2277.8	2173.7	1834.3	2737.5	1296.1	2621.9	1491.1	3147.5	1048.1
7276.3	4082.7	4681.4	4858.3	5490.8	5241.4	4517.4	5273.4	4496.3	6466.7	4570.7
227.3	3136.4	3662.0	4123.8	5983.1	4800.0	3513.4	3482.4	2042.2	4638.0	1837.3
1077.9	4165.7	4645.9	5391.1	4541.6	5561.3	4996.8	4900.7	3519.6	4748.4	3488.3
156.8	4487.1	5230.2	6072.3	4242.2	8428.1	2479.3	5548.6	4388.8	10181.0	3174.0
1292.9	3707.3	4063.7	4296.1	4934.3	7341.1	4777.6	4111.8	3870.2	5750.6	1856.4
411.7	4000.0	4555.4	4685.7	2990.8	6440.6	2184.2	4748.3	4475.3	10285.5	3079.1
1287.7	3270.8	3352.4	3094.4	3685.7	4573.2	2842.1	2992.0	2301.6	3448.3	1675.5
880.2	3486.2	5263.5	4869.6	3024.8	7253.1	2696.9	3870.2	2602.7	13215.6	1923.3

1556.7	1312.7	994.8
4286.3	5041.8	2615.9
5409.4	4013.4	1570.4
6022.0	5013.5	3005.9
302.5	702.6	103.5
820.2	1396.7	291.3
3242.9	2795.9	2159.9
5036.6	3418.4	2013.7
518.5	1119.8	526.6
7887.9	7200.3	5127.5
11288.6	12202.8	10988.1
171.2	555.0	332.6
4329.6	4561.7	2982.3
5031.2	6638.8	4115.0
3907.1	4511.2	1630.5
183.8	256.0	214.2
496.2	1152.1	502.7
4258.7	5265.7	4225.8
1059.3	1634.1	951.3
1147.9	1190.4	470.0
3842.6	3965.2	2155.0
2389.9	3274.0	1242.8
4513.3	5457.1	3226.8
2954.9	4629.6	1430.3
3100.3	4743.2	3286.5
4248.7	5841.3	3599.0
225.6	248.7	54.1
4654.0	4680.8	3156.4
3775.4	4603.4	1886.8
2696.9	3606.7	1883.8
6445.7	5263.8	3610.7
8914.6	7606.7	4470.5
3331.8	2821.8	2154.7
5793.6	6535.9	5115.4
6315.5	5415.1	3692.0
7230.0	5830.4	5389.4
10431.8	8049.8	3581.2
7961.7	7267.1	4218.6
8142.0	6516.9	3068.2
4843.4	4065.8	2886.2
9617.6	6387.6	2568.5

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FN667741.1 gg_id:524492 Xenorhabdus bovienii str. SS-2004
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
GU480990.1 gg_id:529536 Xenorhabdus cabanillasii
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EU190977.1 gg_id:266440 Xenorhabdus kozodoii str. FR48
FJ860884.1 gg_id:591393 Xenorhabdus nematophila str. K97
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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

FN667
AY278
D7800
AY317
GU480
GU480
DQ208
DQ205
D7800
FJ8608
X82252
DQ329
GU480
GU480
EU190
FJ8608
AY278
EU513
DQ211
EU250
GU480
DQ646
AAYR0
AF365
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AJ2322
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EF1791
NC_00
AJ6275
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CP000
AJ2322
X75274
FJ6418
DQ646
EF5154
EF1791
NZ_AA
X75276
X75273

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109.0	2911.0	3234.3	3318.9	2253.3	3560.1	2450.5	4257.7	3340.7	4661.3	2079.8
128.8	3503.8	4116.5	4491.7	3041.8	5275.6	2720.8	4426.9	3851.1	5524.0	2309.9
1635.5	4684.7	5280.5	5406.2	3845.9	6670.1	2876.2	5362.5	5718.8	11279.4	4054.3
4486.6	5042.8	6187.1	6714.5	4394.3	8244.4	3353.2	6359.3	5976.2	13516.4	4618.8
17509.3	7234.9	7596.5	8153.7	7811.2	8731.5	8772.4	7349.3	11891.4	11320.0	10135.7
1642.7	4878.9	5792.1	5979.1	4058.0	7448.9	3024.4	5919.2	6016.7	12709.3	4335.7
6467.7	7842.9	8647.8	9942.6	7218.3	11307.9	6815.1	9360.2	9969.3	18791.9	7568.4
14841.4	7207.8	8556.2	9513.1	6966.4	9728.1	7074.6	8462.6	8930.3	16872.1	9247.4
4484.3	5269.7	6348.4	6670.0	4406.2	8336.4	3421.2	6634.5	6266.2	13899.2	4798.9
7844.9	6681.8	7815.0	8409.2	5994.5	9879.9	5085.4	8118.4	7906.8	15989.0	6878.3
1688.5	4281.9	5337.5	6632.7	4039.4	7085.9	2673.2	5613.9	4601.4	10385.3	4037.5
1784.2	5094.9	6957.9	7016.5	4224.3	8667.6	3485.1	6433.7	5288.0	13333.3	4381.4
1181.9	8551.8	8211.3	8664.3	7623.5	8672.9	5977.1	8279.2	8504.6	10766.0	7057.3
122.7	3231.1	3497.7	3356.1	2452.0	2809.6	2662.5	4271.5	3137.7	3857.5	2526.7
5838.9	6198.2	6751.1	7783.6	5945.9	8848.0	5343.7	7453.7	7201.0	13382.9	6483.1
121.9	4069.0	5495.6	5399.7	3243.0	6784.4	2728.9	5209.5	2891.0	11984.7	3009.9
4193.7	6709.9	6769.0	7206.7	6770.1	7036.7	6059.7	6785.1	7628.7	7959.7	7645.7
614.9	4302.2	4542.5	5161.7	4562.4	5980.5	3201.5	5051.2	3640.1	6133.5	3111.6
47.5	2533.6	2666.4	2740.2	1186.6	4426.4	974.9	4004.1	1617.4	2405.9	1276.7
1296.2	4590.3	5745.0	6287.5	4743.3	8840.6	4026.7	5921.9	4433.1	14989.6	3591.4
2109.8	6743.4	8482.7	8542.5	6148.5	9035.4	5220.6	9401.1	8723.9	15603.7	6943.7
2401.7	1394.2	1445.3	1241.1	925.6	1733.7	1062.7	1328.9	1658.1	2998.7	1137.6
277.6	3242.1	2243.2	1893.2	1499.8	3003.4	1143.3	2612.4	2504.4	3361.7	1025.9
94.3	1268.2	2347.8	2418.6	1468.8	3190.7	764.4	2446.4	1806.7	6153.0	1380.0
290.5	3688.3	5102.2	4257.3	2909.5	4679.2	2614.9	4746.6	4995.6	8909.2	2766.8
139.7	4753.1	6196.0	6512.1	4556.1	8524.6	3097.2	6121.5	3970.0	15452.2	2787.8
66.2	1406.5	2337.3	2530.9	1194.4	3785.0	614.5	2747.8	653.9	5301.5	894.3
6506.3	3149.7	3582.9	3261.8	2756.1	3341.4	3118.0	3141.8	4264.7	5300.8	4166.7
9416.2	6776.5	8168.7	7636.5	5964.5	8054.1	6448.4	7909.5	8897.9	11470.3	7435.7
65.2	1439.9	1585.3	1507.6	1093.7	1951.6	699.1	1814.0	1428.6	2831.8	983.5
81.3	3172.3	4357.1	4321.8	2885.4	6428.2	1801.7	4075.4	2182.5	11678.6	1410.6
126.6	3106.5	4028.8	4200.0	2805.3	5237.0	1952.9	4328.0	4435.0	9868.4	2607.1
172.6	4351.0	4730.0	4630.6	3452.4	5214.9	2879.8	5339.5	5424.9	10405.1	3017.2
133.9	6520.2	7490.2	7848.8	6366.9	9179.9	3881.0	7724.1	8103.2	14245.9	4227.1
9662.3	9285.7	11054.8	11118.6	9736.5	10641.7	10787.1	11714.3	14682.0	13236.7	11206.4
776.1	7630.7	7632.4	7782.6	5996.8	8633.0	5617.4	6967.9	10414.1	13679.6	6995.0
86.2	2053.0	3212.9	3263.6	2527.5	5390.5	1232.4	3294.5	1382.9	11143.2	1169.0
120.3	3094.5	4228.3	4140.6	2770.3	5126.9	2061.9	4571.4	4781.0	9500.1	2557.1
874.9	3187.7	4806.5	3948.1	2538.3	4863.9	1940.7	4262.9	4518.9	8036.2	2604.7
14324.5	6098.6	6935.4	6915.5	4587.3	7995.7	6261.7	6585.7	7736.2	11153.2	6551.0

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5324.0	4805.6	3551.1
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9722.3	7987.1	4303.3
8699.4	9475.6	7026.1
8712.2	7507.6	4057.1
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9877.4	8062.3	4382.1
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8244.1	6921.3	4074.6
9779.0	8049.2	3946.1
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4921.4	4550.2	3201.8
10419.6	9394.4	5756.0
10778.5	6779.5	3352.3
6916.4	8158.5	6573.3
7901.6	5867.0	4341.8
6828.2	4411.4	3518.2
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9054.0	8869.3	5815.3
1623.8	2910.9	874.2
3183.1	2729.3	2074.6
3152.6	2783.3	1595.0
5002.1	4994.6	2864.0
8312.9	6360.5	3829.8
3892.8	2608.2	767.8
3323.0	4388.2	2469.3
8000.1	7987.2	6552.6
1889.9	1896.9	1522.7
6143.1	4570.3	2148.1
5999.5	5426.7	3170.5
5879.5	5382.7	3692.2
9750.5	8612.2	5160.0
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7296.8	9171.1	6177.5
5006.0	3284.3	1765.7
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AAYV01000006.1 gg_id:264324 Yersinia pestis biovar Antiqua str. E1979001 AAYV0
EF179125.1 gg_id:275713 Yersinia aldovae str. CCUG 18770 EF1791
NZ_ABAT01000008.1 gg_id:260769 Yersinia pestis biovar Orientalis str. F1991016 NZ_AB
AJ232237.1 gg_id:10382 Yersinia pestis SS-Yp-115 AJ2322
AJ627597.1 gg_id:107378 Yersinia aleksici str. Y159 AJ6275
NR_027543.1 gg_id:535819 Yersinia bercovieri str. CNY 7506; ATCC 43970 NR_02
U63135.1 gg_id:10347 Yersinia enterocolitica German U63135
AF282308.1 gg_id:41539 Yersinia enterocolitica str. 8081 AF2823
Z49830.1 gg_id:10349 Yersinia enterocolitica str. ER-31406-92 serotype O:5 Z49830
GU596500.1 gg_id:527323 Yersinia enterocolitica str. GP2 GU596
EF179130.1 gg_id:272269 Yersinia enterocolitica str. CCUG 8239A EF1791
X68674.1 gg_id:10341 Yersinia enterocolitica serotype 0:3; strain 11472 Princess Alexandra Hospital Brisbane A X68674
EU523225.1 gg_id:269635 Yersinia enterocolitica str. KM1 EU523
DQ486901.1 gg_id:158291 Yersinia frederiksenii 49 DQ486
AF366384.1 gg_id:34461 Yersinia rohdei str. ATCC 43380 AF3663
EF179123.1 gg_id:265704 Yersinia intermedia str. CCUG 11292 EF1791
DQ917929.1 gg_id:163194 Yersinia intermedia str. H-27 DQ917
NR_027546.1 gg_id:557655 Yersinia mollaretii str. CNY 7263; ATCC 43969 NR_02
NZ_ACCA01000078.1 gg_id:382211 Yersinia kristensenii str. ATCC 33638 NZ_AC
FM955884.1 gg_id:546539 Yersinia kristensenii str. Asd MY-1 FM955
EU401667.1 gg_id:263404 Yersinia ruckeri EU401
X75275.1 gg_id:10363 Yersinia ruckeri X75275
FJ873802.1 gg_id:534783 Yersinia ruckeri str. LY0903 FJ8738
AY359283.1 gg_id:102805 Aquicella siphonis str. SGT-108 AY3592
EF688351.1 gg_id:245537 soil clone F4-96 EF6883
FJ542924.1 gg_id:526380 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone B FJ5429
EU801111.1 gg_id:320125 It's all ranking aquatic Delaware Bay NJ clone 2C229435 EU801
FM877663.1 gg_id:362619 Microbial several mining wastes Bulgaria vicinity uranium mine Sliven clone Sliv-27 FM877
EF019154.1 gg_id:212714 aspen rhizosphere clone Amb_16S_1801 EF0191
FJ382597.1 gg_id:542155 Potentially pathogenic and air stem cell transplant summer hospital shower water BN FJ3825
AY734242.1 gg_id:135830 dynamics aquifers indicates presence stable autochthonous microbial endokarst spri AY7342
AJ252651.1 gg_id:36918 agricultural soil clone SC-I-71 AJ2526
NR_025763.1 gg_id:552844 Aquicella lusitana str. SGT-39; CIP 107650 NR_02
GQ054582.1 gg_id:454783 Topographical and Temporal Human Skin Microbiome skin back clone nbw1092b02c GQ054
FJ793155.1 gg_id:529786 Archaea and Hot Spring Thailand Tao Dam hot spring clone TDB06 FJ7931
FJ542873.1 gg_id:529296 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone A FJ5428
DQ083104.1 gg_id:132329 Fnctnl and rspnss mcrbl cntr-old fld sl cln X174 DQ083
EF540406.1 gg_id:227017 oil-shale semi-coke solid waste clone 4_15MK EF5404
NC_011527.1 gg_id:356835 Coxiella burnetii str. CbuG_Q212 NC_01
EU881324.1 gg_id:314162 (maize-sweet cropping field) Karst region maize-sweet potato cropland soil clone KM EU8813
EU143669.1 gg_id:251151 Coxiella-like infection Psittacine birds liver clone 1358 EU1436

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169.2	3370.5	4765.1	4788.0	3338.4	5309.6	2803.9	5329.9	5567.5	9077.8	3135.1
100.8	1825.5	2812.4	2695.3	1834.2	3529.7	1258.9	3276.8	3012.9	6576.7	1725.8
145.7	3020.5	3971.2	3991.2	2874.1	4971.6	1932.4	4480.5	4603.4	9196.9	2437.7
5034.2	3787.3	4777.3	4126.8	2356.6	5296.5	2441.0	4321.2	4177.7	9385.1	2556.1
536.3	2433.4	3101.0	3125.9	1772.9	4822.8	1106.9	3306.4	3094.6	9582.3	1655.9
239.1	2920.4	4226.4	4021.6	2794.2	5835.1	1980.8	3793.0	2064.8	9977.0	1432.6
49.8	2031.8	3808.0	3622.5	1186.2	4809.1	1242.6	4949.4	4101.9	7694.4	1707.7
998.0	9354.9	8728.7	8999.1	7397.6	10252.6	5469.3	8452.8	10317.9	15549.7	6917.8
66.8	2249.2	3760.0	3458.4	2001.2	5507.0	1259.4	3516.4	1328.5	9912.9	921.1
84.4	2460.5	3720.5	3719.9	1585.2	5278.7	1386.8	3827.7	3167.0	7173.8	1710.3
523.3	3241.4	5427.6	5811.0	3684.2	7992.3	2785.6	5314.0	3841.9	13562.0	2485.1
874.0	5714.8	6601.5	6104.0	5935.5	7578.3	5338.3	6591.5	5744.0	11332.6	3458.5
695.1	2929.1	3653.8	3264.2	2570.0	3941.5	2349.8	4265.7	3467.3	6399.3	2606.7
199.5	2394.0	5239.4	4879.4	2783.8	5650.9	2009.3	5380.7	4928.5	9764.3	3041.9
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138.9	3855.3	5275.2	5439.0	3149.1	7482.4	2213.4	5234.5	3355.2	13720.7	2314.4
814.0	7499.3	8935.4	9753.0	6096.1	11123.5	4098.6	9194.9	8925.0	19868.2	6696.2
37.2	644.8	954.7	731.1	277.4	1749.0	198.0	1242.0	855.1	3179.6	347.9
69.9	1259.0	2485.4	2248.0	1284.2	3184.1	821.7	2586.0	2094.5	6165.0	1358.9
77.7	2549.8	3095.2	3228.6	2621.3	4701.8	1823.8	3746.5	1681.6	6160.3	1566.7
399.9	3187.7	3641.9	3856.5	3146.1	5546.6	2384.0	3950.0	2135.6	7113.3	1982.5
85.3	3290.8	3995.6	4454.5	3356.6	6596.1	1940.7	4423.7	1971.4	8385.6	2144.5
64.9	1655.2	956.7	758.1	860.9	1775.8	515.2	1549.7	728.3	954.0	647.1
7647.2	8330.5	6783.3	6601.2	5817.2	7789.5	5346.3	7159.6	7053.8	6068.7	6908.9
720.1	6111.7	4423.6	4461.5	6179.7	5741.8	4822.9	6486.2	3529.1	3302.9	4832.5
423.6	6022.5	4616.0	3496.8	3780.8	6569.6	2136.1	6791.3	3806.7	2382.8	3724.8
9622.9	9863.7	7765.2	8234.6	7838.6	10212.7	7457.8	9220.9	8354.7	10085.5	9321.3
5792.5	8970.8	6389.0	6230.9	6006.2	8374.3	4755.9	8619.1	6458.6	6675.0	8479.4
8414.7	9658.3	7818.2	8148.0	7952.7	9337.7	7978.7	8743.6	10625.9	10954.3	8602.7
158.3	2064.9	996.9	563.8	729.2	1822.6	517.0	1135.2	1416.8	646.1	568.3
2340.0	4682.4	3995.3	4071.9	3766.7	4473.1	4222.4	4603.1	4112.5	3334.9	3319.6
74.4	1234.9	652.8	835.4	447.8	1007.0	366.8	638.7	225.2	103.8	323.2
1366.2	4826.5	3698.1	3606.8	4425.2	4521.0	3372.7	5114.1	2829.4	3177.8	2234.3
1632.3	8877.4	8007.9	8350.1	8266.7	8280.5	9788.3	8655.1	7386.8	5623.2	9509.1
2868.3	7609.0	6792.3	6985.0	6901.2	6780.6	7822.7	7540.6	4908.7	4217.7	6408.3
115.6	1532.0	857.6	674.8	1073.6	1562.1	587.9	951.4	270.7	347.7	768.8
58.9	2424.2	1168.3	519.8	878.6	3030.6	219.3	1700.1	556.0	377.9	748.6
148.5	2647.6	2432.1	2543.5	2131.3	2593.0	2328.4	3047.5	1056.1	685.3	1154.7
1619.8	4330.1	4293.3	4958.0	4788.6	4767.1	6120.1	7027.7	4377.6	3626.2	5507.0
7793.8	8680.2	8555.7	10041.1	9096.8	8911.2	10753.9	8830.6	8480.9	8516.5	10129.8

3287.0	4241.4	2913.8
5899.8	5691.5	3251.3
4339.5	4020.1	2302.7
5298.6	4930.9	2936.6
4959.2	4780.7	2415.6
5259.4	4557.2	1695.9
5182.0	3950.3	2191.5
4933.7	5442.7	1736.3
9189.3	10279.8	6742.3
4860.3	3686.2	1520.7
4564.1	5112.5	2003.1
7397.3	5683.4	3207.6
7845.3	6761.0	4780.6
4227.1	4654.2	2322.4
5857.0	5346.5	3136.6
4700.8	3830.7	2080.8
6768.2	5333.1	3056.1
11000.8	10691.4	6066.4
1815.7	1489.4	451.1
3161.8	2731.0	1493.2
4313.1	4037.7	2007.6
5056.7	4454.4	1903.7
5751.4	4832.2	2033.6
1452.1	1715.2	1545.4
6948.9	8202.5	7872.3
5821.6	4450.9	6129.4
6799.3	4774.1	6398.6
9856.6	8921.7	10036.6
8507.5	7692.0	8797.1
8545.5	8261.4	8748.4
1157.2	989.1	1472.1
4607.9	4695.3	5327.1
855.2	1046.3	1747.2
4641.2	4260.4	5736.4
8440.7	7543.3	8507.3
7907.6	7579.5	8139.7
1001.3	1067.5	1196.7
2053.7	1627.4	3230.1
3546.2	3108.9	4185.0
6220.1	6765.6	5871.7
8492.8	9010.2	9268.6

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EU143670.1 gg_id:254854 Coxiella-like infection Psittacine birds liver clone 1357 EU143
AB001519.1 gg_id:8016 Haemaphysalis longicornis symbiont AB001
NZ_AAQJ02000001.1 gg_id:237975 Rickettsiella grylli NZ_AA
FJ542982.1 gg_id:524171 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone B FJ5429
FJ542909.1 gg_id:527108 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone A FJ5429
AY447040.1 gg_id:107683 hepatopancreatic symbiont clone 7 AY447
AF286124.1 gg_id:73506 eubacterium Cecidotrioza sozanica AF286
AF327558.1 gg_id:50747 Folsomia candida symbiont AF327
U97547.1 gg_id:8028 Rickettsiella grylli U9754
FJ437936.1 gg_id:574974 Benthic okenone production Fayetteville New York Green Lake surface sediments 16. FJ4379
EU134738.1 gg_id:235968 tallgrass prarie soil clone FFCH12405 EU134
DQ396123.1 gg_id:154082 deep-sea octacoral clone ctg_NISA227 DQ396
AF526927.2 gg_id:55626 Mars Odyssey Orbiter and encapsulation facility clone T5-3 AF526
GQ346963.1 gg_id:547615 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ346
EU491737.1 gg_id:265658 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU491
GQ402591.1 gg_id:587585 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
DQ450792.1 gg_id:160953 Microbial Alpine Tundra Wet Meadow Soil: Chloroflexi Cold Water-Saturated satura DQ450
EU134722.1 gg_id:251564 tallgrass prarie soil clone FFCH7120 EU134
AY326588.1 gg_id:136759 Amazon soil clone 776-1 AY326
GQ339152.1 gg_id:515598 Comprehensive Investigation on Iron Cycling Freshwater Seep ing Microscopy Cultiv GQ339
EU802753.1 gg_id:319778 It's all ranking aquatic Northeast Colon Panama clone 4C230126 EU802
EU050790.1 gg_id:256320 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_07_86 EU050
EU276556.1 gg_id:359663 -DGGE and Approaches Analyze Effect Agricultural Practices on Soil agricultural soil c EU276
EF515889.1 gg_id:218114 grassland soil clone FCPS672 EF5158
EU134752.1 gg_id:255441 tallgrass prarie soil clone FFCH15063 EU134
DQ083100.1 gg_id:137191 Functional and responses microbial century-old field soil clone X14 DQ083
EU881328.1 gg_id:353731 (maize-sweet cropping field) Karst region maize-sweet potato cropland soil clone KM EU881
EU735697.1 gg_id:340556 archaeal structures oil contaminated and soils China pristine soil Jidong Oilfield clone EU735
EF580986.1 gg_id:279663 Survey Microbial Freshwater Calcareous Mats freshwater calcareous mat clone CM6 EF5809
AF255638.1 gg_id:32355 EBPR sludge clone Ebpr13 AF255
FJ638597.1 gg_id:511763 Temperature dependent succession sulfate reducing muddy southwestern Taiwan hc FJ6385
AM746627.1 gg_id:244768 Proteinimicrobium ihbtica str. HMPB3 AM746
AB058914.1 gg_id:49724 Legionella sp. OY6 AB058
EU134756.1 gg_id:240701 tallgrass prarie soil clone FFCH15686 EU134
AB179493.1 gg_id:99390 sedimentary rock clone MIZ02 AB179
AJ536872.1 gg_id:78512 uranium mining waste pile soil sample clone JG30a-KF-94 proteobacterium AJ5368
EU134735.1 gg_id:257122 tallgrass prarie soil clone FFCH11666 EU134
FJ542953.1 gg_id:514449 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone B FJ5429
EU937889.1 gg_id:334207 Biogeochemistry Iron Oxidation Circumneutral Freshwater Habitat riparian iron oxidi EU937
EU328043.1 gg_id:278735 dynamics during bioremediation crude oil contaminated moderate saline soil clone B EU328
EU134784.1 gg_id:239870 tallgrass prarie soil clone FFCH2111 EU134

3149.7	6858.7	6088.4	6394.5	6188.0	6295.4	7389.4	6350.7	7615.0	6872.9	7743.8
370.2	2988.3	3596.1	2893.9	2840.2	3751.8	2175.4	3904.6	1638.0	1169.0	2033.0
6256.4	6966.1	7298.9	7401.5	6576.4	6947.1	8619.1	11180.8	6073.0	4951.3	11933.9
29224.1	11106.5	10813.0	11703.5	10814.7	10873.5	13324.8	14611.8	12795.7	9997.2	19928.9
2709.3	8236.5	8043.8	8486.2	7895.2	8528.9	9781.9	13788.3	6646.4	6794.5	16013.5
15664.9	9786.2	9903.7	10920.4	9734.0	10647.6	12203.2	16013.3	9219.9	8672.4	18411.4
4244.4	5160.7	6482.1	6727.7	5257.1	5331.2	6765.6	8191.4	9348.4	5942.0	9431.7
7011.6	9008.2	9192.7	10001.3	8740.2	8856.9	10319.7	12181.0	8635.0	6443.2	13339.4
2439.0	8814.4	8540.9	9522.5	7865.3	8857.1	10854.9	15710.4	7256.5	7511.1	19407.7
558.6	4509.8	4406.1	4928.1	5131.3	5060.7	4269.7	6718.2	3285.3	1539.5	3549.3
11461.0	9645.3	7109.7	7388.2	7217.9	9237.8	7852.2	11858.5	7628.5	4903.7	11780.8
138.6	772.1	730.8	834.5	599.8	1055.5	444.8	1736.1	470.7	461.8	634.2
317.0	406.5	325.8	508.0	343.5	373.2	230.0	461.8	180.0	107.8	167.3
8062.3	7252.3	7031.0	8380.2	9834.3	7086.6	7858.0	8525.8	8804.3	3257.5	6213.0
18849.5	11529.1	10338.6	11696.0	11312.3	10990.4	12115.1	11625.7	14370.0	9586.0	12563.9
1581.4	6983.2	5595.4	4546.1	5564.2	5113.8	4789.7	5078.0	4512.2	3999.6	4814.2
2941.0	5444.4	4085.4	3986.2	4098.4	4762.5	3748.3	6196.7	3611.8	4055.1	6137.4
1184.6	5607.8	3253.8	2684.9	3593.9	4600.1	2462.0	7422.8	2588.8	816.9	4651.1
327.5	1055.6	931.7	1151.6	1033.6	1378.7	833.8	1698.1	609.3	825.8	1338.7
434.5	4675.7	4911.4	4668.5	5006.4	5254.5	5291.0	5772.8	2741.8	2147.9	5056.0
68.6	609.1	691.1	504.9	356.7	872.7	231.8	841.5	277.2	99.2	184.9
4889.5	6382.5	5630.1	5515.5	5303.0	6326.1	6019.2	5893.2	7073.0	6147.0	5998.4
7572.7	9079.6	7461.7	9253.6	7424.7	8455.0	8195.2	8116.2	9084.6	7787.2	9848.5
76.3	2084.8	1205.2	1332.6	1353.7	2079.2	1042.3	2062.4	679.8	693.7	1081.9
175.4	2154.0	1874.2	1713.4	1698.9	2517.3	1340.9	3189.4	1181.3	1507.7	1833.9
42.5	1687.4	558.4	572.9	470.8	1337.7	156.9	766.3	285.2	177.1	350.5
6507.2	8091.2	6866.1	6828.2	6786.3	7674.4	7766.5	8342.0	7402.5	7879.8	9834.8
10028.7	6889.0	6808.6	7131.2	7275.7	8203.7	7456.4	8668.7	7183.4	5889.7	7438.2
6780.4	6511.6	5070.5	5017.7	5359.8	6133.3	4668.3	6870.1	5725.4	4852.0	5991.0
4702.1	3075.9	2539.4	3128.3	2941.3	3884.5	3356.5	4566.9	2590.9	1907.9	2548.1
4485.7	3493.6	2829.9	2669.9	2696.7	3576.1	1953.4	4835.7	2654.0	1377.1	2579.6
2686.9	4379.2	2850.0	2580.8	2571.0	3200.3	2188.2	4206.8	1702.2	783.2	1726.5
55.4	21.3	31.2	30.2	25.6	54.0	25.8	26.0	29.4	24.0	35.5
1429.2	6372.3	6267.3	6570.2	6933.9	7040.5	7225.1	7872.1	5034.1	2744.9	7178.7
1659.0	5009.5	4767.0	4358.8	5574.2	5644.3	3900.7	5691.0	2698.6	1369.1	4150.5
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1174.5	5398.2	5289.5	5074.8	5494.8	5570.6	5990.0	6145.7	3674.4	3559.8	4260.0
1326.2	3853.5	2534.9	2213.7	1902.7	3853.5	1592.9	4818.2	2008.3	1332.9	3530.6
10427.1	6895.8	6051.6	6440.0	6540.0	6446.9	6884.3	6392.6	8457.6	6311.5	7434.6
497.0	6515.0	5522.3	6419.5	7431.1	5416.8	7610.9	5975.9	7046.9	2878.9	4846.9
6050.0	6287.9	4957.4	3935.7	4286.0	5378.6	3693.6	7443.1	4369.6	3810.3	5037.4

6491.5	7551.3	7147.4
3428.9	4299.9	4392.9
10518.6	8734.9	8347.1
14427.6	12716.1	12008.8
12124.2	9776.4	9509.9
15339.1	11236.9	11233.2
7160.2	6778.7	6724.4
10985.7	10061.0	8348.7
14874.8	10730.6	9558.8
5902.5	5450.2	5569.0
11079.9	10230.5	10399.2
1195.6	1382.1	1825.3
1397.5	464.8	829.4
8258.9	9066.3	7200.7
11619.0	12413.4	11953.4
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4838.2	3967.1	5010.3
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1736.7	1848.2	1684.5
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1406.3	777.8	1534.1
4334.7	6691.5	6432.4
7808.5	7817.1	9247.1
1767.3	2508.6	2230.5
2976.1	3556.3	3067.7
2226.2	760.0	1087.4
8543.9	7511.0	9180.6
8828.2	8837.8	7612.9
5902.6	6081.4	7040.3
4699.6	2782.1	5638.4
4414.8	3732.3	3919.7
4839.5	3781.2	3578.7
98.6	65.1	194.5
7536.6	6496.1	6669.0
5300.0	5255.6	6381.7
3600.7	4796.8	3885.8
6127.0	5439.8	7262.9
3470.2	3152.4	3176.0
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GU362970.1 gg_id:575883 and archaeal biogeochemical cycling genes within Qiongdongnan basin Sea: pilot stu GU362
DQ396109.1 gg_id:156557 deep-sea octacoral clone ctg_NISA135 DQ396
EU803079.1 gg_id:326446 It's all ranking aquatic Northeast Colon Panama clone 4C230497 EU803
AJ252619.1 gg_id:36221 agricultural soil clone SC-I-16 AJ2526
FJ444660.1 gg_id:578973 Cotton Rhizosphere cotton rhizosphere clone 2h-38 FJ4446
FJ444646.1 gg_id:587687 Cotton Rhizosphere cotton rhizosphere clone 2h-15 FJ4446
DQ431905.1 gg_id:207732 microorganisms catalyzing nitrogen removal and organic matter metabolism perme DQ431
GQ349429.1 gg_id:569326 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ349
EF515899.1 gg_id:225991 grassland soil clone FCPT587 EF5158
EU735661.1 gg_id:325840 archaeal structures oil contaminated and soils China pristine soil Jidong Oilfield clone EU735
CU466806.1 gg_id:317285 Evry wastewater treatment plant anoxic basin clone CU466
AB294332.1 gg_id:215917 Microbial structure deep coal seem groundwater stream clone SWB21 AB2943
EU202847.1 gg_id:347934 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo EU2028
FJ545549.1 gg_id:511371 Diveristy Seawater and Sediment Northern North Yel Sea sediment clone S2-5 FJ5455
GU305791.1 gg_id:534111 Research on changes structure during algae outbreak oligotrophic lakes (YangHe res GU305
FJ205343.1 gg_id:535383 Prokaryotic deep-sea hydrothermal region East Lau Spreading Centre deep marine se FJ2053
GQ350354.1 gg_id:587874 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ350
EU925916.1 gg_id:303457 sediments sediment station DBS1 northern Bering Sea clone 152H67 EU9259
AB015255.1 gg_id:8026 deepest cold-seep area Japan Trench clone JTB256 proteobacterium AB015
EF574681.1 gg_id:229650 site S25 near Coco's Island marine clone S25_1025 EF5746
EU644214.1 gg_id:282458 and Samoylov Island Lena active layer -centred polygon near surface horizon; Rim_T EU6442
AF235121.1 gg_id:74504 North Sea clone KTc0924 AF2351
EU134760.1 gg_id:238980 tallgrass prarie soil clone FFCH7560 EU1347
EU249954.1 gg_id:246142 Polyphasic description Pocillopora seawater adjacent Pacillopora meandrina coral co EU2499
EF575249.1 gg_id:232669 site S25 near Coco's Island marine clone S25_1593 EF5752
EU134712.1 gg_id:245968 tallgrass prarie soil clone FFCH5316 EU1347
FJ468390.1 gg_id:555059 Bioaugmentation Pseudomonas sp. strain MHP41 promotes attenuation and changes FJ4683
FJ236047.1 gg_id:334364 three Parisian treatment plants approaches drinking water clone Orly7 FJ2360
FJ437972.1 gg_id:539237 Benthic okenone production Fayetteville New York Green Lake surface sediments 16. FJ4379
EF575079.1 gg_id:237689 site S25 near Coco's Island marine clone S25_1423 EF5750
FJ205338.1 gg_id:555799 Prokaryotic deep-sea hydrothermal region East Lau Spreading Centre deep marine se FJ2053
AF255642.1 gg_id:22253 EBPR sludge clone Ebpr12 AF2556
EU386125.1 gg_id:272458 Biogeographical and microbes sediments on subseafloor sediment South China Sea c EU3861
EU134733.1 gg_id:237253 tallgrass prarie soil clone FFCH11328 EU1347
EU134753.1 gg_id:248221 tallgrass prarie soil clone FFCH15155 EU1347
EF019986.1 gg_id:216743 aspen rhizosphere clone Elev_16S_1373 EF0199
EU805209.1 gg_id:326155 It's all ranking aquatic 250 miles Panama City clone 6C233205 EU8052
EU834797.1 gg_id:541438 Microbiology Aerobic Phosphorus Removal Process aerobic phosphorus-removing se EU8347
FJ712415.1 gg_id:523629 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) K FJ7124
EU193049.1 gg_id:357896 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo EU1930
Z32636.1 gg_id:8006 Legionella brunensis Z32636

347.2	3573.7	2952.1	2559.7	3192.9	3308.3	2809.3	3919.0	2366.7	718.0	2013.0
56.7	102.5	93.0	107.5	85.2	102.7	80.1	112.1	65.7	35.6	63.6
162.5	2228.4	2999.1	2712.7	2331.9	2969.3	3282.1	2894.8	1758.6	1378.8	1403.1
12061.3	8375.2	7052.3	6224.2	5770.4	7032.5	5983.6	6205.6	9018.9	7340.5	7178.9
905.8	7483.1	7444.5	7629.6	9270.3	7164.2	8215.6	7707.2	5632.7	4635.1	6385.9
2161.1	4574.8	3821.8	3987.7	4016.2	4425.8	3767.8	3824.9	3260.6	2753.7	4200.0
62.5	1513.5	909.9	741.0	761.1	1280.7	503.5	1318.9	830.6	485.7	802.7
9416.9	6582.2	6609.9	5860.6	5637.6	5843.7	6008.1	5794.9	7083.3	8522.7	6879.0
1334.6	3059.9	2128.5	2547.7	2640.7	2932.4	2137.6	3857.5	2913.9	1336.0	3148.4
6219.8	5621.2	7038.7	6118.3	6679.2	5769.5	6359.6	7406.8	6513.2	2966.3	4902.0
1308.9	6626.4	5976.8	6060.9	6677.2	6116.3	7018.5	7165.0	5130.9	2916.8	6347.1
42.4	238.0	192.9	211.6	210.1	301.2	168.2	371.9	105.8	42.8	101.0
3609.5	6404.6	4203.5	3445.2	3746.8	5342.4	3128.9	8284.9	3567.6	3681.0	5076.2
2552.8	4787.7	4152.4	5056.4	5136.0	4534.0	4982.5	5893.0	3603.5	3293.2	3181.9
3767.2	6476.9	4744.5	3390.7	3593.8	5504.7	3315.5	3641.4	5140.8	6915.8	3442.9
18695.5	5886.0	5757.3	6575.5	7500.0	6497.9	6445.0	6582.4	5398.6	5350.9	7746.2
6214.3	6727.0	7249.7	8060.4	8602.2	7069.1	8383.9	7138.6	5375.9	6968.9	7474.3
3753.1	6848.9	6414.0	7999.1	5627.4	6413.5	6591.7	6951.5	5751.7	5835.8	7986.7
33.5	122.5	84.9	103.7	92.3	130.5	102.2	121.9	61.5	28.7	58.1
1299.3	3015.9	2873.1	2539.3	2845.8	2636.3	3081.2	3000.9	1501.9	765.8	2061.0
2362.8	6132.2	6401.5	6404.7	6444.9	7052.9	6766.4	8335.1	5195.2	6200.7	7086.2
52.8	240.8	425.8	392.2	250.4	317.1	164.7	691.4	116.0	225.7	153.7
11998.6	11365.2	10536.0	11415.4	11509.2	11263.9	11384.2	12690.6	11060.5	12087.8	16760.3
2891.0	5832.5	5083.6	4739.2	4710.4	5361.4	5833.0	4775.0	6417.7	5821.6	7216.2
130.4	1606.0	1837.2	1168.3	1601.3	1856.8	1818.9	2256.4	1008.9	1685.9	1641.4
2713.0	7280.6	6848.5	6346.4	7669.1	6543.6	6605.2	6932.0	5502.3	8735.9	7557.2
316.2	5270.4	3694.2	3756.9	3271.5	4372.0	3284.4	8016.3	2006.2	947.7	5399.4
10090.5	7695.1	7573.1	8946.4	8746.0	8041.3	7483.5	9705.5	11117.2	6292.6	10071.2
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15454.1	10090.9	8770.4	10057.9	9288.3	9539.5	9971.7	10096.3	9903.3	8463.1	10264.2
279.4	4968.5	3867.4	3568.9	2926.5	5223.3	2923.5	4788.2	3158.3	5014.2	2748.3
140.9	1376.9	1271.0	1157.2	1004.4	1777.0	1139.0	2841.5	861.1	522.6	793.7

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121.1	131.9	118.6
4084.4	2596.0	2487.2
6759.9	7343.2	6832.0
9584.6	7218.6	8590.5
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1392.1	459.4	1535.6
8280.9	5675.6	6551.3
3207.6	2704.3	4255.7
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NR_024969.1 gg_id:575576 Legionella waltersii str. 2074-AUS-E; ATCC 51914 NR_02
AF129524.1 gg_id:51847 Legionella pneumophila str. E5C1; ATCC700713 AF1295
X97361.1 gg_id:7908 Legionella sp str. LLAP8 X97361
NC_006368.1 gg_id:129226 Legionella pneumophila str. Paris NC_00
AB233212.1 gg_id:140544 Legionella landfill str. OA1-4 AB233
FJ542889.1 gg_id:522337 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone A FJ5428
FJ612289.1 gg_id:592165 and Biogeochemistry Dongping Lake Ecosystems lake water clone DP7.5.15 FJ6122
NR_026522.1 gg_id:565488 Legionella tucsonensis str. 087-AZ-H; ATCC 49180 NR_02
EU250236.1 gg_id:246283 acid mine drainage clone GXDC-22 EU250
FJ230896.1 gg_id:315994 under Level Antibiotic Selection Pressures river water clone F20 FJ2308
EU134790.1 gg_id:244967 tallgrass prarie soil clone FFCH3904 EU134
GQ002634.1 gg_id:507027 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbu GQ002
GQ264139.1 gg_id:564434 Structure Simulated Level Waste Site simulated level waste site clone WC3_79 GQ264
DQ814490.1 gg_id:168390 zebrafish digestive tract clone aaa29e09 DQ814
Z49722.1 gg_id:7972 Legionella fairfieldensis Z49722
DQ413099.1 gg_id:154202 Microbial -dependent and Approaches Anaerobic/Aerobic SBR Reactor EBPR sludge DQ413
Z49724.1 gg_id:7994 "Legionella donaldsonii" Z49724
DQ337039.1 gg_id:145455 subsurface water clone EV818EB5CPSAJJ36 DQ337
AY792279.1 gg_id:123281 Humic Lake clone CrystalBog1D4 AY792
FJ744881.1 gg_id:549676 Transporter genes expressed coastal response dissolved organic carbon surface wate FJ7448
AY662002.1 gg_id:137028 uranium-contaminated groundwater clone 300G-C11 AY662
DQ667196.1 gg_id:171418 Legionella taurinensis str. ATCC 700508 DQ667
X97363.1 gg_id:7946 Legionella sp str. LLAP10 X97363
FM877662.1 gg_id:359700 Microbial several mining wastes Bulgaria vicinity uranium mine Sliven clone Sliv-17 FM877
DQ327699.1 gg_id:166988 Biological filtration limits carbon availability affects downstream biofilm formation a DQ327
FJ542894.1 gg_id:518474 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone A FJ5428
X97356.1 gg_id:7948 Legionella sp str. LLAP2 X97356
AF467296.1 gg_id:64661 Xanthomonas sp. clone 88_5_2 AF467
AY598719.2 gg_id:99452 Amoeba proteus symbiotic AY598
AY957913.1 gg_id:114944 drinking water biofilm clone B3NR56D11 AY957
GU062706.1 gg_id:590087 Legionella sp. str. NML 93L054 GU062
Z49720.1 gg_id:7915 Legionella cherrii Z49720
Z49733.1 gg_id:7976 Legionella quinlivanii Z49733
AY050582.1 gg_id:21751 MCB-contaminated groundwater-treating reactor clone GOUTA10 AY0505
Z49739.1 gg_id:7955 Legionella worsliensis Z49739
EU937840.1 gg_id:331322 Biogeochemistry Iron Oxidation Circumneutral Freshwater Habitat riparian iron oxidi EU937
FJ543058.1 gg_id:528709 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone B FJ5430
EU800944.1 gg_id:306074 It's all ranking aquatic Delaware Bay NJ clone 2C229203 EU800
Z49719.1 gg_id:7922 Legionella bozemanii Z49719
AJ969023.1 gg_id:120376 Legionella anisa UCSC 25 AJ969
FJ479065.1 gg_id:590656 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4790

5819.4	6666.0	5364.7	5430.3	4234.1	6989.3	4034.2	8390.1	6488.8	3604.2	4865.4
680.9	2581.4	3316.5	2827.4	1897.1	2528.5	1808.1	3146.8	2343.9	4213.8	2566.7
2136.3	5131.7	5931.1	4793.5	4569.9	5508.8	4166.1	6445.3	7566.9	4105.0	5235.9
22578.7	5677.7	5152.7	6826.0	6888.2	5830.9	6234.8	7534.5	6377.6	4878.9	7055.0
93.3	2568.1	2547.5	2330.5	1419.8	3903.8	1447.7	6261.1	1950.5	716.1	1899.8
1956.0	5873.0	5626.8	6071.6	5202.9	7115.7	4991.5	7323.8	8669.2	7371.3	4909.3
2966.8	5097.8	4794.4	5048.5	5567.7	5140.5	4749.4	5965.6	5706.4	4013.5	4686.5
14309.0	5651.7	5557.1	5972.3	5496.1	5858.3	6416.4	5027.8	5845.7	4730.9	6958.3
1166.5	1930.5	2006.1	1900.0	1694.6	2717.8	1354.6	3787.7	1629.2	621.6	1216.2
1697.4	5244.0	6055.9	5761.6	4401.8	6986.5	2612.0	9103.6	5712.6	3965.3	4533.2
12473.6	5727.1	5498.4	6378.7	5907.9	5881.5	5869.2	6003.5	5634.4	4332.5	5500.4
1337.4	7724.6	7479.1	7070.5	5932.7	6961.8	7373.5	7833.4	8477.4	8651.6	5862.9
11633.3	7821.6	7648.7	8613.8	8695.9	8877.1	9852.1	10596.8	5867.9	7238.3	8176.2
3724.4	3847.3	4138.1	3727.3	2906.2	5365.5	2574.0	7120.8	4128.0	1843.4	3595.6
54.5	664.0	1203.2	922.5	690.6	1154.9	1087.4	1433.4	409.3	152.1	366.0
499.0	2498.1	2879.5	2423.9	2282.7	3427.1	1803.7	4390.4	2460.0	2315.7	2519.8
33.7	1502.6	1957.1	1532.7	1924.4	1862.0	1970.1	2764.0	704.6	365.6	810.3
89.3	827.2	764.8	622.2	647.2	1421.0	611.4	2493.6	1054.8	309.4	397.9
69.4	372.1	212.9	150.2	105.4	723.0	116.9	1041.3	244.6	156.6	173.8
14685.9	5453.3	5251.6	5935.8	4585.2	6508.5	3982.8	8887.7	4768.4	2194.6	4333.6
4737.7	3644.0	2896.6	2929.8	2273.4	3406.4	2417.1	4271.6	3954.7	1553.3	2830.8
725.7	3870.6	3984.9	4620.6	3866.4	5381.2	3600.9	6123.1	4808.3	5188.1	4026.1
3506.8	3176.9	3246.4	2621.1	2655.1	3753.3	2058.9	5350.6	3185.0	1906.2	2920.0
19451.5	8749.8	8633.9	9703.6	8875.9	9394.7	9526.6	11808.0	8646.0	6620.0	10179.2
52.6	628.1	708.4	799.7	748.5	761.7	812.3	1027.6	280.4	158.2	264.4
1794.8	3721.8	3375.6	3575.6	3925.2	4712.2	3168.1	5079.5	1922.9	4704.2	3373.1
7114.3	5308.7	5408.6	5384.3	4430.2	6611.0	4576.2	7878.6	5077.3	3912.7	5157.3
39.9	286.4	396.5	262.6	265.7	665.3	168.2	520.0	195.5	120.8	119.7
49.2	1114.2	1673.0	1417.8	444.8	2055.9	227.4	3375.2	825.8	286.1	649.0
721.8	3407.4	3279.2	2805.3	2035.1	4556.2	1902.4	6154.7	2272.7	1992.8	2789.9
374.7	2439.5	2569.1	2247.2	2043.7	3292.3	1469.6	4069.3	1968.9	809.6	1297.5
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3008.1	3313.4	3779.8	3389.6	4175.2	4191.2	3021.4	5140.5	4256.8	2298.9	2807.2
928.2	5103.2	5892.8	6182.7	4971.1	6892.9	4865.7	7724.9	4634.0	7900.6	7143.0
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8732.4	6047.7	6155.2	6725.9	7862.0	6425.3	7312.0	7346.5	6369.0	5248.8	4906.3
1862.8	3052.2	2710.2	3306.9	3399.9	3734.2	3826.1	4119.1	1553.7	2365.5	2708.7
3352.9	7379.1	6575.8	8165.7	7457.5	7957.5	5350.8	9228.7	6773.1	9070.5	7632.7
1681.3	2908.5	2705.8	2734.1	3036.9	3620.9	2443.2	3515.8	3734.5	2245.6	2309.7
9287.1	4901.8	4963.2	4905.5	5093.8	5486.0	5086.0	5481.6	5280.2	3632.9	5342.2
1655.1	5646.4	4631.7	5523.3	3684.2	5968.2	3338.9	7941.7	6965.8	6257.6	5058.1

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7553.8	6932.4	8543.1
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8535.1	8278.5	7755.5
7422.2	6852.9	7840.6
6838.5	7146.4	8233.1
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7138.5	6624.3	7155.9
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12390.2	10246.5	13512.2
1191.9	678.2	1843.6
6241.5	5155.9	7668.5
9477.2	8291.9	10025.7
602.1	701.9	1171.8
3432.0	2766.4	5178.2
6856.0	5789.9	9241.1
4806.7	4262.2	7012.5
28.7	42.0	25.9
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7320.1	6900.3	7746.7
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9373.3	8775.7	10084.3
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EF516979.1 gg_id:226108 grassland soil clone FCPP464 EF5169
GQ347573.1 gg_id:555343 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ347
DQ327700.1 gg_id:163406 Biological filtration limits carbon availability affects downstream biofilm formation a DQ327
EU835422.1 gg_id:318862 structure and quorum sensing reverse osmosis RO membrane biofilm clone 1B17 EU8354
Z49741.1 gg_id:7937 Legionella lytica str. LLAP-3 legionella like amoebal pathogen Z49741
Z32640.1 gg_id:7984 Legionella israelensis Z32640
EU236319.1 gg_id:298170 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg1bF3 EU2363
GQ054315.1 gg_id:463932 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw1108 GQ054
EU134769.1 gg_id:243485 tallgrass prarie soil clone FFCH9178 EU1347
Z49729.1 gg_id:7954 Legionella moravica Z49729
Z49728.3 gg_id:7971 Legionella londiniensis Z49728
AB255083.1 gg_id:173398 corroded concrete clone IC-85 AB2550
Z49736.1 gg_id:7956 Legionella shakespearei Z49736
Z49725.1 gg_id:7929 Legionella gratiana Z49725
Z49735.1 gg_id:7931 Legionella santicrucis Z49735
DQ413067.1 gg_id:153948 Microbial -dependent and Approaches Anaerobic/Aerobic SBR Reactor EBPR sludge DQ413
EU800974.1 gg_id:311942 It's all ranking aquatic Delaware Bay NJ clone 2C229243 EU8009
FJ382013.1 gg_id:543450 Potentially pathogenic and air stem cell transplant winter hospital shower water BMT FJ3820
Z49727.1 gg_id:7973 Legionella lansingensis Z49727
Z49734.1 gg_id:7927 Legionella sainthelensi Z49734
AM747393.1 gg_id:236913 Legionella dresdeniensis str. W03-356 AM747
EU835407.1 gg_id:318176 structure and quorum sensing reverse osmosis RO membrane biofilm clone 1T17 EU8354
EU835445.1 gg_id:340760 structure and quorum sensing reverse osmosis RO membrane biofilm clone 2B20 EU8354
Z49717.1 gg_id:7974 Legionella birminghamiensis Z49717
Z32641.1 gg_id:7991 Tatlockia maceachernii Z32641
AF227162.1 gg_id:52462 Tatlockia micdadei str. ATCC33218 AF2271
Z32642.1 gg_id:7981 Legionella oakridgenesis Z32642
AJ919271.1 gg_id:114678 Legionella nautarum AJ9192
GQ388900.1 gg_id:551369 quality deterioration drinking system during serious red water outbreak clone Z61 GQ388
FJ236838.1 gg_id:328884 Legionella sp. str. CDC-3041-AUS-E FJ2368
EU134750.1 gg_id:238279 tallgrass prarie soil clone FFCH14647 EU1347
Z49730.3 gg_id:7982 Legionella nautarum Z49730
NR_025196.1 gg_id:556395 Legionella busanensis str. K9951; KCTC 12084 NR_025
AF122884.2 gg_id:8008 Legionella beliardensis str. Montbeliard A1 AF1228
GQ009403.1 gg_id:500261 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw77 GQ009
EF612978.1 gg_id:233794 acid mine drainage clone YSK16S-15 EF6129
EF036512.1 gg_id:191570 Legionella jordanis NML 060502 EF0365
EF471571.1 gg_id:270320 Fast Screening and Estuarine Operon Libraries whole surface water Chesapeake Bay EF4715
EF520577.1 gg_id:229517 structure lakes: what controls ? acid-impacted lake clone ADK-RXe02-02 EF5205
DQ458002.1 gg_id:158776 acid mine drainage clone DX32 DQ458
EU491749.1 gg_id:263538 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU4917

689.6	2224.0	1972.1	2023.1	1995.2	2281.1	1794.8	3155.8	2676.3	2492.4	1954.5
293.0	2605.7	2930.5	2584.1	2245.1	3426.3	3488.1	4343.2	3087.3	1596.6	2234.0
103.8	1005.8	1014.5	856.5	674.4	1578.7	489.1	2554.9	942.8	347.9	557.1
2701.6	6777.9	5632.5	5653.7	5656.1	5593.6	4638.2	6990.6	6953.6	4325.8	6215.4
1597.2	2108.4	2169.2	2761.1	2011.8	2423.9	2050.7	3892.2	2374.0	1853.4	2146.3
55.3	145.4	159.4	129.1	101.9	246.5	72.6	328.4	82.8	47.2	75.3
307.1	3794.8	4494.7	4642.4	4872.5	4896.6	3644.1	6008.5	4574.8	3349.7	3086.6
1231.6	5362.1	4860.1	4748.6	5118.7	5402.9	4622.6	6782.7	4337.7	4274.9	3438.2
539.9	3214.4	2577.6	2247.4	2240.4	3439.2	2221.0	5452.6	2317.5	1209.5	2003.5
11067.4	4433.6	4556.7	4800.6	3864.4	5395.3	4484.9	6451.0	5033.8	6020.7	5554.5
1434.8	2263.2	2439.6	2223.0	1842.2	2735.3	1618.7	4233.2	2198.0	1376.7	2359.5
2134.6	2509.5	2764.0	2522.0	1839.2	3367.1	1754.3	5237.3	2542.1	1316.6	1938.6
15630.0	8225.3	8362.1	8555.5	9328.7	9288.7	10994.2	9789.0	10095.2	9964.2	11020.5
1715.5	7317.3	6880.0	7049.6	7788.8	8012.3	7178.8	7881.2	7832.9	6241.8	10217.9
3398.4	1738.0	1356.8	1459.0	1671.3	1722.3	1282.5	1737.2	1262.7	1069.8	1212.9
727.3	3773.5	3721.0	3515.7	3214.0	3818.2	3146.8	5260.8	3902.9	2892.8	3879.6
3477.4	7154.0	7519.4	8255.5	8200.0	8219.2	6405.0	10065.0	9173.5	6772.8	7240.0
28235.0	8046.6	6631.2	6683.5	5588.5	7430.6	5635.5	8414.5	7036.3	3076.6	6280.6
71.2	251.6	288.8	203.9	110.3	289.2	110.9	350.5	131.9	107.1	159.2
11666.2	4003.2	3704.8	4204.3	3959.3	5357.7	3351.5	6673.7	3731.2	2081.3	3754.7
9766.6	5834.7	4606.5	4885.8	4819.2	5843.6	4305.4	7870.9	4341.3	2875.6	4445.2
4657.1	4427.9	4594.2	4818.8	3820.9	5918.3	3745.6	7576.1	4804.5	3217.3	4981.5
4895.5	5450.6	4883.4	4716.6	4676.0	5528.2	4507.4	6671.6	6646.0	5308.9	5792.4
194.8	2320.2	2198.5	2188.5	1358.5	3240.8	873.9	4906.0	2329.3	1656.9	1783.9
1974.3	2098.6	1955.3	2118.0	2093.1	2375.1	3125.6	2723.3	1708.3	2196.2	2848.5
52.1	309.4	308.2	331.7	309.8	566.8	201.3	982.9	220.6	120.6	166.8
56.0	711.6	745.1	586.7	520.3	993.1	319.2	1424.9	556.6	219.2	436.8
2431.7	6091.7	6184.4	6933.2	6912.5	6623.3	6685.0	7516.0	7488.4	6707.0	6855.3
5033.2	5780.8	4765.2	4849.3	5430.3	5704.3	5122.2	6319.9	3645.8	3855.2	3779.0
771.7	2855.4	2536.7	2265.9	1723.6	3890.2	1473.5	6464.6	2225.6	1100.8	2291.2
4985.7	5928.5	6162.6	5897.9	5479.1	5849.6	6308.8	7090.3	8197.1	4919.0	6531.5
1991.7	6990.5	7505.4	8655.8	7088.9	7979.0	8475.4	9359.3	7449.9	7340.5	8241.0
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8944.5	3626.5	3006.4	3185.4	2581.1	4344.3	2250.8	6137.8	3897.1	1791.0	2757.9
2089.0	1893.4	1794.7	1775.2	1597.1	2394.4	1633.0	3529.2	1540.3	969.3	1905.2
313.1	4345.5	4328.8	4938.0	4253.3	5022.9	4043.3	6945.8	4001.1	3664.5	3768.6
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193.1	3862.3	4119.3	3965.9	3418.6	4248.4	3871.2	4953.9	4024.9	1864.1	2808.2
4529.6	5943.0	4934.7	4845.7	3550.6	6214.8	3643.8	8361.7	5675.4	3541.8	4690.6
42.0	117.2	184.1	115.4	157.0	423.0	79.6	357.2	373.2	145.2	61.4
1370.9	1537.4	1784.6	2158.4	2280.3	2080.3	2002.9	3252.5	1612.1	797.0	1607.8

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6571.1	4890.4	6346.6
9673.5	10575.4	10527.1
9090.4	8130.0	9447.5
1903.9	2069.7	1919.1
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3221.5	3028.7	4096.3
1072.0	727.7	1381.3
1403.9	1293.5	1709.9
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6342.7	6583.4	8500.4
6697.1	4685.7	8066.0
8102.6	7402.5	7971.4
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EU491259.1 gg_id:276006 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak EU491
EU386109.1 gg_id:264331 Biogeographical and microbes sediments on subseafloor sediment South China Sea c EU386
GQ850579.1 gg_id:559606 bottom water northern Bering Sea clone d131 GQ850
AY050590.1 gg_id:52016 MCB-contaminated groundwater-treating reactor clone GOUTB2 AY0505
GQ261748.1 gg_id:550690 shifts taxa and response localized organic loading deep sea sediment whale falls clo GQ261
EU491526.1 gg_id:268607 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR4C EU491
EU491716.1 gg_id:267408 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU491
GQ472814.1 gg_id:574241 Biodiversity planktonic Northern surface water northern Bering Sea clone b45 GQ472
EU735642.1 gg_id:312981 archaeal structures and pristine soils China oil contaminated soil Jidong Oilfield clone EU735
EF520571.1 gg_id:230249 structure lakes: what controls ? acid-impacted lake clone ADK-HDe02-30 EF5205
EF516119.1 gg_id:221947 grassland soil clone FCPU740 EF5161
GU118075.1 gg_id:554366 Threatened Corals Provide Microbial Habitats clone Apal_M08 GU118
EU236332.1 gg_id:297516 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg5a2A5 EU236
FJ744812.1 gg_id:546723 Transporter genes expressed coastal response dissolved organic carbon surface wate FJ7448
EU236289.1 gg_id:292187 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone HgCo16 EU236
Z49726.1 gg_id:8012 Legionella jamestownensis Z49726
Z49723.1 gg_id:7977 Legionella geestiana Z49723
Z49716.1 gg_id:7978 Legionella adelaidensis Z49716
AY536226.1 gg_id:101534 host gut clone LAgut--P14 AY536
DQ295893.1 gg_id:145412 Cohn's Crenothrix filamentous oxidizer unusual methane monooxygenase physical e DQ295
GQ390223.1 gg_id:548160 oxic-anoxic interface meromictic crater lake Lac Pavin clone eub62A8 GQ390
AB504955.1 gg_id:565012 structure microorganisms reddish-brown iron-rich snow clone oze05B47 AB504
DQ837251.1 gg_id:247086 Archaeal and pristine National Park Spain Donana coastal aquifer clone 49S1_2B_45 DQ837
FJ502272.1 gg_id:509929 Co-occurrence denitrification and nitrogen fixation meromictic lake (Switzerland) Lak FJ5022
AF152597.1 gg_id:8098 Methylobacter psychrophilus str. Z-0021 AF1525
AJ583183.1 gg_id:94840 radioactive site ground water clone S15B-MN136 AJ5831
AB240527.1 gg_id:141423 microbial structure rhizosphere biofilm Sapporo root-base (80 160 mm) Phragmites S AB2405
DQ984190.1 gg_id:205851 Clonothrix fusca str. AW-b DQ984
AF351235.1 gg_id:48494 coal tar waste-contaminated groundwater clone 8-4 proteobacterium AF3512
DQ367735.1 gg_id:150338 Fluorescence Situ Hybridization-F Cytometry-Cell Sorting-Based Method Enrichment DQ367
AB240465.1 gg_id:141872 microbial structure rhizosphere biofilm Sapporo root-tip (0 40 mm) Phragmites Sosei AB2404
EF125436.1 gg_id:175001 mangrove soil clone MSB-2D7 EF1254
AB240522.1 gg_id:140993 microbial structure rhizosphere biofilm Sapporo root-base (80 160 mm) Phragmites S AB2405
DQ066944.1 gg_id:135917 Lake Washington sediment clone pLW-18 DQ066
DQ066943.1 gg_id:131019 Lake Washington sediment clone pLW-17 DQ066
M95657.1 gg_id:8104 Methylobacter luteus str. 11914 M9565
AF304195.1 gg_id:40043 Methylobacter luteus str. NCIMB 11914 AF3041
AF304197.1 gg_id:37065 Methylobacter marinus str. A45 AF3041
DQ270621.1 gg_id:142869 hydrothermal carbonate chimney clone LC1133B-99 DQ270
AJ704662.1 gg_id:109268 marine sediment clone HMMVBeg-7 AJ7046
DQ521819.1 gg_id:160617 Anaerobic Methane Oxidizing ANME-1b Archaea Hypersaline Sediments Gulf Mexic DQ521

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3813.7	2363.5	2510.2	2346.2	2629.3	2526.5	2512.3	3417.3	2627.3	1262.1	1845.0
2128.0	5194.8	4755.8	5188.6	5154.6	5452.5	5293.9	6115.3	4467.7	3634.1	4490.8
25506.1	5989.2	6314.4	6858.8	6961.6	6031.8	7853.3	5587.0	7412.0	8357.5	9122.2
1336.7	4361.6	4635.3	5245.4	4965.1	4551.5	5026.8	4996.6	3106.1	2299.1	3566.0
916.9	289.4	289.0	226.4	131.6	535.9	52.2	900.6	269.8	79.5	183.8
2678.4	1621.3	1796.0	1878.0	1674.3	2000.6	1565.3	2243.9	1660.2	1743.5	1371.7
182.3	4496.3	4775.3	5234.0	3723.0	6475.8	3950.6	7491.6	6804.1	6270.4	3878.5
12665.1	5849.9	5076.6	4683.7	4861.3	5726.6	6565.2	7343.4	5485.7	2120.3	4522.9
75.0	302.5	316.7	290.7	263.4	456.2	257.7	645.3	212.3	135.9	220.8
61.4	310.1	476.7	372.0	349.4	816.8	247.6	912.2	229.2	64.6	215.9
8691.0	4624.1	5341.0	4768.2	3951.6	5600.1	3865.0	6430.7	6050.6	4078.4	4743.6
7850.3	3839.1	3460.0	3906.0	4350.6	4151.5	3680.1	5118.7	3503.4	2019.7	3250.0
2683.7	4549.7	4448.4	4558.8	5069.7	4698.1	5167.9	4810.4	3747.5	5513.6	2295.0
2008.0	6513.8	6650.9	6899.5	8735.0	7376.6	7878.0	8473.5	6445.6	4579.5	6138.2
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43.4	807.5	483.6	443.0	172.8	733.2	196.2	1377.8	423.9	187.3	303.5
85.9	1782.2	1706.0	1000.2	206.8	1840.8	130.1	2511.6	548.4	114.5	1019.2
2486.3	3606.7	3314.3	3494.3	2254.4	4685.5	2444.7	6908.1	3231.1	2130.8	2637.3
263.0	920.2	1943.1	1871.5	7059.9	3139.6	1825.9	2829.2	500.0	1162.6	695.8
350.1	3228.5	4547.6	5002.2	9682.4	5420.6	5456.3	5514.1	1691.8	1132.2	2334.3
1663.9	3686.9	4624.5	4489.1	7513.0	5910.3	3078.3	4641.0	2622.0	3311.6	3177.3
329.8	2734.8	2725.5	2870.2	8329.6	3587.4	1764.5	3203.7	1391.0	1354.4	1861.4
2867.0	5802.4	6303.8	6419.5	9947.3	7263.5	7374.6	6442.3	3582.8	3793.8	4419.4
111.0	1489.3	1588.2	1506.0	6972.7	2454.4	1093.5	2056.8	373.6	178.5	1155.4
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3801.0	5665.9	6019.7	6198.3	10256.1	7999.2	6017.3	6640.4	5635.6	3345.3	4987.7
203.8	2788.9	3857.7	3486.1	7481.4	5564.3	4329.0	4934.6	1069.5	301.7	1517.8
940.8	5839.7	7345.5	7369.4	10208.4	8676.1	7177.4	7781.6	5352.8	9414.9	4862.1
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34.8	158.9	199.0	296.4	1110.8	244.0	553.9	282.4	54.8	20.1	100.3
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65.4	2794.3	3129.4	2994.3	4443.2	4062.6	1963.2	3136.4	676.4	500.2	995.1
187.0	4367.8	5072.9	4938.9	8320.3	6709.8	5579.5	5095.6	2672.3	3672.2	3636.1
223.0	577.4	1201.2	1229.0	1106.3	1369.8	956.4	1267.9	316.3	114.3	877.4
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734.4	2293.1	2814.3	3153.9	5587.2	3064.6	2512.4	3571.0	2280.2	975.4	1318.4
2402.7	3134.9	2807.5	3097.8	3767.2	3442.3	3724.7	3890.3	3125.5	3075.9	3070.2
3196.4	2754.2	2699.0	2864.6	2989.6	2989.3	2975.7	2858.9	3236.4	2913.0	2948.5
269.9	2013.1	2485.5	1459.0	2777.7	2867.4	1744.7	2676.1	814.3	1118.5	1116.1

6203.5	6120.6	6739.4
3228.1	3008.2	4386.4
6829.7	5316.1	6587.5
5993.5	7122.0	5624.0
4660.9	4795.7	5245.4
740.2	992.8	1612.2
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7021.6	6152.2	5772.7
7653.3	6078.5	7411.6
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7252.9	6198.4	7458.1
5816.0	5393.2	6287.0
4957.9	4936.5	3873.4
9273.0	8181.0	10649.0
2150.9	1757.6	2164.0
1598.9	1372.5	1827.6
2746.0	2278.8	4534.2
7078.3	4671.5	8188.1
1565.8	1760.6	925.3
3815.4	4826.3	4979.3
3825.8	4637.2	4100.0
2666.3	3091.6	4947.3
6000.6	5578.3	5901.9
1125.0	1671.4	3534.1
1429.6	1283.1	2264.2
6086.2	5234.8	6287.8
3304.7	3401.2	5778.5
8464.0	6698.5	7168.4
8151.2	6896.2	7074.1
144.9	252.6	276.7
802.8	643.9	1463.5
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618.3	891.2	612.7
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2615.5	3325.4	3851.8
3353.0	3386.2	4591.3
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AJ937699.1 gg_id:143230 Microbiological investigation methane- and hydrocarbon-discharging volcanoes Carp AJ9376
AB294954.1 gg_id:223386 -dependent & analyses hydrothermal system off Taketomi Island Japan microbial ma AB2949
FJ712420.1 gg_id:525836 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) k FJ7124
GQ346825.1 gg_id:533281 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ346
EU491680.1 gg_id:269280 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU4916
AB294957.1 gg_id:224998 -dependent & analyses hydrothermal system off Taketomi Island Japan microbial ma AB2949
FJ712568.1 gg_id:525302 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) k FJ7125
FJ712444.1 gg_id:516890 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) k FJ7124
AB294960.1 gg_id:218525 -dependent & analyses hydrothermal system off Taketomi Island Japan microbial ma AB2949
EU700156.1 gg_id:294790 Study on Shantou Bay Marine Sediments Microorganisms sediment clone STU14 EU700
GQ350283.1 gg_id:578592 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ350
AB188770.1 gg_id:113920 Maorithyas hadalis gill thioautotrophic symbiont II AB188
FJ717255.1 gg_id:511065 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United King FJ7172
AB188776.1 gg_id:112716 Maorithyas hadalis gill thioautotrophic symbiont II AB188
AB476280.1 gg_id:549573 Compositional and functional transition epibiotic microbial hydrothermal vent galath AB476
FJ264669.1 gg_id:339219 Manganese and Iron Dependent Anaerobic Oxidation Methane methane seep sedim FJ2646
FJ717256.1 gg_id:555227 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United King FJ7172
DQ070797.1 gg_id:145621 Prokaryotic Structures Seafloor Basalts Varying Age and Juan de Fuca Ridge basalt gl DQ070
DQ270620.1 gg_id:144477 hydrothermal carbonate chimney clone LC1133B-86 DQ270
GU302420.1 gg_id:555130 Spatial structure and activity sedimentary microbial underlying Beggiatoa spp. mat h GU302
AB042414.1 gg_id:24022 Maorithyas hadalis gill thioautotrophic symbiont II gill AB0424
DQ513099.1 gg_id:161529 Microbial life fluids ridge flank crustal fluid clone FS274-37B-03 DQ513
AB245479.1 gg_id:146843 Sulfurivirga caldicularium str. MM1 AB2454
EU528230.1 gg_id:286126 Seasonal Dynamics Mudflat Mouth Major Kentucky Lake Reservoir Tributary sedime EU528
DQ270629.1 gg_id:141697 hydrothermal carbonate chimney clone LC1446B-37 DQ270
GQ350218.1 gg_id:535569 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ350
DQ270612.1 gg_id:142835 hydrothermal carbonate chimney clone LC1133B-5 DQ270
U05595.1 gg_id:8100 methanotrophic symbiont of Louisiana Slope mussel gill U05595
NR_026064.1 gg_id:576044 Methylocaldum szegediense str. OR2 NR_02
AF215632.1 gg_id:71299 Methylocaldum sp. str. dr65 AF2156
EF203191.1 gg_id:208702 phylotypes sediments Lake Kastoria Greece sediment clone Kas146B EF2031
AJ617834.1 gg_id:110041 oxic-anoxic interphase flooded paddy soil clone D14307 AJ6178
U89297.1 gg_id:8046 Methylocaldum tepidum str. LK6 U89297
AF215633.1 gg_id:73918 Methylocaldum sp. str. r6f AF2156
FJ810597.1 gg_id:380204 Subsurface ecosystem resilience: Long-term attenuation subsurface contaminants su FJ8105
NR_026063.1 gg_id:572916 Methylocaldum gracile str. VKM 14L NR_02
NC_002977.6 gg_id:128429 Methylococcus capsulatus str. Bath NC_00
NR_029251.1 gg_id:540868 Methylococcus thermophilus str. IMV-B-3037; ACM 3585 NR_02
X72771.1 gg_id:8036 Methylococcus capsulatus Bath str. ACM 3302 ATCC 33009 NCIBM 1113 X72771
X72769.1 gg_id:8040 Methylococcus sp str. JB140 X72769
AB354618.1 gg_id:273571 Laminated iron texture iron-oxidizing calcite travertine iron-rich deposit clone FD09 AB3546

247.8	1737.9	2277.9	2078.2	2772.9	2689.5	2834.3	2684.4	1679.2	1471.2	1649.8
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2724.8	2778.6	3691.5	3221.6	4560.5	3322.5	3256.9	3471.6	3305.2	2125.0	2542.3
874.3	4794.7	5119.2	5163.5	7136.3	5696.2	6416.8	5218.1	2962.5	1904.4	4175.1
2180.6	5065.4	5415.3	5258.5	7039.5	6354.0	5902.9	5245.9	4185.7	2990.9	4649.1
127.5	2038.3	3495.4	2113.0	4271.6	3244.5	2374.5	2594.3	537.6	223.5	870.0
3975.9	5455.5	6373.7	6088.2	9946.6	7836.8	5940.7	6679.1	4725.2	5713.1	4728.0
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5565.9	3858.6	3869.6	4509.3	7114.8	5459.9	3570.6	4263.5	2691.8	1724.3	3257.6
931.2	3509.5	3903.7	4558.5	6739.3	5347.7	3742.3	4873.9	3598.3	2195.1	3719.4
103.8	1258.0	1402.8	1210.6	2805.6	2187.6	1666.2	1228.3	828.1	2743.6	536.5
3268.4	4363.5	4785.2	5032.2	4601.8	5372.2	4938.8	5162.8	4568.5	5625.9	5398.0
4284.5	5227.8	4030.1	4194.1	3463.5	3619.2	3435.5	3665.1	2695.4	4045.0	3508.3
782.0	2361.2	2629.7	2811.7	2900.6	2626.9	3070.6	3230.8	1458.3	1365.2	1686.1
72.8	672.8	1350.0	1716.4	392.4	874.5	722.3	1369.1	136.3	1674.7	796.0
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48.7	138.0	145.8	147.5	161.6	142.4	186.6	148.3	136.6	117.2	106.4
371.1	1095.0	911.4	658.8	834.7	847.4	767.5	845.9	583.9	648.6	1987.0
9120.6	6866.5	6573.7	7042.5	7112.2	8220.3	6325.7	7270.3	7006.5	6872.1	8164.6
127.1	3078.0	2815.1	3076.7	2652.9	2742.5	2201.0	2879.1	1928.2	2992.0	1504.4
730.5	1604.0	2313.7	2253.8	2211.5	2013.3	2460.0	2554.3	1301.1	1782.0	2718.5
222.4	1523.9	2278.4	2004.3	2664.3	1843.6	3066.7	1995.5	1029.5	336.8	1603.6
1570.1	9008.8	9376.7	10006.0	9849.9	8668.2	10679.9	8319.8	8321.7	10164.7	13191.2
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6476.8	5341.6	5502.4	5530.9	5493.5	5309.3	5237.0	6027.5	6211.8	7613.7	6059.0
511.4	2328.5	3235.3	3301.9	4650.9	3769.8	5542.8	2609.3	2432.4	1377.4	2627.2
135.6	1325.1	1630.6	1535.0	2294.7	2093.0	1317.5	2237.0	554.0	162.7	970.5
753.3	5820.4	5031.0	6083.4	7255.3	6140.5	7039.5	6457.4	4238.9	3701.2	6763.1
7221.3	6210.7	5985.6	7534.4	7595.4	6807.2	7175.9	6518.0	6905.9	9105.9	6813.3
48.6	187.0	323.6	237.8	136.9	246.1	177.9	306.9	131.4	207.6	162.3
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251.9	3106.2	3158.1	3385.1	3958.5	3769.3	3832.1	4303.6	2331.6	2295.5	2588.2
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5645.1	5958.1	6431.7	6138.6	7057.5	5680.3	8139.0	5877.3	5582.6	5415.7	6093.2
1769.7	5718.7	4503.7	6038.3	6427.0	5556.3	7038.7	5206.2	3929.0	6505.9	6019.3
2593.2	4342.0	4060.2	4264.5	4430.1	4210.9	4880.1	4385.8	3194.2	2462.7	4162.4
86.5	2393.9	2564.4	2548.5	4687.6	3106.0	3387.2	2355.3	932.6	1977.9	1096.4
1895.6	4884.9	4307.9	4819.0	5923.6	4713.7	5571.4	5188.0	3807.4	3754.1	5763.1
167.7	3296.7	2909.3	3370.9	4077.3	3175.4	4116.9	3529.7	2131.1	2132.2	2196.7

2372.8	3291.0	1691.4
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3643.4	2995.8	3226.5
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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
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
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria

o__Methylococcales	f__Methylococcaceae
o__Methylococcales	f__Methylococcaceae
o__Methylococcales	f__Methylococcaceae
o__Methylococcales	f__Methylococcaceae
o__Methylococcales	f__Methylococcaceae
o__Methylococcales	f__Methylococcaceae
o__Methylococcales	f__Methylococcaceae
o__Methylococcales	f__Methylococcaceae
o__Methylococcales	f__Methylococcaceae
o__Methylococcales	f__Methylococcaceae
o__Methylococcales	f__Methylococcaceae
o__Methylococcales	f__Methylococcaceae
o__Methylococcales	f__Methylococcaceae
o__Methylococcales	f__Methylococcaceae
o__Methylococcales	f__Methylococcaceae
o__Methylococcales	f__Methylococcaceae
o__Methylococcales	f__Methylococcaceae
o__Methylococcales	f__Methylococcaceae
o__Methylococcales	f__Methylococcaceae
o__Methylococcales	f__Methylococcaceae
o__Methylococcales	f__Methylococcaceae
o__Methylococcales	f__Methylococcaceae
o__Methylococcales	f__Methylococcaceae
o__Methylococcales	f__Methylococcaceae
o__Methylococcales	f__Methylococcaceae
o__Methylococcales	f__Methylococcaceae
o__Methylococcales	f__Methylococcaceae
o__Methylococcales	f__Methylococcaceae
o__Methylococcales	f__Methylococcaceae
o__Methylococcales	f__Methylococcaceae
o__Methylococcales	f__Methylococcaceae
o__Methylococcales	f__Methylococcaceae
o__Methylococcales	f__Methylococcaceae
o__Methylococcales	f__Methylococcaceae
o__Methylococcales	f__Methylococcaceae
o__Methylococcales	f__Piscirickettsiaceae
o__Methylococcales	f__Piscirickettsiaceae
o__Methylococcales	f__Piscirickettsiaceae
o__Methylococcales	f__Piscirickettsiaceae
o__Methylococcales	f__Piscirickettsiaceae
o__Methylococcales	f__Piscirickettsiaceae
o__Methylococcales	f__Piscirickettsiaceae

g__Methylococcus
g__Methylomicrobium
g__Methylomicrobium
g__Methylomicrobium
g__Methylomicrobium
g__Methylomonas
g__Methylomonas
g__Methylomonas
g__Methylomonas
g__Methylomonas
g__Methylomonas
g__Methylomonas
g__Methylosarcina
g__Methylosarcina
g__Methylosphaera
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__Cycloclasticus
g__Cycloclasticus
g__Thioalkalimicrobium
g__Thioalkalimicrobium
g__Thiomicrospira
g__Thiomicrospira
g__Thiomicrospira

s__unclassified	3275
s__Methylomicrobium buryatense	1641
s__unclassified	1275
s__unclassified	1590
s__unclassified	2073
s__Methylomonas rubra	1306
s__Methylomonas rubra	232
s__Methylomonas rubra	779
s__unclassified	1123
s__unclassified	1188
s__unclassified	1549
s__unclassified	891
s__unclassified	1102
s__unclassified	380
s__Methylosphaera hansonii	1899
s__unclassified	1059
s__unclassified	1111
s__unclassified	1342
s__unclassified	1483
s__unclassified	1654
s__unclassified	1723
s__unclassified	1822
s__unclassified	1880
s__unclassified	1970
s__unclassified	2007
s__unclassified	2020
s__unclassified	249
s__unclassified	25
s__unclassified	33
s__unclassified	609
s__unclassified	656
s__unclassified	681
s__unclassified	714
s__unclassified	743
s__Cycloclasticus pugetii	2394
s__unclassified	3058
s__unclassified	3387
s__unclassified	3564
s__Thiomicrospira crunogena	3408
s__unclassified	3325
s__unclassified	3336

AJ563935.1 gg_id:100913 Methylococcus capsulatus str. Texas = NCIMB 11853 AJ5639
AF307138.1 gg_id:39461 Methylomicrobium buryatense str. 5B AF307
U05570.1 gg_id:8080 Methylomicrobium pelagicum U0557
AF096091.1 gg_id:8060 Methylobacter alcaliphilus str. 5z AF096
EF495157.1 gg_id:222556 Methylobacter alcaliphilus str. 20Z EF4951
AF304194.1 gg_id:38046 Methylomonas rubra str. NCIMB 11913 AF304
AF150807.1 gg_id:8055 Methylomonas rubra AF150
AY995198.1 gg_id:119789 Methylomonas rubra str. UCM B-3075; NCIMB 11913; ACM3303; VKM-15m AY995
X72776.1 gg_id:8084 Methylomonas aurantiaca str. JB103 (phenon3) X72776
X72778.1 gg_id:8090 Methylomonas fodinarum str. ACM 3268 JB13 (phenon2) X72778
DQ837263.1 gg_id:245267 Archaeal and pristine National Park Spain Donana coastal aquifer clone 56S_1B_6 DQ837
GQ340208.1 gg_id:544467 Prokaryotic Marathonas Reservoir Greece water column clone VE07-15-BAC GQ340
NR_025040.1 gg_id:550440 Methylosarcina quisquiliarum str. AML-D4; ATCC 700908 NR_02
AF177296.1 gg_id:8051 Methylosarcina fibrata AML-C10 AF177
U67929.1 gg_id:8101 Methylosphaera hansonii str. AM6 U6792
DQ337085.1 gg_id:145089 subsurface water clone EV818SWSAP61 DQ337
DQ001669.1 gg_id:157473 Microbial seeps asphalt seep clone B91-30 DQ001
AM935153.1 gg_id:534315 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM935
AB486440.1 gg_id:585666 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC AB486
EU144025.1 gg_id:235630 Methylomicrobium album str. BG8 EU144
AM936189.1 gg_id:537819 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM936
X72775.1 gg_id:8059 Methylomicrobium pelagicum str. ACM 3505 NCIMB 2265 X72775
X72773.1 gg_id:8091 Methylobacter whittenburyi str. 3310 NCIMB 11128 ACM 3306 X72773
EU328101.1 gg_id:278818 dynamics during bioremediation crude oil contaminated moderate saline soil clone Y EU328
FM242408.1 gg_id:308594 sequences sediment clone 65 T12d-oil FM242
X72772.1 gg_id:8086 Methylobacter luteus str. ACM 3304 NCIMB 11914 X72772
AM936083.1 gg_id:539835 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM936
EF157165.1 gg_id:247809 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon EF1571
NR_029240.1 gg_id:594166 Methylomicrobium agile str. A30; ATCC 35068 NR_02
EU144026.1 gg_id:252662 Methylomicrobium agile str. ATCC 35068 EU144
AM936065.1 gg_id:564002 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM936
EF648094.1 gg_id:254304 dynamics during produced water treatment aerobic activated sludge clone HB102 EF648
EU735633.1 gg_id:353064 archaeal structures and pristine soils China oil contaminated soil Jidong Oilfield clone EU735
AY007295.1 gg_id:22040 Methylobacter sp. str. LW12 AY007
NR_025955.1 gg_id:555220 Cycloclasticus pugetii str. PS-1; ATCC 51542 NR_02
AF148215.1 gg_id:7712 Cycloclasticus oligotrophus AF148
AF126548.1 gg_id:7703 Thialkalimicrobium aerophilum str. AL3 AF126
AF126549.1 gg_id:7704 Thialkalimicrobium sibericum str. AL7 AF126
CP000109.2 gg_id:141093 Thiomicrospira crunogena str. XCL-2 CP000
AB166731.1 gg_id:99742 Thiomicrospira thermophila str. I78 AB166
FJ792079.1 gg_id:548362 Unexpectedly archaeal species shift between rare and dominant over thousand year FJ7920