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D_6_Arthrobacter sp. F15, KR088550.1.1442	KR088550.1.1442	D_0_Bacteria, D_1_Actinobacteria, D_2_Actinobacteria, D_3_Micrococcales, D_4_Micrococaceae, D_5_Arthrobacter, D_6_Arthrobacter sp. F15	1	1	8	0	0	3	GTCGAACGATGAACCTCACTTGTGGGGGATTAGTGGCGAACGGGTGAAGTACAGTGAAGTACCTGCCCTTGACTCGGGATAAGCTGGGAACCGGGTCTAATACTGGATACGACCTCTGCGCATGCCATGTGTGGTGAAGACCTTTGTGGTGTGGTGGTGAAGGCTACCAAGCGACGACGGGTAGCGCCCTGAGAGGGTGGACCGGGCCACACTGGGAGTGAAGACGGCCACAGCTCTCACGGGAGGACAGCTGGGAATATTCACAACTGGGCGCAAGCTCGATGACGACGCGCCGATGAGGGATGAAGCGGTCTCGGGTGTAAACCTCTTTTCAGTAGGGAAGAGCTGGCTTTCTGGGGTGTGGTACGGTACCTGCAGAGAAGAGCGCCGGCTAACTGTCGACGACGCGCGGTAATACGTAGGGCCGCCGCTTAATCTGGGAATATTGCATATGGCGGAGCGCTGATGACGCTGATGATGAAGAAGGCTTCGGGTGTAAAGTACTTCGAGGGGAGAGCGGTGAATTAACCTGATGACCTTACCGCAGAGAAGCACCGCTAACTCGTGCCAGCAGCGCGGTAAATACGAGGGTCAACGCTTAATCGGAATTAACCTGGCGCTAAAGCGCACGACGCGCTTTGTAAAGTCAGATGTGAATCCCGGGCTCAACTGGGAAGCTCATTTGAACTGGCAAGCTTGAGTCTCGTAGAGGGGGTAAGTTCAGGTGTAGCGGTGAAATGCGTAGAGATCTGGAGGAATACCGGTGGCGAAGCGGGCCCCGTGACGAAGACTGACGCTAGGTGCGGAAGCGTGGGGAGCAACA
Ambiguous_taxa, JX134630.1.1439	JX134630.1.1439	D_0_Bacteria, D_1_Proteobacteria, D_2_Gammaproteobacteria, D_3_Enterobacteriales, D_4_Enterobacteriaceae, Ambiguous_taxa, D_0_Bacteria, D_1_Bacteroidetes, D_2_Bacteroidia, D_3_Bacteroidales, D_4_Prevotellaceae, D_5_Prevotella, D_6_uncultured bacterium	0	7	0	0	0	0	TGAGGAATATTGGTCAATGGCGAGCGCTGAAGCAGCCAGTGAAGCTGACGAGTACGCGCCCTATGGGTGTAAAGCTGTTTATAAGGGAATAAAGTGAAGTCTCGTAGAGCTTTTGCATGTACTCTATGATAAAGGACCGCGTAATCTCGTGCCAGCAGCGGTAAATCGGAAGGTCGGGCTTATCCGGATTATTTGGTTTAAAGGCGAGTGAAGCGGTGTGTGAAGTAGACGCTCAACGTCTGACGCGGAACCTGGTTTCTTGATAGCACAAGGTGGCGGAATCTGGTGTAGCGGTGAAATGCTAGATATCAACGAAGAACCTCGATTGCGAAGCAGCTTCACTGGAGCGCAACTGACGTGAAGCTCGAAATGCGGGTATCAACA
D_6_uncultured bacterium, KF842094.1.1435	KF842094.1.1435	D_0_Bacteria, D_1_Bacteroidetes, D_2_Bacteroidia, D_3_Bacteroidales, D_4_Prevotellaceae, D_5_Prevotella, D_6_uncultured bacterium	0	0	3	0	5	5	TGAGGAATATTGGTCAATGGCGAGCGCTGAAGCAGCCAGTGAAGCTGACGAGTACGCGCCCTATGGGTGTAAAGCTGTTTATAAGGGAATAAAGTGAAGTCTCGTAGAGCTTTTGCATGTACTCTATGATAAAGGACCGCGTAATCTCGTGCCAGCAGCGGTAAATCGGAAGGTCGGGCTTATCCGGATTATTTGGTTTAAAGGCGAGTGAAGCGGTGTGTGAAGTAGACGCTCAACGTCTGACGCGGAACCTGGTTTCTTGATAGCACAAGGTGGCGGAATCTGGTGTAGCGGTGAAATGCTAGATATCAACGAAGAACCTCGATTGCGAAGCAGCTTCACTGGAGCGCAACTGACGTGAAGCTCGAAATGCGGGTATCAACA
Ambiguous_taxa, AB218348.1.1430	AB218348.1.1430	D_0_Bacteria, D_1_Lentisphaerae, D_2_Lentisphaeria, D_3_Victivallales, D_4_Victivallaceae, D_5_Victivallis, Ambiguous_taxa	0	0	0	0	0	2	TGAGGAATATTGGTCAATGGCGAGCGCTGAAGCAGCCAGTGAAGCTGACGAGTACGCGCCCTATGGGTGTAAAGCTGTTTATAAGGGAATAAAGTGAAGTCTCGTAGAGCTTTTGCATGTACTCTATGATAAAGGACCGCGTAATCTCGTGCCAGCAGCGGTAAATCGGAAGGTCGGGCTTATCCGGATTATTTGGTTTAAAGGCGAGTGAAGCGGTGTGTGAAGTAGACGCTCAACGTCTGACGCGGAACCTGGTTTCTTGATAGCACAAGGTGGCGGAATCTGGTGTAGCGGTGAAATGCTAGATATCAACGAAGAACCTCGATTGCGAAGCAGCTTCACTGGAGCGCAACTGACGTGAAGCTCGAAATGCGGGTATCAACA
D_6_Cronobacter sp. BYP, KM088092.1.1428	KM088092.1.1428	D_0_Bacteria, D_1_Proteobacteria, D_2_Gammaproteobacteria, D_3_Enterobacteriales, D_4_Enterobacteriaceae, D_5_Enterwinia, D_6_uncultured bacterium	0	1	0	0	0	0	TGAGGAATATTGGTCAATGGCGAGCGCTGAAGCAGCCAGTGAAGCTGACGAGTACGCGCCCTATGGGTGTAAAGCTGTTTATAAGGGAATAAAGTGAAGTCTCGTAGAGCTTTTGCATGTACTCTATGATAAAGGACCGCGTAATCTCGTGCCAGCAGCGGTAAATCGGAAGGTCGGGCTTATCCGGATTATTTGGTTTAAAGGCGAGTGAAGCGGTGTGTGAAGTAGACGCTCAACGTCTGACGCGGAACCTGGTTTCTTGATAGCACAAGGTGGCGGAATCTGGTGTAGCGGTGAAATGCTAGATATCAACGAAGAACCTCGATTGCGAAGCAGCTTCACTGGAGCGCAACTGACGTGAAGCTCGAAATGCGGGTATCAACA
Ambiguous_taxa, JQ723715.1.1431	JQ723715.1.1431	D_0_Bacteria, D_1_Proteobacteria, D_2_Alphaproteobacteria, D_3_Sphingomonadales, D_4_Sphingomonadaceae	7	3	14	0	0	10	TGAGGAATATTGGTCAATGGCGAGCGCTGAAGCAGCCAGTGAAGCTGACGAGTACGCGCCCTATGGGTGTAAAGCTGTTTATAAGGGAATAAAGTGAAGTCTCGTAGAGCTTTTGCATGTACTCTATGATAAAGGACCGCGTAATCTCGTGCCAGCAGCGGTAAATCGGAAGGTCGGGCTTATCCGGATTATTTGGTTTAAAGGCGAGTGAAGCGGTGTGTGAAGTAGACGCTCAACGTCTGACGCGGAACCTGGTTTCTTGATAGCACAAGGTGGCGGAATCTGGTGTAGCGGTGAAATGCTAGATATCAACGAAGAACCTCGATTGCGAAGCAGCTTCACTGGAGCGCAACTGACGTGAAGCTCGAAATGCGGGTATCAACA
D_6_Candidatus Liberibacter asiaticus, FJ196314.1.2284	FJ196314.1.2284	D_0_Bacteria, D_1_Proteobacteria, D_2_Alphaproteobacteria, D_3_Rhizobiales, D_4_Rhizobiaceae, D_5_Candidatus Liberibacter, D_6_Candidatus Liberibacter	0	25	1	691	4	1	TGAGGAATATTGGTCAATGGCGAGCGCTGAAGCAGCCAGTGAAGCTGACGAGTACGCGCCCTATGGGTGTAAAGCTGTTTATAAGGGAATAAAGTGAAGTCTCGTAGAGCTTTTGCATGTACTCTATGATAAAGGACCGCGTAATCTCGTGCCAGCAGCGGTAAATCGGAAGGTCGGGCTTATCCGGATTATTTGGTTTAAAGGCGAGTGAAGCGGTGTGTGAAGTAGACGCTCAACGTCTGACGCGGAACCTGGTTTCTTGATAGCACAAGGTGGCGGAATCTGGTGTAGCGGTGAAATGCTAGATATCAACGAAGAACCTCGATTGCGAAGCAGCTTCACTGGAGCGCAACTGACGTGAAGCTCGAAATGCGGGTATCAACA
Ambiguous_taxa, JX945363.1.1425	JX945363.1.1425	D_0_Bacteria, D_1_Proteobacteria, D_2_Gammaproteobacteria, D_3_Pseudomonadales, D_4_Moraxellaceae, D_5_Acinetobacter	0	0	0	0	2	0	TGAGGAATATTGGTCAATGGCGAGCGCTGAAGCAGCCAGTGAAGCTGACGAGTACGCGCCCTATGGGTGTAAAGCTGTTTATAAGGGAATAAAGTGAAGTCTCGTAGAGCTTTTGCATGTACTCTATGATAAAGGACCGCGTAATCTCGTGCCAGCAGCGGTAAATCGGAAGGTCGGGCTTATCCGGATTATTTGGTTTAAAGGCGAGTGAAGCGGTGTGTGAAGTAGACGCTCAACGTCTGACGCGGAACCTGGTTTCTTGATAGCACAAGGTGGCGGAATCTGGTGTAGCGGTGAAATGCTAGATATCAACGAAGAACCTCGATTGCGAAGCAGCTTCACTGGAGCGCAACTGACGTGAAGCTCGAAATGCGGGTATCAACA
Ambiguous_taxa, EF102823.1.1419	EF102823.1.1419	D_0_Bacteria, D_1_Proteobacteria, D_2_Gammaproteobacteria, D_3_Betaproteobacteriales, D_4_Burkholderiaceae, D_5_Delftia, D_6_uncultured bacterium, FJ557934.1.1411	3	1	0	0	2	2	TGAGGAATATTGGTCAATGGCGAGCGCTGAAGCAGCCAGTGAAGCTGACGAGTACGCGCCCTATGGGTGTAAAGCTGTTTATAAGGGAATAAAGTGAAGTCTCGTAGAGCTTTTGCATGTACTCTATGATAAAGGACCGCGTAATCTCGTGCCAGCAGCGGTAAATCGGAAGGTCGGGCTTATCCGGATTATTTGGTTTAAAGGCGAGTGAAGCGGTGTGTGAAGTAGACGCTCAACGTCTGACGCGGAACCTGGTTTCTTGATAGCACAAGGTGGCGGAATCTGGTGTAGCGGTGAAATGCTAGATATCAACGAAGAACCTCGATTGCGAAGCAGCTTCACTGGAGCGCAACTGACGTGAAGCTCGAAATGCGGGTATCAACA
D_6_uncultured bacterium, FJ557934.1.1411	FJ557934.1.1411	D_0_Bacteria, D_1_Firmicutes, D_2_Bacilli, D_3_Bacillales, D_4_Staphylococcaceae, D_5_Staphylococcus, D_6_uncultured bacterium	0	0	1	0	0	0	TGAGGAATATTGGTCAATGGCGAGCGCTGAAGCAGCCAGTGAAGCTGACGAGTACGCGCCCTATGGGTGTAAAGCTGTTTATAAGGGAATAAAGTGAAGTCTCGTAGAGCTTTTGCATGTACTCTATGATAAAGGACCGCGTAATCTCGTGCCAGCAGCGGTAAATCGGAAGGTCGGGCTTATCCGGATTATTTGGTTTAAAGGCGAGTGAAGCGGTGTGTGAAGTAGACGCTCAACGTCTGACGCGGAACCTGGTTTCTTGATAGCACAAGGTGGCGGAATCTGGTGTAGCGGTGAAATGCTAGATATCAACGAAGAACCTCGATTGCGAAGCAGCTTCACTGGAGCGCAACTGACGTGAAGCTCGAAATGCGGGTATCAACA
Ambiguous_taxa, GQ149483.1.1484	GQ149483.1.1484	D_0_Bacteria, D_1_Actinobacteria, D_2_Actinobacteria, D_3_Micrococcales, D_4_Micrococaceae, D_5_Arthrobacter, Ambiguous_taxa	0	0	1	0	0	0	TGAGGAATATTGGTCAATGGCGAGCGCTGAAGCAGCCAGTGAAGCTGACGAGTACGCGCCCTATGGGTGTAAAGCTGTTTATAAGGGAATAAAGTGAAGTCTCGTAGAGCTTTTGCATGTACTCTATGATAAAGGACCGCGTAATCTCGTGCCAGCAGCGGTAAATCGGAAGGTCGGGCTTATCCGGATTATTTGGTTTAAAGGCGAGTGAAGCGGTGTGTGAAGTAGACGCTCAACGTCTGACGCGGAACCTGGTTTCTTGATAGCACAAGGTGGCGGAATCTGGTGTAGCGGTGAAATGCTAGATATCAACGAAGAACCTCGATTGCGAAGCAGCTTCACTGGAGCGCAACTGACGTGAAGCTCGAAATGCGGGTATCAACA
Ambiguous_taxa, KF941208.1.1402	KF941208.1.1402	D_0_Bacteria, D_1_Proteobacteria, D_2_Gammaproteobacteria, D_3_Enterobacteriales, D_4_Enterobacteriaceae, D_5_Pantoea, D_6_Arthrobacter agilis	0	0	0	0	1	0	TGAGGAATATTGGTCAATGGCGAGCGCTGAAGCAGCCAGTGAAGCTGACGAGTACGCGCCCTATGGGTGTAAAGCTGTTTATAAGGGAATAAAGTGAAGTCTCGTAGAGCTTTTGCATGTACTCTATGATAAAGGACCGCGTAATCTCGTGCCAGCAGCGGTAAATCGGAAGGTCGGGCTTATCCGGATTATTTGGTTTAAAGGCGAGTGAAGCGGTGTGTGAAGTAGACGCTCAACGTCTGACGCGGAACCTGGTTTCTTGATAGCACAAGGTGGCGGAATCTGGTGTAGCGGTGAAATGCTAGATATCAACGAAGAACCTCGATTGCGAAGCAGCTTCACTGGAGCGCAACTGACGTGAAGCTCGAAATGCGGGTATCAACA
D_6_Arthrobacter agilis, KY859788.1.1402	KY859788.1.1402	D_0_Bacteria, D_1_Actinobacteria, D_2_Actinobacteria, D_3_Micrococcales, D_4_Micrococaceae, D_5_Arthrobacter, D_6_Arthrobacter agilis	0	0	2	0	0	0	TGAGGAATATTGGTCAATGGCGAGCGCTGAAGCAGCCAGTGAAGCTGACGAGTACGCGCCCTATGGGTGTAAAGCTGTTTATAAGGGAATAAAGTGAAGTCTCGTAGAGCTTTTGCATGTACTCTATGATAAAGGACCGCGTAATCTCGTGCCAGCAGCGGTAAATCGGAAGGTCGGGCTTATCCGGATTATTTGGTTTAAAGGCGAGTGAAGCGGTGTGTGAAGTAGACGCTCAACGTCTGACGCGGAACCTGGTTTCTTGATAGCACAAGGTGGCGGAATCTGGTGTAGCGGTGAAATGCTAGATATCAACGAAGAACCTCGATTGCGAAGCAGCTTCACTGGAGCGCAACTGACGTGAAGCTCGAAATGCGGGTATCAACA
D_6_uncultured bacterium, EU775986.1.1401	EU775986.1.1401	D_0_Bacteria, D_1_Bacteroidetes, D_2_Bacteroidia, D_3_Bacteroidales, D_4_Bacteroidaceae, D_5_Bacteroides, D_6_uncultured bacterium	0	0	3	0	0	0	TGAGGAATATTGGTCAATGGCGAGCGCTGAAGCAGCCAGTGAAGCTGACGAGTACGCGCCCTATGGGTGTAAAGCTGTTTATAAGGGAATAAAGTGAAGTCTCGTAGAGCTTTTGCATGTACTCTATGATAAAGGACCGCGTAATCTCGTGCCAGCAGCGGTAAATCGGAAGGTCGGGCTTATCCGGATTATTTGGTTTAAAGGCGAGTGAAGCGGTGTGTGAAGTAGACGCTCAACGTCTGACGCGGAACCTGGTTTCTTGATAGCACAAGGTGGCGGAATCTGGTGTAGCGGTGAAATGCTAGATATCAACGAAGAACCTCGATTGCGAAGCAGCTTCACTGGAGCGCAACTGACGTGAAGCTCGAAATGCGGGTATCAACA
Ambiguous_taxa, FJ164058.1.1400	FJ164058.1.1400	D_0_Bacteria, D_1_Actinobacteria, D_2_Actinobacteria, D_3_Micrococcales, D_4_Microbacteriaceae, D_5_Lefsonia, Ambiguous_taxa	0	0	2	0	0	0	TGAGGAATATTGGTCAATGGCGAGCGCTGAAGCAGCCAGTGAAGCTGACGAGTACGCGCCCTATGGGTGTAAAGCTGTTTATAAGGGAATAAAGTGAAGTCTCGTAGAGCTTTTGCATGTACTCTATGATAAAGGACCGCGTAATCTCGTGCCAGCAGCGGTAAATCGGAAGGTCGGGCTTATCCGGATTATTTGGTTTAAAGGCGAGTGAAGCGGTGTGTGAAGTAGACGCTCAACGTCTGACGCGGAACCTGGTTTCTTGATAGCACAAGGTGGCGGAATCTGGTGTAGCGGTGAAATGCTAGATATCAACGAAGAACCTCGATTGCGAAGCAGCTTCACTGGAGCGCAACTGACGTGAAGCTCGAAATGCGGGTATCAACA
D_6_uncultured bacterium, DQ793727.1.1397	DQ793727.1.1397	D_0_Bacteria, D_1_Firmicutes, D_2_Clostridia, D_3_Clostridiales, D_4_Ruminococcaceae, D_5_Ruminococcus, D_6_uncultured bacterium	0	0	1	0	0	0	TGAGGAATATTGGTCAATGGCGAGCGCTGAAGCAGCCAGTGAAGCTGACGAGTACGCGCCCTATGGGTGTAAAGCTGTTTATAAGGGAATAAAGTGAAGTCTCGTAGAGCTTTTGCATGTACTCTATGATAAAGGACCGCGTAATCTCGTGCCAGCAGCGGTAAATCGGAAGGTCGGGCTTATCCGGATTATTTGGTTTAAAGGCGAGTGAAGCGGTGTGTGAAGTAGACGCTCAACGTCTGACGCGGAACCTGGTTTCTTGATAGCACAAGGTGGCGGAATCTGGTGTAGCGGTGAAATGCTAGATATCAACGAAGAACCTCGATTGCGAAGCAGCTTCACTGGAGCGCAACTGACGTGAAGCTCGAAATGCGGGTATCAACA
D_6_uncultured bacterium, DQ795254.1.1395	DQ795254.1.1395	D_0_Bacteria, D_1_Firmicutes, D_2_Clostridia, D_3_Clostridiales, D_4_Lachnospiraceae, D_5_Eubacterium] hallii group, D_6_uncultured bacterium	0	0	2	0	0	0	TGAGGAATATTGGTCAATGGCGAGCGCTGAAGCAGCCAGTGAAGCTGACGAGTACGCGCCCTATGGGTGTAAAGCTGTTTATAAGGGAATAAAGTGAAGTCTCGTAGAGCTTTTGCATGTACTCTATGATAAAGGACCGCGTAATCTCGTGCCAGCAGCGGTAAATCGGAAGGTCGGGCTTATCCGGATTATTTGGTTTAAAGGCGAGTGAAGCGGTGTGTGAAGTAGACGCTCAACGTCTGACGCGGAACCTGGTTTCTTGATAGCACAAGGTGGCGGAATCTGGTGTAGCGGTGAAATGCTAGATATCAACGAAGAACCTCGATTGCGAAGCAGCTTCACTGGAGCGCAACTGACGTGAAGCTCGAAATGCGGGTATCAACA
D_6_uncultured bacterium, JN904060.1.1395	JN904060.1.1395	D_0_Bacteria, D_1_Proteobacteria, D_2_Gammaproteobacteria, D_3_Pseudomonadales, D_4_Moraxellaceae, D_5_Acinetobacter	0	5	0	0	0	0	TGAGGAATATTGGTCAATGGCGAGCGCTGAAGCAGCCAGTGAAGCTGACGAGTACGCGCCCTATGGGTGTAAAGCTGTTTATAAGGGAATAAAGTGAAGTCTCGTAGAGCTTTTGCATGTACTCTATGATAAAGGACCGCGTAATCTCGTGCCAGCAGCGGTAAATCGGAAGGTCGGGCTTATCCGGATTATTTGGTTTAAAGGCGAGTGAAGCGGTGTGTGAAGTAGACGCTCAACGTCTGACGCGGAACCTGGTTTCTTGATAGCACAAGGTGGCGGAATCTGGTGTAGCGGTGAAATGCTAGATATCAACGAAGAACCTCGATTGCGAAGCAGCTTCACTGGAGCGCAACTGACGTGAAGCTCGAAATGCGGGTATCAACA

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