# Phylochip Data for Region 5

**Samples:** S16, S17, S18, S19, S20, S21

**Date samples received:** 12/13/2017
**Date of analysis:** 1/11/2018
**Date of report:** 1/18/2018

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|---|
| **Task 1)** Was there a chain of custody? Y / N |
| If yes, is it attached? Y / N |
| Any anomalies? (e.g. Inconsistencies, samples received at unacceptable temperature.) |
| No anomalies. Samples arrived frozen. |
| Were samples stored at -80 until analysis? Y / N |
| Any anomalies? (e.g. Power outages, equipment failure.) |
| No anomalies |
| **Task 2)** Were samples processed in accordance with standard procedure? Y / N |
| Any anomalies? (e.g. Poor DNA recovery, amplification inhibition.) |
| No anomalies |
| **Task 3)** Were samples analyzed in accordance with procedure? Y / N |
| Any anomalies? (e.g. Chip defects, hybridization problems.) |
| No anomalies |
| **Task 4)** Was community analysis performed? Y / N |
| Any anomalies: (e.g. Contamination observed) |
| No anomalies |
| **Task 5)** Was Fecal Source Identification Preformed? Y / N |
| Any anomalies: (e.g. Custom reference used, poor signals.) |
| No anomalies |
| **Task 6)** Have the Raw Data Files been transferred? Y / N |
| Any anomalies: (e.g. Will data be transferred at a later date.) |
| No anomalies |
| Is the Final Report Attached? Y / N |
| Any anomalies: (e.g. Any reason the report wouldn't be attached.) |
| No anomalies |
| Have the requirements of the QASP been met? Y / N |

## Fecal Source Results

| Sample_ID | Organization | Received_date | Sample_type | Extracted_matrix | Analysis_date | Extraction_method | Method_name |
|---|---|---|---|---|---|---|---|
| R5_S16 | EPA_R5 | 12/13/2017 | Field | Filter | 1/11/2018 | MP FastDNA | PhyloChip_G3 |
| R5_S17 | EPA_R5 | 12/13/2017 | Field | Filter | 1/11/2018 | MP FastDNA | PhyloChip_G3 |
| R5_S18 | EPA_R5 | 12/13/2017 | Field | Filter | 1/11/2018 | MP FastDNA | PhyloChip_G3 |
| R5_S19 | EPA_R5 | 12/13/2017 | Field | Filter | 1/11/2018 | MP FastDNA | PhyloChip_G3 |
| R5_S20 | EPA_R5 | 12/13/2017 | Field | Filter | 1/11/2018 | MP FastDNA | PhyloChip_G3 |
| R5_S21 | EPA_R5 | 12/13/2017 | Field | Filter | 1/11/2018 | MP FastDNA | PhyloChip_G3 |

* Values >=0.2 (red) indicate strong source signal. Likely source.
Values >=0.1 and <0.2 (yellow) indicate marginal source signal: Possible source, recommer
Values <0.1 indicate low source signal. Unlikely source.

| Classifier | Spike_mix | #Diagnostic_probes | Unit_name | Result_Bird | Result_Dog | Result_Horse | Result_Human | Result_Pig | Result_Ruminant | Notes* |
|---|---|---|---|---|---|---|---|---|---|---|
| SourceTracker_6057 | Second Genome 2017 | 65 | proportion | 0.11 | 0.03 | 0.03 | 0.05 | 0.02 | 0.02 | |
| SourceTracker_6057 | Second Genome 2017 | 2 | proportion | 0.12 | 0.03 | 0.03 | 0.05 | 0.02 | 0.02 | |
| SourceTracker_6057 | Second Genome 2017 | 106 | proportion | 0.04 | 0.02 | 0.04 | 0.02 | 0.03 | 0.05 | |
| SourceTracker_6057 | Second Genome 2017 | 148 | proportion | 0.07 | 0.01 | 0.02 | 0.01 | 0.00 | 0.01 | |
| SourceTracker_6057 | Second Genome 2017 | 47 | proportion | 0.14 | 0.01 | 0.03 | 0.02 | 0.01 | 0.01 | |
| SourceTracker_6057 | Second Genome 2017 | 70 | proportion | 0.18 | 0.02 | 0.04 | 0.03 | 0.01 | 0.03 | |

ıd additional testing.

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## Diagnostic probe quartets used for SourceTracker analysis (presence/abs

| #Quartet ID |
|---|
| 36044 |
| 36043 |
| 115103 |
| 115102 |
| 115105 |
| 115104 |
| 106169 |
| 106168 |
| 114776 |
| 114775 |
| 115108 |
| 92463 |
| 66683 |
| 66682 |
| 82819 |
| 82818 |
| 115109 |
| 66690 |
| 63373 |
| 63372 |
| 66701 |
| 106198 |
| 106197 |
| 66716 |
| 66715 |
| 115111 |
| 115110 |
| 114786 |
| 114785 |
| 16917 |
| 82875 |
| 88488 |
| 88487 |
| 115697 |
| 114601 |
| 114600 |
| 80258 |
| 80257 |
| 82894 |
| 82893 |
| 66754 |

## sence)

| | Binary (presence/absence) | | | | | |
|---|---|---|---|---|---|---|
| Common source | R5_S16 | R5_S17 | R5_S18 | R5_S19 | R5_S20 | R5_S21 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 1 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 1 | 1 | 0 | 0 | 1 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |

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66753
115119
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87873
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|---|---|---|---|---|---|---|
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 1 | 0 |
| Bird | 0 | 0 | 0 | 0 | 1 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 1 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 1 | 0 |
| Bird | 0 | 0 | 0 | 0 | 1 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |

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114216
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|---|---|---|---|---|---|---|
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 1 | 1 | 0 | 0 | 1 | 1 |
| Bird | 1 | 1 | 0 | 0 | 1 | 1 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 1 |
| Bird | 0 | 0 | 0 | 0 | 0 | 1 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 1 | 0 | 0 |
| Bird | 0 | 0 | 0 | 1 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |

83155
63642
67091
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83255
109040
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110518
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38188
38187
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70700
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115728
110013
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|---|---|---|---|---|---|---|
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 1 | 0 | 0 | 0 | 0 | 0 |
| Bird | 1 | 0 | 0 | 0 | 0 | 0 |
| Bird | 1 | 1 | 0 | 0 | 0 | 0 |
| Bird | 1 | 1 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 1 | 0 | 0 | 0 |
| Bird | 0 | 0 | 1 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 1 | 0 |
| Bird | 0 | 0 | 0 | 0 | 1 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 1 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 1 | 0 | 0 | 0 |
| Bird | 0 | 0 | 1 | 0 | 0 | 0 |
| Bird | 0 | 1 | 0 | 0 | 1 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 1 |
| Bird | 0 | 0 | 0 | 0 | 0 | 1 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 1 | 0 |
| Bird | 0 | 0 | 0 | 0 | 1 | 0 |
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| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 1 | 1 | 0 | 0 | 0 | 0 |

115195
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|---|---|---|---|---|---|---|
| Bird | 1 | 1 | 0 | 0 | 0 | 0 |
| Bird | 1 | 1 | 0 | 1 | 0 | 0 |
| Bird | 1 | 1 | 0 | 1 | 0 | 0 |
| Bird | 0 | 0 | 1 | 0 | 0 | 0 |
| Bird | 0 | 0 | 1 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 1 | 0 | 0 | 0 | 0 | 0 |
| Bird | 1 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 1 | 1 | 0 | 1 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 1 | 0 |
| Bird | 0 | 0 | 0 | 0 | 1 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |

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|---|---|---|---|---|---|---|
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 1 | 0 | 0 | 0 | 0 | 0 |
| Bird | 1 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |

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67506
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115761
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|---|---|---|---|---|---|---|
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 1 | 1 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 1 | 1 |
| Bird | 0 | 0 | 0 | 0 | 1 | 1 |
| Bird | 0 | 0 | 0 | 0 | 1 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 1 |
| Bird | 0 | 0 | 0 | 0 | 0 | 1 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |

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|---|---|---|---|---|---|---|
| Bird | 0 | 0 | 1 | 0 | 0 | 0 |
| Bird | 0 | 0 | 1 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 1 | 1 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 1 |
| Bird | 0 | 0 | 0 | 0 | 0 | 1 |
| Bird | 0 | 1 | 0 | 0 | 0 | 0 |
| Bird | 0 | 1 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 1 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 1 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |

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|---|---|---|---|---|---|---|
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
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| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
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| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 1 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
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| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |

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|---|---|---|---|---|---|---|
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 1 | 1 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 1 | 1 |
| Bird | 0 | 0 | 0 | 0 | 1 | 1 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 1 |
| Bird | 1 | 0 | 0 | 0 | 0 | 1 |
| Bird | 1 | 0 | 0 | 0 | 0 | 1 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
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| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |

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91361
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|---|---|---|---|---|---|---|
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
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| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
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| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 1 | 0 |
| Bird | 0 | 0 | 0 | 0 | 1 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |

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|---|---|---|---|---|---|---|
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 1 |
| Bird | 0 | 0 | 0 | 0 | 0 | 1 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 1 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |

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|---|---|---|---|---|---|---|
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 1 |
| Bird | 0 | 0 | 0 | 0 | 0 | 1 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 1 | 0 | 0 | 0 |
| Bird | 0 | 0 | 1 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
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| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
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| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
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| Bird | 0 | 0 | 0 | 0 | 0 | 0 |

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|---|---|---|---|---|---|---|
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
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| Bird | 0 | 0 | 0 | 1 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 1 | 0 | 0 |
| Bird | 0 | 0 | 0 | 1 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
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| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
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| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
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| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
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| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 1 | 1 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 1 |

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|---|---|---|---|---|---|---|
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| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
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| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
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| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
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| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Bird | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
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| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
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| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
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| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 1 | 0 | 0 | 0 | 0 | 1 |

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| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 1 | 1 | 0 | 0 | 0 | 1 |
| Dog | 1 | 1 | 0 | 0 | 0 | 1 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
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| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 1 | 0 | 0 | 0 | 0 |
| Dog | 0 | 1 | 0 | 0 | 0 | 0 |
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| Dog | 1 | 0 | 0 | 1 | 0 | 0 |
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| Dog | 0 | 0 | 0 | 0 | 0 | 1 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
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| Dog | 1 | 0 | 0 | 0 | 1 | 1 |
| Dog | 1 | 0 | 0 | 0 | 1 | 1 |
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|---|---|---|---|---|---|---|
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
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| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 1 | 1 | 0 | 1 | 1 |
| Dog | 0 | 1 | 1 | 0 | 1 | 1 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 1 |
| Dog | 0 | 0 | 0 | 0 | 0 | 1 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 1 |
| Dog | 0 | 0 | 0 | 0 | 0 | 1 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 1 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |

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|---|---|---|---|---|---|---|
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| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 1 | 1 | 0 | 1 | 0 | 1 |
| Dog | 1 | 1 | 0 | 1 | 0 | 1 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
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| Dog | 0 | 0 | 0 | 0 | 0 | 1 |
| Dog | 0 | 0 | 0 | 1 | 0 | 0 |
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| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
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| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 1 | 1 | 1 | 0 | 0 | 0 |
| Dog | 1 | 1 | 1 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
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|---|---|---|---|---|---|---|
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| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
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| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
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| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
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| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
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| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
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| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 1 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
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| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
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| Dog | 0 | 0 | 0 | 0 | 0 | 0 |

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|---|---|---|---|---|---|---|
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| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
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| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
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| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
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| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
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| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
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| Dog | 0 | 0 | 0 | 0 | 0 | 0 |

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|---|---|---|---|---|---|---|
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| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 1 | 1 | 0 | 0 | 0 | 0 |
| Dog | 1 | 1 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
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| Dog | 0 | 0 | 1 | 0 | 0 | 0 |
| Dog | 0 | 0 | 1 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
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| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
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| Dog | 0 | 0 | 0 | 0 | 0 | 0 |

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|---|---|---|---|---|---|---|
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| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
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| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
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| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
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| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
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| Dog | 1 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
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| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
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| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
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|---|---|---|---|---|---|---|
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| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
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| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
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| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
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|---|---|---|---|---|---|---|
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| Dog | 0 | 0 | 0 | 0 | 0 | 0 |

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|---|---|---|---|---|---|---|
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| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
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| Dog | 1 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
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| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
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| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
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| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
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| Dog | 0 | 0 | 0 | 0 | 0 | 0 |
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| Ruminant | 0 | 0 | 0 | 0 | 0 | 0 |
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| Ruminant | 0 | 0 | 0 | 0 | 0 | 0 |
| Ruminant | 1 | 0 | 0 | 0 | 0 | 0 |

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79032
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| Ruminant | 0 | 0 | 0 | 0 | 0 | 1 |
| Ruminant | 0 | 0 | 0 | 0 | 1 | 1 |
| Ruminant | 0 | 0 | 0 | 0 | 1 | 1 |
| Ruminant | 0 | 0 | 0 | 0 | 0 | 0 |
| Ruminant | 0 | 0 | 0 | 0 | 0 | 0 |
| Ruminant | 0 | 0 | 0 | 0 | 0 | 0 |
| Ruminant | 0 | 0 | 0 | 0 | 0 | 0 |
| Ruminant | 0 | 0 | 0 | 0 | 0 | 0 |
| Ruminant | 0 | 0 | 0 | 0 | 0 | 0 |
| Ruminant | 0 | 0 | 0 | 0 | 0 | 0 |

## Community Analysis: Binary (presence/absence)

| lineage | kingdom | phylum | class |
|---|---|---|---|
| k__Bacteria | k__Bacteria | p__ABY1_OD1 | c__unclassified |
| k__Bacteria | k__Bacteria | p__ABY1_OD1 | c__unclassified |
| k__Bacteria | k__Bacteria | p__ABY1_OD1 | c__unclassified |
| k__Bacteria | k__Bacteria | p__ABY1_OD1 | c__unclassified |
| k__Bacteria | k__Bacteria | p__ABY1_OD1 | c__unclassified |
| k__Bacteria | k__Bacteria | p__ABY1_OD1 | c__unclassified |
| k__Bacteria | k__Bacteria | p__ABY1_OD1 | c__unclassified |
| k__Bacteria | k__Bacteria | p__ABY1_OD1 | c__unclassified |
| k__Bacteria | k__Bacteria | p__ABY1_OD1 | c__unclassified |
| k__Bacteria | k__Bacteria | p__ABY1_OD1 | c__unclassified |
| k__Bacteria | k__Bacteria | p__ABY1_OD1 | c__unclassified |
| k__Bacteria | k__Bacteria | p__ABY1_OD1 | c__unclassified |
| k__Bacteria | k__Bacteria | p__AC1 | c__LC-1 |
| k__Bacteria | k__Bacteria | p__AC1 | c__LC-1 |
| k__Bacteria | k__Bacteria | p__AC1 | c__LC-1 |
| k__Bacteria | k__Bacteria | p__AC1 | c__SHA-114 |
| k__Bacteria | k__Bacteria | p__AC1 | c__SHA-114 |
| k__Bacteria | k__Bacteria | p__AC1 | c__SHA-114 |
| k__Bacteria | k__Bacteria | p__AC1 | c__SHA-114 |
| k__Bacteria | k__Bacteria | p__AC1 | c__SHA-114 |
| k__Bacteria | k__Bacteria | p__AC1 | c__SHA-114 |
| k__Bacteria | k__Bacteria | p__AC1 | c__SHA-114 |
| k__Bacteria | k__Bacteria | p__Acidobacteria | c__Acidobacteria-5 |
| k__Bacteria | k__Bacteria | p__Acidobacteria | c__Acidobacteria-5 |
| k__Bacteria | k__Bacteria | p__Acidobacteria | c__Acidobacteria-5 |
| k__Bacteria | k__Bacteria | p__Acidobacteria | c__Acidobacteria-5 |
| k__Bacteria | k__Bacteria | p__Acidobacteria | c__Acidobacteria-5 |
| k__Bacteria | k__Bacteria | p__Acidobacteria | c__Acidobacteria-5 |
| k__Bacteria | k__Bacteria | p__Acidobacteria | c__Acidobacteria-5 |
| k__Bacteria | k__Bacteria | p__Acidobacteria | c__Acidobacteria-5 |
| k__Bacteria | k__Bacteria | p__Acidobacteria | c__Acidobacteria-5 |
| k__Bacteria | k__Bacteria | p__Acidobacteria | c__Acidobacteria-5 |
| k__Bacteria | k__Bacteria | p__Acidobacteria | c__Acidobacteria-5 |
| k__Bacteria | k__Bacteria | p__Acidobacteria | c__Acidobacteria-5 |
| k__Bacteria | k__Bacteria | p__Acidobacteria | c__Acidobacteria-5 |
| k__Bacteria | k__Bacteria | p__Acidobacteria | c__Acidobacteria-5 |
| k__Bacteria | k__Bacteria | p__Acidobacteria | c__Acidobacteria-5 |

| order | family |
|---|---|
| o__unclassified | f__unclassified |
| o__unclassified | f__unclassified |
| o__unclassified | f__unclassified |
| o__unclassified | f__unclassified |
| o__unclassified | f__unclassified |
| o__unclassified | f__unclassified |
| o__unclassified | f__unclassified |
| o__unclassified | f__unclassified |
| o__unclassified | f__unclassified |
| o__unclassified | f__unclassified |
| o__unclassified | f__unclassified |
| o__unclassified | f__unclassified |
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| o__unclassified | f__unclassified |
| o__unclassified | f__unclassified |
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| o__unclassified | f__unclassified |
| o__unclassified | f__unclassified |
| o__unclassified | f__unclassified |
| o__unclassified | f__unclassified |
| o__unclassified | f__unclassified |
| o__unclassified | f__unclassified |

| | Taxo |
|---|---|
| genus | |
| g__sfA | |
| g__sfA | |
| g__sfB | |
| g__sfB | |
| g__sfC | |
| g__sfD | |
| g__sfE | |
| g__sfF | |
| g__sfG | |
| g__sfH | |
| g__sfI | |
| g__sfJ | |
| g__sfA | |
| g__sfB | |
| g__sfC | |
| g__sfA | |
| g__sfA | |
| g__sfB | |
| g__sfC | |
| g__sfD | |
| g__sfE | |
| g__sfF | |
| g__sfA | |
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| g__sfA | |
| g__sfA | |
| g__sfA | |
| g__sfA | |
| g__sfA | |

| nomic Lineage<br>species | otu |
|---|---|
| s__unclassified | 74875 |
| s__unclassified | 75813 |
| s__unclassified | 74776 |
| s__unclassified | 75651 |
| s__unclassified | 75265 |
| s__unclassified | 75712 |
| s__unclassified | 74874 |
| s__unclassified | 75667 |
| s__unclassified | 75150 |
| s__unclassified | 75140 |
| s__unclassified | 75366 |
| s__unclassified | 74670 |
| s__unclassified | 51307 |
| s__unclassified | 51526 |
| s__unclassified | 51609 |
| s__unclassified | 51109 |
| s__unclassified | 51299 |
| s__unclassified | 51641 |
| s__unclassified | 51353 |
| s__unclassified | 51472 |
| s__unclassified | 51121 |
| s__unclassified | 51644 |
| s__unclassified | 51096 |
| s__unclassified | 51159 |
| s__unclassified | 51167 |
| s__unclassified | 51217 |
| s__unclassified | 51241 |
| s__unclassified | 51242 |
| s__unclassified | 51253 |
| s__unclassified | 51256 |
| s__unclassified | 51326 |
| s__unclassified | 51351 |
| s__unclassified | 51380 |
| s__unclassified | 51494 |
| s__unclassified | 51513 |
| s__unclassified | 51543 |
| s__unclassified | 51557 |

| representative gene | accessi |
|---|---|
| GQ354923.1 gg_id:540167 structure between two geochemically distinct springs Alum Rock Park spring clone M | GQ354 |
| DQ676460.1 gg_id:220280 Archaeal sediment and plankton freshwater pond suboxic freshwater-pond clone M | DQ676 |
| EU644237.1 gg_id:284266 and Samoylov Island Lena active layer -centred polygon near surface horizon; Rim_T | EU644 |
| DQ676456.1 gg_id:224443 Archaeal sediment and plankton freshwater pond suboxic freshwater-pond clone M | DQ676 |
| GQ339139.1 gg_id:528049 Comprehensive Investigation on Iron Cycling Freshwater Seep ing Microscopy Cultiv | GQ339 |
| AB179495.1 gg_id:99699 sedimentary rock clone MIZ04 | AB179 |
| AB193900.1 gg_id:108824 deep-sea vent clone Mb-NB06 | AB193 |
| DQ676475.1 gg_id:223552 Archaeal sediment and plankton freshwater pond suboxic freshwater-pond clone M | DQ676 |
| GQ346852.1 gg_id:562467 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich | GQ346 |
| GQ348940.1 gg_id:577547 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich | GQ348 |
| EU283579.1 gg_id:278529 Model Early Earth Harbors Deeply Divergent Divisions Anderson Lake clone A285 | EU283 |
| FJ234919.1 gg_id:346434 Microbial structure mesophilic biogas mesophil anaerobic reactors fed corne silage cl | FJ2349 |
| GU196235.1 gg_id:578115 Bioaugmentation improved recovery digesters after toxicant exposure lab-scale ana | GU196 |
| AJ543755.1 gg_id:96419 anoxic sediment Lake Cadagno clone 1 | AJ5437 |
| EF192905.1 gg_id:202214 sediments temperate artificial lake Rapel reservoir sediment clone Rap2_24C | EF1929 |
| AJ290978.1 gg_id:112449 anaerobic bioreactor clone SHA-114 | AJ2909 |
| AB186797.1 gg_id:105224 polychlorinated dioxin dechlorinating microcosm clone TSBZ04 | AB186 |
| AY297964.1 gg_id:88282 thermophilic anaerobic terephthalate-degrading sludge clone TTA_B4 | AY2979 |
| EU385779.1 gg_id:267654 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S | EU385 |
| AM712334.1 gg_id:254942 detection and ly microbial Brothers Seamount Kermadec Arc New Zealand biofilm h | AM712 |
| AY592377.1 gg_id:106589 deep-sea mud volcano clone Amsterdam-2B-17; BC20-2B-17 | AY5923 |
| EU385806.1 gg_id:261876 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S | EU3858 |
| EF492945.1 gg_id:241470 Iron-manganese Nodule and Its Surrounding Soil soil around iron-manganese nodule | EF4929 |
| AF245036.1 gg_id:44004 soil metagenomic library clone 17F9 | AF2450 |
| FJ793158.1 gg_id:529323 Archaea and Hot Spring Thailand Tao Dam hot spring clone TDB13 | FJ7931 |
| EF516094.1 gg_id:226261 grassland soil clone FCPS413 | EF5160 |
| FJ004718.1 gg_id:561968 Acidobacteria former agricultural soil rhizosphere clone 1Fe | FJ0047 |
| EU132222.1 gg_id:246947 tallgrass prarie soil clone FFCH14447 | EU132 |
| EU925922.1 gg_id:347057 sediments sediment station DBS1 northern Bering Sea clone 160I37 | EU9259 |
| Z95707.1 gg_id:1740 soil clone 11-14 | Z95707 |
| EU881247.1 gg_id:352805 (long-term grazing and burned annual) Karst region serious disturbance field soil clor | EU8812 |
| GU230433.1 gg_id:556512 Multilevel approach along Rio de la Plata-South Atlantic Ocean coastal sediment clo | GU230 |
| AY703459.1 gg_id:138920 Detection and ly acidobacterial analyses Altamira Cave clone ALT24 | AY7034 |
| EF516178.1 gg_id:222997 grassland soil clone FCPT460 | EF5161 |
| FJ004643.1 gg_id:533715 Acidobacteria former agricultural bulk soil clone 72L1B | FJ0046 |
| AY922011.1 gg_id:113257 farm soil clone AKYG433 | AY9220 |
| EF516869.1 gg_id:219766 grassland soil clone FCPU565 | EF5168 |

| Binary (presence/absence) | | | | |
|---|---|---|---|---|
| R5_S17 | R5_S18 | R5_S19 | R5_S20 | R5_S21 |
| 0 | 0 | 0 | 0 | 0 |
| 0 | 0 | 0 | 0 | 0 |
| 0 | 0 | 0 | 0 | 0 |
| 0 | 0 | 0 | 0 | 0 |
| 0 | 0 | 0 | 1 | 1 |
| 0 | 0 | 0 | 0 | 0 |
| 0 | 1 | 0 | 0 | 0 |
| 0 | 0 | 0 | 0 | 0 |
| 0 | 0 | 0 | 0 | 0 |
| 0 | 0 | 0 | 0 | 0 |
| 0 | 0 | 0 | 0 | 0 |
| 1 | 1 | 0 | 0 | 0 |
| 1 | 0 | 0 | 0 | 0 |
| 0 | 0 | 0 | 0 | 0 |
| 0 | 0 | 0 | 0 | 0 |
| 0 | 0 | 0 | 0 | 0 |
| 1 | 0 | 0 | 0 | 0 |
| 0 | 0 | 0 | 0 | 0 |
| 0 | 0 | 0 | 0 | 0 |
| 0 | 0 | 0 | 0 | 0 |
| 0 | 0 | 0 | 0 | 0 |
| 0 | 0 | 0 | 0 | 0 |
| 0 | 0 | 0 | 0 | 0 |
| 0 | 0 | 0 | 0 | 1 |
| 0 | 0 | 0 | 0 | 0 |
| 0 | 0 | 0 | 0 | 0 |
| 0 | 0 | 0 | 0 | 0 |
| 0 | 1 | 0 | 1 | 0 |
| 0 | 0 | 0 | 0 | 0 |
| 0 | 0 | 0 | 0 | 0 |
| 0 | 0 | 0 | 0 | 1 |
| 0 | 0 | 0 | 0 | 0 |
| 0 | 0 | 0 | 0 | 0 |
| 0 | 0 | 0 | 0 | 0 |
| 0 | 1 | 0 | 0 | 0 |
| 0 | 0 | 0 | 0 | 0 |
| 0 | 0 | 0 | 0 | 0 |

| | | | |
|---|---|---|---|
| k__Bacteria | k__Bacteria | p__Acidobacteria | c__Acidobacteria-5 |
| k__Bacteria | k__Bacteria | p__Acidobacteria | c__Acidobacteria-5 |
| k__Bacteria | k__Bacteria | p__Acidobacteria | c__Acidobacteria-5 |
| k__Bacteria | k__Bacteria | p__Acidobacteria | c__Acidobacteria-5 |
| k__Bacteria | k__Bacteria | p__Acidobacteria | c__Acidobacteria-5 |
| k__Bacteria | k__Bacteria | p__Acidobacteria | c__Acidobacteria-5 |
| k__Bacteria | k__Bacteria | p__Acidobacteria | c__Acidobacteria |
| k__Bacteria | k__Bacteria | p__Acidobacteria | c__Acidobacteria |
| k__Bacteria | k__Bacteria | p__Acidobacteria | c__Acidobacteria |
| k__Bacteria | k__Bacteria | p__Acidobacteria | c__Acidobacteria |
| k__Bacteria | k__Bacteria | p__Acidobacteria | c__Acidobacteria |
| k__Bacteria | k__Bacteria | p__Acidobacteria | c__Acidobacteria |
| k__Bacteria | k__Bacteria | p__Acidobacteria | c__Acidobacteria |
| k__Bacteria | k__Bacteria | p__Acidobacteria | c__Acidobacteria |
| k__Bacteria | k__Bacteria | p__Acidobacteria | c__Acidobacteria |
| k__Bacteria | k__Bacteria | p__Acidobacteria | c__Acidobacteria |
| k__Bacteria | k__Bacteria | p__Acidobacteria | c__Acidobacteria |
| k__Bacteria | k__Bacteria | p__Acidobacteria | c__Acidobacteria |
| k__Bacteria | k__Bacteria | p__Acidobacteria | c__Acidobacteria |
| k__Bacteria | k__Bacteria | p__Acidobacteria | c__Acidobacteria |
| k__Bacteria | k__Bacteria | p__Acidobacteria | c__Acidobacteria |
| k__Bacteria | k__Bacteria | p__Acidobacteria | c__Acidobacteria |
| k__Bacteria | k__Bacteria | p__Acidobacteria | c__Acidobacteria |
| k__Bacteria | k__Bacteria | p__Acidobacteria | c__Acidobacteria |
| k__Bacteria | k__Bacteria | p__Acidobacteria | c__Acidobacteria |
| k__Bacteria | k__Bacteria | p__Acidobacteria | c__Acidobacteria |
| k__Bacteria | k__Bacteria | p__Acidobacteria | c__Acidobacteria |
| k__Bacteria | k__Bacteria | p__Acidobacteria | c__Acidobacteria |
| k__Bacteria | k__Bacteria | p__Acidobacteria | c__Acidobacteria |
| k__Bacteria | k__Bacteria | p__Acidobacteria | c__Acidobacteria |
| k__Bacteria | k__Bacteria | p__Acidobacteria | c__Acidobacteria |
| k__Bacteria | k__Bacteria | p__Acidobacteria | c__Acidobacteria |
| k__Bacteria | k__Bacteria | p__Acidobacteria | c__Acidobacteria |
| k__Bacteria | k__Bacteria | p__Acidobacteria | c__Acidobacteria |
| k__Bacteria | k__Bacteria | p__Acidobacteria | c__Acidobacteria |
| k__Bacteria | k__Bacteria | p__Acidobacteria | c__Acidobacteria |
| k__Bacteria | k__Bacteria | p__Acidobacteria | c__Acidobacteria |
| k__Bacteria | k__Bacteria | p__Acidobacteria | c__Acidobacteria |

| | |
|---|---|
| o__unclassified | f__unclassified |
| o__unclassified | f__unclassified |
| o__unclassified | f__unclassified |
| o__unclassified | f__unclassified |
| o__unclassified | f__unclassified |
| o__unclassified | f__unclassified |
| o__Acidobacteriales | f__Acidobacteriaceae |
| o__Acidobacteriales | f__Acidobacteriaceae |
| o__Acidobacteriales | f__Acidobacteriaceae |
| o__Acidobacteriales | f__Acidobacteriaceae |
| o__Acidobacteriales | f__Acidobacteriaceae |
| o__Acidobacteriales | f__Acidobacteriaceae |
| o__Acidobacteriales | f__Acidobacteriaceae |
| o__Acidobacteriales | f__Acidobacteriaceae |
| o__Acidobacteriales | f__Acidobacteriaceae |
| o__Acidobacteriales | f__Acidobacteriaceae |
| o__Acidobacteriales | f__Acidobacteriaceae |
| o__Acidobacteriales | f__Acidobacteriaceae |
| o__Acidobacteriales | f__Acidobacteriaceae |
| o__Acidobacteriales | f__Acidobacteriaceae |
| o__Acidobacteriales | f__Acidobacteriaceae |
| o__Acidobacteriales | f__Acidobacteriaceae |
| o__Acidobacteriales | f__Acidobacteriaceae |
| o__Acidobacteriales | f__Acidobacteriaceae |
| o__Acidobacteriales | f__Acidobacteriaceae |
| o__Acidobacteriales | f__Acidobacteriaceae |
| o__Acidobacteriales | f__Acidobacteriaceae |
| o__Acidobacteriales | f__Acidobacteriaceae |
| o__Acidobacteriales | f__Acidobacteriaceae |
| o__Acidobacteriales | f__Acidobacteriaceae |
| o__Acidobacteriales | f__Acidobacteriaceae |
| o__Acidobacteriales | f__Acidobacteriaceae |
| o__Acidobacteriales | f__Acidobacteriaceae |
| o__Acidobacteriales | f__Acidobacteriaceae |
| o__Acidobacteriales | f__Acidobacteriaceae |
| o__Acidobacteriales | f__Acidobacteriaceae |
| o__Acidobacteriales | f__Acidobacteriaceae |
| o__Acidobacteriales | f__Acidobacteriaceae |
| o__Acidobacteriales | f__Acidobacteriaceae |
| o__Acidobacteriales | f__Acidobacteriaceae |

g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__Acidobacterium
g__Acidobacterium
g__Candidatus Koribacter
g__Candidatus Koribacter
g__Candidatus Koribacter
g__Candidatus Koribacter
g__Candidatus Koribacter
g__Candidatus Koribacter
g__Candidatus Koribacter
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g__Edaphobacter
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g__unclassified

| | |
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| s__unclassified | 51626 |
| s__unclassified | 51658 |
| s__unclassified | 51723 |
| s__unclassified | 51755 |
| s__unclassified | 51773 |
| s__unclassified | 51795 |
| s__unclassified | 51516 |
| s__unclassified | 51694 |
| s__Candidatus Koribacter versatilis | 51166 |
| s__Candidatus Koribacter versatilis | 51240 |
| s__unclassified | 51045 |
| s__unclassified | 51098 |
| s__unclassified | 51207 |
| s__unclassified | 51371 |
| s__unclassified | 51443 |
| s__unclassified | 51482 |
| s__unclassified | 51518 |
| s__unclassified | 51657 |
| s__unclassified | 51675 |
| s__unclassified | 51757 |
| s__unclassified | 51759 |
| s__unclassified | 51767 |
| s__unclassified | 51786 |
| s__unclassified | 51802 |
| s__Edaphobacter modestus | 51137 |
| s__Edaphobacter modestus | 51792 |
| s__unclassified | 51158 |
| s__unclassified | 51215 |
| s__unclassified | 51338 |
| s__Terriglobus roseus | 51347 |
| s__unclassified | 51348 |
| s__unclassified | 51613 |
| s__unclassified | 50971 |
| s__unclassified | 50973 |
| s__unclassified | 50974 |
| s__unclassified | 50982 |
| s__unclassified | 50986 |
| s__unclassified | 50990 |
| s__unclassified | 50992 |
| s__unclassified | 50993 |
| s__unclassified | 50994 |

DQ906800.1 gg_id:240618 Oman subsurface soil clone 5A-4 DQ906
DQ984540.1 gg_id:240646 Mt. Nan-Jen soil clone IFD_04 DQ984
EF018279.1 gg_id:212863 aspen rhizosphere clone Amb_16S_639 EF0182
EU193029.1 gg_id:329690 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo EU193
DQ513087.1 gg_id:161093 Microbial life fluids ridge flank crustal fluid clone FS266-72B-03 DQ513
EF516647.1 gg_id:222528 grassland soil clone FCPU544 EF5166
DQ463182.1 gg_id:157927 Acid Drainage Tong Lushan Copper Mine China acid mine drainage clone tls1-4 DQ463
D26171.1 gg_id:3704 Acidobacterium capsulatum D2617
AJ292576.1 gg_id:38048 PCB-polluted soil clone WD217 AJ2925
NC_008009.1 gg_id:159436 Korebacter versatilis Ellin345 NC_00
EF020028.1 gg_id:211355 aspen rhizosphere clone Elev_16S_1423 EF020
AM934736.1 gg_id:564102 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM934
AB486931.1 gg_id:540833 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCOR AB486
AB240248.1 gg_id:143307 microbial structure rhizosphere Phragmites bulk soil reed bed reactor laboratory clo AB240
GQ402790.1 gg_id:535450 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
AY234523.1 gg_id:112314 soil isolate Ellin5106 AY2345
EF018237.1 gg_id:206267 aspen rhizosphere clone Amb_16S_588 EF0182
AB240373.1 gg_id:144577 microbial structure Phragmites rhizosphere biofilm reed bed reactor laboratory clon AB2403
EF516733.1 gg_id:222434 grassland soil clone FCPP762 EF5167
AY963401.1 gg_id:156032 structures and correlated ecological factors soils two evergreen broad-leaved forests AY9634
EU680441.1 gg_id:285726 unculturable forest Gaoligong Mountains Yunnan soil clone S5-14 EU680
EU680442.1 gg_id:284815 unculturable forest Gaoligong Mountains Yunnan soil clone S5-16 EU680
EF516334.1 gg_id:223904 grassland soil clone FCPO423 EF5163
AB307653.1 gg_id:267261 clay wall used Japanese traditional buildings clone B45 AB307
AY963484.1 gg_id:150977 structures and correlated ecological factors soils two evergreen broad-leaved forests AY9634
DQ528761.1 gg_id:160117 Edaphobacter modestum str. Wbg-1 DQ528
AY963496.1 gg_id:155420 structures and correlated ecological factors soils two evergreen broad-leaved forests AY9634
AY326573.1 gg_id:136280 Amazon soil clone 81-2 AY3265
FJ466338.1 gg_id:571120 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea FJ4663
DQ660894.1 gg_id:162763 Terriglobus roseus str. KBS 68 DQ660
EF018694.1 gg_id:212239 aspen rhizosphere clone Amb_16S_988 EF0186
DQ532229.1 gg_id:168599 Geographical Variation Microbial Burden and Spacecraft Assembly Johnson Space C DQ532
EU035939.2 gg_id:320478 Insight microbial structure Norwegian deep-water Desmacidon sponge deep-sea cor EU0359
EF516123.1 gg_id:221631 grassland soil clone FCPN626 EF5161
FJ466377.1 gg_id:509471 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea FJ4663
EF492914.1 gg_id:243138 Iron-manganese Nodule and Its Surrounding Soil soil around iron-manganese nodule EF4929
EF516926.1 gg_id:220395 grassland soil clone FCPP741 EF5169
AY963394.1 gg_id:153608 structures and correlated ecological factors soils two evergreen broad-leaved forests AY9633
EU132221.1 gg_id:239485 tallgrass prarie soil clone FFCH14327 EU132
FJ902583.1 gg_id:587792 phreatic limestone sinkholes northeastern Mexico biofilm 1m deep hydrothermal ver FJ9025
EU440640.1 gg_id:540618 Soil are Changed Agricultural Practices agricultural soil clone Plot17-H09 EU440

| | | | | |
|---|---|---|---|---|
| 0 | 0 | 0 | 0 | 0 |
| 0 | 0 | 0 | 0 | 0 |
| 0 | 0 | 0 | 0 | 0 |
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AF465659.1 gg_id:41797 Acidobacterium group clone YNPRH72A AF4656
FJ269341.1 gg_id:588263 Microbes marine sponges sponge tissue clone XC1E08 FJ2693
EF019289.1 gg_id:209203 aspen rhizosphere clone Elev_16S_476 EF0192
EU491200.1 gg_id:262940 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak EU491
EU132218.1 gg_id:257702 tallgrass prarie soil clone FFCH13847 EU132
EF492905.1 gg_id:248553 Iron-manganese Nodule and Its Surrounding Soil soil around iron-manganese nodule EF4929
EF494349.1 gg_id:223415 Nunnock River granitic landscape clone NR.1.090 EF4943
AY395361.1 gg_id:106724 pasture soil clone EB1042 AY3953
AY913359.1 gg_id:114204 forest soil clone DUNssu152 (+7A) (OTU#097) AY9133
EU250262.1 gg_id:235484 acid mine drainage clone GXDC-48 EU250
EF612359.1 gg_id:245188 historic semiarid lead-zinc mine tailings site soil clone OS-C161 EF6123
DQ451440.1 gg_id:156686 forest soil clone FAC1 DQ451
AY922122.1 gg_id:113404 farm soil clone AKYH1493 AY9221
AY212587.1 gg_id:104490 water 10 m downstream manure clone 137ds10 AY2125
AM072423.1 gg_id:138534 Untersuchung Verschiebung der bakteriellen Populationen mit U(VI) inokulierten Bc AM072
AF465656.1 gg_id:46677 Acidobacterium group clone YNPRH46A AF4656
AF200698.1 gg_id:16327 soil clone UA2 AF2006
FJ536905.1 gg_id:535248 Linking performance microbiology biofilters treating dimethyl sulphide presence and FJ5369
DQ906061.1 gg_id:223389 nickel resistance genes metagenome Tinto River rhizosphere clone ERF-1H5 DQ906
DQ404598.1 gg_id:151613 contaminated sediment clone 656042 DQ404
FJ479257.1 gg_id:577226 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4792
AY395347.1 gg_id:106465 pasture soil clone EB1028 AY3953
AY587227.1 gg_id:102666 soil clone AY5872
AY326572.1 gg_id:136267 Amazon soil clone 1031-2 AY3265
AJ292587.1 gg_id:39070 PCB-polluted soil clone WD277 AJ2925
AY234608.1 gg_id:112338 soil isolate Ellin5257 AY2346
AB240272.1 gg_id:143367 microbial structure rhizosphere Phragmites bulk soil reed bed reactor laboratory clo AB240
GQ500876.1 gg_id:564241 Surveys Biofilms and Sediments Mammoth Karst Aquifers Bio-Sep beads containing GQ500
GQ264031.1 gg_id:592891 Structure Simulated Level Waste Site simulated level waste site clone WC3_122 GQ264
FM873307.1 gg_id:362254 occupant source house floor dust clone FD01E01 FM873
GU359061.1 gg_id:518576 rhizosphere soil peanut clone 1S9 GU359
GU134916.1 gg_id:584087 Acid-tolerant microaerophilic oxdizing enhance Fe(III) accumulation Fe(II) oxidizing e GU134
GQ487990.1 gg_id:556931 Microbial metal soil polluted heavy metals clone V20-30 GQ487
DQ395032.1 gg_id:151522 harbor sediment clone VHS-B5-13 DQ395
EU150215.1 gg_id:278437 acidobacteria and soil Niwot Ridge LTER; spruce fir forest clone NiA_SF_26 EU150
EU132259.1 gg_id:244025 tallgrass prarie soil clone FFCH8685 EU132
FJ478546.1 gg_id:582523 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4785
AY289389.1 gg_id:88072 soil clone ABS-318 AY2893
EU669640.1 gg_id:308898 soil clone S8-19 EU6696
AY225650.1 gg_id:97371 Mid-Atlantic Ridge hydrothermal sediment clone AT-s2-57 AY2256

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EF018405.1 gg_id:212293 aspen rhizosphere clone Amb_16S_1019 EF0184
FJ810547.1 gg_id:405751 Subsurface ecosystem resilience: Long-term attenuation subsurface contaminants su FJ8105
GQ487992.1 gg_id:546910 Microbial metal soil polluted heavy metals clone V8-11 GQ487
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EF019762.1 gg_id:216690 aspen rhizosphere clone Elev_16S_943 EF0197
GQ500711.1 gg_id:557097 Surveys Biofilms and Sediments Mammoth Cave Karst Aquifers Charon's Cascade sa GQ500
GU363035.1 gg_id:543451 and archaeal biogeochemical cycling genes within Qiongdongnan basin Sea: pilot stu GU363
EU735013.1 gg_id:347978 assemblages sediment station DBSE Northern Bering Sea clone 109A50 EU735
DQ458047.1 gg_id:158731 acid mine drainage clone DX6 DQ458
FM872925.1 gg_id:369871 occupant source house floor dust clone FB04F12 FM872
AY922132.1 gg_id:114129 farm soil clone AKYH511 AY9221
FM872996.1 gg_id:359837 occupant source house floor dust clone FB02F09 FM872
AJ863211.1 gg_id:126401 poplar tree microcosm bulk soil unflooded clone 20BSU25 AJ8632
FM866297.1 gg_id:360249 Microbial several mining wastes Bulgaria uranium mill tailings clone BuhC-173 FM866
EU276526.1 gg_id:358489 -DGGE and Approaches Analyze Effect Agricultural Practices on Soil agricultural soil c EU2765
EU150201.1 gg_id:279537 acidobacteria and soil Niwot Ridge LTER; spruce fir forest clone NiA_SF_12 EU1502
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EU132307.1 gg_id:244850 tallgrass prarie soil clone FFCH7214 EU1323
EU491340.1 gg_id:271398 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X3 clone EU4913
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DQ395960.1 gg_id:155016 deep-sea octacoral clone ctg_CGOGA68 DQ395
EU335199.1 gg_id:241341 Changes microbial metabolic and along hydrogeochemically variable profile saturate EU3351
FJ203529.1 gg_id:352218 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h FJ2035
AY326582.1 gg_id:136930 Amazon soil clone 31-1 AY3265
EU665054.1 gg_id:541146 Soil are Changed Agricultural Practices agricultural soil clone Plot22-B06 EU6650
FJ466242.1 gg_id:547399 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea FJ4662
AF154085.1 gg_id:1813 hydrocarbon seep clone BPC015 AF1540
AY963491.1 gg_id:153165 structures and correlated ecological factors soils two evergreen broad-leaved forests AY9634
EF492949.1 gg_id:255562 Iron-manganese Nodule and Its Surrounding Soil soil around iron-manganese nodule EF4929
AM935750.1 gg_id:538422 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM935
EU881222.1 gg_id:336433 Karst region natural restoration land soil clone KNR200711-030 EU8812
AB192240.1 gg_id:144515 termite gut homogenate clone RsTu1-92 AB1922
EU250256.1 gg_id:257823 acid mine drainage clone GXDC-42 EU2502
EU335409.1 gg_id:253648 Changes microbial metabolic and along hydrogeochemically variable profile unsatura EU3354
EF018918.1 gg_id:213165 aspen rhizosphere clone Amb_16S_1420 EF0189
FJ478490.1 gg_id:568935 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4784

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EF018439.1 gg_id:212726 aspen rhizosphere clone Amb_16S_1060 EF0184
AF013534.2 gg_id:1828 soil clone C112 AF0135
DQ660878.1 gg_id:251359 DongChuan copper pyrites PRC determined acid mine drainage (AMD) clone DCK-I-1 DQ660
GQ500739.1 gg_id:538176 Surveys Biofilms and Sediments Mammoth Cave Karst Aquifers Bio-Sep beads conta GQ500
AJ581628.1 gg_id:100705 soil near uranium mill tailings clone KCM-C-25 AJ5816
AY922137.1 gg_id:113301 farm soil clone AKYH551 AY9221
FM872961.1 gg_id:361264 occupant source house floor dust clone FB02B12 FM872
AF234701.1 gg_id:28670 sludge clone A22 AF2347
EU193040.1 gg_id:334337 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo EU1930
EU700181.1 gg_id:297788 Study on Shantou Bay Marine Sediments Microorganisms sediment clone STU39 EU7001
AY963351.1 gg_id:154229 structures and correlated ecological factors soils two evergreen broad-leaved forests AY9633
EF597706.1 gg_id:238131 Metagenomics deep mediterranean warm bathypelagic habitat 3010m depth Ionian EF5977
EU050884.1 gg_id:250701 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_04_20 EU0508
AY921956.1 gg_id:113944 farm soil clone AKYG1148 AY9219
EU589288.1 gg_id:270648 China Ningxia rice paddy field soil clone 2_B10 EU5892
EU132175.1 gg_id:256235 tallgrass prarie soil clone FFCH11537 EU1321
DQ017915.1 gg_id:129839 upland stream clone S-Btb7_44 DQ017
EF612353.1 gg_id:243634 historic semiarid lead-zinc site mine tailings clone K6-C86 EF6123
EU449736.1 gg_id:551546 Soil are Changed Agricultural Practices agricultural soil clone Plot4-H05 EU4497
EU449671.1 gg_id:545542 Soil are Changed Agricultural Practices agricultural soil clone Plot4-2E07 EU4496
EU276508.1 gg_id:359433 -DGGE and Approaches Analyze Effect Agricultural Practices on Soil agricultural soil c EU2765
DQ289915.1 gg_id:172055 Microbial Carbon and Nitrogen Cycling Sediments South Atlantic Bight Permeable Sh DQ289
EF019507.1 gg_id:216553 aspen rhizosphere clone Elev_16S_1009 EF0195
AJ863210.1 gg_id:124071 poplar tree microcosm bulk soil unflooded clone 20BSU7 AJ8632
GU118680.1 gg_id:539508 Threatened Corals Provide Microbial Habitats clone Mfav_G07 GU118
EU881185.1 gg_id:310755 Karst region natural restoration land soil clone KNR200711-117 EU8811
EU202779.1 gg_id:319420 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo EU2027
EU440593.1 gg_id:553987 Soil are Changed Agricultural Practices agricultural soil clone Plot17-2H08 EU4405
EF061945.1 gg_id:180033 Xiamen China mangrove sediment clone XME61 EF0619
DQ811916.1 gg_id:169706 mangrove soil clone MSB-3H10 DQ811
AF280856.1 gg_id:71241 bioreactor clone mle1-25 AF2808
AJ536875.1 gg_id:78582 uranium mining waste pile soil sample clone JG30a-KF-145 sp. AJ5368
EF208702.1 gg_id:202031 Vertical and horizontal structure microbial sandy carbonate sediment clone CI75cm.2 EF2087
EF019194.1 gg_id:213048 aspen rhizosphere clone Amb_16S_1868 EF0191
AY963461.1 gg_id:155408 structures and correlated ecological factors soils two evergreen broad-leaved forests AY9634
EU449729.1 gg_id:571898 Soil are Changed Agricultural Practices agricultural soil clone Plot4-G06 EU4497
AY963360.1 gg_id:154596 structures and correlated ecological factors soils two evergreen broad-leaved forests AY9633
EF494338.1 gg_id:226552 Nunnock River granitic landscape clone NR.1.045 EF4943
EF516272.1 gg_id:224515 grassland soil clone FCPN628 EF5162
DQ833470.1 gg_id:162661 detected analyses depth sediment Guanting Reservoir clone 5-35 DQ833
AY289378.1 gg_id:88876 soil clone DS-231 AY2893

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EF492967.1 gg_id:251273 Iron-manganese Nodule and Its Surrounding Soil soil around iron-manganese nodule EF4929
EU491617.1 gg_id:258921 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU491
EF020018.1 gg_id:211775 aspen rhizosphere clone Elev_16S_1409 EF020
AJ519379.1 gg_id:75044 uranium mining waste pile clone JG37-AG-73 sp. AJ5193
EU276472.1 gg_id:359394 -DGGE and Approaches Analyze Effect Agricultural Practices on Soil agricultural soil c EU276
EF018874.1 gg_id:212877 aspen rhizosphere clone Amb_16S_1358 EF0188
DQ837260.1 gg_id:256297 Archaeal and pristine National Park Spain Donana coastal aquifer clone 49S1_2B_67 DQ837
EU202778.1 gg_id:316315 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo EU202
AY913238.1 gg_id:112964 forest soil clone DUNssu017 (+1B) (OTU#052) AY913
EU680459.1 gg_id:280233 unculturable forest Gaoligong Mountains Yunnan soil clone S13-37 EU680
DQ984553.1 gg_id:240236 Mt. Nan-Jen soil clone IFD_41 DQ984
FJ466387.1 gg_id:553417 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea FJ4663
EF018503.1 gg_id:204592 aspen rhizosphere clone Amb_16S_1139 EF0185
FJ466241.1 gg_id:512006 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea FJ4662
DQ202227.1 gg_id:140433 Enrichment s Type II Methane-Oxidizing Inhabiting Northern Peatlands peatland clo DQ202
EF042585.2 gg_id:232738 Microbial and geochemical dynamics extremely acidic metal-rich stream massive sulf EF0425
AY289385.1 gg_id:90452 soil clone DS-87 AY289
EF018868.1 gg_id:215513 aspen rhizosphere clone Amb_16S_1351 EF0188
AY963368.1 gg_id:155297 structures and correlated ecological factors soils two evergreen broad-leaved forests AY963
AJ581608.1 gg_id:93865 soil near uranium mill tailings clone KCM-B-77 AJ5816
EU050885.1 gg_id:256652 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_02_91 EU050
EF999370.1 gg_id:252534 Vertical and Methanotrophs Estuarine Sediments Pearl River Estuary sediments 22cn EF9993
EU202826.1 gg_id:314799 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo EU202
FJ465984.1 gg_id:553387 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea FJ4659
EF061943.1 gg_id:194730 Xiamen China mangrove sediment clone XME2 EF0619
FJ466047.1 gg_id:559379 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea FJ4660
AY922048.1 gg_id:112734 farm soil clone AKYG647 AY922
EF516699.1 gg_id:224638 grassland soil clone FCPN431 EF5166
GQ402710.1 gg_id:566158 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
DQ917891.1 gg_id:226056 Microbial profiles bleached and wild-type Muricea elongata Acidobacteria clone ME DQ917
EU881286.1 gg_id:331724 (long-term grazing and burned annual) Karst region serious disturbance field soil clo EU881
AF524859.1 gg_id:77390 sphagnum peat bog clone K-5b10 AF5248
AY963390.1 gg_id:154565 structures and correlated ecological factors soils two evergreen broad-leaved forests AY963
EF600574.1 gg_id:302530 soil clone E5-34 EF6005
EF018170.1 gg_id:211684 aspen rhizosphere clone Amb_16S_507 EF0181
AY765992.1 gg_id:108645 Acidobacteriaceae KP3 AY765
DQ984543.1 gg_id:256036 Mt. Nan-Jen soil clone IFD_19 DQ984
EF019556.1 gg_id:213076 aspen rhizosphere clone Elev_16S_1065 EF0195
EF600563.1 gg_id:291339 soil clone E5-8 EF6005

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AY922010.1 gg_id:113782 farm soil clone AKYG420 AY922
AY922151.1 gg_id:114240 farm soil clone AKYH715 AY922
DQ450715.1 gg_id:160091 Microbial Alpine Tundra Wet Meadow Soil: Chloroflexi Cold Water-Saturated satura DQ450
DQ058684.1 gg_id:138816 Identification biofilm and bulk s nonchlorinated model system: detection large nitrit DQ058
EF018355.1 gg_id:215113 aspen rhizosphere clone Amb_16S_728 EF0183
AY963471.1 gg_id:154234 structures and correlated ecological factors soils two evergreen broad-leaved forests AY9634
AY234636.1 gg_id:111882 soil isolate Ellin5285 AY2346
EF580946.1 gg_id:278766 Survey Microbial Freshwater Calcareous Mats freshwater calcareous mat clone CM6 EF5809
EU150213.1 gg_id:278429 acidobacteria and soil Niwot Ridge LTER; spruce fir forest clone NiA_SF_24 EU150
FJ478852.1 gg_id:545536 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4788
EU491650.1 gg_id:265935 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU491
FM877546.1 gg_id:357743 Microbial several mining wastes Bulgaria uranium mill tailings clone BuhD-119 FM877
FJ466293.1 gg_id:541280 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea FJ4662
EU132210.1 gg_id:247003 tallgrass prarie soil clone FFCH13193 EU132
EF516049.1 gg_id:217420 grassland soil clone FCPS633 EF5160
GQ120646.1 gg_id:375577 rhizosphere pioneer plants (Bahia xylopoda and Viguiera linearis) growing on heavy GQ120
FJ479234.1 gg_id:582150 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4792
AF234142.1 gg_id:28512 Sturt arid-zone soil clone #0319-7F19 AF2341
FJ478926.1 gg_id:578528 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4789
FM877548.1 gg_id:369088 Microbial several mining wastes Bulgaria uranium mill tailings clone BuhD-130 FM877
AY289399.1 gg_id:90674 soil clone ABS-10 AY2893
DQ906060.1 gg_id:220544 nickel resistance genes metagenome Tinto River rhizosphere clone ERF-1H3 DQ906
FJ152605.1 gg_id:311752 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX1A_ FJ1526
EU335268.1 gg_id:257461 Changes microbial metabolic and along hydrogeochemically variable profile unsatura EU335
EU449702.1 gg_id:567134 Soil are Changed Agricultural Practices agricultural soil clone Plot4-C01 EU449
FJ205234.1 gg_id:570312 Prokaryotic deep-sea region East Lau Spreading Centre inactive hydrothermal field se FJ2052
AY963500.1 gg_id:152510 structures and correlated ecological factors soils two evergreen broad-leaved forests AY9635
EF597694.1 gg_id:248253 Metagenomics deep mediterranean warm bathypelagic habitat 3010m depth Ionian EF5976
FJ466210.1 gg_id:544431 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea FJ4662
AJ292578.1 gg_id:45591 PCB-polluted soil clone WD228 AJ2925
DQ829645.1 gg_id:249932 Acidobacteria (Spain) Donana National Park clone DON6 DQ829
GQ402674.1 gg_id:567036 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
FJ466400.1 gg_id:571342 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea FJ4664
EU202738.1 gg_id:327251 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo EU202
FJ466332.1 gg_id:544403 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea FJ4663
EU370269.1 gg_id:363971 structure photosynthetic complex biofilm acidophilic streams Rio Tinto (SW Spain) e EU370
EU202782.1 gg_id:309400 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo EU202
FJ466085.1 gg_id:548939 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea FJ4660
AJ850100.1 gg_id:198267 Sponge Italy:Lingurian Sea clone SLIIK0 AJ8501
FJ466166.1 gg_id:552854 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea FJ4661
FJ466014.1 gg_id:575126 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea FJ4660

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FJ466050.1 gg_id:545180 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea FJ4660
EF018357.1 gg_id:205244 aspen rhizosphere clone Amb_16S_732 EF0183
DQ404735.1 gg_id:151798 contaminated sediment clone 655075 DQ404
DQ906783.1 gg_id:241820 Oman subsurface soil clone 2B-4 DQ906
EF516149.1 gg_id:223221 grassland soil clone FCPU726 EF5161
AY922112.1 gg_id:114322 farm soil clone AKYH1441 AY9221
EU276532.1 gg_id:370090 -DGGE and Approaches Analyze Effect Agricultural Practices on Soil agricultural soil c EU2765
DQ451491.1 gg_id:156804 forest soil clone FAC52 DQ451
EU335330.1 gg_id:254143 Changes microbial metabolic and along hydrogeochemically variable profile unsatura EU3353
FJ529274.1 gg_id:554828 Evidence vertical transmission symbionts adult embryo Caribbean sponge Svenzea ze FJ5292
EU491480.1 gg_id:260260 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X4 clone EU4914
AY395324.1 gg_id:104834 pasture soil clone EB1005 AY3953
FM873305.1 gg_id:363171 occupant source house floor dust clone FD01D10 FM873
DQ451496.1 gg_id:156857 forest soil clone FAC57 DQ451
AM162414.1 gg_id:151114 and situ identification acidic sphagnum peat bog clone B59 AM162
EF999388.1 gg_id:252185 Vertical and Methanotrophs Estuarine Sediments Pearl River Estuary sediments 22cn EF9993
EU150228.1 gg_id:279590 acidobacteria and dry meadow soil Niwot Ridge LTER clone NiA_DM_1 EU1502
FJ466428.1 gg_id:563945 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea FJ4664
EU193005.1 gg_id:321058 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo EU1930
AJ292581.1 gg_id:25003 PCB-polluted soil clone WD247 AJ2925
GU208393.1 gg_id:582704 Study on Sediment Dongping Lake sediment clone Fh1-6 GU208
AY963503.1 gg_id:154268 structures and correlated ecological factors soils two evergreen broad-leaved forests AY9635
AM162415.1 gg_id:152327 and situ identification acidic sphagnum peat bog clone B62 AM162
EF688384.1 gg_id:241619 soil clone F6-100 EF6883
EU373956.1 gg_id:261742 southern Cretan margin (eastern Mediterranean Sea) canyon and slope sediment clc EU3739
EU276529.1 gg_id:362467 -DGGE and Approaches Analyze Effect Agricultural Practices on Soil agricultural soil c EU2765
Z95710.1 gg_id:22391 Holophaga/Acidobacterium phylum clone 32-10 Z95710
EU117175.1 gg_id:238372 Scratching surface rare biosphere tag primers recent progress made toward microbi EU1171
AY493928.1 gg_id:136996 Fingerprinting aggregates soil clone 537 AY4939
AY922148.1 gg_id:113191 farm soil clone AKYH694 AY9221
FJ479477.1 gg_id:577222 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4794
AY289380.1 gg_id:89699 soil clone ABS-150 AY2893
EF494364.1 gg_id:220562 Nunnock River granitic landscape clone NR.1.008 EF4943
FJ478491.1 gg_id:553968 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4784
EU449733.1 gg_id:548647 Soil are Changed Agricultural Practices agricultural soil clone Plot4-G12 EU4497
DQ829644.1 gg_id:236775 Acidobacteria (Spain) Donana National Park clone DON5 DQ829
GU061236.1 gg_id:584106 Evaluation culturing methods cultivate previously Yel Sea intertidal beach seawater GU061
EF018559.1 gg_id:211201 aspen rhizosphere clone Amb_16S_822 EF0185
AY289382.1 gg_id:89580 soil clone DS-130 AY2893
FJ004671.1 gg_id:566891 Acidobacteria former agricultural soil rhizosphere clone 246 FJ0046
EU373917.1 gg_id:264000 southern Cretan margin (eastern Mediterranean Sea) canyon and slope sediment clc EU3739

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FJ466328.1 gg_id:533475 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea FJ4663
DQ310740.1 gg_id:145786 Recurring seasonal dynamics microbial stream habitats riverine sediment clone WC( DQ310
AB240247.1 gg_id:144789 microbial structure rhizosphere Phragmites bulk soil reed bed reactor laboratory clo AB240
EF492906.1 gg_id:248716 Iron-manganese Nodule and Its Surrounding Soil soil around iron-manganese nodule EF4929
DQ083303.1 gg_id:128109 Acidobacteria pasture soil clone EC1113 DQ083
EF516913.1 gg_id:226506 grassland soil clone FCPT635 EF5169
DQ837256.1 gg_id:242275 Archaeal and pristine National Park Spain Donana coastal aquifer clone 49S1_2B_56 DQ837
AY703470.1 gg_id:139008 Detection and ly acidobacterial analyses Altamira Cave clone ALT5 AY7034
AY921764.1 gg_id:113851 farm soil clone AKYG1603 AY9217
EU335387.1 gg_id:244133 Changes microbial metabolic and along hydrogeochemically variable profile unsatura EU3353
AJ532720.1 gg_id:75652 uranium mining waste pile clone JG34-KF-135 AJ5327
AJ519368.1 gg_id:75679 uranium mining waste pile clone JG37-AG-31 sp. AJ5193
EU925917.1 gg_id:315699 sediments sediment station DBS1 northern Bering Sea clone 154H76 EU9259
AB240301.1 gg_id:142005 microbial structure Phragmites rhizosphere biofilm reed bed reactor laboratory clon AB2403
FN396687.1 gg_id:543863 constant flux thermophilic cold seabed Arctic marine surface sediment clone s5_0_V FN3966
EF999365.1 gg_id:254954 Vertical and Methanotrophs Estuarine Sediments Pearl River Estuary sediments 22cn EF9993
DQ451492.1 gg_id:156776 forest soil clone FAC53 DQ451
FM872485.1 gg_id:362116 occupant source house floor dust clone FA01A05 FM872
DQ648903.1 gg_id:183276 biodiversity and rhizosphere polluted site TGGE screening libraries PCB contaminate DQ648
EF019375.1 gg_id:213210 aspen rhizosphere clone Elev_16S_601 EF0193
DQ811917.1 gg_id:161945 mangrove soil clone MSB-4dx5 DQ811
AY913329.1 gg_id:114314 forest soil clone DUNssu124 (+1B) (OTU#092) AY9133
AY921985.1 gg_id:112801 farm soil clone AKYG1765 AY9219
EF018706.1 gg_id:212676 aspen rhizosphere clone Amb_16S_1157 EF0187
EF061944.1 gg_id:193841 Xiamen China mangrove sediment clone XME31 EF0619
GQ264340.1 gg_id:539385 Structure Simulated Level Waste Site simulated level waste site clone WW2_174 GQ264
GU205312.1 gg_id:531776 unusual Microbial Venezuelan Tepui (Orthoquartzite) Cave: Dominance Chloroflexal GU205
GQ402599.1 gg_id:508855 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
AY963463.1 gg_id:150792 structures and correlated ecological factors soils two evergreen broad-leaved forests AY9634
FJ152824.1 gg_id:331686 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX5A_ FJ1528
AY703461.1 gg_id:139345 Detection and ly acidobacterial analyses Altamira Cave clone ALT21 AY7034
AF317741.1 gg_id:136924 Nullarbor cave clone wb1_A08 AF3177
AB486755.1 gg_id:565220 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCOR( AB4867
EF492944.1 gg_id:245527 Iron-manganese Nodule and Its Surrounding Soil soil around iron-manganese nodule EF4929
FJ004689.1 gg_id:560014 Acidobacteria former agricultural soil rhizosphere clone 6Fe FJ0046
EU276463.1 gg_id:361472 -DGGE and Approaches Analyze Effect Agricultural Practices on Soil agricultural soil c EU2764
AY493932.1 gg_id:136838 Fingerprinting aggregates soil clone 1283 AY4939
FJ479104.1 gg_id:538113 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4791
GQ500793.1 gg_id:540282 Surveys Biofilms and Sediments Mammoth Cave Karst Aquifers Bio-Sep beads conta GQ500
X97098.1 gg_id:3730 peat bog clone TM2 X97098
EF597699.1 gg_id:240765 Metagenomics deep mediterranean warm bathypelagic habitat 3010m depth Ionian EF5976

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EF018530.1 gg_id:209723 aspen rhizosphere clone Amb_16S_790 EF0185
AY922154.1 gg_id:113332 farm soil clone AKYH735 AY922
EF125431.1 gg_id:195246 mangrove soil clone MSB-2D12 EF1254
AY850302.1 gg_id:136684 depending on what microbial treatment present soil clone cw7 AY8503
DQ906775.1 gg_id:236062 Oman subsurface soil clone 2A-3 DQ906
EU676420.1 gg_id:302540 rhizosphere pioneer plants (Bahia xylopoda and Viguiera linearis) growing on metals EU676
EF018157.1 gg_id:212760 aspen rhizosphere clone Amb_16S_492 EF0181
EF173346.1 gg_id:182111 Options situ remediation contaminated mixture chlorinated hydrocarbons hydrocarb EF1733
GU172193.1 gg_id:582540 Microbial Eucalyptus plantation soil clone DSM-R21 GU172
DQ451525.1 gg_id:156611 forest soil clone FAC86 DQ451
FJ465992.1 gg_id:546843 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea FJ4659
EF516950.1 gg_id:221187 grassland soil clone FCPP719 EF5169
FJ152801.1 gg_id:346446 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX5A_ FJ1528
EU132094.1 gg_id:253652 tallgrass prarie soil clone FFCH4380 EU132
EU734939.1 gg_id:322030 assemblages sediment station DBSE Northern Bering Sea clone 030C26 EU7349
EF600570.1 gg_id:291945 soil clone E5-24 EF6005
EF494374.1 gg_id:217344 Nunnock River granitic landscape clone NR.1.127 EF4943
GQ402697.1 gg_id:538729 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
AY963323.1 gg_id:155327 structures and correlated ecological factors soils two evergreen broad-leaved forests AY9633
AB262723.1 gg_id:243925 microorganisms shal subsurface Sarobetsu mire peat soil clone HSM050P-B-12 AB2627
EU421852.1 gg_id:271460 Un-culturable Indian Himalayas soil under glacier Lahaul-Spiti Valley clone KC-27 EU4218
FJ517001.1 gg_id:551640 semiarid 'Tablas de Daimiel National Park' wetland (Central Spain) unravelled water c FJ5170
EF019493.1 gg_id:206727 aspen rhizosphere clone Elev_16S_761 EF0194
AB300068.1 gg_id:220849 Wide ancient microbial DNAs Quaternary sediments holocene mud sediment clone S AB300
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GQ246334.1 gg_id:590912 Temporal and spatial China North Yel Sea sediments clone Sd1-53 GQ246
AY225646.1 gg_id:97685 Mid-Atlantic Ridge hydrothermal sediment clone AT-s3-28 AY2256
EU385737.1 gg_id:276636 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S EU3857
AB177178.1 gg_id:133702 seafloor methane hydrate clone ODP1230B23.02 AB177
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GQ246376.1 gg_id:587607 Temporal and spatial China North Yel Sea sediments clone Cm1-39 GQ246
EU386023.1 gg_id:267584 Biogeographical and microbes sediments on subseafloor sediment South China Sea c EU3860
EU925841.1 gg_id:323947 sediments sediment station DBS1 northern Bering Sea clone 022E38 EU9258
EU287157.1 gg_id:236701 Pacific arctic surface sediment clone P13-64 EU287
GQ246383.1 gg_id:558182 Temporal and spatial China North Yel Sea sediments clone Cm1-46 GQ246
EU734964.1 gg_id:342871 assemblages sediment station DBSE Northern Bering Sea clone 058D16 EU7349
AM176872.1 gg_id:160549 Recovery mangrove sediment clone SZB79 AM176
EU246285.1 gg_id:242979 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-P6-C11 EU2462

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FJ205355.1 gg_id:555830 Prokaryotic deep-sea hydrothermal region East Lau Spreading Centre deep marine se FJ2053
EU373945.1 gg_id:259584 southern Cretan margin (eastern Mediterranean Sea) canyon and slope sediment clc EU3739
EU328055.1 gg_id:279230 dynamics during bioremediation crude oil contaminated moderate saline soil clone B EU3280
FJ748804.1 gg_id:512374 Vertical and sulfate-reducing prokaryotes estuarine Southern China Pearl River Estuar FJ7488
FJ269346.1 gg_id:587166 Microbes marine sponges sponge tissue clone XE1A06 FJ2693
DQ297966.1 gg_id:144752 Microbial hydrocarbon contaminated soil clone UD7 DQ297
EF127615.1 gg_id:208380 Fossil Genes and Microbes Entombed Oldest Ice on Earth ice clone DLE014 EF1276
EF492965.1 gg_id:256992 Iron-manganese Nodule and Its Surrounding Soil soil around iron-manganese nodule EF4929
AB240484.1 gg_id:141861 microbial structure rhizosphere biofilm Sapporo root-tip (0 40 mm) Phragmites Sosei AB2404
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EU150230.1 gg_id:279384 acidobacteria and dry meadow soil Niwot Ridge LTER clone NiA_DM_4 EU1502
FJ592765.1 gg_id:511315 Fumarole-supported islands biodiversity within hyperarid -elevation landscape on Pur FJ5927
AM116734.1 gg_id:142650 Interactions U(VI) added natural dependance on various incubation conditions soil u AM116
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EU132395.1 gg_id:253431 tallgrass prarie soil clone FFCH1720 EU1323
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EU223961.1 gg_id:247010 -RFLP microbes Qinghai-Tin rail soil clone 149 EU2239
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AY921973.1 gg_id:113400 farm soil clone AKYG1698 AY9219
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AY289372.1 gg_id:112292 soil clone DS-13 AY2893
EF516486.1 gg_id:221484 grassland soil clone FCPP426 EF5164
EU669595.1 gg_id:351338 soil clone S11-2 EU6695
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EU335391.1 gg_id:239226 Changes microbial metabolic and along hydrogeochemically variable profile unsatura EU3353
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AM777958.1 gg_id:246222 nonsaline . Influence pore-size filters determination structure alkaline groundwater AM777
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EF127618.1 gg_id:204154 Fossil Genes and Microbes Entombed Oldest Ice on Earth ice clone DLE075 EF1276
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Z95720.1 gg_id:3697 soil clone RB30 Z95720
EU669608.1 gg_id:322898 soil clone S11-33 EU669
DQ648925.1 gg_id:197697 biodiversity and rhizosphere polluted site TGGE screening libraries PCB contaminate DQ648
FJ004727.1 gg_id:573937 Acidobacteria former agricultural bulk soil clone 1L2B FJ0047
AF097766.1 gg_id:1776 activated sludge clone 2951 AF097
FJ790561.1 gg_id:549105 Chasmolithic microbial niches -altitude arid tuff Tibet desert clone VB43 FJ7905
AY493926.1 gg_id:136943 Fingerprinting aggregates soil clone 539 AY493
FJ479201.1 gg_id:513643 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4792
EF494321.1 gg_id:218151 Nunnock River granitic landscape clone NR.4.007 EF4943
DQ450705.1 gg_id:161241 Microbial Alpine Tundra Wet Meadow Soil: Chloroflexi Cold Water-Saturated satura DQ450
EF516128.1 gg_id:224218 grassland soil clone FCPT565 EF5161
FJ479029.1 gg_id:556814 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4790
GQ264352.1 gg_id:567627 Structure Simulated Level Waste Site simulated level waste site clone WW2_25 GQ264
DQ532357.2 gg_id:164562 Geographical Variation Microbial Burden and Spacecraft Assembly Kennedy Space C DQ532
FJ479240.1 gg_id:589151 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4792
FJ478618.1 gg_id:590565 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4786
EU979032.1 gg_id:340207 Effects intercropping Rhizobium inoculation on microbial biomass and rhizosphere b EU979
DQ648920.1 gg_id:191363 biodiversity and rhizosphere polluted site TGGE screening libraries PCB contaminate DQ648
DQ083266.1 gg_id:128164 Acidobacteria pasture soil clone EC1038 DQ083
AF173824.1 gg_id:1767 Antarctic clone LB3-92 AF1738
DQ532263.1 gg_id:171397 Geographical Variation Microbial Burden and Spacecraft Assembly Johnson Space C DQ532
EU150244.1 gg_id:277931 acidobacteria and dry meadow soil Niwot Ridge LTER clone NiA_DM_21 EU150
EU669596.1 gg_id:341165 soil clone S11-7 EU669
GQ029460.1 gg_id:401741 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw861f09 GQ029
CU921698.1 gg_id:565019 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU921
GQ275099.1 gg_id:586270 gut symbionts are tightly linked herbivory ants extract single ant clone #123 GQ275
EU131955.1 gg_id:242792 tallgrass prarie soil clone FFCH15207 EU1319
EF019535.1 gg_id:209516 aspen rhizosphere clone Elev_16S_1040 EF0195
FJ479597.1 gg_id:588240 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4795
EF018479.1 gg_id:216034 aspen rhizosphere clone Amb_16S_1107 EF0184
EF019534.1 gg_id:206841 aspen rhizosphere clone Elev_16S_1038 EF0195
EU276488.1 gg_id:367606 -DGGE and Approaches Analyze Effect Agricultural Practices on Soil agricultural soil c EU2764
EF492911.1 gg_id:247203 Iron-manganese Nodule and Its Surrounding Soil soil around iron-manganese nodule EF4929
FJ466180.1 gg_id:566535 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea FJ4661
EU132318.1 gg_id:257472 tallgrass prarie soil clone FFCH10172 EU1323
FJ152715.1 gg_id:315631 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX5A_ FJ1527
EU335388.1 gg_id:255794 Changes microbial metabolic and along hydrogeochemically variable profile unsatura EU3353
EU335275.1 gg_id:250547 Changes microbial metabolic and along hydrogeochemically variable profile unsatura EU3352
AY509523.1 gg_id:136325 cyanobacterial blooms four Swedish lakes freshwater clone LiUU-11-191 AY5095
EU202757.1 gg_id:340218 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo EU2027
EU131979.1 gg_id:236098 tallgrass prarie soil clone FFCH2893 EU1319

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EU132025.1 gg_id:240289 tallgrass prarie soil clone FFCH8759 EU132
FJ535093.1 gg_id:556648 microbial colonizing walls Karstic Slovenia cave wall biofilm clone 3PJM88 FJ5350
EF612356.1 gg_id:238966 historic semiarid lead-zinc mine tailings site soil clone OS-C85 EF6123
AM902631.1 gg_id:237774 Acidobacteria and Planctomycetes radioactive mineral Central Alps Austria subsurfa AM902
EU669607.1 gg_id:336301 soil clone S11-31 EU669
EU192989.1 gg_id:353698 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo EU192
EU131934.1 gg_id:249598 tallgrass prarie soil clone FFCH11145 EU131
FJ478812.1 gg_id:558300 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4788
EU881303.1 gg_id:307883 (maize-sweet cropping field) Karst region maize-sweet potato cropland soil clone KM EU8813
EU132097.1 gg_id:242038 tallgrass prarie soil clone FFCH1205 EU132
DQ532341.1 gg_id:166649 Geographical Variation Microbial Burden and Spacecraft Assembly Kennedy Space C DQ532
FJ790570.1 gg_id:568934 Chasmolithic microbial niches -altitude arid tuff Tibet desert clone VB74 FJ7905
EF205575.1 gg_id:210897 among geographically regions central Tibet geothermal spring mat clone TP32 EF2055
EF205532.1 gg_id:208981 among geographically regions central Tibet geothermal spring mat clone DTB48 EF2055
FJ478484.1 gg_id:543361 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4784
EU335287.1 gg_id:251244 Changes microbial metabolic and along hydrogeochemically variable profile unsatura EU335
FN396738.1 gg_id:575010 constant flux thermophilic cold seabed Arctic marine surface sediment clone s5_8_II FN396
AB303221.1 gg_id:289370 Acanthopleuribacter pedis str. NBRC 101209 AB303
U41563.1 gg_id:1736 "Geothrix fermentans" U4156
DQ660831.1 gg_id:237050 DongChuan copper pyrites PRC determined acid mine drainage (AMD) clone DCN-I-4 DQ660
GQ390238.1 gg_id:562850 oxic-anoxic interface meromictic crater lake Lac Pavin clone eub62A6 GQ390
DQ660849.1 gg_id:240444 DongChuan copper pyrites PRC determined acid mine drainage (AMD) clone DCN-I-2 DQ660
AB240350.1 gg_id:144899 microbial structure Phragmites rhizosphere biofilm reed bed reactor laboratory clon AB240
EU803304.1 gg_id:322696 It's all ranking aquatic Lake Gatun clone 5C230854 EU803
AB240249.1 gg_id:142414 microbial structure rhizosphere Phragmites bulk soil reed bed reactor laboratory clo AB240
FJ810540.1 gg_id:373070 Subsurface ecosystem resilience: Long-term attenuation subsurface contaminants su FJ8105
EU156148.1 gg_id:252532 thermal spring microbial and functional genes Coffee Pots Hot Spring clone pCOF_65 EU156
AM086131.1 gg_id:149184 Abundance and archaea mesotrophic Lake Kinneret lake profundal sediment clone AM086
AB192122.1 gg_id:142455 termite gut homogenate clone M1PL1-36 AB192
FJ810545.1 gg_id:433880 Subsurface ecosystem resilience: Long-term attenuation subsurface contaminants su FJ8105
GQ472456.1 gg_id:542134 Microbial Dongping Lake lake sediment clone 5F1-11 GQ472
AM180887.1 gg_id:149516 situ detection Acidobacteria mats chemoautotrophic cave (Lower Kane Cave WY US AM180
EU169840.1 gg_id:361234 Bio-reduction Trichloroethene Hydrogen-Based Membrane Biofilm Reactor membra EU169
X77215.1 gg_id:1732 Holophaga foetida X77215
EU340170.1 gg_id:235707 on Aquatic Macrophytes Geothermally Active Area Sedge Bay Yellowstone Lake WY EU340
AJ009478.1 gg_id:1733 anaerobic TCB-transforming consortium clone SJA-87 AJ0094
AB192121.1 gg_id:144303 termite gut homogenate clone M1NP1-62 AB192
DQ066997.1 gg_id:133176 Lake Washington sediment clone pLW-59 DQ066
FN554392.1 gg_id:554680 Isolation members group 8 Acidobacteria subdivision 1 Verrucomicrobia and other h FN5543
GQ487951.1 gg_id:553643 Microbial metal soil polluted heavy metals clone T7-99 GQ487
GU169059.1 gg_id:592179 Biofilms formed on substances: response f conditions and carbon concentrations sy GU169

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EU360308.1 gg_id:274047 microbial fuel cell enriched sediment clone FWS 726 EU3603
EF032758.1 gg_id:194029 cyanobacterial mat in lava cave clone HAVOmat71 EF0327
EU404024.1 gg_id:311763 Microbial septic tank effluent and soil biozone infiltrative surface clean water clone ( EU404(
AY963514.1 gg_id:154909 structures and correlated ecological factors soils two evergreen broad-leaved forests AY9635
EF494334.1 gg_id:225918 Nunnock River granitic landscape clone NR.1.031 EF4943
AB240310.1 gg_id:144019 microbial structure Phragmites rhizosphere biofilm reed bed reactor laboratory clone AB2403
AB486063.1 gg_id:586133 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC AB486(
EF516537.1 gg_id:218957 grassland soil clone FCPT436 EF5165
EU132113.1 gg_id:251439 tallgrass prarie soil clone FFCH10391 EU1321
Z95713.1 gg_id:1728 soil clone 32-20 Z95713
AB486378.1 gg_id:588194 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC AB4863
DQ906890.1 gg_id:251805 Oman subsurface soil clone 11B-20 DQ906
AY395447.1 gg_id:103470 pasture soil clone EB1128 AY3954
AB488104.1 gg_id:578435 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSSURC AB4881
EF516616.1 gg_id:224372 grassland soil clone FCPN715 EF5166
DQ450820.1 gg_id:160986 Microbial Alpine Tundra Wet Meadow Soil: Chloroflexi Cold Water-Saturated saturat DQ450
EF515929.1 gg_id:218370 grassland soil clone FCPS615 EF5159
GQ397044.1 gg_id:586275 Functional unvegetated perhumid recently-deglaciated soils do not correlate shifts s GQ397
GQ302583.1 gg_id:542433 prokaryotic sediment Shawan methods cold spring clone sw-xj162 GQ302
AY921868.1 gg_id:113021 farm soil clone AKYG1139 AY9218
EF492961.1 gg_id:250693 Iron-manganese Nodule and Its Surrounding Soil soil around iron-manganese nodule EF4929
Z95729.1 gg_id:1718 soil clone iii1-8 Z95729
FJ545583.1 gg_id:565231 Diveristy Seawater and Sediment Northern North Yel Sea sediment clone S2-65 FJ5455
FJ479007.1 gg_id:509899 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4790
DQ378223.1 gg_id:151990 oil-polluted soil clone M01_Pitesti DQ378
EF632944.1 gg_id:237284 Unique microbial contrasting aquatic altitude Andean Altiplano (northern Chile) fresh EF6329
EF515913.1 gg_id:224501 grassland soil clone FCPP604 EF5159
EU925899.1 gg_id:324084 sediments sediment station DBS1 northern Bering Sea clone 124H8 EU9258
EF516669.1 gg_id:219348 grassland soil clone FCPN472 EF5166
AB488081.1 gg_id:592475 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSSURC AB4880
AY289394.1 gg_id:111806 soil clone DS-215 AY2893
FN424397.1 gg_id:565655 structure sediments Bizerte (Tunisia) southern Mediterranean coastal anthropized la FN4243
FJ479328.1 gg_id:511937 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4793
DQ228377.1 gg_id:143029 microbial compositions two subglacial possible role microbes chemical weathering p DQ228
FJ868852.1 gg_id:509795 Effects nitrogen form on excessive fertilization soil Earth-cumuli-orthic anthrosols clo FJ8688
AY493935.1 gg_id:136569 Fingerprinting aggregates soil clone 869 AY4939
DQ001620.1 gg_id:157110 Microbial seeps asphalt seep clone E91-12 DQ001
GQ016556.1 gg_id:493114 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ016
GQ302580.1 gg_id:563979 prokaryotic sediment Shawan methods cold spring clone sw-xj147 GQ302
AB128876.1 gg_id:103558 deep marine sediments Nankai Trough Japan; ODP Leg 190 clone 1174-1091-17 AB1288

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EU132022.1 gg_id:244993 tallgrass prarie soil clone FFCH16206 EU132
EF516758.1 gg_id:217242 grassland soil clone FCPN518 EF5167
AB240376.1 gg_id:141305 microbial structure Phragmites rhizosphere biofilm reed bed reactor laboratory clon AB240
DQ415770.1 gg_id:158462 Dominant microbial limestone-corroding biofilms frasassi system Italy Frasassi sulfid DQ415
AB426221.1 gg_id:272259 -situ identification study benzene-degrading s under methanogenic condition anaerc AB426
AB426190.1 gg_id:263608 -situ identification study benzene-degrading s under methanogenic condition anaerc AB426
AY177760.1 gg_id:78424 subsurface soil beneath grassland clone AY177
GQ402795.1 gg_id:584529 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
AB240315.1 gg_id:142591 microbial structure Phragmites rhizosphere biofilm reed bed reactor laboratory clon AB240
FJ825470.1 gg_id:532951 Microbial during start-up mesophilic biogas plant clone 150b_BE4_38 FJ8254
AM902640.1 gg_id:252937 Acidobacteria and Planctomycetes radioactive mineral Central Alps Austria subsurfa AM902
AB426230.1 gg_id:263257 -situ identification study benzene-degrading s under methanogenic condition anaerc AB426
FJ478644.1 gg_id:543083 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4786
AF523992.1 gg_id:63234 forested wetland clone FW32 AF523
EU132238.1 gg_id:237679 tallgrass prarie soil clone FFCH15579 EU132
AY222310.1 gg_id:113738 host hindgut caecum clone Aci 1 AY222
AB300113.1 gg_id:226421 Wide ancient microbial DNAs Quaternary sediments holocene mud sediment clone K AB300
EF688201.1 gg_id:333448 Detection microbial sludge anaerobic wastewater treatment system clone 4F4_cons EF6882
DQ811915.1 gg_id:170193 mangrove soil clone MSB-3G5 DQ811
GU208397.1 gg_id:583865 Study on Sediment Dongping Lake sediment clone Fh1-16 GU208
DQ676398.1 gg_id:222747 Archaeal and plankton freshwater pond suboxic freshwater-pond sediment clone M DQ676
AJ240998.1 gg_id:1724 marine sediment clone Sva0450 AJ2409
EU617730.1 gg_id:310379 Seasonal variation microbial Yel Sea sediment clone C13S-4 EU617
FJ416122.1 gg_id:361045 sediments sediment station NEC5 Northern Bering Sea clone 111N77 FJ4161
EF125429.1 gg_id:178099 mangrove soil clone MSB-2C8 EF1254
DQ154825.1 gg_id:138946 Diel Migration Restructures Hypersaline Microbial Mat hypersaline microbial mat cl DQ154
GQ472454.1 gg_id:556802 Microbial Dongping Lake lake sediment clone 5F4-8 GQ472
GQ249526.1 gg_id:556154 Microbial anaerobic sediments Bay Cadiz (Spain) marine sediment: 6-8 cm layer clor GQ249
EU925849.1 gg_id:333078 sediments sediment station DBS1 northern Bering Sea clone 041E69 EU9258
AB525453.1 gg_id:541520 Segregated ANME-1 and -2 cold-seep marine sediments deep-sea methane seep sed AB5254
FM242439.1 gg_id:318951 sequences sediment clone 20 T12d+oil FM242
GQ259274.1 gg_id:576470 Microbial activities coastal marine sediments and water column Svalbard deep sedir GQ259
GU180169.1 gg_id:583825 Impact coplanar PCBs on microbial activity anaerobic estuarine sediments sediment GU180
EU617731.1 gg_id:309253 Seasonal variation microbial Yel Sea sediment clone C13S-111 EU617
GQ356996.1 gg_id:584697 Metal Dependent Marine Methane Oxidation methane seep sediment clone FeLive GQ356
AB426217.1 gg_id:261015 -situ identification study benzene-degrading s under methanogenic condition anaerc AB426
EF597692.1 gg_id:257405 Metagenomics deep mediterranean warm bathypelagic habitat 3010m depth Ionian EF5976
FJ902087.1 gg_id:555433 phreatic limestone sinkholes northeastern Mexico orange biomat 8m deep cenote Ca FJ9020
EU132182.1 gg_id:236707 tallgrass prarie soil clone FFCH11809 EU132
FJ269274.1 gg_id:580045 Microbes marine sponges sponge tissue clone XA2D09F FJ2692
FJ535081.1 gg_id:539336 microbial colonizing walls Karstic Slovenia cave wall biofilm clone 2PJM22 FJ5350

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FJ205358.1 gg_id:508870 Prokaryotic deep-sea hydrothermal region East Lau Spreading Centre deep marine se FJ2053
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EU652505.1 gg_id:277687 Seasonal variation microbial Yel Sea sediment clone D8S-107 EU6525
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EU202817.1 gg_id:329074 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo EU2028
EU287123.1 gg_id:256935 Pacific arctic surface sediment clone P13-30 EU287
AY225649.1 gg_id:95646 Mid-Atlantic Ridge hydrothermal sediment clone AT-s54 AY2256
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FJ484816.1 gg_id:513563 microbial autonomous rover world's deepest phreatic sinkhole wall biomat El Zacator FJ4848
GQ487923.1 gg_id:581733 Microbial metal soil polluted heavy metals clone T1-98 GQ487
EU652507.1 gg_id:278012 Seasonal variation microbial Yel Sea sediment clone B8S-56 EU6525
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FJ466104.1 gg_id:557785 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea FJ4661
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GQ264513.1 gg_id:590045 Structure Simulated Level Waste Site simulated level waste site clone WW3_65 GQ264
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GQ402596.1 gg_id:559586 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
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EF018600.1 gg_id:213933 aspen rhizosphere clone Amb_16S_874 EF0186
AY963431.1 gg_id:154089 structures and correlated ecological factors soils two evergreen broad-leaved forests AY9634
AY963354.1 gg_id:154309 structures and correlated ecological factors soils two evergreen broad-leaved forests AY9633
EF520625.1 gg_id:231211 structure lakes: what controls ? acid-impacted lake clone ADK-SGh02-62 EF5206
AB262728.1 gg_id:245506 microorganisms shal subsurface Sarobetsu mire peat soil clone HSM050P-B-17 AB2627
EF515945.1 gg_id:217695 grassland soil clone FCPN757 EF5159
AB486891.1 gg_id:580183 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCOR AB4868
DQ451519.1 gg_id:156650 forest soil clone FAC80 DQ451
EF019301.1 gg_id:203801 aspen rhizosphere clone Elev_16S_492 EF0193
AY913513.1 gg_id:113638 forest soil clone DUNssu336 (+7B) (OTU#091) AY9135
EU399672.1 gg_id:272782 and localization microbial consortium full-scale granular activated carbon anaerobic EU3996
EU445204.1 gg_id:532631 Isolation Weight Forest Topsoil Metagenomic tropical forest topsoil clone R17 EU4452
AY395354.1 gg_id:102185 pasture soil clone EB1035 AY3953
EF492952.1 gg_id:245898 Iron-manganese Nodule and Its Surrounding Soil soil around iron-manganese nodule EF4929
AY234723.1 gg_id:111405 soil isolate Ellin6071 AY2347
FN594692.1 gg_id:581422 and arsenic mobilization rock biofilms ancient biofilom gold mine Zloty Stok clone a8 FN5946
FJ461997.1 gg_id:581847 Microbial ecology industrial digestor mesophilic anaerobic reactor fed effluent chemi FJ4619
AM162425.1 gg_id:156359 and situ identification acidic sphagnum peat bog clone B119 AM162
GQ340081.1 gg_id:588765 Prokaryotic Marathonas Reservoir Greece water column clone A07-42-BAC GQ340
GQ263798.1 gg_id:540293 Structure Simulated Level Waste Site simulated level waste site clone WC1_b37 GQ263
EU861915.1 gg_id:332934 effects chronic fertilization on alpine tundra microbial implications carbon and cyclin EU8619
GQ402586.1 gg_id:556383 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
EF018723.1 gg_id:207760 aspen rhizosphere clone Amb_16S_1178 EF0187
EU202741.1 gg_id:347427 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo EU2027
AM749736.1 gg_id:256750 Isolation ing candidate division soils New Zealand steam-affected geothermal soil cl AM749
AM935398.1 gg_id:534931 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM935
AY963366.1 gg_id:154125 structures and correlated ecological factors soils two evergreen broad-leaved forests AY9633
EF018819.1 gg_id:210872 aspen rhizosphere clone Amb_16S_1297 EF0188
AY963393.1 gg_id:152086 structures and correlated ecological factors soils two evergreen broad-leaved forests AY9633
DQ451511.1 gg_id:156603 forest soil clone FAC72 DQ451
GQ402695.1 gg_id:574269 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
AJ536873.1 gg_id:79020 uranium mining waste pile soil sample clone JG30a-KF-40 sp. AJ5368
GQ402805.1 gg_id:513782 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
DQ066995.1 gg_id:131970 Lake Washington sediment clone pLW-63 DQ066
AY963443.1 gg_id:152545 structures and correlated ecological factors soils two evergreen broad-leaved forests AY9634
AY963420.1 gg_id:156507 structures and correlated ecological factors soils two evergreen broad-leaved forests AY9634
EF126260.1 gg_id:263285 Phototrophic microbial build laminated Fe-formations on Sulawesi Indonesia mesoph EF1262
AY493924.1 gg_id:136281 Fingerprinting aggregates soil clone 355 AY4939

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EU676415.1 gg_id:287625 rhizosphere pioneer plants (Bahia xylopoda and Viguiera linearis) growing on metals- EU6764
EU044116.1 gg_id:237652 luences structure fosters richness subtropical Altamaha Ohopee River Valley inland c EU0441
AB254784.1 gg_id:161597 Biogenic Fe-oxyhydroxides nodules (takashikozo) encrusted iron-oxide reducing sedi AB2547
FJ466097.1 gg_id:557180 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea FJ4660
GU205285.1 gg_id:525931 unusual Microbial Venezuelan Tepui (Orthoquartzite) Cave: Dominance Chloroflexal GU205
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AY212581.1 gg_id:103580 water 10 m downstream manure clone 130ds10 AY2125
AJ306764.1 gg_id:66935 DCP-dechlorinating consortium clone SHA-261 AJ3067
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EF019821.1 gg_id:209523 aspen rhizosphere clone Elev_16S_1166 EF0198
AM162421.1 gg_id:155041 and situ identification acidic sphagnum peat bog clone B18 AM162
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FM877544.1 gg_id:369392 Microbial several mining wastes Bulgaria uranium mill tailings clone BuhD-110 FM877
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EU132409.1 gg_id:237818 tallgrass prarie soil clone FFCH2202 EU1324
AJ536863.1 gg_id:78832 uranium mining waste pile soil sample clone JG30-KF-C5 sp. AJ5368
AM162419.1 gg_id:152963 and situ identification acidic sphagnum peat bog clone B15 AM162
AY963364.1 gg_id:153346 structures and correlated ecological factors soils two evergreen broad-leaved forests AY9633
FJ479149.1 gg_id:572184 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4791
AB179516.1 gg_id:101119 sedimentary rock clone MIZ25 AB1795
FJ535085.1 gg_id:593912 microbial colonizing walls Karstic Slovenia cave wall biofilm clone 3PJM113 FJ5350
FJ462107.1 gg_id:592473 Microbial ecology industrial digestor mesophilic anaerobic reactor fed effluent chemi FJ4621
AY493921.1 gg_id:136304 Fingerprinting aggregates soil clone 351 AY4939
AM935004.1 gg_id:545992 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM935
FJ466071.1 gg_id:564195 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea FJ4660
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DQ906868.1 gg_id:256303 Oman subsurface soil clone 11A-3 DQ906
EF018657.1 gg_id:204324 aspen rhizosphere clone Amb_16S_943 EF0186
GQ402789.1 gg_id:582679 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
AB486182.1 gg_id:584693 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC AB486
FJ466148.1 gg_id:544575 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea FJ4661
AY963331.1 gg_id:154822 structures and correlated ecological factors soils two evergreen broad-leaved forests AY9633
FJ466083.1 gg_id:533572 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea FJ4660
EU676414.1 gg_id:299684 rhizosphere pioneer plants (Bahia xylopoda and Viguiera linearis) growing on metals- EU6764
FJ466197.1 gg_id:513591 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea FJ4661
EF018283.1 gg_id:210615 aspen rhizosphere clone Amb_16S_644 EF0182
EU335379.1 gg_id:240295 Changes microbial metabolic and along hydrogeochemically variable profile unsatura EU3353

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EU132045.1 gg_id:240983 tallgrass prarie soil clone FFCH9825 EU132
EF516126.1 gg_id:226281 grassland soil clone FCPT514 EF5161
DQ129637.1 gg_id:138184 microarray level air two cities Texas urban aerosol clone AKIW659 DQ129
EF019147.1 gg_id:208718 aspen rhizosphere clone Amb_16S_1790 EF0191
GQ263218.1 gg_id:592008 Structure Simulated Level Waste Site simulated level waste site clone F3_25X GQ263
FJ152859.1 gg_id:350446 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX5A_ FJ1528
EF018719.1 gg_id:210677 aspen rhizosphere clone Amb_16S_1170 EF0187
GQ264287.1 gg_id:544353 Structure Simulated Level Waste Site simulated level waste site clone WW2_101 GQ264
EU881125.1 gg_id:322588 Karst region primary forest soil clone KPF200711-143 EU881
EF018078.1 gg_id:204993 aspen rhizosphere clone Amb_16S_404 EF0180
GQ402709.1 gg_id:587893 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
EF020033.1 gg_id:215120 aspen rhizosphere clone Elev_16S_1428 EF0200
EF516689.1 gg_id:226313 grassland soil clone FCPN758 EF5166
EU150203.1 gg_id:278495 acidobacteria and soil Niwot Ridge LTER; spruce fir forest clone NiA_SF_14 EU150
FJ901511.1 gg_id:568755 phreatic limestone sinkholes northeastern Mexico biomat 80m deep cenote La Palita FJ9015
DQ833485.1 gg_id:161914 detected analyses depth sediment Guanting Reservoir clone 35-19 DQ833
FJ004679.1 gg_id:553090 Acidobacteria former agricultural soil rhizosphere clone 89 FJ0046
DQ404851.1 gg_id:153227 contaminated sediment clone 655981 DQ404
EU044114.1 gg_id:249968 luences structure fosters richness subtropical Altamaha Ohopee River Valley inland c EU044
GQ402578.1 gg_id:545323 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
EU132362.1 gg_id:242626 tallgrass prarie soil clone FFCH13873 EU132
EF516577.1 gg_id:221845 grassland soil clone FCPT524 EF5165
EF019667.1 gg_id:205391 aspen rhizosphere clone Elev_16S_822 EF0196
FJ466067.1 gg_id:575896 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea FJ4660
EF516304.1 gg_id:222573 grassland soil clone FCPT689 EF5163
DQ017939.1 gg_id:134417 upland stream clone S-Jos_51 DQ017
DQ001647.1 gg_id:158148 Microbial seeps asphalt seep clone E101-54 DQ001
AM749754.1 gg_id:246440 Isolation ing candidate division soils New Zealand steam-affected geothermal soil cl AM749
AY963377.1 gg_id:150731 structures and correlated ecological factors soils two evergreen broad-leaved forests AY9633
FJ004775.1 gg_id:554827 Acidobacteria former agricultural bulk soil clone 31L2B FJ0047
DQ984552.1 gg_id:241889 Mt. Nan-Jen soil clone IFD_30 DQ984
EF516032.1 gg_id:219884 grassland soil clone FCPP523 EF5160
AY963418.1 gg_id:154876 structures and correlated ecological factors soils two evergreen broad-leaved forests AY9634
EU150229.1 gg_id:278164 acidobacteria and dry meadow soil Niwot Ridge LTER clone NiA_DM_2 EU150
FJ465995.1 gg_id:544523 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea FJ4659
EU331380.1 gg_id:250740 Influence Nitrate on Microbial Reduction Pertechnetate microcosm sediment contan EU3313
EF516947.1 gg_id:227230 grassland soil clone FCPS681 EF5169
AJ009495.1 gg_id:3677 chlorobenzene-degrading consortium clone SJA-149 AJ0094
EF019981.1 gg_id:206392 aspen rhizosphere clone Elev_16S_1368 EF0199
AM935451.1 gg_id:557468 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM935
EF494337.1 gg_id:222398 Nunnock River granitic landscape clone NR.1.044 EF4943

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AY913265.1 gg_id:114356 forest soil clone DUNssu045 (-2B) (OTU#121) AY913
FJ478535.1 gg_id:583760 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4785
FJ205213.1 gg_id:549259 Prokaryotic deep-sea region East Lau Spreading Centre inactive hydrothermal field se FJ2052
EF492968.1 gg_id:247708 Iron-manganese Nodule and Its Surrounding Soil soil around iron-manganese nodule EF4929
AY922037.1 gg_id:112776 farm soil clone AKYG600 AY922
AF465650.1 gg_id:17775 thermal soil clone YNPRH2B AF465
GU172173.1 gg_id:536567 Microbial Eucalyptus plantation soil clone DSM-R1 GU172
EU445207.1 gg_id:541749 Isolation Weight Forest Topsoil Metagenomic tropical forest topsoil clone R20 EU445
EF492956.1 gg_id:241718 Iron-manganese Nodule and Its Surrounding Soil soil around iron-manganese nodule EF4929
EF515983.1 gg_id:226166 grassland soil clone FCPS403 EF5159
FJ479535.1 gg_id:553939 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4795
DQ450706.1 gg_id:161275 Microbial Alpine Tundra Wet Meadow Soil: Chloroflexi Cold Water-Saturated satura DQ450
EU150248.1 gg_id:278253 acidobacteria and dry meadow soil Niwot Ridge LTER clone NiA_DM_26 EU150
FJ793181.1 gg_id:526228 Archaea and Hot Spring Thailand Tao Dam hot spring clone TDB66 FJ7931
AY963425.1 gg_id:151183 structures and correlated ecological factors soils two evergreen broad-leaved forests AY963
FJ004745.1 gg_id:575745 Acidobacteria former agricultural bulk soil clone 26L2B FJ0047
EF157254.1 gg_id:241324 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon EF1572
EF032754.1 gg_id:190912 cyanobacterial mat in lava cave clone HAVOmat42 EF0327
FJ466195.1 gg_id:543818 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea FJ4661
EU202739.1 gg_id:343210 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo EU202
GU444079.1 gg_id:519245 Effects amendments on fertility and microbial structure cucumber Cucumis sativus L GU444
FJ624931.1 gg_id:566511 Influence lead contamination on boreal pine forest soil clone HF_C_58 FJ6249
FJ710779.1 gg_id:510168 Abundance and microbial long-term operated anammox biofilm reactors initiated ino FJ7107
EF018396.1 gg_id:205033 aspen rhizosphere clone Amb_16S_1009 EF0183
GQ264426.1 gg_id:589387 Structure Simulated Level Waste Site simulated level waste site clone WW3_116 GQ264
FJ479270.1 gg_id:594169 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4792
AB186882.1 gg_id:105319 polychlorinated dioxin dechlorinating microcosm clone TSBb06 AB186
EF019361.1 gg_id:216341 aspen rhizosphere clone Elev_16S_581 EF0193
GU118588.1 gg_id:588882 Threatened Corals Provide Microbial Habitats clone Mfav_P18 GU118
AB240298.1 gg_id:141801 microbial structure Phragmites rhizosphere biofilm reed bed reactor laboratory clon AB240
FJ592762.1 gg_id:562807 Fumarole-supported islands biodiversity within hyperarid -elevation landscape on Pu FJ5927
AM935189.1 gg_id:558353 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM935
AY703464.1 gg_id:139346 Detection and ly acidobacterial analyses Altamira Cave clone ALT40 AY7034
GU187034.1 gg_id:578443 Isolation -yet Acidobacteria on solid dilute media surface soil clone IGE-015 GU187
EF018402.1 gg_id:210745 aspen rhizosphere clone Amb_16S_1015 EF0184
EU132316.1 gg_id:240950 tallgrass prarie soil clone FFCH1016 EU132
EF516154.1 gg_id:221233 grassland soil clone FCPO684 EF5161
EF494368.1 gg_id:225293 Nunnock River granitic landscape clone NR.1.042 EF4943
EF018351.1 gg_id:209415 aspen rhizosphere clone Amb_16S_723 EF0183
EF494344.1 gg_id:220327 Nunnock River granitic landscape clone NR.1.077 EF4943
DQ066994.1 gg_id:136128 Lake Washington sediment clone pLW-64 DQ066

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AY963419.1 gg_id:156406 structures and correlated ecological factors soils two evergreen broad-leaved forests AY9634
AY963359.1 gg_id:151094 structures and correlated ecological factors soils two evergreen broad-leaved forests AY9633
EU491161.1 gg_id:272414 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak EU491
GQ263191.1 gg_id:577141 Structure Simulated Level Waste Site simulated level waste site clone F3_152X GQ263
EF018769.1 gg_id:211221 aspen rhizosphere clone Amb_16S_1230 EF0187
AY913237.1 gg_id:113212 forest soil clone DUNssu016 (+1B) (OTU#120) AY9132
EU665077.1 gg_id:545745 Soil are Changed Agricultural Practices agricultural soil clone Plot22-H02 EU6650
EU132291.1 gg_id:254271 tallgrass prarie soil clone FFCH4169 EU1322
EF020317.1 gg_id:204462 aspen rhizosphere clone Elev_16S_1890 EF0203
EF688388.1 gg_id:245809 soil clone F6-128 EF6883
AY963374.1 gg_id:151872 structures and correlated ecological factors soils two evergreen broad-leaved forests AY9633
EU335292.1 gg_id:250451 Changes microbial metabolic and along hydrogeochemically variable profile unsatura EU3352
EU881304.1 gg_id:305083 (maize-sweet cropping field) Karst region maize-sweet potato cropland soil clone KM EU8813
AY913231.1 gg_id:113763 forest soil clone DUNssu010 (+1B) (OTU#116) AY9132
EF492904.1 gg_id:254383 Iron-manganese Nodule and Its Surrounding Soil soil around iron-manganese nodule EF4929
AY118153.1 gg_id:60816 anaerobic benzene-degrading clone Cart-N4 AY1181
EF516655.1 gg_id:221341 grassland soil clone FCPU664 EF5166
AM162427.1 gg_id:151955 and situ identification acidic sphagnum peat bog clone B22 AM162
AB234235.1 gg_id:145554 Biotransformation Polychlorinated Dioxins Microbial Dynamics Sediment Microcosm AB2342
AB426196.1 gg_id:274878 -situ identification study benzene-degrading s under methanogenic condition anaerc AB4261
EU132276.1 gg_id:253770 tallgrass prarie soil clone FFCH2719 EU1322
AY963303.1 gg_id:153327 structures and correlated ecological factors soils two evergreen broad-leaved forests AY9633
EU881313.1 gg_id:339795 (maize-sweet cropping field) Karst region maize-sweet potato cropland soil clone KM EU8813
AY555784.1 gg_id:101141 Bor Khlueng hot spring clone PK34 AY5557
AJ519364.1 gg_id:75894 uranium mining waste pile near Johanngeorgenstadt soil clone JG37-AG-5 AJ5193
AJ617858.1 gg_id:110291 oxic-anoxic interphase flooded paddy soil clone D282110 AJ6178
EU404033.1 gg_id:313796 Microbial septic tank effluent and soil biozone infiltrative surface clean water clone ( EU4040
FJ197547.1 gg_id:310970 deep Pacific Ocean and Eastern Mediterranean Sea sediment clone ALVIN29a_4C_ FL FJ1975
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EF018300.1 gg_id:212449 aspen rhizosphere clone Amb_16S_662 EF0183
DQ328617.1 gg_id:145959 microorganisms populating site extreme acid mine drainage sediment clone H5 DQ328
AY963324.1 gg_id:156453 structures and correlated ecological factors soils two evergreen broad-leaved forests AY9633
EF516650.1 gg_id:222943 grassland soil clone FCPP504 EF5166
AB369160.1 gg_id:241567 Microbiological Assessment Circulation Mud Fluids During First Operation Drilling De AB3691
FJ625319.1 gg_id:570620 Influence lead contamination on boreal pine forest soil clone HF_M_16 FJ6253
DQ129640.1 gg_id:137789 microarray level air two cities Texas urban aerosol clone AKIW863 DQ129
EU780449.1 gg_id:316355 modern freshwater stromatolites Ruidera Pools Natural Park Spain dry stromatolite ( EU7804
EF494361.1 gg_id:223616 Nunnock River granitic landscape clone NR.1.005 EF4943
GU183624.1 gg_id:557366 Structures Reduced and Oxidized Aquifer lower Aqueous Arsenic Titas Bangladesh a GU183
AM997648.1 gg_id:542627 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A AM997

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AY225643.1 gg_id:96804 Mid-Atlantic Ridge hydrothermal sediment clone AT-s3-37 AY2256
AM040133.1 gg_id:149857 sandy sediments clone Sylt 37 AM040
DQ070820.1 gg_id:149756 Prokaryotic Structures Seafloor Basalts Varying Age East Pacific Rise and Ridge basal DQ070
GQ246348.1 gg_id:535475 Temporal and spatial China North Yel Sea sediments clone Cm1-11 GQ246
EU734999.1 gg_id:311554 assemblages sediment station DBSE Northern Bering Sea clone 093B48 EU7349
EU491394.1 gg_id:259756 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X3 clone EU4913
EU652606.1 gg_id:279002 Seasonal variation microbial Yel Sea sediment clone D8S-76 EU6526
FJ205208.1 gg_id:574895 Prokaryotic deep-sea region East Lau Spreading Centre inactive hydrothermal field se FJ2052
FJ358923.1 gg_id:550228 and redox-stratified sediments marine reef sandy sediment clone SO13 FJ3589
EF125465.1 gg_id:187788 mangrove soil clone MSB-2Y4 EF1254
AJ241003.1 gg_id:1702 Norway:(Svalbard)Hornsund clone Sva0725 AJ2410
EU287099.1 gg_id:251889 Pacific arctic surface sediment clone P13-6 EU2870
GQ984352.1 gg_id:590289 surface water Northern Bering Sea clone DBS1g27 GQ984
GU369908.1 gg_id:532228 and mats vents Arc white microbial film on pebble aphotic zone shal hydrothermal v GU369
EU734944.1 gg_id:320242 assemblages sediment station DBSE Northern Bering Sea clone 036C37 EU7349
EU132194.1 gg_id:255963 tallgrass prarie soil clone FFCH12382 EU1321
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AY703465.1 gg_id:139386 Detection and ly acidobacterial analyses Altamira Cave clone ALT41 AY7034
EF516971.1 gg_id:223577 grassland soil clone FCPU401 EF5169
FJ444736.1 gg_id:588064 Cotton Rhizosphere cotton rhizosphere clone 4h-60 FJ4447
EF516941.1 gg_id:223804 grassland soil clone FCPP416 EF5169
AY921811.1 gg_id:113092 farm soil clone AKYG1685 AY9218
EF516929.1 gg_id:224421 grassland soil clone FCPO720 EF5169
FJ269289.1 gg_id:568362 Microbes marine sponges sponge tissue clone XA3A05F FJ2692
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FJ269329.1 gg_id:585767 Microbes marine sponges sponge tissue clone XB3C09F FJ2693
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FJ269338.1 gg_id:576211 Microbes marine sponges sponge tissue clone XB3A12F FJ2693
DQ070804.1 gg_id:147802 Prokaryotic Structures Seafloor Basalts Varying Age and Juan de Fuca Ridge basalt gl DQ070
EU491423.1 gg_id:259892 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X4 clone EU4914
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EU735010.1 gg_id:328268 assemblages sediment station DBSE Northern Bering Sea clone 106A42 EU735
EF125415.1 gg_id:185747 soil naked tidal flat sediment near mangrove clone MSB-1F2 EF1254
GU454881.1 gg_id:522212 Understanding short-chain fatty acids accumulation enhanced alkaline digestion: kir GU454
FJ437927.1 gg_id:543301 Benthic okenone production Fayetteville New York Green Lake surface sediments 16. FJ4379
EU755076.1 gg_id:351025 and Dioxygenase Genes Coal Tar Contaminated Soils coal tar-contaminated soil clon EU755
EF020070.1 gg_id:213078 aspen rhizosphere clone Elev_16S_1477 EF020
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EU132115.1 gg_id:241435 tallgrass prarie soil clone FFCH1005 EU132
EF092234.1 gg_id:264224 Persistent Axinella corrugata Geobacter clone B2706_E4 EF0922
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FJ358922.1 gg_id:594049 and redox-stratified sediments marine reef sandy sediment clone AO15 FJ3589
EU735636.1 gg_id:326715 archaeal structures and pristine soils China oil contaminated soil Jidong Oilfield clone EU735
AM259858.1 gg_id:204709 Spatial sponge- Mediterranean Tethya aurantium sponge cortex clone TAA-10-23 AM259
AF385537.1 gg_id:73910 swab advanced noma lesion clone CA002 AF385
DQ833472.1 gg_id:169792 detected analyses depth sediment Guanting Reservoir clone 5-38 DQ833
EU528207.1 gg_id:286946 Seasonal Dynamics Mudflat Mouth Major Kentucky Lake Reservoir Tributary sedime EU528
DQ129284.1 gg_id:137747 microarray level air two cities Texas urban aerosol clone AKIW896 DQ129
EU133029.1 gg_id:249727 tallgrass prarie soil clone FFCH18764 EU133
FJ478643.1 gg_id:581307 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4786
FJ479273.1 gg_id:591093 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4792
GQ263231.1 gg_id:574576 Structure Simulated Level Waste Site simulated level waste site clone F3_41X GQ263
EU132594.1 gg_id:253941 tallgrass prarie soil clone FFCH10110 EU132
EU133117.1 gg_id:237496 tallgrass prarie soil clone FFCH5344 EU133
EU132829.1 gg_id:253573 tallgrass prarie soil clone FFCH13720 EU132
AY093463.1 gg_id:55589 deep marine sediment clone MB-A2-108 AY093
EF018262.1 gg_id:215928 aspen rhizosphere clone Amb_16S_619 EF0182
EF516773.1 gg_id:224718 grassland soil clone FCPT593 EF5167
AJ863190.1 gg_id:121375 poplar tree microcosm bulk soil unflooded clone 20BSU18 AJ8631
AB486164.1 gg_id:532857 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC AB486
DQ067014.1 gg_id:128299 Lake Washington sediment clone pLW-76 DQ067
FJ479558.1 gg_id:577549 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4795
EU133207.1 gg_id:236133 tallgrass prarie soil clone FFCH8340 EU133
FJ479097.1 gg_id:545487 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4790
FJ478871.1 gg_id:513347 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4788
EU132575.1 gg_id:238110 tallgrass prarie soil clone FFCH10523 EU132
GQ263065.1 gg_id:547749 Structure Simulated Level Waste Site simulated level waste site clone F2_188X GQ263

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FJ444654.1 gg_id:577683 Cotton Rhizosphere cotton rhizosphere clone 2h-26 FJ4446
EU132482.1 gg_id:248375 tallgrass prarie soil clone FFCH5992 EU1324
U75647.1 gg_id:11419 Acidimicrobium ferrooxidans U7564
EF621760.1 gg_id:240050 Acidimicrobium ferrooxidans str. TH3 EF6217
AF251436.2 gg_id:37993 Ferrimicrobium acidiphilum str. T23 AF2514
GQ402621.1 gg_id:540625 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
GQ402557.1 gg_id:582560 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
X92698.1 gg_id:11631 peat bog clone TM112 X92698
X92710.1 gg_id:11426 peat bog clone TM262 X92710
AJ290022.1 gg_id:39131 Germany: Lake Fuchskuhle south basin clone FukuS5 FukuS5 AJ2900
AB254795.1 gg_id:160047 Biogenic Fe-oxyhydroxides nodules (takashikozo) encrusted iron-oxide reducing sedi AB2547
X92702.1 gg_id:11632 peat bog clone TM187 X92702
EU370318.1 gg_id:360360 structure photosynthetic complex biofilm acidophilic streams Rio Tinto (SW Spain) e EU3703
X92701.1 gg_id:13505 peat bog clone TM177 X92701
AY792236.1 gg_id:128358 Temporal Variation and Humic Lake clone CrystalBog2A8 AY7922
X92700.1 gg_id:11536 peat bog clone TM167 X92700
EU372631.1 gg_id:548811 Evaluation Leptospirillum spp. Rio Tinto basin model interest biohydrometallurgy se EU3726
EU370302.1 gg_id:357619 structure photosynthetic complex biofilm acidophilic streams Rio Tinto (SW Spain) e EU3703
AM936856.1 gg_id:573254 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM936
AY913578.1 gg_id:113656 forest soil clone DUNssu437 (-7A) (OTU#187) AY9135
X92703.1 gg_id:11394 peat bog clone TM208 X92703
EF019399.1 gg_id:207124 aspen rhizosphere clone Elev_16S_634 EF0193
GQ060701.1 gg_id:434040 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw04d05 GQ060
AJ347027.1 gg_id:56660 sponge clone TK14 AJ3470
AY093455.1 gg_id:63126 marine sediment clone MB-A2-100 AY0934
FJ674692.1 gg_id:509223 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface FJ6746
DQ906064.1 gg_id:225385 nickel resistance genes metagenome Tinto River rhizosphere clone ERF-B9 DQ906
DQ450881.1 gg_id:156584 acidophile waste ore deposits acid mine drainage site clone S5 DQ450
GQ487905.1 gg_id:582749 Microbial metal soil polluted heavy metals clone T1-39 GQ487
EU050926.1 gg_id:254366 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_04_15 EU0509
AF454307.1 gg_id:56545 actinobacterium clone ML817J-10 AF4543
DQ458034.1 gg_id:157830 acid mine drainage clone DX65 DQ458
EF516779.1 gg_id:225319 grassland soil clone FCPP721 EF5167
GU168002.1 gg_id:578668 Iron Oxidizing Various Sulfidic Mine Waste Dumps heap soil GU168
X92708.1 gg_id:11397 peat bog clone TM226 X92708
EU370274.1 gg_id:364140 structure photosynthetic complex biofilm acidophilic streams Rio Tinto (SW Spain) e EU3702
AM749756.1 gg_id:249582 Isolation ing candidate division soils New Zealand steam-affected geothermal soil cl AM749
EU340182.1 gg_id:251247 on Aquatic Macrophytes Geothermally Active Area Sedge Bay Yellowstone Lake WY EU3401
FJ152940.1 gg_id:328654 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX4C FJ1529
FJ466121.1 gg_id:557394 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea FJ4661

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GQ225722.1 gg_id:573091 Acidophilic acidic coal spoil clone BC10 GQ225
AB254796.1 gg_id:159923 Biogenic Fe-oxyhydroxides nodules (takashikozo) encrusted iron-oxide reducing sedi AB254
EF613015.1 gg_id:235014 acid mine drainage clone YSK16S-52 EF6130
DQ906055.1 gg_id:217588 nickel resistance genes metagenome Tinto River rhizosphere clone ERF-1C5 DQ906
AM749739.1 gg_id:236029 Isolation ing candidate division soils New Zealand steam-affected geothermal soil cl AM749
EU287048.1 gg_id:237721 Pacific arctic surface sediment clone B78-84 EU2870
AM889149.1 gg_id:532624 structure superficial sediments Bizerte (Tunisia) southern Mediterranean coastal an AM889
EU491799.1 gg_id:266217 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU4917
X92705.1 gg_id:11396 peat bog clone TM213 X92705
FJ592827.1 gg_id:559669 Fumarole-supported islands biodiversity within hyperarid -elevation landscape on Pu FJ5928
AM749755.1 gg_id:253790 Isolation ing candidate division soils New Zealand steam-affected geothermal soil cl AM749
GQ263011.1 gg_id:590427 Structure Simulated Level Waste Site simulated level waste site clone F2_135X GQ263
DQ906070.1 gg_id:221609 nickel resistance genes metagenome Tinto River rhizosphere clone ERF-D12 DQ906
GU167995.1 gg_id:562452 Iron Oxidizing Various Sulfidic Mine Waste Dumps heap soil GU167
EF127609.1 gg_id:209725 Fossil Genes and Microbes Entombed Oldest Ice on Earth ice clone DLE037 EF1276
DQ906083.1 gg_id:222011 nickel resistance genes metagenome Tinto River rhizosphere clone ERF-H10 DQ906
EF464627.1 gg_id:215003 Identification sulfate reducing methylmercury contaminated SSU genes gold mine tai EF4646
DQ451514.1 gg_id:156655 forest soil clone FAC75 DQ451
GQ402597.1 gg_id:569556 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
DQ316372.2 gg_id:151098 and seasonal dynamics Actinobacteria four lakes Northeastern Germany freshwater DQ316
EU236409.1 gg_id:289344 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg92E9 EU2364
EU117171.1 gg_id:250067 Scratching surface rare biosphere tag primers recent progress made toward microbi EU1171
AM936079.1 gg_id:562332 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM936
AM935566.1 gg_id:536920 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM935
EF516519.1 gg_id:223441 grassland soil clone FCPS579 EF5165
EF409867.1 gg_id:211564 acid mine drainage clone YSK21-06 EF4098
AF047642.1 gg_id:11393 acid mine drainage clone TRA2-10 AF0476
EU133154.1 gg_id:256166 tallgrass prarie soil clone FFCH677 EU1331
FJ478790.1 gg_id:539421 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4787
AY395429.1 gg_id:102636 pasture soil clone EB1110 AY3954
EU491711.1 gg_id:265696 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU4917
GQ402759.1 gg_id:590637 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
GQ225721.1 gg_id:582989 Acidithiomicrobium sp. str. P2 GQ225
AF523913.1 gg_id:63307 forested wetland clone RCP2-105 AF5239
FJ479261.1 gg_id:556910 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4792
AJ347031.1 gg_id:60177 sponge clone TK39 AJ3470
AJ581605.1 gg_id:94227 soil near uranium mill tailings clone KCM-B-10 AJ5816
DQ458030.1 gg_id:157129 acid mine drainage clone DX38 DQ458
EU286995.1 gg_id:251178 Pacific arctic surface sediment clone B78-31 EU2869

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EU132486.1 gg_id:254897 tallgrass prarie soil clone FFCH10951 EU1324
AJ241005.1 gg_id:11418 marine sediment clone Sva0996 AJ2410
DQ521532.1 gg_id:174445 Antarctic lake ice cover clone ANTLV2_H11 DQ521
AM259924.1 gg_id:245061 Chondrilla nucula-specific sponge mesohyl clone CN81 AM259
GQ094396.1 gg_id:410072 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ094
FJ478712.1 gg_id:548077 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4787
EU491192.1 gg_id:260851 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak EU491
FJ592832.1 gg_id:562817 Fumarole-supported islands biodiversity within hyperarid -elevation landscape on Pu FJ5928
GU167997.1 gg_id:575724 Iron Oxidizing Various Sulfidic Mine Waste Dumps heap soil GU167
DQ906077.1 gg_id:221218 nickel resistance genes metagenome Tinto River rhizosphere clone ERF-F5 DQ906
AB254776.1 gg_id:160500 Biogenic Fe-oxyhydroxides nodules (takashikozo) encrusted iron-oxide reducing sedi AB254
EF516392.1 gg_id:225849 grassland soil clone FCPT402 EF5163
EU440648.1 gg_id:564553 Soil are Changed Agricultural Practices agricultural soil clone Plot17-A07 EU440
EU419132.1 gg_id:269564 Microbial and ecology selected andesitic hydrothermal acidic hydrothermally modifi EU419
EU440646.1 gg_id:538728 Soil are Changed Agricultural Practices agricultural soil clone Plot17-2B10 EU440
X92695.1 gg_id:11399 peat bog clone TM56 X92695
DQ814564.1 gg_id:167937 zebrafish digestive tract clone aaa31f03 DQ814
FJ477629.1 gg_id:512880 gut symbionts are tightly linked herbivory ants whole extracted single ant clone 98I FJ4776
AY882848.2 gg_id:111607 hot spring clone SK299 AY8828
DQ451513.1 gg_id:156849 forest soil clone FAC74 DQ451
AJ581606.1 gg_id:94128 soil near uranium mill tailings clone KCM-B-37 AJ5816
GQ246415.1 gg_id:592877 Temporal and spatial China North Yel Sea sediments clone Ld1-20 GQ246
FJ543054.1 gg_id:518645 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone B FJ5430
EF157185.1 gg_id:238707 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon EF1571
EU369127.1 gg_id:315138 libraries oyster shell clone MBIOS-11 EU369
AM936704.1 gg_id:573814 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM936
DQ129383.1 gg_id:138117 microarray level air two cities Texas urban aerosol clone AKIW874 DQ129
AM936076.1 gg_id:535146 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM936
AM936378.1 gg_id:558057 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM936
FJ479385.1 gg_id:534888 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4793
AM936749.1 gg_id:535040 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM936
AM936452.1 gg_id:564695 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM936
AM936677.1 gg_id:537218 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM936
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AM935941.1 gg_id:575680 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM935
AM936815.1 gg_id:537760 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM936
AM935557.1 gg_id:536057 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM935
EU133198.1 gg_id:252462 tallgrass prarie soil clone FFCH8237 EU1331
AM936649.1 gg_id:542020 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM936

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FJ670881.1 gg_id:525442 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6708
FJ479142.1 gg_id:574692 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4791
EU132696.1 gg_id:254130 tallgrass prarie soil clone FFCH11231 EU1326
GQ093936.1 gg_id:424457 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ093
DQ521525.1 gg_id:197548 Antarctic lake ice cover clone ANTLV2_G03 DQ521
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EU803985.1 gg_id:310703 It's all ranking aquatic Lake Gatun clone 5C231663 EU8039
DQ316378.2 gg_id:153262 and seasonal dynamics Actinobacteria four lakes Northeastern Germany freshwater DQ316
GQ340246.1 gg_id:534170 Prokaryotic Marathonas Reservoir Greece water column clone VE07-96-BAC GQ340
AY921917.1 gg_id:113190 farm soil clone AKYH901 AY9219
EU236418.1 gg_id:298250 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg92G4 EU2364
GQ850547.1 gg_id:563246 surface water northern Bering Sea clone u72 GQ850
AJ863196.1 gg_id:125157 poplar tree microcosm bulk soil unflooded clone 20BSU6 AJ8631
DQ463715.2 gg_id:169756 distinct Lake Tanganyika oxic epilimnion clone TK-SE2 DQ463
DQ316383.2 gg_id:156257 and seasonal dynamics Actinobacteria four lakes Northeastern Germany freshwater DQ316
GU118194.1 gg_id:590548 Threatened Corals Provide Microbial Habitats clone Dstr_N17 GU118
GQ396937.1 gg_id:575662 Functional unvegetated perhumid recently-deglaciated soils do not correlate shifts s GQ396
FJ827859.1 gg_id:548521 Seasonal nutrient additions eutrophic integrated lake epilimnion clone ME002B4 FJ8278
DQ316381.2 gg_id:150770 and seasonal dynamics Actinobacteria four lakes Northeastern Germany freshwater DQ316
EU132614.1 gg_id:244549 tallgrass prarie soil clone FFCH10283 EU1326
DQ316363.2 gg_id:155077 and seasonal dynamics Actinobacteria four lakes Northeastern Germany freshwater DQ316
AF418962.1 gg_id:39516 USA: Colorado Fort collins Horsetooth Reservoir clone HTG5 AF4189
EU234292.1 gg_id:253600 penicillin G production wastewater receiving river and un techniques upstream Wan EU2342
EU801921.1 gg_id:324132 It's all ranking aquatic Chesapeake Bay MD clone 3C003302 EU8019
EU592386.1 gg_id:592515 Seasonal changes Salton Sea hypersaline water clone SSW178N EU5923
EU234258.1 gg_id:237217 river and un techniques downstream Wang Yang River receiving penicillin G producti EU2342
EU803621.1 gg_id:346911 It's all ranking aquatic Lake Gatun clone 5C231220 EU8036
EU703218.1 gg_id:392975 lakes on Eastern Tin Plateau oligosaline lake altitude 4718 masl clone XZNMC66 EU7032
AB491851.1 gg_id:554927 affiliation (Litopenaeus vannamei) Banyuwangi East Java microbial flocs floating brac AB4918
EU528238.1 gg_id:282746 Seasonal Dynamics Mudflat Mouth Major Kentucky Lake Reservoir Tributary sedime EU5282
AY921723.1 gg_id:113149 farm soil clone AKYG1901 AY9217
FJ152677.1 gg_id:354357 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX1A_ FJ1526
EF019264.1 gg_id:211255 aspen rhizosphere clone Elev_16S_446 EF0192
GQ021461.1 gg_id:488207 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbu27 GQ021
AJ575535.1 gg_id:98733 freshwater clone NM2 AJ5755
GQ016492.1 gg_id:493175 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ016
FJ827871.1 gg_id:550926 Seasonal nutrient additions eutrophic integrated lake epilimnion clone ME012F1 FJ8278
GU119245.1 gg_id:548930 Threatened Corals Provide Microbial Habitats reef water clone Reef_K06 GU119
DQ520183.1 gg_id:161639 shal China sequences hypertrophic freshwater lake clone ML-7-116.2 DQ520

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GQ340213.1 gg_id:584272 Prokaryotic Marathonas Reservoir Greece water column clone VE07-28-BAC GQ340
EU132590.1 gg_id:255512 tallgrass prarie soil clone FFCH1008 EU132
EU132666.1 gg_id:257176 tallgrass prarie soil clone FFCH1091 EU132
EU340186.1 gg_id:256498 on Aquatic Macrophytes Geothermally Active Area Sedge Bay Yellowstone Lake WY EU340
EF516030.1 gg_id:222035 grassland soil clone FCPT456 EF516
AM935299.1 gg_id:542933 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM935
EU132977.1 gg_id:255449 tallgrass prarie soil clone FFCH17424 EU132
EF019232.1 gg_id:207912 aspen rhizosphere clone Elev_16S_404 EF0192
EU925881.1 gg_id:350536 sediments sediment station DBS1 northern Bering Sea clone 087F85 EU925
AM935740.1 gg_id:559985 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM935
FJ478803.1 gg_id:584385 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4788
EU132782.1 gg_id:235653 tallgrass prarie soil clone FFCH12764 EU132
AY221045.1 gg_id:84258 Mammoth cave clone CCM13a AY221
EF516604.1 gg_id:218712 grassland soil clone FCPO472 EF5166
DQ316376.2 gg_id:155271 and seasonal dynamics Actinobacteria four lakes Northeastern Germany freshwater DQ316
EF516535.1 gg_id:219570 grassland soil clone FCPS488 EF5165
AY395413.1 gg_id:105527 pasture soil clone EB1094 AY3954
EF019813.1 gg_id:213344 aspen rhizosphere clone Elev_16S_1157 EF0198
DQ128808.2 gg_id:180978 no tillage soil clone HSB NT53_D06 DQ128
FJ478634.1 gg_id:562659 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4786
EU335429.1 gg_id:251886 Changes microbial metabolic and along hydrogeochemically variable profile unsatura EU335
EU335147.1 gg_id:243610 Changes microbial metabolic and along hydrogeochemically variable profile saturate EU335
AB487439.1 gg_id:559205 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNIR0 AB487
DQ395955.1 gg_id:152101 deep-sea octacoral clone ctg_CGOGA19 DQ395
EF157223.1 gg_id:257150 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon EF1572
AM935802.1 gg_id:543152 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM935
EU440650.1 gg_id:537124 Soil are Changed Agricultural Practices agricultural soil clone Plot17-H03 EU440
AJ581630.1 gg_id:93175 soil near uranium mill tailings clone KCM-C-53 AJ5816
FM209069.1 gg_id:533501 Dynamics during identified and SSU libraries pilot-scale bioremediation process hydr FM209
AB360448.1 gg_id:265034 Iamibacter majanohamensis str. NBRC 102561 AB360
GQ500878.1 gg_id:593462 Surveys Biofilms and Sediments Mammoth Karst Aquifers Bio-Sep beads containing GQ500
CU466698.1 gg_id:342630 Evry wastewater treatment plant anoxic basin clone CU466
EU133138.1 gg_id:244545 tallgrass prarie soil clone FFCH604 EU133
AY102341.1 gg_id:65445 heavy metal-contaminated soil clone a13156 AY1023
AM935499.1 gg_id:548072 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM935
FJ478585.1 gg_id:512041 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4785
AY921951.1 gg_id:113885 farm soil clone AKYG1106 AY9219
EF020060.1 gg_id:217034 aspen rhizosphere clone Elev_16S_1467 EF0200
AY234598.1 gg_id:112160 soil isolate Ellin5247 AY2345
EU669633.1 gg_id:333608 soil clone S1-9 EU669

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AY921962.1 gg_id:113586 farm soil clone AKYG1583 AY9219
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FJ999602.1 gg_id:389275 sponge Haliclona simulans South China Sea clone B55 FJ9996
FJ202465.1 gg_id:335185 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2024
AM911370.1 gg_id:369680 Phenotype-specific (Scleractinia) their implications coral's nutrition health and cold- AM911
DQ070822.1 gg_id:146815 Prokaryotic Structures Seafloor Basalts Varying Age East Pacific Rise and Ridge basal DQ070
AB476265.1 gg_id:574727 Compositional and functional transition epibiotic microbial hydrothermal vent galath AB476
FN424398.1 gg_id:576054 structure sediments Bizerte (Tunisia) southern Mediterranean coastal anthropized la FN4243
GU118878.1 gg_id:542569 Threatened Corals Provide Microbial Habitats clone Past_I10 GU118
DQ270650.1 gg_id:142032 hydrothermal carbonate chimney clone LC1228B-35 DQ270
EU491619.1 gg_id:264768 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU491
CU917839.1 gg_id:546297 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU917
AB286641.1 gg_id:210507 Reducing production and domination comamonadaceae reducing oxygen supply was AB286
CU466705.1 gg_id:331084 Evry wastewater treatment plant anoxic basin clone CU466
DQ316384.1 gg_id:151097 and seasonal dynamics Actinobacteria four lakes Northeastern Germany freshwater DQ316
EU488068.1 gg_id:540668 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU488
DQ450797.1 gg_id:160075 Microbial Alpine Tundra Wet Meadow Soil: Chloroflexi Cold Water-Saturated satura DQ450
GQ340284.1 gg_id:591444 Prokaryotic Marathonas Reservoir Greece water column clone B08-103-BAC GQ340
AM176889.1 gg_id:160187 Recovery mangrove sediment clone SZB6 AM176
EF019788.1 gg_id:215846 aspen rhizosphere clone Elev_16S_974 EF0197
FJ356666.1 gg_id:556595 Intra- Microheterogeneity Multiple Displacement Single-cells Marine Cyanobacteria L FJ3566
DQ289932.1 gg_id:172264 Microbial Carbon and Nitrogen Cycling Sediments South Atlantic Bight Permeable Sh DQ289
GU061197.1 gg_id:575752 Evaluation culturing methods cultivate previously Yel Sea intertidal beach surface se GU061
FJ615171.1 gg_id:578870 Microbial dynamics seasonally fjord: British Columbia Saanich Inlet depth 10m anoxic FJ6151
FJ529346.1 gg_id:573369 Evidence vertical transmission symbionts adult embryo Caribbean sponge Svenzea ze FJ5293
FJ229956.1 gg_id:566439 Microbes marine sponges Indonesia: Manado clone XC1C08 FJ2299
FJ229949.1 gg_id:575087 Microbes marine sponges USA: Key Largo Florida clone XB3E12F FJ2299
AJ347026.1 gg_id:60183 sponge clone TK06 AJ3470
AF317769.1 gg_id:136346 Nullarbor cave clone wb1_P06 AF3177
FJ203303.1 gg_id:331758 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c FJ2033
EU491133.1 gg_id:276243 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak EU491
DQ070807.1 gg_id:148554 Prokaryotic Structures Seafloor Basalts Varying Age and Juan de Fuca Ridge basalt gl DQ070
FJ203322.1 gg_id:344834 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c FJ2033
GU369911.1 gg_id:521448 and mats vents Arc white microbial film on pebble aphotic zone shal hydrothermal v GU369
FJ203655.1 gg_id:315494 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h FJ2036
EU374087.1 gg_id:272708 southern Cretan margin (eastern Mediterranean Sea) canyon and slope sediment clc EU3740
GQ350187.1 gg_id:550067 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ350
AF382122.1 gg_id:79134 bacterioplankton clone ZA3409c AF3821

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GQ348064.1 gg_id:556769 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ348
DQ009431.1 gg_id:119667 bacterioplankton clone SPOTSFEB02_70m35 DQ009
GQ351092.1 gg_id:548197 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ351
GQ347207.1 gg_id:563738 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ347
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GQ350379.1 gg_id:543378 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ350
GQ346944.1 gg_id:577150 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ346
GQ350844.1 gg_id:535697 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ350
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GQ348458.1 gg_id:534913 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ348
AF382139.1 gg_id:100695 bacterioplankton clone ZA3635c AF382
GU061498.1 gg_id:589639 and function microbial mesoscale eddy perturbations South China Sea clone CE1-DC GU061
GQ350624.1 gg_id:581082 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ350
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GQ340205.1 gg_id:588079 Prokaryotic Marathonas Reservoir Greece water column clone VE07-10-BAC GQ340
GQ340275.1 gg_id:585868 Prokaryotic Marathonas Reservoir Greece water column clone A08-156-BAC GQ340
GQ340192.1 gg_id:548098 Prokaryotic Marathonas Reservoir Greece water column clone K07-91-BAC GQ340
EU117943.1 gg_id:239240 Ecology Freshwater Actinobacteria acI Lineage lake epilimnion clone TR1C3 EU117
DQ316345.1 gg_id:153606 and seasonal dynamics Actinobacteria four lakes Northeastern Germany freshwater DQ316
AY792229.1 gg_id:123628 Humic Lake clone CrystalBog022E4 AY792
AJ575546.1 gg_id:97083 freshwater clone SW1 AJ5755
EU803672.1 gg_id:323127 It's all ranking aquatic Lake Gatun clone 5C231277 EU803
EU117813.1 gg_id:241892 Ecology Freshwater Actinobacteria acI Lineage lake epilimnion clone LT1A9 EU117
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AY863101.1 gg_id:111721 wastewater treatment pool clone SXAU070 AY863
EU117607.1 gg_id:255862 Ecology Freshwater Actinobacteria acI Lineage lake epilimnion clone CH1B9 EU117
GU305764.1 gg_id:555795 Research on changes structure during algae outbreak oligotrophic lakes (YangHe res GU305

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EU800635.1 gg_id:322266 It's all ranking aquatic Delaware Bay NJ clone 2C228795 EU800
EU117835.1 gg_id:255319 Ecology Freshwater Actinobacteria acI Lineage lake epilimnion clone LT1E10 EU1178
GQ020257.1 gg_id:489410 Topographical and Temporal Human Skin Microbiome skin glabella clone nbu266d07 GQ020
EU117736.1 gg_id:235280 Ecology Freshwater Actinobacteria acI Lineage lake epilimnion clone IW1D3 EU117
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EU117793.1 gg_id:242895 Ecology Freshwater Actinobacteria acI Lineage lake epilimnion clone LA1D3 EU117
EU117597.1 gg_id:243443 Ecology Freshwater Actinobacteria acI Lineage lake epilimnion clone CL1D8 EU1175
EU117981.1 gg_id:254057 Ecology Freshwater Actinobacteria acI Lineage lake epilimnion clone TW1D9 EU1179
AJ575555.1 gg_id:97386 freshwater clone NO1 AJ5755
AY792226.1 gg_id:120109 Humic Lake clone CrystalBog1D1 AY792
EU803598.1 gg_id:347586 It's all ranking aquatic Lake Gatun clone 5C231197 EU8035
EU735737.1 gg_id:352333 Biological Arsenic Remediation Project Groundwater Aquifer soil clone C_M47 EU735
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AJ575513.1 gg_id:96722 freshwater clone S12 AJ5755
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DQ316343.2 gg_id:153128 and seasonal dynamics Actinobacteria four lakes Northeastern Germany freshwater DQ316
EU117975.1 gg_id:236670 Ecology Freshwater Actinobacteria acI Lineage lake epilimnion clone TW1B9 EU1179
EU117634.1 gg_id:251604 Ecology Freshwater Actinobacteria acI Lineage lake epilimnion clone CB7E2 EU1176
EU801039.1 gg_id:331093 It's all ranking aquatic Delaware Bay NJ clone 2C229336 EU801
EU117886.1 gg_id:235511 Ecology Freshwater Actinobacteria acI Lineage lake epilimnion clone RC1A7 EU1178
EU117746.1 gg_id:247629 Ecology Freshwater Actinobacteria acI Lineage lake epilimnion clone IW1G7 EU117
AF418967.1 gg_id:30680 USA: Colorado Fort collins Horsetooth Reservoir clone HT2E3 AF4189
EU117775.1 gg_id:239896 Ecology Freshwater Actinobacteria acI Lineage lake epilimnion clone ME7F6 EU117
DQ316346.1 gg_id:151307 and seasonal dynamics Actinobacteria four lakes Northeastern Germany freshwater DQ316
EU117689.1 gg_id:244911 Ecology Freshwater Actinobacteria acI Lineage lake epilimnion clone GR1A4 EU1176
GU305811.1 gg_id:557202 Research on changes structure during algae outbreak oligotrophic lakes (YangHe res GU305
EU117655.1 gg_id:257661 Ecology Freshwater Actinobacteria acI Lineage lake epilimnion clone FF1A7 EU1176
EU117873.1 gg_id:255402 Ecology Freshwater Actinobacteria acI Lineage lake epilimnion clone MI1E8 EU1178
EU117795.1 gg_id:246865 Ecology Freshwater Actinobacteria acI Lineage lake epilimnion clone LA1E10 EU117
EU117757.1 gg_id:241264 Ecology Freshwater Actinobacteria acI Lineage lake epilimnion clone JB3G11 EU117
EU117806.1 gg_id:252598 Ecology Freshwater Actinobacteria acI Lineage lake epilimnion clone LA1H10 EU1178
EU801147.1 gg_id:324019 It's all ranking aquatic Delaware Bay NJ clone 2C229494 EU801
EU703381.1 gg_id:431445 lakes on Eastern Tin Plateau freshwater lake altitude 4298 masl clone XZTSH87 EU703
EU117698.1 gg_id:256870 Ecology Freshwater Actinobacteria acI Lineage lake epilimnion clone GR1C5 EU1176
AY792223.1 gg_id:122328 Humic Lake clone CrystalBog5G8 AY792
EU117557.1 gg_id:249857 Ecology Freshwater Actinobacteria acI Lineage lake epilimnion clone BR1A5 EU1175
EU117988.1 gg_id:254459 Ecology Freshwater Actinobacteria acI Lineage lake epilimnion clone TW1H4 EU1179
EU117652.1 gg_id:242933 Ecology Freshwater Actinobacteria acI Lineage lake epilimnion clone FF1A1 EU1176
EU117776.1 gg_id:249545 Ecology Freshwater Actinobacteria acI Lineage lake epilimnion clone ME7G10 EU117
EU234301.1 gg_id:248946 penicillin G production wastewater receiving river and un techniques upstream Wan EU2343

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EU800363.1 gg_id:307023 It's all ranking aquatic Delaware Bay NJ clone 2C228427 EU800
EU803878.1 gg_id:324989 It's all ranking aquatic Lake Gatun clone 5C231522 EU803
EU117741.1 gg_id:253508 Ecology Freshwater Actinobacteria acI Lineage lake epilimnion clone IW1F2 EU117
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FJ711180.1 gg_id:574249 Actinobaculum schaalii str. NML 99A018 FJ7111
NR_028978.1 gg_id:582466 Actinobaculum urinale str. R9242; CCUG 46093 NR_02
AJ276805.1 gg_id:47874 Actinomyces catuli str. CCUG 41709 AJ2768
NR_026181.1 gg_id:547861 Actinomyces denticolens str. NCTC 11490 NR_02
Y08828.1 gg_id:12562 Actinomyces europaeus str. CCUG 32789A Y08828
AF489584.1 gg_id:94067 Actinomyces hyovaginalis str. D3 AF4895
AJ276405.1 gg_id:33765 Actinomyces marimammalium str. CCUG 41710 AJ2764
AY244766.1 gg_id:104354 Actinomyces sp. str. 2002-2301122 AY2447
X78721.1 gg_id:12574 Actinomyces turicensis str. APL11 X78721
X82451.1 gg_id:12571 Actinomyces meyeri str. C.I.P. 103148T X82451
AJ234040.1 gg_id:52899 Actinomyces odontolyticus str. CCUG 20536T AJ2340
GQ048196.1 gg_id:439901 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbu GQ048
GQ074395.1 gg_id:448385 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw162c GQ074
AJ234049.1 gg_id:23267 Actinomyces sp. str. CCUG 33931 AJ2340
X82453.1 gg_id:12545 Actinomyces viscosus str. NCTC 10951 X82453
GQ421314.1 gg_id:542967 Actinomyces oris str. A19A1 GQ421
AF543282.1 gg_id:58296 Actinomyces naeslundii str. ChDC B204 AF5432
FJ823139.1 gg_id:556324 Actinomyces viscosus str. TeTC FJ8231
GQ067994.1 gg_id:397505 Topographical and Temporal Human Skin Microbiome skin alar crease clone nbw145 GQ067
X81062.1 gg_id:12551 Actinomyces naeslundii str. NCTC 10301 X81062
GQ063069.1 gg_id:458238 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ063
NZ_ACUY02000007.1 gg_id:484320 Actinomyces sp. oral taxon 848 str. F0332 NZ_AC
AJ243791.1 gg_id:40580 Actinomyces urogenitalis AJ2437
AJ427451.1 gg_id:82476 Actinomyces vaccimaxillae str. R10176T AJ4274
GQ014220.1 gg_id:495445 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw760c GQ014
AJ271894.1 gg_id:44463 Actinomyces lingnae str. CCUG 32865 AJ2718
NR_028905.1 gg_id:588670 Actinomyces coleocanis str. M343/98/2; CCUG 41708 NR_02
AJ277385.1 gg_id:67513 Actinomyces suimastitidis str. CCUG 39276 AJ2773
FJ393117.1 gg_id:357502 Fusing Biology Engineering Improve Power Output Microbial Fuel Cells microbial fuel FJ3931
AY221601.1 gg_id:90040 metal and hydrocarbon contaminated soil clone HN1-52 AY2216
NR_028960.1 gg_id:541935 Actinomyces funkei str. CCUG 42773 NR_02
X78720.1 gg_id:12567 Actinomyces sp str. APL10 X78720
GQ091902.1 gg_id:389728 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ091
AJ421779.1 gg_id:60136 Actinomyces cardiffensis str. CCUG 44997 AJ4217
AJ243892.1 gg_id:44425 Actinomyces canis AJ2438
AB490162.1 gg_id:560661 Actinomyces sp. str. GTC3949 AB490

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DQ378185.1 gg_id:151007 oil-polluted soil clone F21_Pitesti DQ378
DQ278863.1 gg_id:152869 Actinomyces sp. 152R-3 DQ278
GQ004952.1 gg_id:504710 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu65b0 GQ004
GQ091872.1 gg_id:437735 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ091
FJ542912.1 gg_id:522040 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone A FJ5429
FJ542871.1 gg_id:527314 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone A FJ5428
NR_026182.1 gg_id:561441 Actinomyces georgiae str. DSM 6843 NR_02
DQ378174.1 gg_id:153783 oil-polluted soil clone F09_Pitesti DQ378
AF287750.1 gg_id:29001 Actinomyces sp. oral strain str. B27SC AF287
AF433168.1 gg_id:19270 Actinomyces hongkongensis str. HKU8 AF433
AY207066.1 gg_id:83011 Actinobaculum sp. P1 str. P2P_19 AY207
FJ234422.1 gg_id:545415 Actinomyces naturae sp. nov. able grow presence concentrations chlorinated solvent FJ2344
AJ507295.1 gg_id:58541 Actinomyces oricola str. CCUG 46090 AJ5072
FM873627.1 gg_id:368710 occupant source house mattress dust clone MA01G06 FM873
AJ697609.1 gg_id:109929 Actinomyces dentalis str. R18165 AJ6976
EF558367.1 gg_id:278919 Actinomyces massiliensis str. 4401292 EF5583
GQ010287.1 gg_id:499378 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ010
GU227166.1 gg_id:551431 Microbiological immunological Adolescent Moroccan Aggressive Periodontitis Patier GU227
GQ421317.1 gg_id:593883 Actinomyces oris str. CCUG 33920 GQ421
GU227175.1 gg_id:571103 Microbiological immunological Adolescent Moroccan Aggressive Periodontitis Patier GU227
AB545933.1 gg_id:541516 Actinomyces johnsonii str. JCM 16129 AB5459
AJ234056.1 gg_id:27124 Actinomyces viscosus str. CCUG 35332 AJ2340
AJ243792.1 gg_id:16513 Actinomyces cf. urogenitalis M560/98/1 AJ2437
AJ540309.1 gg_id:79234 Actinomyces graevenitzii str. CCUG 27294 AJ5403
X81061.1 gg_id:12548 Actinomyces bovis str. NCTC 11535 X81061
AJ251986.1 gg_id:26223 Actinomyces radicidentis str. CCUG 36733T AJ2519
GQ073149.1 gg_id:441099 Topographical and Temporal Human Skin Microbiome skin palm clone nbw205f08c1 GQ073
GQ099503.1 gg_id:450107 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw51 GQ099
AJ234066.1 gg_id:40753 Actinomyces slackii str. CCUG 32792 AJ2340
X80414.1 gg_id:12560 Actinomyces gerencseriae str. DSM 6844 X80414
AJ234039.1 gg_id:24150 Actinomyces bowdenii str. M1956/95/1 AJ2340
FM873536.1 gg_id:366843 occupant source house mattress dust clone MA01H12 FM873
AJ234048.1 gg_id:30901 Actinomyces naeslundii str. CCUG 33914 AJ2340
AJ635359.1 gg_id:106166 Actinomyces naeslundii AJ6353
FM873274.1 gg_id:358736 occupant source house floor dust clone FC04H05 FM873
EU484334.1 gg_id:539951 Actinomyces sp. str. 7400942 EU484
X80411.1 gg_id:12558 Actinomyces howellii str. NCTC 11636 X80411
AM696983.1 gg_id:223408 sequencing libraries indoor dust clone BF0001B009 AM696
GQ077230.1 gg_id:416528 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw115 GQ077
AF543286.1 gg_id:58292 Actinomyces viscosus str. ChDC OS34 AF543
GQ017278.1 gg_id:492389 Topographical and Temporal Human Skin Microbiome skin alar crease clone nbu116 GQ017

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| s__Arcanobacterium pluranimalium | 39361 |
| s__Arcanobacterium pyogenes | 38641 |
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AY349363.1 gg_id:92262 human oral cavity clone IO076 AY3493
EU409526.1 gg_id:275066 Arcanobacterium haemolyticum str. 3801 EU4095
EU915469.1 gg_id:309072 Arcanobacterium pluranimalium str. 1128 EU9154
X79224.1 gg_id:12595 Arcanobacterium bernardiae str. LCDC 89/0504 = DSM 9152 X79224
EU267795.1 gg_id:253789 Arcanobacterium pyogenes RY 11-3 EU2677
EU268191.1 gg_id:247375 Arcanobacterium pyogenes HC-H 13-2 EU2681
EU268193.1 gg_id:257909 Arcanobacterium pyogenes HC-H 10 EU2681
EF061225.1 gg_id:192142 Arcanobacterium sp. str. NML 06501 EF0612
EU289136.1 gg_id:239780 microbiome cloacal openings urogenital and anal tracts tammar wallaby Macropus e EU2891
AJ243794.1 gg_id:25077 Arcanobacterium sp. CCUG 41705 AJ2437
AJ879697.1 gg_id:112481 Arcanobacterium sp. 106-04 AJ8796
AJ576076.1 gg_id:94295 Mobiluncus mulieris str. CCUG 22331 AJ5760
EU289072.1 gg_id:258140 microbiome cloacal openings urogenital and anal tracts tammar wallaby Macropus e EU2890
FJ672024.1 gg_id:516662 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6720
CU914909.1 gg_id:384164 and dynamics adapted microbiota during degradation Tunisian zarzatine enriched se CU9149
FJ671401.1 gg_id:517932 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6714
EF419390.1 gg_id:215248 Substantial alterations cutaneous biota psoriatic lesions human skin clone 4P2-49 EF4193
FJ672120.1 gg_id:516856 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6721
FJ671584.1 gg_id:509470 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6715
FJ675566.1 gg_id:524033 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6755
FJ671451.1 gg_id:514203 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6714
EU535629.1 gg_id:285786 profile human microbiota antecubital fossa (inner elbow) skin clone nbt28d02 EU5356
EF063623.1 gg_id:181971 Microbial ecology autotrophic denitrifying anaerobic methanogenic UASB reactor clo EF0636
AB062818.1 gg_id:33488 termite gut homogenate clone BCf3-22 AB0628
NR_026225.1 gg_id:533806 Actinomyces hordeovulneris str. CIP 103149 NR_026
EF688243.1 gg_id:303554 Detection microbial sludge anaerobic wastewater treatment system clone 6B10_con EF6882
AJ508455.1 gg_id:58582 Actinomyces nasicola str. CCUG 46092 AJ5084
AY959048.1 gg_id:131712 Microbes on human vaginal epithelium clone rRNA275 AY9590
FJ169868.1 gg_id:327484 Varibaculum cambriense str. M398 FJ1698
FJ169869.1 gg_id:328472 Varibaculum cambriense str. M380 FJ1698
DQ923134.1 gg_id:181134 Actinopolyspora xinjiangensis str. YIM 90829 DQ923
GQ263862.1 gg_id:574018 Structure Simulated Level Waste Site simulated level waste site clone WC2_107 GQ263
FJ152655.1 gg_id:343126 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX1A_ FJ1526
AY234439.1 gg_id:111971 soil isolate Ellin5022 AY2344
AB048864.1 gg_id:47825 Actinokineospora sp. str. YU 923-201 AB0488
AF114799.1 gg_id:12995 Actinokineospora inagensis str. NRRL B-24050T AF1147
EU570742.1 gg_id:259282 Actinokineospora terrae str. 173846 EU5707
GQ166953.1 gg_id:552367 Amycolatopsis fastidiosa str. LCB1001 GQ166
X84447.1 gg_id:12969 Actinosynnema mirum str. DSM 43827 X84447
D85475.1 gg_id:12986 Actinosynnema mirum str. IFO14064 D85475
AJ512464.1 gg_id:57769 Kibdelosporangium philippinense str. DSM 44226 AJ5124

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| s__Lentzea albidocapillata | 38144 |
| s__Lentzea albidocapillata | 38342 |
| s__Lentzea violacea | 37642 |
| s__Lentzea violacea | 37683 |
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| s__Saccharothrix xinjiangensis | 37993 |
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DQ298331.1 gg_id:155487 studies on and nifH Lasiurus sindicus Sewan grass Thar Desert Rajasthan India rhizos DQ298
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Y09158.1 gg_id:12966 IMSNU 50711T) Y09158
AJ242633.1 gg_id:46572 Lentzea violacea str. LM 036T (=IMSNU 50388T) AJ2426
X84321.1 gg_id:12965 Lentzea albidocapillata str. IMMIB D-958 X84321
AJ242634.1 gg_id:30376 Lentzea violacea str. LM 044 AJ2426
AF183957.4 gg_id:12967 Lentzea flaviverrucosa str. AS4.0578 AF1839
AF183958.1 gg_id:12968 Lentzea flavoverrucoides AF1839
AF114813.1 gg_id:12972 Lentzea waywayandensis str. NRRL B-16159T AF1148
EU593719.1 gg_id:267698 Lentzea violacea str. 174493 EU593
EU570340.1 gg_id:271073 Lentzea sp. str. 173316 EU5703
AB020029.1 gg_id:12982 Lentzea waywayandensis str. JCM 9114 AB0200
AB006176.1 gg_id:12981 Lentzea albida str. IFO16102 AB0061
AF114815.1 gg_id:12970 Saccharothrix texasensis str. NRRL B-16107T AF1148
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EU570355.1 gg_id:276163 Saccharothrix texasensis str. 173789 EU5703
EU593595.1 gg_id:277548 Saccharothrix xinjiangensis str. 173800 EU5935
AF114803.1 gg_id:12960 Saccharothrix australiensis str. NRRL 11239T AF1148
AF114812.1 gg_id:12973 Saccharothrix syringae str. NRRL B-16468T AF1148
X53193.1 gg_id:136685 Saccharothrix australiensis X53193
AB284261.2 gg_id:206788 Actinosynnema violaceoruber str. NBRC 102064 AB2842
GQ917213.1 gg_id:582929 Dactylosporangium variesporum GQ917
AY135693.3 gg_id:60437 Saccharothrix xinjiangensis str. AS 4.1731 AY1356
AF114805.1 gg_id:12963 Saccharothrix coeruleofusca str. NRRL B-16115T AF1148
FJ486394.1 gg_id:560514 Saccharothrix espanaensis str. HBUM174894 FJ4863
AF114807.1 gg_id:12959 Saccharothrix espanaensis str. NRRL 15764T AF1148
EU841603.1 gg_id:306457 Saccharothrix longispora str. HBUM174878 EU8416
AF114809.1 gg_id:12975 Saccharothrix longispora str. NRRL B-116116T AF1148
EU570357.1 gg_id:265885 Saccharothrix longispora str. 173645 EU5703
AB297962.1 gg_id:248764 Streptomyces tenebrarius str. NBRC 16177 AB2979
AF114800.1 gg_id:12978 Actinosynnema subsp. pretiosum str. NRRL B-16060T subsp. AF1148
EU841595.1 gg_id:329490 Lechevalieria aerocolonigenes str. HBUM174553 EU8415
NR_028738.1 gg_id:548297 Lechevalieria aerocolonigenes str. NRRL B-3298 NR_028
EU593584.1 gg_id:272843 Lechevalieria aerocolonigenes str. 173443 EU5935
AJ512462.1 gg_id:57772 Kibdelosporangium albatum str. DSM 44149 AJ5124
EU570361.1 gg_id:259817 Lentzea waywayandensis str. 173621 EU5703
AB020031.1 gg_id:12984 Saccharothrix tangerinus str. MK27-91F2 AB0200
DQ898283.2 gg_id:161869 Lechevalieria xinjiangensis str. R24 DQ898
EU570744.1 gg_id:261512 Lentzea albidocapillata str. 173856 EU5707
AF114808.1 gg_id:12976 Lechevalieria flava str. NRRL B-16131T AF1148

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AB303365.1 gg_id:225758 Actinosynnema subsp. pretiosum str. NBRC 15621 AB3033
DQ298327.1 gg_id:151750 studies on and nifH Lasiurus sindicus Sewan grass Thar Desert Rajasthan India rhizos DQ298
DQ298350.1 gg_id:152567 studies on and nifH Lasiurus sindicus Sewan grass Thar Desert Rajasthan India rhizos DQ298
EU221376.1 gg_id:244196 Salana multivorans str. Y2S8 EU2213
NR_027613.1 gg_id:542896 Beutenbergia cavernae str. HKI 0122; DSM 12333 NR_027
NR_025495.1 gg_id:568991 Salana multivorans str. Se-3111; DSM 13521; NRRL B-24118 NR_025
EU863843.1 gg_id:338853 Georgenia sp. E9 EU8638
X94155.2 gg_id:73976 Georgenia muralis str. 1A-C X94155
EU095256.1 gg_id:241541 Georgenia ferrireducens str. F64 EU0952
AY880044.1 gg_id:111575 Georgenia sp. T04-04 AY8800
FJ671468.1 gg_id:521907 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6714
DQ203185.1 gg_id:139651 Ruania flava str. YIM 004 DQ203
EF601725.1 gg_id:232214 Georgenia deserti str. YIM 80691 EF6017
FJ671531.1 gg_id:511138 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6715
FJ670794.1 gg_id:515169 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6707
FJ672173.1 gg_id:509013 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6721
Y09911.1 gg_id:12542 Bogoriella caseolytica str. HKI0088T Y09911
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AY243343.1 gg_id:107500 Brevibacterium permense str. VKM Ac-2280 AY2433
AM937247.2 gg_id:276481 oligotrophic riverine carrying -cassette capturing genetic devices their genome river AM937
X83813.1 gg_id:12522 Brevibacterium iodinum str. DSM 2062T X83813
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EU086802.1 gg_id:236962 Brevibacterium casei str. 60 EU0868
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AJ488509.2 gg_id:73538 Brevibacterium luteolum str. CF87 AJ4885
AB210987.2 gg_id:145220 Brevibacterium luteolum str. SSCS1-2 AB2109
D88212.1 gg_id:12518 Brevibacterium sp D88212
EU086822.1 gg_id:251743 Brevibacterium otitidis str. G696 EU0868
NR_025375.1 gg_id:554922 Brevibacterium paucivorans str. CF 62; DSM 13657 NR_025
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AB288106.1 gg_id:178942 Brevibacterium sanguinis I-16 AB2881
FJ672800.1 gg_id:522372 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6728
DQ344485.1 gg_id:172245 Brevibacterium samyangensis str. SST-8 DQ344
FJ675524.1 gg_id:529096 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6755
EF459545.1 gg_id:204447 Brevibacterium antiquum KFC-74 EF4595
EF035139.1 gg_id:176058 Brevibacterium sp. str. MT5-11 EF0351
DQ223419.1 gg_id:140760 Brevibacterium sp. LB12 DQ223
GQ040457.1 gg_id:430434 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw954g GQ040

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| o__Actinomycetales | f__Brevibacteriaceae |
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| o__Actinomycetales | f__Cellulomonadaceae |

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g__Demequina
g__Demequina
g__Oerskovia
g__Tropheryma
g__Tropheryma

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| s__Cellulomonas denverensis | 40468 |
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| s__Cellulomonas parahominis | 40860 |
| s__Cellulomonas uda | 40284 |
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| s__Tropheryma whipplei | 38988 |
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EU099382.1 gg_id:258101 Brevibacterium sp. str. SC9 EU099
X76567.1 gg_id:12520 Brevibacterium iodinum str. NCDO 613 X76567
FJ670694.1 gg_id:516893 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6706
X77451.1 gg_id:12521 Brevibacterium linens str. DSM 20425 X77451
FJ674759.1 gg_id:529325 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6747
EF419416.1 gg_id:206826 Substantial alterations cutaneous biota psoriatic lesions human skin clone 6PN34 EF4194
AM421807.1 gg_id:216329 Brevibacterium mariniaquaticum str. HFW-26 AM421
DQ361016.1 gg_id:146469 Brevibacterium linens str. 1MF DQ361
EU868814.1 gg_id:592745 Brevibacterium sp. str. 5401308 EU8688
AB327249.1 gg_id:254761 Catenulispora subtropica str. TT 01-19 (= NBRC 103396) AB3272
EF451662.1 gg_id:217192 Cellulomonas sp. str. KAR32 EF4516
EF063610.1 gg_id:177558 Microbial ecology autotrophic denitrifying anaerobic methanogenic UASB reactor clo EF0636
AJ229245.1 gg_id:12346 Actinobacteria str. VeCb6 AJ2292
X79458.1 gg_id:12343 Cellulomonas fermentans str. DSM 3133 X79458
AJ863164.1 gg_id:159316 Cellulomonas bogoriensis str. 69B4 AJ8631
AY554419.1 gg_id:104027 Cellulomonas sp. 9A1 AY5544
AY655726.1 gg_id:105859 Cellulomonas denverensis str. W6124 AY6557
FJ200381.1 gg_id:315369 Cellulomonas hominis str. 3089BRRJ FJ2003
EU373531.1 gg_id:564028 Cellulomonas hominis str. FR1_148_P EU3735
AY655731.1 gg_id:101233 Cellulomonas parahominis str. W7336 AY6557
AB259960.1 gg_id:159820 Cellulomonas uda AB2599
NR_029095.1 gg_id:556569 Cellulomonas xylanilytica str. XIL11; LMG 21723 NR_029
X79463.1 gg_id:12315 Cellulomonas flavigena str. NCIMB 8073 X79463
EU834248.1 gg_id:350859 Cellulomonas denverensis str. DS21 EU8342
AB268586.1 gg_id:173567 Cellulomonas chitinilytica str. X.bu-b AB2685
AF064702.1 gg_id:12319 Cellulomonas iranensis str. O AF0647
X79462.1 gg_id:12331 Cellulomonas biazotea str. DSM 20112 X79462
NR_024913.1 gg_id:535428 Cellulomonas persica str. I; ATCC 700642 NR_024
AF282627.1 gg_id:47463 Cellulomonas gelida AF2826
AJ245568.1 gg_id:12332 Cellulomonas sp. str. GM13 AJ2455
AJ292035.1 gg_id:61987 Cellulomonas sp. str. d6 AJ2920
X83799.1 gg_id:12323 Cellulomonas flavigena str. DSM 20109T X83799
EF688360.1 gg_id:235695 soil clone F4-169 EF6883
AM902253.3 gg_id:326434 Cellulomonas sp. str. KB23 AM902
AB166884.1 gg_id:104614 Cellulomonas gelida str. T5-10 AB1668
EU050924.1 gg_id:252063 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_01_15 EU0509
EU697083.1 gg_id:289962 Cellulomonas sp. str. F11 EU6970
AB471560.1 gg_id:534681 Demequina sp. str. KV-811 AB4715
AJ314849.1 gg_id:54867 Oerskovia jenensis str. DSM 46001 AJ3148
AF251035.1 gg_id:39437 Tropheryma whipplei Twist str. twist AF2510
AF190688.1 gg_id:25685 Tropheryma whipplei AF1906

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| o__Actinomycetales | f__Cellulomonadaceae |
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AY250865.1 gg_id:83082 lichen-dominated Antarctic cryptoendolithic community clone FBP218 AY2508
GU205277.1 gg_id:525009 unusual Microbial Venezuelan Tepui (Orthoquartzite) Cave: Dominance Chloroflexal GU205
GQ502471.1 gg_id:571864 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf1- GQ502
DQ366005.1 gg_id:151679 Dominant soils Marble Point and Wright Valley Victoria Land Antarctica soil clone DQ366
EU132492.1 gg_id:246070 tallgrass prarie soil clone FFCH14477 EU1324
EU276542.1 gg_id:366196 -DGGE and Approaches Analyze Effect Agricultural Practices on Soil agricultural soil c EU2765
AY250882.1 gg_id:86523 lichen-dominated Antarctic cryptoendolithic community clone FBP406 AY2508
CU920319.1 gg_id:575392 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU9201
GQ088433.1 gg_id:373239 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw: GQ088
AY250885.1 gg_id:83120 lichen-dominated Antarctic cryptoendolithic community clone FBP468 AY2508
FM874115.1 gg_id:360829 occupant source house mattress dust clone MC01G06 FM874
AM697088.1 gg_id:223578 sequencing libraries indoor dust clone BF0002B038 AM697
GU205310.1 gg_id:515585 unusual Microbial Venezuelan Tepui (Orthoquartzite) Cave: Dominance Chloroflexal GU205
AF408985.1 gg_id:104265 Actinomycetales str. Ellin143 AF4089
AB491284.1 gg_id:514224 Tomitella biformata str. AHU 1820 AB4912
FJ592823.1 gg_id:574265 Fumarole-supported islands biodiversity within hyperarid -elevation landscape on Pu FJ5928
EF016822.1 gg_id:246415 Hyper-Arid Atacama Desert Soils soil clone E1B-F6-114 EF0168
FM877676.1 gg_id:356915 Microbial several mining wastes Bulgaria vicinity uranium mine Sliven clone Sliv-78 FM877
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EF157260.1 gg_id:247211 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon EF1572
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EU133122.1 gg_id:237583 tallgrass prarie soil clone FFCH5509 EU1331
EU289493.1 gg_id:253651 metagenomic approach biosynthesis ansamycin endophytes or symbionts enriched s EU2894
AY234441.1 gg_id:112349 soil isolate Ellin5024 AY2344
EF016810.1 gg_id:256178 Hyper-Arid Atacama Desert Soils soil clone E1B-C1-114 EF0168
DQ298144.1 gg_id:142506 -dependent and microbial assemblages silkworm midgut clone swm98 DQ298
AY250880.1 gg_id:86480 lichen-dominated Antarctic cryptoendolithic community clone FBP402 AY2508
DQ366003.1 gg_id:153548 Dominant soils Marble Point and Wright Valley Victoria Land Antarctica soil clone DQ366
FJ592817.1 gg_id:559986 Fumarole-supported islands biodiversity within hyperarid -elevation landscape on Pu FJ5928
GQ088228.1 gg_id:390260 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw: GQ088
AB234237.1 gg_id:148806 Biotransformation Polychlorinated Dioxins Microbial Dynamics Sediment Microcosm AB2342
AY534743.1 gg_id:99194 Millisia brevis str. J82 AY5347
AY250883.1 gg_id:83514 lichen-dominated Antarctic cryptoendolithic community clone FBP417 AY2508
EF127613.1 gg_id:213535 Fossil Genes and Microbes Entombed Oldest Ice on Earth ice clone DLE090 EF1276
AB288888.1 gg_id:201506 termite gut homogenate clone BOf2-16 AB2888
DQ125551.1 gg_id:130787 uranium contaminated soil clone AKAU3527 DQ125
EU104204.1 gg_id:331234 Evidence Comamonadaceae determinants settling performance activated sludge clo EU1042
EF471701.1 gg_id:267662 Fast Screening and Estuarine Operon Libraries whole surface water Chesapeake Bay ( EF4717
AJ867924.1 gg_id:142681 Fluctuations Significantly Influence Microbial Present Nival Lakes lake water clone D3 AJ8679
EU803916.1 gg_id:346841 It's all ranking aquatic Lake Gatun clone 5C231574 EU8039

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CR933228.1 gg_id:110305 Evry municipal wastewater treatment plant clone 054C09_B_DI_P58 CR933
FJ769434.1 gg_id:568643 Changes Methanogenic Microbial After Sludge Pre-treatment full-scale municipal ana FJ7694
GQ017242.1 gg_id:492424 Topographical and Temporal Human Skin Microbiome skin alar crease clone nbu116 GQ017
DQ015810.1 gg_id:139725 Antarctic lake water clone ELB16-113 DQ015
GQ340357.1 gg_id:553793 Prokaryotic Marathonas Reservoir Greece water column clone VE08-149-BAC GQ340
GQ111879.1 gg_id:451456 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw GQ111
DQ347943.1 gg_id:200646 Specificity Soil-Feeding Termite Mounds and Putative Origin these soil-feeding termi DQ347
AF227165.1 gg_id:111731 Propioniferax innocua str. ATCC49929 AF2271
AY566575.1 gg_id:108722 sp. str. PG-02 AY5665
FJ916097.1 gg_id:586357 Evidence structuring organic carbon source temperate lakes integrated lake epilimnic FJ9160
AM980985.1 gg_id:311573 Ponticoccus gilvus str. MSW-19 AM980
GQ340189.1 gg_id:548357 Prokaryotic Marathonas Reservoir Greece water column clone K07-85-BAC GQ340
DQ520173.1 gg_id:160626 shal China sequences hypertrophic freshwater lake clone ML-7-10.2 DQ520
DQ316366.2 gg_id:156400 and seasonal dynamics Actinobacteria four lakes Northeastern Germany freshwater DQ316
EF125420.1 gg_id:193229 soil naked tidal flat sediment near mangrove clone MSB-1F9 EF1254
EU812989.1 gg_id:305551 Microbial structure thermophilic reactors biogas reactor fed corn silage clone TUM-M EU8129
EU801210.1 gg_id:318920 It's all ranking aquatic Chesapeake Bay MD clone 3C002457 EU8012
FJ479550.1 gg_id:550173 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4795
FJ937869.1 gg_id:467626 Marine Sponge Gelliodes carnosa coastal waters Lingshui Bay Hainan Island South Ch FJ9378
GQ357647.1 gg_id:575785 Streptomyces sp. str. YIM 75704 GQ357
GU227180.1 gg_id:592605 Microbiological immunological Adolescent Moroccan Aggressive Periodontitis Patier GU227
AB198453.1 gg_id:135406 termite gut wall fraction clone RsW01-014 AB1984
AJ576385.1 gg_id:104294 midgut homogenate Pachnoda ephippiata larva clone PeM15 AJ5763
GQ850574.1 gg_id:557602 bottom water northern Bering Sea clone d118 GQ850
AY948059.1 gg_id:142745 Synchrony and seasonality two temperate rivers USA: Massachusetts Parker River cl AY9480
EU907900.1 gg_id:323949 Identification hexahydro-135-trinitro-135-triazine (RDX)-degrading microorganisms v EU9079
FJ542902.1 gg_id:525816 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone A FJ5429
EF520362.1 gg_id:234186 structure lakes: what controls ? acid-impacted lake clone ADK-MOh02-65 EF5203
FM874965.1 gg_id:359343 occupant source house dust skin surface swab clone SB01D12 FM874
AY566577.1 gg_id:108724 Eubacterium sp. str. PG-04 AY5665
EF471698.1 gg_id:277468 Fast Screening and Estuarine Operon Libraries whole surface water Chesapeake Bay EF4716
GU305824.1 gg_id:556516 Research on changes structure during algae outbreak oligotrophic lakes (YangHe res GU305
AF513101.1 gg_id:65420 activated sludge foam clone 7 AF5131
GQ340111.1 gg_id:586558 Prokaryotic Marathonas Reservoir Greece water column clone B07-05-BAC GQ340
EU930868.1 gg_id:315328 Jannaschia sp. str. psc3 EU9308
DQ062659.1 gg_id:133829 Kribbia dieselivorans str. R33 DQ062
EU467938.1 gg_id:296510 cheetah feces clone CE2_e12 EU4679
EF157137.1 gg_id:254649 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon EF1571
EU179735.1 gg_id:263649 Cellulosimicrobium sp. str. HY-12 EU1797
X83804.1 gg_id:12330 Cellulomonas cellasea str. DSM 20118T X83804
EF451632.1 gg_id:208675 Cellulomonas sp. str. KAR2 EF4516

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| s__Corynebacterium bovis | 37015 |
| s__Corynebacterium bovis | 37323 |
| s__Corynebacterium confusum | 36798 |
| s__Corynebacterium cystitidis | 36795 |
| s__Corynebacterium diphtheriae | 37211 |

FM955877.1 gg_id:593259 Cellulomonas sp. str. Asd M7A1 FM955
FJ971722.1 gg_id:429838 microbial autrotrophic denitrification granular sludge clone E-B7 FJ9717
EF688154.1 gg_id:326817 Detection microbial sludge anaerobic wastewater treatment system clone 1F4_cons EF6881
DQ223670.1 gg_id:161011 Cellulomonas sp. zf-IIRht4 DQ223
FN397670.1 gg_id:386689 Arsenicicoccus sp. str. AMV4 FN397
FJ230840.1 gg_id:338568 Oerskovia sp. str. SB3 FJ2308
EU560979.1 gg_id:259886 Cellulomonas sp. str. 5420S-23 EU560
EU644102.1 gg_id:280631 and Samoylov Island Lena active layer -centred polygon near permafrost table; Rim_ EU644
FJ005066.1 gg_id:344364 Cellulomonas sp. str. RCML-44 FJ0050
NR_028904.1 gg_id:575780 Dermatophilus chelonae str. W16; DSM 44178 NR_02
DQ521505.1 gg_id:193536 Antarctic lake ice cover clone ANTLV2_A07 DQ521
GQ094386.1 gg_id:381291 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ094
AF527583.1 gg_id:62967 EBPR sludge lab scale clone LPB21 AF5275
EF451634.1 gg_id:215481 Cellulomonas sp. str. KAR4 EF4516
DQ303278.1 gg_id:141216 Microbial ecology macroscopic filaments extreme Tinto River acidic river clone fc3 DQ303
AB193570.1 gg_id:108280 Actinomadura sp. str. Shinshu-MS-03 AB1935
EF019023.1 gg_id:203722 aspen rhizosphere clone Amb_16S_1562 EF0190
DQ985164.1 gg_id:194841 Actinomadura alba str. YIM 45681 DQ985
EU133137.1 gg_id:250813 tallgrass prarie soil clone FFCH598 EU133
EU335334.1 gg_id:246169 Changes microbial metabolic and along hydrogeochemically variable profile unsatura EU3353
AY234546.1 gg_id:111386 soil isolate Ellin5129 AY2345
EU861937.1 gg_id:334140 effects chronic fertilization on alpine tundra microbial implications carbon and cyclin EU861
GQ263304.1 gg_id:511050 Structure Simulated Level Waste Site simulated level waste site clone FW1_a52 GQ263
AF498716.1 gg_id:72811 soil isolate Ellin334 AF4987
Y07606.2 gg_id:12061 Drentse grassland soil clone DA016 Y07606
EU038018.1 gg_id:251707 Episodic subaerial speleogenesis controlled mineralogy microbial colonization and cc EU0380
GU205304.1 gg_id:525863 unusual Microbial Venezuelan Tepui (Orthoquartzite) Cave: Dominance Chloroflexal GU205
GQ001448.1 gg_id:508215 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu173b04 GQ001
GQ014722.1 gg_id:494944 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw763c GQ014
GQ002396.1 gg_id:507265 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu176h09 GQ002
AY230773.1 gg_id:83313 Corynebacterium sp. 'Smarlab BioMol-2301292' str. Smarlab BioMol 2301292 'Smarlal AY2307
AF537589.1 gg_id:69384 Corynebacterium argentoratense National Microbiology Laboratory Special identifier AF5375
X83955.1 gg_id:13418 Corynebacterium argentoratense str. CIP 104296 X83955
AM990811.1 gg_id:278095 Corynebacterium sp. MOLA 35 AM990
Y13777.2 gg_id:13372 Corynebacterium auriscanis str. M135/96/2 Y13777
AF311390.1 gg_id:37493 Corynebacterium bovis str. 33 AF3113
AF311389.1 gg_id:23997 Corynebacterium bovis str. 32 AF3113
AF311415.1 gg_id:33060 Corynebacterium bovis str. 115 AF3114
Y15887.1 gg_id:13500 Corynebacterium confusum str. DMMZ 3259 Y15887
X82058.1 gg_id:13421 Corynebacterium cystitidis str. CIP 103424T X82058
AF145257.1 gg_id:13348 Corynebacterium xerosis str. 71376 AF1452

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| s__Corynebacterium diphtheriae | 37282 |
| s__Corynebacterium durum | 37145 |
| s__Corynebacterium efficiens | 37256 |
| s__Corynebacterium flavescens | 36899 |
| s__Corynebacterium freneyi | 36816 |
| s__Corynebacterium freneyi | 36854 |
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| s__Corynebacterium freneyi | 37011 |
| s__Corynebacterium freneyi | 37215 |
| s__Corynebacterium freneyi | 37267 |
| s__Corynebacterium glucuronolyticum | 36923 |
| s__Corynebacterium jeikeium | 37247 |
| s__Corynebacterium kroppenstedtii | 37205 |
| s__Corynebacterium lipophiloflavum | 36882 |
| s__Corynebacterium lipophiloflavum | 37305 |
| s__Corynebacterium lubricantis | 36874 |
| s__Corynebacterium lubricantis | 37055 |
| s__Corynebacterium macginleyi | 33708 |
| s__Corynebacterium mastitidis | 37378 |
| s__Corynebacterium matruchotii | 36965 |
| s__Corynebacterium pilosum | 37047 |
| s__Corynebacterium pseudogenitalium | 28928 |
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| s__Corynebacterium pseudogenitalium | 36213 |
| s__Corynebacterium pseudotuberculosis | 37095 |
| s__Corynebacterium pseudotuberculosis | 37342 |
| s__Corynebacterium pseudotuberculosis | 37347 |
| s__Corynebacterium renale | 37040 |
| s__Corynebacterium riegelii | 37280 |
| s__Corynebacterium simulans | 36764 |
| s__Corynebacterium simulans | 36820 |
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| s__Corynebacterium simulans | 37317 |
| s__Corynebacterium stationis | 36848 |
| s__Corynebacterium tuberculostearicum | 29149 |
| s__Corynebacterium tuberculostearicum | 30359 |
| s__Corynebacterium tuberculostearicum | 34167 |
| s__Corynebacterium urealyticum | 37117 |

BX248360.1 gg_id:136033 Corynebacterium diphtheriae str. NCTC13129 BX248
AF543285.1 gg_id:58295 Corynebacterium durum str. ChDC OS33 AF543
BA000035.2 gg_id:107869 Corynebacterium efficiens str. YS-314 BA000
X84441.1 gg_id:13463 Corynebacterium flavescens str. NCDO 1320 X84441
AJ292762.1 gg_id:73485 Corynebacterium freneyi str. 20695110 AJ2927
FM213375.1 gg_id:335388 Corynebacterium xerosis str. St51377/1 FM213
AJ292763.1 gg_id:37739 Corynebacterium freneyi str. 20395347 AJ2927
FN179322.1 gg_id:565070 Corynebacterium xerosis str. St53244 FN1793
FN179328.1 gg_id:536505 Corynebacterium xerosis str. St47126 FN1793
EF462413.1 gg_id:250643 Corynebacterium freneyi 3526 EF4624
X86688.1 gg_id:13425 Corynebacterium glucuronolyticum str. GF 838 (=DSM 44120) X86688
CR931997.1 gg_id:137456 Corynebacterium jeikeium str. K411 = NCTC 11915 CR9319
AY524774.1 gg_id:105080 Corynebacterium kroppenstedtii VA1719_2000 AY5247
EU540561.1 gg_id:285399 profile human microbiota antecubital fossa (inner elbow) skin clone nbt119g01 EU5405
NR_026370.1 gg_id:550368 Corynebacterium lipophiloflavum str. DMMZ 1944; CCUG 37336; DSM 44291 NR_02
FM173121.1 gg_id:351541 Corynebacterium sp. str. KSS-10Se FM173
FM173119.1 gg_id:304633 Corynebacterium sp. str. KSS-3Se FM173
AB354691.1 gg_id:244209 Corynebacterium macginleyi str. EC009 AB3546
AB359408.1 gg_id:255771 Corynebacterium mastitidis str. TBS-19 AB3594
ACEB01000045.1 gg_id:548125 Corynebacterium matruchotii str. ATCC 33806 ACEB0
X84246.1 gg_id:13467 Corynebacterium pilosum str. NCTC 11862 X84246
GQ051353.1 gg_id:389984 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl GQ051
GQ026272.1 gg_id:414000 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl GQ026
GQ051205.1 gg_id:412681 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl GQ051
GQ047349.1 gg_id:377112 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbu5( GQ047
X81911.1 gg_id:13397 Corynebacterium diphtheriae str. CCUG 2708 X81911
X84255.1 gg_id:13414 Corynebacterium pseudotuberculosis str. NCTC 3450 X84255
GQ118343.1 gg_id:445441 Corynebacterium ulcerans str. CD074; NCTC 12077 GQ118
D37806.1 gg_id:70082 Corynebacterium renale str. HR59 D37806
GQ009105.1 gg_id:500560 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw827c0: GQ009
GQ030945.1 gg_id:417964 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ030
GQ031548.1 gg_id:395038 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ031
GQ030984.1 gg_id:449470 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ030
GQ031648.1 gg_id:452484 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ031
GQ028326.1 gg_id:378263 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw' GQ028
GQ065486.1 gg_id:392448 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw GQ065
FJ671806.1 gg_id:512806 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6718
AJ438043.1 gg_id:85890 Corynebacterium tuberculostearicum str. CIP102622 AJ4380
GQ034989.1 gg_id:426313 Topographical and Temporal Human Skin Microbiome skin glabella clone nbu330e11 GQ034
GQ015980.1 gg_id:493683 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv GQ015
NR_027597.1 gg_id:543063 Corynebacterium urealyticum 7109 str. DSM 7109; ATCC 43042 NR_02

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AJ222816.1 gg_id:13387 Corynebacterium variabile str. DSM 20536 AJ2228
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GQ029080.1 gg_id:460444 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw85 GQ029
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GQ029974.1 gg_id:407125 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw865d1 GQ029
GQ032817.1 gg_id:446381 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw918f01 GQ032
GQ036404.1 gg_id:386016 Topographical and Temporal Human Skin Microbiome skin palm clone nbu364a11c1 GQ036
GQ034944.1 gg_id:383236 Topographical and Temporal Human Skin Microbiome skin glabella clone nbu329h08 GQ034
GQ074780.1 gg_id:457016 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv GQ074
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GQ029018.1 gg_id:395610 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw85 GQ029
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GQ112809.1 gg_id:386007 Topographical and Temporal Human Skin Microbiome skin nare clone nbw588e05c1 GQ112
GQ005142.1 gg_id:504520 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbu GQ005
GQ005156.1 gg_id:504507 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbu GQ005
GQ041775.1 gg_id:373458 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw932d1 GQ041
GQ097241.1 gg_id:407663 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw GQ097
GQ005197.1 gg_id:504466 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbu GQ005
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GQ030435.1 gg_id:421168 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw878b09 GQ030
GQ050842.1 gg_id:459757 Topographical and Temporal Human Skin Microbiome skin nare clone nbu439f11c1 GQ050
GQ028533.1 gg_id:409185 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ028
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GQ048156.1 gg_id:414186 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbu GQ048
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GQ003777.1 gg_id:505883 Topographical and Temporal Human Skin Microbiome skin nare clone nbu57b10c1 GQ003
GQ051358.1 gg_id:407108 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl GQ051
GQ028496.1 gg_id:416489 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ028
GQ050873.1 gg_id:441175 Topographical and Temporal Human Skin Microbiome skin nare clone nbu440c01c1 GQ050
GQ066205.1 gg_id:404066 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw GQ066
GQ048273.1 gg_id:454240 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbu GQ048
GQ096870.1 gg_id:381920 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw GQ096

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| k__Bacteria | k__Bacteria | p__Actinobacteria | c__Actinobacteria |
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GQ054303.1 gg_id:426934 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw1107 GQ054
GQ028139.1 gg_id:386868 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ028
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GQ047866.1 gg_id:418352 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbu GQ047
FM875252.1 gg_id:364849 occupant source house dust skin surface swab clone SB04F12 FM875
GQ009903.1 gg_id:499762 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ009

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GQ051849.1 gg_id:380776 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ051

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GQ062726.1 gg_id:400298 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ062
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GQ005086.1 gg_id:504576 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbu GQ005
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GQ062029.1 gg_id:467668 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw27b1 GQ062
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GQ041178.1 gg_id:423065 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv GQ041
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GQ064342.1 gg_id:375206 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw7 GQ064
GQ027623.1 gg_id:402796 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv GQ027
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GQ041299.1 gg_id:465471 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv GQ041

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GQ071683.1 gg_id:378896 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw GQ071
GQ017802.1 gg_id:491866 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbu GQ017
GQ029980.1 gg_id:396355 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw865e0 GQ029
GQ029387.1 gg_id:464508 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw925d07 GQ029
GQ027569.1 gg_id:448735 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv GQ027

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GQ047102.1 gg_id:409651 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw GQ047
GQ072324.1 gg_id:399169 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw194h03 GQ072
GQ031835.1 gg_id:417337 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ031
GQ028499.1 gg_id:465434 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ028
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GQ028754.1 gg_id:447719 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw919h0 GQ028
GQ048745.1 gg_id:409748 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu5 GQ048
GQ094740.1 gg_id:432317 Topographical and Temporal Human Skin Microbiome skin nare clone nbw374c03c1 GQ094
GQ031656.1 gg_id:418110 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ031
GQ057432.1 gg_id:415439 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ057

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GQ073762.1 gg_id:383590 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor GQ073
GQ071814.1 gg_id:454390 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw GQ071
GQ039707.1 gg_id:422671 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu426g11 GQ039
GQ057074.1 gg_id:408191 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw10 GQ057
GQ074132.1 gg_id:383918 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ074
GQ050866.1 gg_id:376977 Topographical and Temporal Human Skin Microbiome skin nare clone nbu440b01c1 GQ050
GQ064455.1 gg_id:390603 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw7 GQ064
GQ028427.1 gg_id:447121 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ028
GQ077406.1 gg_id:467332 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv GQ077
GQ056353.1 gg_id:407051 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor GQ056
GQ013221.1 gg_id:496445 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw8 GQ013
GQ061551.1 gg_id:453508 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw22 GQ061
GQ059401.1 gg_id:439539 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw1 GQ059
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GQ009914.1 gg_id:499751 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ009
GQ037107.1 gg_id:390130 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu388h11 GQ037
GQ050520.1 gg_id:417150 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu486g GQ050
GQ087396.1 gg_id:428327 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw GQ087
GQ023136.1 gg_id:486535 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbu30 GQ023
GQ038284.1 gg_id:415126 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbu GQ038
GQ028554.1 gg_id:375016 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ028
GQ031207.1 gg_id:443238 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor GQ031
GQ054887.1 gg_id:451706 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv GQ054

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GQ078757.1 gg_id:428563 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ078

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GQ005228.1 gg_id:504435 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbu GQ005

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GQ002148.1 gg_id:507514 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbu16 GQ002
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GQ038309.1 gg_id:454859 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbu GQ038
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GQ036544.1 gg_id:401261 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbu GQ036
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GQ035219.1 gg_id:393781 Topographical and Temporal Human Skin Microbiome skin alar crease clone nbu334 GQ035
GQ031590.1 gg_id:462488 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ031
GQ029250.1 gg_id:386365 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw GQ029
GQ065395.1 gg_id:396081 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw GQ065
GQ051264.1 gg_id:422086 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl GQ051
GQ055030.1 gg_id:395375 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv GQ055
GQ034027.1 gg_id:408097 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor GQ034
GQ035639.1 gg_id:371495 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbu3 GQ035

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GQ020534.1 gg_id:489134 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl GQ020
GQ049171.1 gg_id:424244 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu470b01 GQ049
GQ005053.1 gg_id:504609 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbu GQ005
GQ075730.1 gg_id:430659 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ075
GQ035730.1 gg_id:432727 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbu GQ035
GQ042005.1 gg_id:457256 Topographical and Temporal Human Skin Microbiome skin alar crease clone nbw935 GQ042
GQ040001.1 gg_id:411614 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw94 GQ040
GQ028442.1 gg_id:425297 Topographical and Temporal Human Skin Microbiome skin interdigital web space cl GQ028
GQ031988.1 gg_id:390961 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ031
GQ043989.1 gg_id:381277 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ043
GQ029398.1 gg_id:452300 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw925e1 GQ029
GQ112781.1 gg_id:388217 Topographical and Temporal Human Skin Microbiome skin nare clone nbw588b07c1 GQ112
GQ027220.1 gg_id:374347 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ027
GQ062662.1 gg_id:371934 Topographical and Temporal Human Skin Microbiome skin interdigital web space cl GQ062
GQ112782.1 gg_id:442041 Topographical and Temporal Human Skin Microbiome skin nare clone nbw588b08c1 GQ112
GQ115532.1 gg_id:376959 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw687b0 GQ115
GQ036608.1 gg_id:442231 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbu GQ036

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GQ075322.1 gg_id:371021 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ075
GQ060707.1 gg_id:376521 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw04e01 GQ060
GQ038766.1 gg_id:373026 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu522g11 GQ038
GQ022610.1 gg_id:487059 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbu31 GQ022
GQ047011.1 gg_id:393489 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw GQ047
GQ051178.1 gg_id:456610 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl GQ051
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GQ054118.1 gg_id:432811 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1098g GQ054
GQ051237.1 gg_id:424755 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl GQ051
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GQ031316.1 gg_id:400951 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor GQ031
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GQ066185.1 gg_id:455647 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw GQ066
GQ000370.1 gg_id:468936 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbu11 GQ000
GQ030161.1 gg_id:456999 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw868b0 GQ030
GQ039672.1 gg_id:437374 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu426a12 GQ039
GQ067407.1 gg_id:399123 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1 GQ067
GQ060559.1 gg_id:438949 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw03c08 GQ060
GQ048807.1 gg_id:445120 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu5 GQ048
GQ054957.1 gg_id:423098 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv GQ054
GQ056847.1 gg_id:381784 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl GQ056

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GQ048424.1 gg_id:395126 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu4 GQ048
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GQ080155.1 gg_id:463719 Topographical and Temporal Human Skin Microbiome skin alar crease clone nbw11: GQ080
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GQ031008.1 gg_id:430471 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ031

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GQ060703.1 gg_id:437541 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw04d08 GQ060
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GQ010081.1 gg_id:499584 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ010
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GQ009248.1 gg_id:500417 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw GQ009
GQ016166.1 gg_id:493501 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw GQ016

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GQ005262.1 gg_id:504402 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbu GQ005
GQ037233.1 gg_id:415256 Topographical and Temporal Human Skin Microbiome skin palm clone nbu390f02c1 GQ037
GQ031017.1 gg_id:450491 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ031
GQ027228.1 gg_id:422836 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ027
GQ041786.1 gg_id:423664 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw932e1 GQ041
GQ061557.1 gg_id:448953 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw22 GQ061
GQ112746.1 gg_id:462567 Topographical and Temporal Human Skin Microbiome skin nare clone nbw587e08c1 GQ112
GQ075702.1 gg_id:425846 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ075

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GQ048133.1 gg_id:401917 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbu45( GQ048
GQ071529.1 gg_id:376963 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw GQ071
GQ100277.1 gg_id:440048 Topographical and Temporal Human Skin Microbiome skin nare clone nbw480a10c1 GQ100
GQ000924.1 gg_id:508738 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbu10 GQ000
GQ020482.1 gg_id:489186 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl GQ020
GQ031178.1 gg_id:420098 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor GQ031
GQ051222.1 gg_id:432784 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl GQ051
GQ031201.1 gg_id:409184 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor GQ031
GQ035289.1 gg_id:435610 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbu35( GQ035
GQ100266.1 gg_id:395558 Topographical and Temporal Human Skin Microbiome skin nare clone nbw479h10c1 GQ100
GQ066215.1 gg_id:409656 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw GQ066
GQ036474.1 gg_id:450581 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbu GQ036
GQ032744.1 gg_id:377043 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw917f04 GQ032
GQ020449.1 gg_id:489219 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl GQ020
GQ033899.1 gg_id:391597 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor GQ033
GQ050614.1 gg_id:409775 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu488b GQ050
GQ069880.1 gg_id:400254 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw242g0 GQ069
GQ097252.1 gg_id:389528 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw GQ097
GQ016005.1 gg_id:493661 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw GQ016
GQ036678.1 gg_id:386753 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbu GQ036
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GQ050388.1 gg_id:424784 Topographical and Temporal Human Skin Microbiome skin nare clone nbu437b05c1 GQ050
GQ072367.1 gg_id:422966 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw195d05 GQ072
GQ092413.1 gg_id:464439 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv GQ092
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GQ000213.1 gg_id:468778 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbu11 GQ000
GQ052333.1 gg_id:396092 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu534d11 GQ052
GQ054983.1 gg_id:377164 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv GQ054
FM875156.1 gg_id:358619 occupant source house dust skin surface swab clone SB03F03 FM875
GQ025621.1 gg_id:417762 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ025
GQ100245.1 gg_id:426110 Topographical and Temporal Human Skin Microbiome skin nare clone nbw479f11c1 GQ100
GQ028134.1 gg_id:444501 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ028
GQ112825.1 gg_id:468130 Topographical and Temporal Human Skin Microbiome skin nare clone nbw588g06c1 GQ112
GQ022039.1 gg_id:487630 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu3 GQ022
GQ024642.1 gg_id:485030 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ024
GQ050551.1 gg_id:386879 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu487c( GQ050
GQ075227.1 gg_id:391143 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ075
GQ015010.1 gg_id:494656 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw8 GQ015

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GQ094796.1 gg_id:425920 Topographical and Temporal Human Skin Microbiome skin nare clone nbw374h04c1 GQ094
GQ088651.1 gg_id:375711 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv GQ088

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GQ000940.1 gg_id:508722 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbu10 GQ000

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GQ051197.1 gg_id:444172 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl GQ051
GQ036409.1 gg_id:389166 Topographical and Temporal Human Skin Microbiome skin palm clone nbu364b05c1 GQ036
GQ044822.1 gg_id:410513 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw GQ044
GQ040808.1 gg_id:401172 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw958h06 GQ040
GQ036465.1 gg_id:382332 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbu GQ036
GQ042060.1 gg_id:405635 Topographical and Temporal Human Skin Microbiome skin alar crease clone nbw935 GQ042
GQ036497.1 gg_id:373797 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbu GQ036
GQ036704.1 gg_id:407982 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbu GQ036
GQ005098.1 gg_id:504564 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbu GQ005
GQ071731.1 gg_id:386054 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw GQ071
GQ048554.1 gg_id:426643 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu4 GQ048
GQ009313.1 gg_id:500351 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw GQ009
GQ041728.1 gg_id:400735 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw931g0 GQ041
GQ005081.1 gg_id:504581 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbu GQ005
GQ059677.1 gg_id:441464 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw38 GQ059
GQ041693.1 gg_id:373878 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw931c1 GQ041
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GQ048382.1 gg_id:418318 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbu GQ048
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GQ028975.1 gg_id:424438 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw85 GQ028
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GQ004401.1 gg_id:505261 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbu GQ004
GQ018067.1 gg_id:491601 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbu GQ018
GQ035288.1 gg_id:412430 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbu35 GQ035
GQ036543.1 gg_id:387151 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbu GQ036
GQ028888.1 gg_id:424234 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw GQ028
GQ048596.1 gg_id:428430 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu4 GQ048
GQ062619.1 gg_id:419990 Topographical and Temporal Human Skin Microbiome skin interdigital web space cl GQ062
GQ034778.1 gg_id:414265 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clo GQ034
GQ100165.1 gg_id:372371 Topographical and Temporal Human Skin Microbiome skin nare clone nbw478f10c1 GQ100
GQ011516.1 gg_id:498150 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw792h0 GQ011
GQ021344.1 gg_id:488324 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbu27 GQ021
GQ075220.1 gg_id:380153 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ075
GQ028050.1 gg_id:451829 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv GQ028
GQ062795.1 gg_id:408506 Topographical and Temporal Human Skin Microbiome skin interdigital web space cl GQ062
GQ045651.1 gg_id:383982 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ045

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GQ038325.1 gg_id:411998 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbu GQ038
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GQ088028.1 gg_id:436364 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ088

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GQ100836.1 gg_id:379994 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor GQ100
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GQ032030.1 gg_id:465843 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ032
GQ026334.1 gg_id:373103 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl GQ026

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GQ041339.1 gg_id:419478 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv GQ041
GQ087768.1 gg_id:381008 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ087
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GQ038336.1 gg_id:413292 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbu GQ038
GQ036586.1 gg_id:454799 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbu GQ036
FM874927.1 gg_id:357938 occupant source house dust skin surface swab clone SB01A08 FM874
AJ438041.1 gg_id:83125 Corynebacterium tuberculostearicum str. CIP102857 AJ438
GQ053693.1 gg_id:437259 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbu GQ053
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GQ026469.1 gg_id:418754 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl GQ026
GQ097047.1 gg_id:439117 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw GQ097
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GQ062565.1 gg_id:405059 Topographical and Temporal Human Skin Microbiome skin nare clone nbw12d03c1 GQ062
GQ062014.1 gg_id:416027 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw27a0 GQ062
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GQ015073.1 gg_id:494596 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw8 GQ015
GQ058952.1 gg_id:376937 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbu58 GQ058
GQ046167.1 gg_id:440673 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw GQ046
GQ042203.1 gg_id:404023 Topographical and Temporal Human Skin Microbiome skin nare clone nbw937e03c1 GQ042
GQ070145.1 gg_id:454856 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1 GQ070

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GQ047640.1 gg_id:378669 Topographical and Temporal Human Skin Microbiome skin palm clone nbw137b09c GQ047
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GQ035603.1 gg_id:378276 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbu GQ035
GQ013409.1 gg_id:496257 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw8( GQ013
GQ013334.1 gg_id:496332 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw8( GQ013
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GQ042622.1 gg_id:380445 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl GQ042
GQ019602.1 gg_id:490066 Topographical and Temporal Human Skin Microbiome skin nare clone nbu204g01c1 GQ019
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GQ020696.1 gg_id:488972 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ020
GQ006536.1 gg_id:503128 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbu GQ006

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| k__Bacteria | k__Bacteria | p__Actinobacteria | c__Actinobacteria |
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