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JOB ID: 87890587-719a-497a-a90d-1e29a2032cba

RESULT PAGE: https://tygs.dsmz.de/user_results/show?guid=87890587-719a-497a-a90d-1e29a2032cba

Table 1: Phylogenies

Publication-ready versions of both the genome-scale GBDP tree and the 16S rRNA gene sequence tree can be customized and exported either in SVG (vector graphic) or PNG format from within the phylogeny viewers in your TYGS result page. For publications the **SVG format is recommended** because it is lossless, always keeps its high resolution and can also be easily converted to other popular formats such as PDF or EPS. Please follow the link provided above!

Table 2: Identification

The below list contains the result of the TYGS species identification routine.

Explanation of remarks that might occur in the below table:

remark [R1]: The TYGS type strain database is automatically updated on an almost daily basis. However, if a particular type strain genome is not available in the TYGS database, this can have several reasons which are detailed in the FAQ. You can request an extended 16S rRNA gene analysis via the 16S tree viewer found in your result page to detect **not yet genome-sequenced** type strains relevant for your study.

remark [R2]: > 70% dDDH value (formula d_4) and (almost) minimal dDDH values for gene-content formulae d_0 and d_6 indicate a potentially unreliable identification result and should thus be checked via the 16S rRNA gene sequence similarity. Such strong deviations can, in principle, be caused by sequence contamination.

remark [R3]: G+C content difference of > 1 % indicates a potentially unreliable identification result because within species G+C content varies no more than 1 %, if computed from genome sequences (PMID: 24505073).

Strain	Conclusion	Identification result	Remark
'GCF_001267175.1_ASM126717v1_genomic'	belongs to known species	<i>Thiopseudomonas alkaliphila</i>	
'GCF_001267195.1_ASM126719v1_genomic'	belongs to known species	<i>Thiopseudomonas alkaliphila</i>	
'GCF_001267215.1_ASM126721v1_genomic'	belongs to known species	<i>Thiopseudomonas alkaliphila</i>	
'GCF_001267255.1_ASM126725v1_genomic'	belongs to known species	<i>Thiopseudomonas alkaliphila</i>	
'GCF_001267275.1_ASM126727v1_genomic'	belongs to known species	<i>Thiopseudomonas alkaliphila</i>	
'GCF_001267295.1_ASM126729v1_genomic'	belongs to known species	<i>Thiopseudomonas alkaliphila</i>	
'GCF_001267315.1_ASM126731v1_genomic'	belongs to known species	<i>Thiopseudomonas alkaliphila</i>	
'GCF_030328955.1_ASM3032895v1_genomic'	belongs to known species	<i>Thiopseudomonas alkaliphila</i>	
'GCF_030329025.1_ASM3032902v1_genomic'	belongs to known species	<i>Thiopseudomonas alkaliphila</i>	
'GCF_030328995.1_ASM3032899v1_genomic'	potential new species		see [R1]

Table 3: Pairwise comparisons of user genomes vs. type-strain genomes

The following table contains the pairwise dDDH values between your user genomes and the selected type-strain genomes. The dDDH values are provided along with their confidence intervals (C.I.) for the three different GBDP formulas:

- formula d_0 (a.k.a. GGDC formula 1): length of all HSPs divided by total genome length
- formula d_4 (a.k.a. GGDC formula 2): sum of all identities found in HSPs divided by overall HSP length
- formula d_6 (a.k.a. GGDC formula 3): sum of all identities found in HSPs divided by total genome length

Note: Formula d_4 is independent of genome length and is thus robust against the use of incomplete draft genomes. For other reasons for preferring formula d_4 , see the FAQ.

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'GCF_001267175.1_ASM126717v1_genomic.fna'	<i>Thiopseudomonas alkaliphila</i> B4199	100.0	[100.0 - 100.0]	100.0	[100.0 - 100.0]	100.0	[100.0 - 100.0]	0.0
'GCF_001267195.1_ASM126719v1_genomic.fna'	'GCF_001267215.1_ASM126721v1_genomic.fna'	94.3	[91.8 - 96.1]	96.7	[95.4 - 97.6]	96.5	[94.9 - 97.6]	0.05
'GCF_001267195.1_ASM126719v1_genomic.fna'	'GCF_001267255.1_ASM126725v1_genomic.fna'	91.9	[88.9 - 94.1]	94.5	[92.8 - 95.8]	94.5	[92.5 - 96.0]	0.03
'GCF_001267215.1_ASM126721v1_genomic.fna'	'GCF_001267255.1_ASM126725v1_genomic.fna'	95.0	[92.7 - 96.6]	94.5	[92.8 - 95.8]	96.7	[95.2 - 97.7]	0.08
'GCF_001267215.1_ASM126721v1_genomic.fna'	<i>Thiopseudomonas alkaliphila</i> B4199	89.7	[86.5 - 92.3]	93.7	[91.8 - 95.1]	92.9	[90.5 - 94.7]	0.14
'GCF_001267175.1_ASM126717v1_genomic.fna'	'GCF_001267215.1_ASM126721v1_genomic.fna'	89.7	[86.5 - 92.3]	93.7	[91.8 - 95.1]	92.9	[90.5 - 94.7]	0.14
'GCF_001267195.1_ASM126719v1_genomic.fna'	<i>Thiopseudomonas alkaliphila</i> B4199	85.2	[81.4 - 88.2]	93.1	[91.2 - 94.6]	89.3	[86.4 - 91.6]	0.1
'GCF_001267175.1_ASM126717v1_genomic.fna'	'GCF_001267195.1_ASM126719v1_genomic.fna'	85.2	[81.4 - 88.2]	93.1	[91.2 - 94.6]	89.3	[86.4 - 91.6]	0.1
'GCF_001267175.1_ASM126717v1_genomic.fna'	'GCF_001267255.1_ASM126725v1_genomic.fna'	86.2	[82.5 - 89.2]	92.7	[90.7 - 94.2]	90.0	[87.3 - 92.2]	0.07
'GCF_001267255.1_ASM126725v1_genomic.fna'	<i>Thiopseudomonas alkaliphila</i> B4199	86.2	[82.5 - 89.2]	92.7	[90.7 - 94.2]	90.0	[87.3 - 92.2]	0.07
'GCF_001267315.1_ASM126731v1_genomic.fna'	'GCF_030329025.1_ASM3032902v1_genomic.fna'	83.1	[79.3 - 86.4]	91.1	[88.9 - 92.9]	87.4	[84.3 - 89.9]	0.1
'GCF_001267215.1_ASM126721v1_genomic.fna'	'GCF_001267275.1_ASM126727v1_genomic.fna'	90.6	[87.4 - 93.0]	89.6	[87.2 - 91.5]	92.9	[90.6 - 94.7]	0.12
'GCF_001267195.1_ASM126719v1_genomic.fna'	'GCF_001267275.1_ASM126727v1_genomic.fna'	87.5	[84.0 - 90.3]	89.6	[87.3 - 91.6]	90.6	[87.9 - 92.7]	0.08
'GCF_001267255.1_ASM126725v1_genomic.fna'	'GCF_001267275.1_ASM126727v1_genomic.fna'	89.4	[86.1 - 92.0]	89.5	[87.1 - 91.5]	92.0	[89.6 - 94.0]	0.04
'GCF_001267175.1_ASM126717v1_genomic.fna'	'GCF_001267275.1_ASM126727v1_genomic.fna'	83.1	[79.3 - 86.3]	89.2	[86.8 - 91.2]	87.0	[84.0 - 89.6]	0.02
'GCF_001267275.1_ASM126727v1_genomic.fna'	<i>Thiopseudomonas alkaliphila</i> B4199	83.1	[79.3 - 86.3]	89.2	[86.8 - 91.2]	87.0	[84.0 - 89.6]	0.02
'GCF_001267275.1_ASM126727v1_genomic.fna'	'GCF_001267295.1_ASM126729v1_genomic.fna'	85.5	[81.8 - 88.5]	89.1	[86.7 - 91.1]	88.9	[86.1 - 91.3]	0.06
'GCF_001267255.1_ASM126725v1_genomic.fna'	'GCF_001267295.1_ASM126729v1_genomic.fna'	89.1	[85.7 - 91.7]	88.6	[86.1 - 90.7]	91.7	[89.1 - 93.6]	0.02
'GCF_001267215.1_ASM126721v1_genomic.fna'	'GCF_001267295.1_ASM126729v1_genomic.fna'	90.8	[87.6 - 93.2]	88.6	[86.1 - 90.6]	92.9	[90.6 - 94.7]	0.06
'GCF_001267195.1_ASM126719v1_genomic.fna'	'GCF_001267295.1_ASM126729v1_genomic.fna'	87.0	[83.4 - 89.9]	88.4	[86.0 - 90.5]	90.0	[87.2 - 92.2]	0.01
'GCF_001267295.1_ASM126729v1_genomic.fna'	<i>Thiopseudomonas alkaliphila</i> B4199	91.0	[87.9 - 93.3]	88.3	[85.9 - 90.4]	93.0	[90.7 - 94.8]	0.08

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'GCF_001267175.1_ASM126717v1_genomic.fna'	'GCF_001267295.1_ASM126729v1_genomic.fna'	91.0	[87.9 - 93.3]	88.3	[85.9 - 90.4]	93.0	[90.7 - 94.8]	0.08
'GCF_001267255.1_ASM126725v1_genomic.fna'	'GCF_001267315.1_ASM126731v1_genomic.fna'	84.2	[80.4 - 87.4]	86.8	[84.2 - 89.0]	87.5	[84.5 - 90.0]	0.22
'GCF_001267255.1_ASM126725v1_genomic.fna'	'GCF_030329025.1_ASM3032902v1_genomic.fna'	82.9	[79.1 - 86.2]	86.7	[84.1 - 88.9]	86.5	[83.4 - 89.1]	0.32
'GCF_001267195.1_ASM126719v1_genomic.fna'	'GCF_030329025.1_ASM3032902v1_genomic.fna'	79.7	[75.8 - 83.2]	86.7	[84.1 - 88.9]	83.8	[80.6 - 86.6]	0.36
'GCF_001267215.1_ASM126721v1_genomic.fna'	'GCF_001267315.1_ASM126731v1_genomic.fna'	87.8	[84.3 - 90.6]	86.6	[84.0 - 88.9]	90.4	[87.7 - 92.6]	0.3
'GCF_001267215.1_ASM126721v1_genomic.fna'	'GCF_030329025.1_ASM3032902v1_genomic.fna'	84.5	[80.7 - 87.6]	86.6	[83.9 - 88.8]	87.7	[84.7 - 90.2]	0.4
'GCF_001267315.1_ASM126731v1_genomic.fna'	<i>Thiopseudomonas alkaliphila</i> B4199	84.1	[80.3 - 87.3]	86.5	[83.8 - 88.7]	87.4	[84.4 - 89.9]	0.16
'GCF_001267175.1_ASM126717v1_genomic.fna'	'GCF_001267315.1_ASM126731v1_genomic.fna'	84.1	[80.3 - 87.3]	86.5	[83.8 - 88.7]	87.4	[84.4 - 89.9]	0.16
'GCF_001267195.1_ASM126719v1_genomic.fna'	'GCF_001267315.1_ASM126731v1_genomic.fna'	85.0	[81.3 - 88.1]	86.4	[83.7 - 88.6]	88.1	[85.2 - 90.5]	0.26
'GCF_001267275.1_ASM126727v1_genomic.fna'	'GCF_030329025.1_ASM3032902v1_genomic.fna'	82.0	[78.1 - 85.3]	85.9	[83.2 - 88.2]	85.6	[82.4 - 88.2]	0.28
'GCF_001267275.1_ASM126727v1_genomic.fna'	'GCF_001267315.1_ASM126731v1_genomic.fna'	84.0	[80.2 - 87.2]	85.9	[83.2 - 88.2]	87.3	[84.2 - 89.8]	0.18
'GCF_001267175.1_ASM126717v1_genomic.fna'	'GCF_030329025.1_ASM3032902v1_genomic.fna'	77.8	[73.8 - 81.3]	85.7	[83.0 - 88.0]	82.0	[78.7 - 85.0]	0.26
'GCF_030329025.1_ASM3032902v1_genomic.fna'	<i>Thiopseudomonas alkaliphila</i> B4199	77.8	[73.8 - 81.3]	85.7	[83.0 - 88.0]	82.0	[78.7 - 85.0]	0.26
'GCF_001267295.1_ASM126729v1_genomic.fna'	'GCF_001267315.1_ASM126731v1_genomic.fna'	84.8	[81.0 - 87.9]	85.4	[82.7 - 87.7]	87.8	[84.8 - 90.2]	0.24
'GCF_001267295.1_ASM126729v1_genomic.fna'	'GCF_030329025.1_ASM3032902v1_genomic.fna'	83.3	[79.4 - 86.5]	85.2	[82.5 - 87.5]	86.5	[83.4 - 89.1]	0.34
'GCF_001267315.1_ASM126731v1_genomic.fna'	'GCF_030328955.1_ASM3032895v1_genomic.fna'	81.2	[77.3 - 84.6]	80.4	[77.5 - 83.1]	84.0	[80.8 - 86.8]	0.4
'GCF_030328955.1_ASM3032895v1_genomic.fna'	'GCF_030329025.1_ASM3032902v1_genomic.fna'	76.7	[72.7 - 80.2]	79.7	[76.8 - 82.4]	80.0	[76.6 - 83.1]	0.5
'GCF_001267215.1_ASM126721v1_genomic.fna'	'GCF_030328955.1_ASM3032895v1_genomic.fna'	78.4	[74.4 - 81.9]	79.0	[76.0 - 81.7]	81.4	[78.0 - 84.3]	0.1
'GCF_001267255.1_ASM126725v1_genomic.fna'	'GCF_030328955.1_ASM3032895v1_genomic.fna'	76.5	[72.5 - 80.1]	78.7	[75.7 - 81.4]	79.7	[76.3 - 82.7]	0.18
'GCF_001267175.1_ASM126717v1_genomic.fna'	'GCF_030328955.1_ASM3032895v1_genomic.fna'	71.9	[67.9 - 75.5]	78.6	[75.6 - 81.3]	75.6	[72.1 - 78.8]	0.24
'GCF_030328955.1_ASM3032895v1_genomic.fna'	<i>Thiopseudomonas alkaliphila</i> B4199	71.9	[67.9 - 75.5]	78.6	[75.6 - 81.3]	75.6	[72.1 - 78.8]	0.24
'GCF_001267195.1_ASM126719v1_genomic.fna'	'GCF_030328955.1_ASM3032895v1_genomic.fna'	74.4	[70.5 - 78.1]	78.1	[75.1 - 80.8]	77.8	[74.3 - 80.9]	0.15
'GCF_001267275.1_ASM126727v1_genomic.fna'	'GCF_030328955.1_ASM3032895v1_genomic.fna'	78.2	[74.2 - 81.7]	77.8	[74.8 - 80.5]	81.0	[77.6 - 84.0]	0.22

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'GCF_001267295.1_ASM126729v1_genomic.fna'	'GCF_030328955.1_ASM3032895v1_genomic.fna'	75.6	[71.6 - 79.1]	77.4	[74.4 - 80.2]	78.7	[75.2 - 81.7]	0.16
'GCF_030328955.1_ASM3032895v1_genomic.fna'	'GCF_030328995.1_ASM3032899v1_genomic.fna'	77.7	[73.7 - 81.2]	65.7	[62.8 - 68.5]	78.1	[74.7 - 81.2]	0.55
'GCF_001267315.1_ASM126731v1_genomic.fna'	'GCF_030328995.1_ASM3032899v1_genomic.fna'	77.3	[73.3 - 80.8]	65.4	[62.4 - 68.2]	77.7	[74.2 - 80.8]	0.96
'GCF_030328995.1_ASM3032899v1_genomic.fna'	'GCF_030329025.1_ASM3032902v1_genomic.fna'	74.1	[70.2 - 77.8]	64.7	[61.8 - 67.6]	74.8	[71.4 - 78.0]	1.05
'GCF_030328995.1_ASM3032899v1_genomic.fna'	<i>Thiopseudomonas alkaliphila</i> B4199	71.5	[67.5 - 75.1]	64.3	[61.4 - 67.1]	72.4	[68.9 - 75.6]	0.8
'GCF_001267175.1_ASM126717v1_genomic.fna'	'GCF_030328995.1_ASM3032899v1_genomic.fna'	71.5	[67.5 - 75.1]	64.3	[61.4 - 67.1]	72.4	[68.9 - 75.6]	0.8
'GCF_001267275.1_ASM126727v1_genomic.fna'	'GCF_030328995.1_ASM3032899v1_genomic.fna'	76.3	[72.4 - 79.9]	63.9	[61.0 - 66.8]	76.5	[73.1 - 79.7]	0.77
'GCF_001267215.1_ASM126721v1_genomic.fna'	'GCF_030328995.1_ASM3032899v1_genomic.fna'	77.7	[73.7 - 81.3]	63.8	[60.9 - 66.6]	77.7	[74.2 - 80.8]	0.65
'GCF_001267295.1_ASM126729v1_genomic.fna'	'GCF_030328995.1_ASM3032899v1_genomic.fna'	75.6	[71.6 - 79.2]	63.8	[60.9 - 66.6]	75.9	[72.4 - 79.1]	0.71
'GCF_001267255.1_ASM126725v1_genomic.fna'	'GCF_030328995.1_ASM3032899v1_genomic.fna'	78.2	[74.2 - 81.7]	63.7	[60.8 - 66.6]	78.0	[74.6 - 81.1]	0.73
'GCF_001267195.1_ASM126719v1_genomic.fna'	'GCF_030328995.1_ASM3032899v1_genomic.fna'	76.1	[72.2 - 79.7]	63.0	[60.1 - 65.8]	76.2	[72.7 - 79.3]	0.7
'GCF_030329025.1_ASM3032902v1_genomic.fna'	<i>Acinetobacter towneri</i> DSM 14962	12.8	[10.1 - 16.1]	53.8	[51.1 - 56.5]	13.3	[10.9 - 16.0]	5.93
'GCF_030328955.1_ASM3032895v1_genomic.fna'	<i>Acinetobacter rongchengensis</i> WCHAc060115 T	12.5	[9.9 - 15.8]	53.8	[51.1 - 56.5]	13.0	[10.6 - 15.7]	9.99
'GCF_001267315.1_ASM126731v1_genomic.fna'	<i>Nitrosomonas stercoris</i> ATCC BAA-2718	13.0	[10.3 - 16.3]	53.5	[50.8 - 56.2]	13.4	[11.0 - 16.2]	2.4
'GCF_030328995.1_ASM3032899v1_genomic.fna'	<i>Acinetobacter defluvii</i> WCHA30	12.6	[9.9 - 15.8]	51.1	[48.5 - 53.8]	13.0	[10.6 - 15.7]	10.18
'GCF_030328995.1_ASM3032899v1_genomic.fna'	<i>Thauera butanivorans</i> NBRC 103042	12.5	[9.9 - 15.8]	49.5	[46.9 - 52.1]	13.0	[10.6 - 15.7]	17.94
'GCF_030328995.1_ASM3032899v1_genomic.fna'	<i>Nitrosomonas stercoris</i> ATCC BAA-2718	12.7	[10.0 - 16.0]	47.9	[45.3 - 50.5]	13.1	[10.8 - 15.9]	3.36
'GCF_030329025.1_ASM3032902v1_genomic.fna'	<i>Acinetobacter seohaensis</i> DSM 16313	12.9	[10.2 - 16.2]	47.5	[44.9 - 50.1]	13.3	[11.0 - 16.1]	5.76
'GCF_001267315.1_ASM126731v1_genomic.fna'	<i>Thauera butanivorans</i> NBRC 103042	12.6	[10.0 - 15.9]	47.2	[44.6 - 49.8]	13.1	[10.7 - 15.8]	18.9
'GCF_030328995.1_ASM3032899v1_genomic.fna'	<i>Acinetobacter rongchengensis</i> WCHAc060115 T	12.5	[9.9 - 15.8]	44.9	[42.4 - 47.5]	12.9	[10.6 - 15.7]	10.54
'GCF_030328955.1_ASM3032895v1_genomic.fna'	<i>Nitrosomonas stercoris</i> ATCC BAA-2718	12.7	[10.0 - 15.9]	43.9	[41.4 - 46.5]	13.1	[10.8 - 15.8]	2.81

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'GCF_001267315.1_ASM126731v1_genomic.fna'	<i>Acinetobacter baumannii</i> ATCC 19606	12.7	[10.1 - 16.0]	43.1	[40.6 - 45.7]	13.2	[10.8 - 15.9]	8.1
'GCF_001267315.1_ASM126731v1_genomic.fna'	<i>Ignatzschineria cameli</i> UAE-HKU57	12.8	[10.1 - 16.0]	41.2	[38.7 - 43.8]	13.2	[10.8 - 15.9]	5.51
'GCF_030329025.1_ASM3032902v1_genomic.fna'	<i>Nitrosomonas stercoris</i> ATCC BAA-2718	12.6	[9.9 - 15.9]	40.9	[38.4 - 43.4]	13.0	[10.7 - 15.8]	2.31
'GCF_001267315.1_ASM126731v1_genomic.fna'	<i>Psychrobacter fulvigenes</i> KC40T	12.8	[10.1 - 16.0]	40.7	[38.2 - 43.2]	13.2	[10.8 - 15.9]	3.12
'GCF_030328955.1_ASM3032895v1_genomic.fna'	<i>Thauera butanivorans</i> NBRC 103042	12.5	[9.9 - 15.8]	40.5	[38.0 - 43.0]	12.9	[10.6 - 15.7]	18.49
'GCF_030328955.1_ASM3032895v1_genomic.fna'	<i>Acinetobacter defluvii</i> WCHA30	12.6	[9.9 - 15.9]	39.6	[37.2 - 42.2]	13.0	[10.7 - 15.8]	9.62
'GCF_030329025.1_ASM3032902v1_genomic.fna'	<i>Acinetobacter rongchengensis</i> WCHAc060115 T	12.6	[9.9 - 15.9]	38.9	[36.4 - 41.4]	13.0	[10.7 - 15.8]	9.49
'GCF_030329025.1_ASM3032902v1_genomic.fna'	<i>Thauera butanivorans</i> NBRC 103042	12.5	[9.9 - 15.8]	38.9	[36.4 - 41.4]	12.9	[10.6 - 15.7]	19.0
'GCF_030328995.1_ASM3032899v1_genomic.fna'	<i>Acinetobacter baumannii</i> ATCC 19606	12.6	[10.0 - 15.9]	38.5	[36.1 - 41.0]	13.1	[10.7 - 15.8]	9.05
'GCF_030329025.1_ASM3032902v1_genomic.fna'	<i>Psychrobacter fulvigenes</i> KC40T	12.6	[10.0 - 15.9]	38.0	[35.5 - 40.5]	13.0	[10.7 - 15.8]	3.02
'GCF_030329025.1_ASM3032902v1_genomic.fna'	<i>Citrobacter tructae</i> SNU WT2	12.7	[10.0 - 15.9]	37.5	[35.0 - 40.0]	13.1	[10.7 - 15.8]	4.85
'GCF_001267315.1_ASM126731v1_genomic.fna'	<i>Acinetobacter rongchengensis</i> WCHAc060115 T	12.6	[9.9 - 15.8]	35.9	[33.4 - 38.4]	13.0	[10.7 - 15.7]	9.59
'GCF_030329025.1_ASM3032902v1_genomic.fna'	<i>Acinetobacter defluvii</i> WCHA30	12.7	[10.0 - 16.0]	35.7	[33.2 - 38.2]	13.1	[10.8 - 15.8]	9.12
'GCF_001267195.1_ASM126719v1_genomic.fna'	<i>Nitrosomonas stercoris</i> ATCC BAA-2718	12.7	[10.0 - 15.9]	35.6	[33.1 - 38.1]	13.1	[10.7 - 15.8]	2.66
'GCF_030328955.1_ASM3032895v1_genomic.fna'	<i>Psychrobacter fulvigenes</i> KC40T	12.6	[9.9 - 15.9]	35.6	[33.2 - 38.2]	13.0	[10.7 - 15.8]	3.52
'GCF_030328995.1_ASM3032899v1_genomic.fna'	<i>Psychrobacter fulvigenes</i> KC40T	12.6	[10.0 - 15.9]	35.5	[33.1 - 38.0]	13.0	[10.7 - 15.8]	4.07
'GCF_030329025.1_ASM3032902v1_genomic.fna'	<i>Acinetobacter baumannii</i> ATCC 19606	12.6	[10.0 - 15.9]	35.3	[32.9 - 37.8]	13.0	[10.7 - 15.8]	8.0
'GCF_030328955.1_ASM3032895v1_genomic.fna'	<i>Citrobacter tructae</i> SNU WT2	12.7	[10.0 - 15.9]	35.3	[32.8 - 37.8]	13.1	[10.7 - 15.8]	4.34
'GCF_030328955.1_ASM3032895v1_genomic.fna'	<i>Acinetobacter baumannii</i> ATCC 19606	12.6	[9.9 - 15.9]	35.1	[32.7 - 37.6]	13.0	[10.7 - 15.8]	8.5
'GCF_030328995.1_ASM3032899v1_genomic.fna'	<i>Citrobacter tructae</i> SNU WT2	12.7	[10.0 - 15.9]	33.5	[31.1 - 36.0]	13.1	[10.7 - 15.8]	3.79
'GCF_001267295.1_ASM126729v1_genomic.fna'	<i>Nitrosomonas stercoris</i> ATCC BAA-2718	12.7	[10.0 - 15.9]	33.2	[30.8 - 35.7]	13.1	[10.8 - 15.8]	2.65
'GCF_001267295.1_ASM126729v1_genomic.fna'	<i>Acinetobacter baumannii</i> ATCC 19606	12.7	[10.0 - 15.9]	31.4	[29.0 - 33.9]	13.1	[10.7 - 15.8]	8.34

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'GCF_001267315.1_ASM126731v1_genomic.fna'	<i>Citrobacter tructae</i> SNU WT2	12.7	[10.0 - 15.9]	30.8	[28.4 - 33.3]	13.1	[10.7 - 15.8]	4.75
'GCF_001267175.1_ASM126717v1_genomic.fna'	<i>Acinetobacter baumannii</i> ATCC 19606	12.7	[10.0 - 15.9]	30.5	[28.1 - 33.0]	13.1	[10.7 - 15.8]	8.26
'GCF_001267215.1_ASM126721v1_genomic.fna'	<i>Acinetobacter baumannii</i> ATCC 19606	12.7	[10.0 - 15.9]	30.5	[28.1 - 33.0]	13.1	[10.7 - 15.8]	8.4
'GCF_001267315.1_ASM126731v1_genomic.fna'	<i>Enterobacter cloacae</i> ATCC 13047	12.8	[10.1 - 16.0]	30.4	[28.0 - 32.9]	13.2	[10.8 - 15.9]	7.38
'GCF_001267275.1_ASM126727v1_genomic.fna'	<i>Acinetobacter baumannii</i> ATCC 19606	12.7	[10.0 - 15.9]	30.4	[28.0 - 32.9]	13.1	[10.7 - 15.8]	8.28
'GCF_001267195.1_ASM126719v1_genomic.fna'	<i>Acinetobacter baumannii</i> ATCC 19606	12.6	[10.0 - 15.9]	30.4	[28.0 - 32.9]	13.1	[10.7 - 15.8]	8.36
'GCF_001267315.1_ASM126731v1_genomic.fna'	<i>Shigella flexneri</i> ATCC 29903	12.8	[10.1 - 16.0]	30.4	[28.0 - 32.9]	13.2	[10.8 - 15.9]	3.46
'GCF_001267255.1_ASM126725v1_genomic.fna'	<i>Acinetobacter baumannii</i> ATCC 19606	12.7	[10.0 - 15.9]	30.3	[27.9 - 32.8]	13.1	[10.7 - 15.8]	8.32
'GCF_001267295.1_ASM126729v1_genomic.fna'	<i>Acinetobacter rongchengensis</i> WCHAc060115 T	12.6	[9.9 - 15.8]	30.2	[27.8 - 32.7]	13.0	[10.6 - 15.7]	9.83
'GCF_030328995.1_ASM3032899v1_genomic.fna'	<i>Ignatzschineria cameli</i> UAE-HKU57	12.6	[9.9 - 15.9]	30.0	[27.6 - 32.5]	13.0	[10.7 - 15.8]	6.46
'GCF_030328955.1_ASM3032895v1_genomic.fna'	<i>Ignatzschineria cameli</i> UAE-HKU57	12.6	[9.9 - 15.8]	30.0	[27.6 - 32.5]	13.0	[10.7 - 15.7]	5.91
'GCF_001267215.1_ASM126721v1_genomic.fna'	<i>Acinetobacter rongchengensis</i> WCHAc060115 T	12.6	[9.9 - 15.8]	29.2	[26.8 - 31.7]	13.0	[10.7 - 15.7]	9.89
'GCF_001267175.1_ASM126717v1_genomic.fna'	<i>Acinetobacter rongchengensis</i> WCHAc060115 T	12.6	[9.9 - 15.8]	29.2	[26.8 - 31.7]	13.0	[10.7 - 15.7]	9.75
'GCF_001267255.1_ASM126725v1_genomic.fna'	<i>Acinetobacter rongchengensis</i> WCHAc060115 T	12.6	[9.9 - 15.8]	28.9	[26.5 - 31.4]	13.0	[10.6 - 15.7]	9.81
'GCF_001267195.1_ASM126719v1_genomic.fna'	<i>Acinetobacter rongchengensis</i> WCHAc060115 T	12.5	[9.9 - 15.8]	28.7	[26.3 - 31.2]	13.0	[10.6 - 15.7]	9.84
'GCF_001267195.1_ASM126719v1_genomic.fna'	<i>Citrobacter tructae</i> SNU WT2	12.6	[9.9 - 15.9]	28.5	[26.1 - 31.0]	13.0	[10.7 - 15.8]	4.49
'GCF_001267315.1_ASM126731v1_genomic.fna'	<i>Acinetobacter defluvii</i> WCHA30	12.6	[9.9 - 15.9]	28.2	[25.8 - 30.7]	13.0	[10.7 - 15.8]	9.22
'GCF_001267195.1_ASM126719v1_genomic.fna'	<i>Psychrobacter fulvigenes</i> KC40T	12.6	[9.9 - 15.9]	27.9	[25.6 - 30.4]	13.0	[10.7 - 15.8]	3.37
'GCF_001267215.1_ASM126721v1_genomic.fna'	<i>Citrobacter tructae</i> SNU WT2	12.7	[10.0 - 15.9]	27.6	[25.3 - 30.1]	13.1	[10.7 - 15.8]	4.44
'GCF_001267175.1_ASM126717v1_genomic.fna'	<i>Citrobacter tructae</i> SNU WT2	12.6	[10.0 - 15.9]	27.6	[25.3 - 30.1]	13.1	[10.7 - 15.8]	4.59
'GCF_001267275.1_ASM126727v1_genomic.fna'	<i>Nitrosomonas stercoris</i> ATCC BAA-2718	12.6	[9.9 - 15.9]	27.5	[25.1 - 29.9]	13.0	[10.7 - 15.7]	2.59
'GCF_030329025.1_ASM3032902v1_genomic.fna'	<i>Ignatzschineria cameli</i> UAE-HKU57	12.6	[9.9 - 15.8]	27.5	[25.1 - 30.0]	13.0	[10.7 - 15.7]	5.41
'GCF_001267255.1_ASM126725v1_genomic.fna'	<i>Nitrosomonas stercoris</i> ATCC BAA-2718	12.6	[9.9 - 15.9]	27.5	[25.1 - 30.0]	13.0	[10.7 - 15.7]	2.63
'GCF_001267295.1_ASM126729v1_genomic.fna'	<i>Psychrobacter fulvigenes</i> KC40T	12.6	[10.0 - 15.9]	27.5	[25.1 - 30.0]	13.0	[10.7 - 15.8]	3.36
'GCF_001267175.1_ASM126717v1_genomic.fna'	<i>Psychrobacter fulvigenes</i> KC40T	12.6	[10.0 - 15.9]	27.5	[25.1 - 30.0]	13.0	[10.7 - 15.8]	3.28

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'GCF_001267255.1_ASM126725v1_genomic.fna'	<i>Citrobacter tructae</i> SNU WT2	12.6	[10.0 - 15.9]	27.5	[25.2 - 30.0]	13.0	[10.7 - 15.8]	4.52
'GCF_001267175.1_ASM126717v1_genomic.fna'	<i>Nitrosomonas stercoris</i> ATCC BAA-2718	12.6	[10.0 - 15.9]	27.5	[25.1 - 29.9]	13.0	[10.7 - 15.8]	2.56
'GCF_001267275.1_ASM126727v1_genomic.fna'	<i>Citrobacter tructae</i> SNU WT2	12.6	[10.0 - 15.9]	27.5	[25.1 - 30.0]	13.0	[10.7 - 15.8]	4.56
'GCF_001267215.1_ASM126721v1_genomic.fna'	<i>Psychrobacter fulvigenes</i> KC40T	12.6	[10.0 - 15.9]	27.4	[25.1 - 29.9]	13.0	[10.7 - 15.8]	3.42
'GCF_030328955.1_ASM3032895v1_genomic.fna'	<i>Enterobacter cloacae</i> ATCC 13047	12.7	[10.0 - 15.9]	27.2	[24.8 - 29.7]	13.1	[10.7 - 15.8]	6.98
'GCF_030329025.1_ASM3032902v1_genomic.fna'	<i>Enterobacter cloacae</i> ATCC 13047	12.7	[10.0 - 15.9]	27.2	[24.9 - 29.7]	13.1	[10.7 - 15.8]	7.48
'GCF_001267315.1_ASM126731v1_genomic.fna'	<i>Acinetobacter towneri</i> DSM 14962	12.6	[9.9 - 15.8]	27.2	[24.9 - 29.7]	13.0	[10.7 - 15.7]	6.03
'GCF_001267275.1_ASM126727v1_genomic.fna'	<i>Psychrobacter fulvigenes</i> KC40T	12.6	[10.0 - 15.9]	27.1	[24.7 - 29.5]	13.0	[10.7 - 15.8]	3.3
'GCF_001267255.1_ASM126725v1_genomic.fna'	<i>Psychrobacter fulvigenes</i> KC40T	12.6	[10.0 - 15.9]	27.1	[24.8 - 29.6]	13.0	[10.7 - 15.8]	3.34
'GCF_001267295.1_ASM126729v1_genomic.fna'	<i>Acinetobacter seohaensis</i> DSM 16313	12.6	[9.9 - 15.9]	27.0	[24.6 - 29.4]	13.0	[10.7 - 15.8]	6.11
'GCF_001267315.1_ASM126731v1_genomic.fna'	<i>Acinetobacter seohaensis</i> DSM 16313	12.6	[9.9 - 15.9]	26.9	[24.6 - 29.4]	13.0	[10.7 - 15.8]	5.86
'GCF_030328995.1_ASM3032899v1_genomic.fna'	<i>Enterobacter cloacae</i> ATCC 13047	12.7	[10.0 - 16.0]	26.6	[24.2 - 29.1]	13.1	[10.8 - 15.8]	6.42
'GCF_030328955.1_ASM3032895v1_genomic.fna'	<i>Shigella flexneri</i> ATCC 29903	12.6	[10.0 - 15.9]	26.6	[24.3 - 29.1]	13.0	[10.7 - 15.8]	3.06
'GCF_001267215.1_ASM126721v1_genomic.fna'	<i>Acinetobacter seohaensis</i> DSM 16313	12.6	[9.9 - 15.9]	26.5	[24.1 - 29.0]	13.0	[10.7 - 15.8]	6.17
'GCF_001267175.1_ASM126717v1_genomic.fna'	<i>Acinetobacter seohaensis</i> DSM 16313	12.6	[9.9 - 15.9]	26.5	[24.1 - 29.0]	13.0	[10.7 - 15.8]	6.02
'GCF_001267175.1_ASM126717v1_genomic.fna'	<i>Thauera butanivorans</i> NBRC 103042	12.6	[9.9 - 15.8]	26.3	[23.9 - 28.7]	13.0	[10.6 - 15.7]	18.74
'GCF_001267195.1_ASM126719v1_genomic.fna'	<i>Ignatzschineria cameli</i> UAE-HKU57	12.6	[9.9 - 15.8]	26.2	[23.9 - 28.7]	13.0	[10.7 - 15.7]	5.76
'GCF_001267255.1_ASM126725v1_genomic.fna'	<i>Thauera butanivorans</i> NBRC 103042	12.5	[9.9 - 15.8]	26.2	[23.8 - 28.7]	13.0	[10.6 - 15.7]	18.67
'GCF_001267195.1_ASM126719v1_genomic.fna'	<i>Thauera butanivorans</i> NBRC 103042	12.5	[9.9 - 15.8]	26.2	[23.9 - 28.7]	12.9	[10.6 - 15.7]	18.64
'GCF_001267215.1_ASM126721v1_genomic.fna'	<i>Thauera butanivorans</i> NBRC 103042	12.6	[9.9 - 15.8]	26.2	[23.9 - 28.7]	13.0	[10.6 - 15.7]	18.59
'GCF_001267295.1_ASM126729v1_genomic.fna'	<i>Thauera butanivorans</i> NBRC 103042	12.6	[9.9 - 15.8]	26.1	[23.7 - 28.6]	13.0	[10.6 - 15.7]	18.66
'GCF_001267295.1_ASM126729v1_genomic.fna'	<i>Citrobacter tructae</i> SNU WT2	12.7	[10.0 - 15.9]	25.9	[23.6 - 28.4]	13.1	[10.7 - 15.8]	4.5
'GCF_001267215.1_ASM126721v1_genomic.fna'	<i>Nitrosomonas stercoris</i> ATCC BAA-2718	12.6	[9.9 - 15.9]	25.8	[23.5 - 28.3]	13.0	[10.7 - 15.8]	2.71
'GCF_001267255.1_ASM126725v1_genomic.fna'	<i>Acinetobacter seohaensis</i> DSM 16313	12.6	[9.9 - 15.9]	25.7	[23.4 - 28.2]	13.0	[10.7 - 15.8]	6.09
'GCF_001267275.1_ASM126727v1_genomic.fna'	<i>Acinetobacter seohaensis</i> DSM 16313	12.6	[9.9 - 15.9]	25.7	[23.4 - 28.2]	13.0	[10.7 - 15.8]	6.05
'GCF_001267275.1_ASM126727v1_genomic.fna'	<i>Thauera butanivorans</i> NBRC 103042	12.5	[9.9 - 15.8]	25.7	[23.4 - 28.2]	13.0	[10.6 - 15.7]	18.72

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'GCF_001267275.1_ASM126727v1_genomic.fna'	<i>Acinetobacter rongchengensis</i> WCHAc060115 T	12.6	[9.9 - 15.8]	25.6	[23.3 - 28.1]	13.0	[10.6 - 15.7]	9.77
'GCF_001267175.1_ASM126717v1_genomic.fna'	<i>Ignatzschineria cameli</i> UAE-HKU57	12.6	[9.9 - 15.9]	25.6	[23.2 - 28.0]	13.0	[10.7 - 15.8]	5.66
'GCF_030328995.1_ASM3032899v1_genomic.fna'	<i>Shigella flexneri</i> ATCC 29903	12.7	[10.0 - 15.9]	25.5	[23.1 - 27.9]	13.1	[10.7 - 15.8]	2.51
'GCF_001267215.1_ASM126721v1_genomic.fna'	<i>Ignatzschineria cameli</i> UAE-HKU57	12.6	[9.9 - 15.9]	25.5	[23.2 - 28.0]	13.0	[10.7 - 15.8]	5.81
'GCF_001267295.1_ASM126729v1_genomic.fna'	<i>Shigella flexneri</i> ATCC 29903	12.7	[10.0 - 15.9]	25.3	[23.0 - 27.8]	13.1	[10.7 - 15.8]	3.22
'GCF_030329025.1_ASM3032902v1_genomic.fna'	<i>Shigella flexneri</i> ATCC 29903	12.6	[10.0 - 15.9]	25.3	[23.0 - 27.8]	13.0	[10.7 - 15.8]	3.56
'GCF_001267295.1_ASM126729v1_genomic.fna'	<i>Acinetobacter towneri</i> DSM 14962	12.6	[9.9 - 15.8]	25.2	[22.8 - 27.6]	13.0	[10.7 - 15.7]	6.27
'GCF_001267215.1_ASM126721v1_genomic.fna'	<i>Acinetobacter towneri</i> DSM 14962	12.6	[9.9 - 15.8]	25.1	[22.7 - 27.5]	13.0	[10.7 - 15.7]	6.33
'GCF_001267175.1_ASM126717v1_genomic.fna'	<i>Acinetobacter towneri</i> DSM 14962	12.6	[9.9 - 15.8]	25.1	[22.8 - 27.6]	13.0	[10.7 - 15.7]	6.19
'GCF_001267195.1_ASM126719v1_genomic.fna'	<i>Acinetobacter seohaensis</i> DSM 16313	12.6	[9.9 - 15.9]	25.0	[22.6 - 27.4]	13.0	[10.7 - 15.7]	6.12
'GCF_001267255.1_ASM126725v1_genomic.fna'	<i>Ignatzschineria cameli</i> UAE-HKU57	12.6	[9.9 - 15.9]	25.0	[22.7 - 27.5]	13.0	[10.7 - 15.7]	5.73
'GCF_001267175.1_ASM126717v1_genomic.fna'	<i>Shigella flexneri</i> ATCC 29903	12.7	[10.0 - 15.9]	24.9	[22.6 - 27.4]	13.1	[10.7 - 15.8]	3.3
'GCF_001267215.1_ASM126721v1_genomic.fna'	<i>Shigella flexneri</i> ATCC 29903	12.7	[10.0 - 15.9]	24.9	[22.6 - 27.4]	13.1	[10.7 - 15.8]	3.16
'GCF_030328955.1_ASM3032895v1_genomic.fna'	<i>Acinetobacter towneri</i> DSM 14962	12.6	[9.9 - 15.8]	24.7	[22.3 - 27.1]	13.0	[10.6 - 15.7]	6.43
'GCF_001267195.1_ASM126719v1_genomic.fna'	<i>Enterobacter cloacae</i> ATCC 13047	12.6	[10.0 - 15.9]	24.7	[22.4 - 27.2]	13.0	[10.7 - 15.8]	7.12
'GCF_001267255.1_ASM126725v1_genomic.fna'	<i>Shigella flexneri</i> ATCC 29903	12.7	[10.0 - 15.9]	24.7	[22.4 - 27.2]	13.1	[10.7 - 15.8]	3.24
'GCF_001267215.1_ASM126721v1_genomic.fna'	<i>Enterobacter cloacae</i> ATCC 13047	12.7	[10.0 - 15.9]	24.6	[22.3 - 27.1]	13.1	[10.7 - 15.8]	7.08
'GCF_001267215.1_ASM126721v1_genomic.fna'	<i>Acinetobacter defluvii</i> WCHA30	12.6	[9.9 - 15.9]	24.6	[22.3 - 27.1]	13.0	[10.7 - 15.7]	9.52
'GCF_001267175.1_ASM126717v1_genomic.fna'	<i>Enterobacter cloacae</i> ATCC 13047	12.7	[10.0 - 15.9]	24.6	[22.3 - 27.1]	13.1	[10.7 - 15.8]	7.22
'GCF_001267295.1_ASM126729v1_genomic.fna'	<i>Enterobacter cloacae</i> ATCC 13047	12.7	[10.0 - 15.9]	24.6	[22.3 - 27.1]	13.1	[10.7 - 15.8]	7.14
'GCF_001267275.1_ASM126727v1_genomic.fna'	<i>Enterobacter cloacae</i> ATCC 13047	12.7	[10.0 - 15.9]	24.5	[22.2 - 27.0]	13.1	[10.7 - 15.8]	7.2
'GCF_001267255.1_ASM126725v1_genomic.fna'	<i>Enterobacter cloacae</i> ATCC 13047	12.7	[10.0 - 15.9]	24.4	[22.1 - 26.9]	13.1	[10.7 - 15.8]	7.15
'GCF_001267175.1_ASM126717v1_genomic.fna'	<i>Acinetobacter defluvii</i> WCHA30	12.6	[9.9 - 15.9]	24.3	[22.0 - 26.8]	13.0	[10.7 - 15.7]	9.38
'GCF_001267295.1_ASM126729v1_genomic.fna'	<i>Acinetobacter defluvii</i> WCHA30	12.6	[9.9 - 15.9]	24.3	[22.0 - 26.8]	13.0	[10.7 - 15.7]	9.46
'GCF_001267255.1_ASM126725v1_genomic.fna'	<i>Acinetobacter towneri</i> DSM 14962	12.6	[9.9 - 15.8]	24.2	[21.9 - 26.7]	13.0	[10.6 - 15.7]	6.25
'GCF_001267275.1_ASM126727v1_genomic.fna'	<i>Acinetobacter towneri</i> DSM 14962	12.6	[9.9 - 15.8]	24.2	[21.9 - 26.7]	13.0	[10.6 - 15.7]	6.21

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'GCF_001267275.1_ASM126727v1_genomic.fna'	<i>Shigella flexneri</i> ATCC 29903	12.7	[10.0 - 15.9]	23.9	[21.6 - 26.4]	13.1	[10.7 - 15.8]	3.28
'GCF_030328995.1_ASM3032899v1_genomic.fna'	<i>Acinetobacter towneri</i> DSM 14962	12.5	[9.9 - 15.8]	23.9	[21.6 - 26.4]	12.9	[10.6 - 15.7]	6.98
'GCF_001267195.1_ASM126719v1_genomic.fna'	<i>Shigella flexneri</i> ATCC 29903	12.7	[10.0 - 15.9]	23.8	[21.5 - 26.3]	13.0	[10.7 - 15.8]	3.21
'GCF_001267275.1_ASM126727v1_genomic.fna'	<i>Ignatzschineria cameli</i> UAE-HKU57	12.6	[9.9 - 15.9]	23.7	[21.4 - 26.2]	13.0	[10.7 - 15.8]	5.69
'GCF_030329025.1_ASM3032902v1_genomic.fna'	<i>Pseudomonas yangonensis</i> JCM 33396	12.8	[10.1 - 16.1]	23.6	[21.3 - 26.0]	13.2	[10.9 - 16.0]	15.81
'GCF_001267275.1_ASM126727v1_genomic.fna'	<i>Acinetobacter defluvii</i> WCHA30	12.6	[9.9 - 15.8]	23.6	[21.3 - 26.1]	13.0	[10.7 - 15.7]	9.4
'GCF_001267295.1_ASM126729v1_genomic.fna'	<i>Pseudomonas shirazensis</i> SWRI56	12.9	[10.2 - 16.2]	23.6	[21.3 - 26.0]	13.3	[11.0 - 16.1]	14.41
'GCF_001267215.1_ASM126721v1_genomic.fna'	<i>Pseudomonas shirazensis</i> SWRI56	12.9	[10.2 - 16.2]	23.5	[21.2 - 26.0]	13.3	[11.0 - 16.1]	14.35
'GCF_001267175.1_ASM126717v1_genomic.fna'	<i>Pseudomonas shirazensis</i> SWRI56	12.9	[10.2 - 16.2]	23.5	[21.2 - 26.0]	13.3	[11.0 - 16.1]	14.5
'GCF_001267255.1_ASM126725v1_genomic.fna'	<i>Acinetobacter defluvii</i> WCHA30	12.6	[9.9 - 15.8]	23.5	[21.2 - 26.0]	13.0	[10.7 - 15.7]	9.44
'GCF_001267315.1_ASM126731v1_genomic.fna'	<i>Pseudomonas straminea</i> JCM 2783	12.7	[10.0 - 16.0]	23.4	[21.1 - 25.9]	13.1	[10.8 - 15.9]	16.02
'GCF_030328995.1_ASM3032899v1_genomic.fna'	<i>Chryseomonas asuensis</i> JCM 13501	12.7	[10.1 - 16.0]	23.4	[21.1 - 25.8]	13.1	[10.8 - 15.9]	5.42
'GCF_001267195.1_ASM126719v1_genomic.fna'	<i>Acinetobacter towneri</i> DSM 14962	12.6	[9.9 - 15.8]	23.3	[21.0 - 25.8]	13.0	[10.6 - 15.7]	6.28
'GCF_001267295.1_ASM126729v1_genomic.fna'	<i>Pseudomonas straminea</i> JCM 2783	12.7	[10.1 - 16.0]	23.1	[20.8 - 25.6]	13.1	[10.8 - 15.9]	15.78
'GCF_001267275.1_ASM126727v1_genomic.fna'	<i>Pseudomonas shirazensis</i> SWRI56	12.9	[10.2 - 16.2]	23.1	[20.8 - 25.6]	13.3	[10.9 - 16.1]	14.47
'GCF_001267195.1_ASM126719v1_genomic.fna'	<i>Acinetobacter defluvii</i> WCHA30	12.6	[9.9 - 15.8]	23.1	[20.8 - 25.5]	13.0	[10.6 - 15.7]	9.48
'GCF_001267255.1_ASM126725v1_genomic.fna'	<i>Pseudomonas shirazensis</i> SWRI56	12.9	[10.2 - 16.2]	23.1	[20.8 - 25.6]	13.3	[10.9 - 16.1]	14.43
'GCF_001267175.1_ASM126717v1_genomic.fna'	<i>Pseudomonas straminea</i> JCM 2783	12.7	[10.1 - 16.0]	23.1	[20.8 - 25.5]	13.1	[10.8 - 15.9]	15.86
'GCF_001267315.1_ASM126731v1_genomic.fna'	<i>Pseudomonas shirazensis</i> SWRI56	12.9	[10.2 - 16.2]	23.0	[20.7 - 25.4]	13.3	[11.0 - 16.1]	14.65
'GCF_001267195.1_ASM126719v1_genomic.fna'	<i>Pseudomonas tensinigenes</i> ZA 5.3	12.8	[10.1 - 16.1]	23.0	[20.7 - 25.5]	13.2	[10.9 - 16.0]	11.71
'GCF_001267215.1_ASM126721v1_genomic.fna'	<i>Pseudomonas straminea</i> JCM 2783	12.7	[10.1 - 16.0]	23.0	[20.8 - 25.5]	13.1	[10.8 - 15.9]	15.72
'GCF_001267175.1_ASM126717v1_genomic.fna'	<i>Pseudomonas tensinigenes</i> ZA 5.3	12.9	[10.2 - 16.1]	23.0	[20.8 - 25.5]	13.2	[10.9 - 16.0]	11.81
'GCF_001267315.1_ASM126731v1_genomic.fna'	<i>Pseudomonas yangonensis</i> JCM 33396	12.9	[10.2 - 16.2]	22.9	[20.6 - 25.4]	13.3	[10.9 - 16.0]	15.71
'GCF_001267295.1_ASM126729v1_genomic.fna'	<i>Chryseomonas asuensis</i> JCM 13501	12.7	[10.0 - 16.0]	22.9	[20.6 - 25.3]	13.1	[10.8 - 15.9]	6.13
'GCF_001267215.1_ASM126721v1_genomic.fna'	<i>Pseudomonas tensinigenes</i> ZA 5.3	12.9	[10.2 - 16.1]	22.9	[20.6 - 25.3]	13.2	[10.9 - 16.0]	11.66
'GCF_001267195.1_ASM126719v1_genomic.fna'	<i>Pseudomonas shirazensis</i> SWRI56	12.9	[10.2 - 16.2]	22.9	[20.6 - 25.4]	13.3	[10.9 - 16.0]	14.4

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'GCF_001267175.1_ASM126717v1_genomic.fna'	<i>Chryseomonas asuensis</i> JCM 13501	12.7	[10.0 - 16.0]	22.8	[20.5 - 25.3]	13.1	[10.8 - 15.9]	6.22
'GCF_001267315.1_ASM126731v1_genomic.fna'	<i>Chryseomonas asuensis</i> JCM 13501	12.7	[10.0 - 16.0]	22.8	[20.5 - 25.3]	13.1	[10.8 - 15.9]	6.37
'GCF_001267315.1_ASM126731v1_genomic.fna'	<i>Pseudomonas indoloxydans</i> JCM 14246	12.8	[10.1 - 16.1]	22.8	[20.5 - 25.2]	13.2	[10.8 - 16.0]	15.04
'GCF_001267215.1_ASM126721v1_genomic.fna'	<i>Chryseomonas asuensis</i> JCM 13501	12.7	[10.0 - 16.0]	22.8	[20.5 - 25.3]	13.1	[10.8 - 15.9]	6.07
'GCF_001267175.1_ASM126717v1_genomic.fna'	<i>Pseudomonas matsuisoli</i> JCM 30078	12.8	[10.1 - 16.0]	22.7	[20.4 - 25.1]	13.2	[10.8 - 15.9]	12.12
'GCF_030328995.1_ASM3032899v1_genomic.fna'	<i>Acinetobacter seohaensis</i> DSM 16313	12.5	[9.9 - 15.8]	22.7	[20.4 - 25.2]	13.0	[10.6 - 15.7]	6.82
'GCF_001267295.1_ASM126729v1_genomic.fna'	<i>Pseudomonas tensinigenes</i> ZA 5.3	12.9	[10.2 - 16.2]	22.6	[20.3 - 25.0]	13.3	[10.9 - 16.0]	11.73
'GCF_001267295.1_ASM126729v1_genomic.fna'	<i>Pseudomonas indoloxydans</i> JCM 14246	12.8	[10.1 - 16.1]	22.6	[20.3 - 25.0]	13.2	[10.9 - 16.0]	14.8
'GCF_001267215.1_ASM126721v1_genomic.fna'	<i>Pseudomonas matsuisoli</i> JCM 30078	12.8	[10.1 - 16.0]	22.6	[20.4 - 25.1]	13.2	[10.8 - 15.9]	11.97
'GCF_001267215.1_ASM126721v1_genomic.fna'	<i>Pseudomonas indoloxydans</i> JCM 14246	12.8	[10.1 - 16.1]	22.6	[20.3 - 25.0]	13.2	[10.9 - 16.0]	14.74
'GCF_001267255.1_ASM126725v1_genomic.fna'	<i>Pseudomonas tensinigenes</i> ZA 5.3	12.9	[10.2 - 16.1]	22.5	[20.3 - 25.0]	13.2	[10.9 - 16.0]	11.74
'GCF_001267175.1_ASM126717v1_genomic.fna'	<i>Pseudomonas indoloxydans</i> JCM 14246	12.8	[10.1 - 16.1]	22.5	[20.3 - 25.0]	13.2	[10.9 - 16.0]	14.89
'GCF_001267255.1_ASM126725v1_genomic.fna'	<i>Pseudomonas straminea</i> JCM 2783	12.7	[10.0 - 16.0]	22.5	[20.2 - 24.9]	13.1	[10.8 - 15.9]	15.8
'GCF_001267315.1_ASM126731v1_genomic.fna'	<i>Pseudomonas tensinigenes</i> ZA 5.3	12.9	[10.2 - 16.2]	22.4	[20.1 - 24.8]	13.3	[10.9 - 16.0]	11.97
'GCF_001267275.1_ASM126727v1_genomic.fna'	<i>Pseudomonas straminea</i> JCM 2783	12.7	[10.0 - 16.0]	22.4	[20.1 - 24.9]	13.1	[10.8 - 15.9]	15.84
'GCF_001267295.1_ASM126729v1_genomic.fna'	<i>Pseudomonas indica</i> NBRC 103045	12.8	[10.1 - 16.0]	22.3	[20.0 - 24.8]	13.1	[10.8 - 15.9]	16.69
'GCF_001267275.1_ASM126727v1_genomic.fna'	<i>Pseudomonas tensinigenes</i> ZA 5.3	12.9	[10.2 - 16.1]	22.3	[20.0 - 24.7]	13.2	[10.9 - 16.0]	11.79
'GCF_001267315.1_ASM126731v1_genomic.fna'	<i>Pseudomonas sediminis</i> PI11	12.8	[10.1 - 16.1]	22.3	[20.1 - 24.8]	13.2	[10.9 - 16.0]	15.28
'GCF_001267275.1_ASM126727v1_genomic.fna'	<i>Chryseomonas asuensis</i> JCM 13501	12.7	[10.0 - 16.0]	22.2	[19.9 - 24.6]	13.1	[10.8 - 15.9]	6.19
'GCF_001267215.1_ASM126721v1_genomic.fna'	<i>Pseudomonas indica</i> NBRC 103045	12.8	[10.1 - 16.0]	22.2	[19.9 - 24.7]	13.2	[10.8 - 15.9]	16.62
'GCF_001267255.1_ASM126725v1_genomic.fna'	<i>Chryseomonas asuensis</i> JCM 13501	12.7	[10.0 - 16.0]	22.2	[19.9 - 24.6]	13.1	[10.8 - 15.9]	6.15
'GCF_001267175.1_ASM126717v1_genomic.fna'	<i>Pseudomonas indica</i> NBRC 103045	12.8	[10.1 - 16.0]	22.2	[20.0 - 24.7]	13.1	[10.8 - 15.9]	16.77
'GCF_001267315.1_ASM126731v1_genomic.fna'	<i>Pseudomonas matsuisoli</i> JCM 30078	12.8	[10.1 - 16.1]	22.2	[20.0 - 24.7]	13.2	[10.8 - 15.9]	12.27
'GCF_001267295.1_ASM126729v1_genomic.fna'	<i>Ignatzschineria cameli</i> UAE-HKU57	12.6	[10.0 - 15.9]	22.2	[19.9 - 24.6]	13.0	[10.7 - 15.8]	5.75
'GCF_030328955.1_ASM3032895v1_genomic.fna'	<i>Pseudomonas yangonensis</i> JCM 33396	12.8	[10.1 - 16.1]	22.2	[19.9 - 24.6]	13.2	[10.9 - 16.0]	15.31
'GCF_001267195.1_ASM126719v1_genomic.fna'	<i>Pseudomonas straminea</i> JCM 2783	12.7	[10.0 - 16.0]	22.2	[19.9 - 24.6]	13.1	[10.8 - 15.8]	15.76
'GCF_001267215.1_ASM126721v1_genomic.fna'	<i>Atopomonas hussainii</i> JCM 19513	12.9	[10.2 - 16.1]	22.1	[19.9 - 24.6]	13.2	[10.9 - 16.0]	11.32

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'GCF_001267175.1_ASM126717v1_genomic.fna'	<i>Pseudomonas pseudoalcaligenes</i> NBRC 14167	12.8	[10.2 - 16.1]	22.1	[19.8 - 24.6]	13.2	[10.9 - 16.0]	14.88
'GCF_001267195.1_ASM126719v1_genomic.fna'	<i>Pseudomonas indoloxydans</i> JCM 14246	12.8	[10.1 - 16.0]	22.1	[19.8 - 24.5]	13.1	[10.8 - 15.9]	14.79
'GCF_001267315.1_ASM126731v1_genomic.fna'	<i>Pseudomonas indica</i> NBRC 103045	12.8	[10.1 - 16.0]	22.0	[19.8 - 24.5]	13.2	[10.8 - 15.9]	16.93
'GCF_030328955.1_ASM3032895v1_genomic.fna'	<i>Pseudomonas shirazensis</i> SWRI56	12.8	[10.1 - 16.1]	22.0	[19.7 - 24.4]	13.2	[10.9 - 16.0]	14.25
'GCF_030328955.1_ASM3032895v1_genomic.fna'	<i>Acinetobacter seohaensis</i> DSM 16313	12.6	[9.9 - 15.8]	22.0	[19.7 - 24.4]	13.0	[10.6 - 15.7]	6.27
'GCF_001267275.1_ASM126727v1_genomic.fna'	<i>Pseudomonas indoloxydans</i> JCM 14246	12.8	[10.1 - 16.1]	22.0	[19.8 - 24.5]	13.2	[10.8 - 15.9]	14.86
'GCF_001267215.1_ASM126721v1_genomic.fna'	<i>Pseudomonas sediminis</i> PI11	12.8	[10.2 - 16.1]	22.0	[19.8 - 24.5]	13.2	[10.9 - 16.0]	14.97
'GCF_001267215.1_ASM126721v1_genomic.fna'	<i>Pseudomonas pseudoalcaligenes</i> NBRC 14167	12.9	[10.2 - 16.1]	22.0	[19.8 - 24.5]	13.2	[10.9 - 16.0]	14.74
'GCF_001267275.1_ASM126727v1_genomic.fna'	<i>Pseudomonas matsuisoli</i> JCM 30078	12.8	[10.1 - 16.0]	22.0	[19.7 - 24.4]	13.1	[10.8 - 15.9]	12.09
'GCF_001267215.1_ASM126721v1_genomic.fna'	<i>Halopseudomonas sabulinigri</i> JCM 14963	12.9	[10.2 - 16.2]	22.0	[19.7 - 24.4]	13.3	[10.9 - 16.0]	12.41
'GCF_001267295.1_ASM126729v1_genomic.fna'	<i>Pseudomonas sediminis</i> PI11	12.9	[10.2 - 16.1]	22.0	[19.8 - 24.5]	13.2	[10.9 - 16.0]	15.04
'GCF_001267255.1_ASM126725v1_genomic.fna'	<i>Pseudomonas matsuisoli</i> JCM 30078	12.8	[10.1 - 16.0]	22.0	[19.7 - 24.4]	13.1	[10.8 - 15.9]	12.05
'GCF_001267315.1_ASM126731v1_genomic.fna'	<i>Pseudomonas pseudoalcaligenes</i> NBRC 14167	12.8	[10.2 - 16.1]	22.0	[19.8 - 24.5]	13.2	[10.9 - 16.0]	15.04
'GCF_001267255.1_ASM126725v1_genomic.fna'	<i>Pseudomonas indoloxydans</i> JCM 14246	12.8	[10.1 - 16.1]	22.0	[19.8 - 24.5]	13.2	[10.8 - 16.0]	14.82
'GCF_001267175.1_ASM126717v1_genomic.fna'	<i>Pseudomonas sediminis</i> PI11	12.9	[10.2 - 16.1]	22.0	[19.8 - 24.5]	13.2	[10.9 - 16.0]	15.12
'GCF_001267195.1_ASM126719v1_genomic.fna'	<i>Pseudomonas sediminis</i> PI11	12.8	[10.1 - 16.1]	21.9	[19.6 - 24.3]	13.2	[10.8 - 15.9]	15.02
'GCF_001267295.1_ASM126729v1_genomic.fna'	<i>Pseudomonas yangonensis</i> JCM 33396	12.8	[10.1 - 16.1]	21.9	[19.6 - 24.3]	13.2	[10.9 - 16.0]	15.47
'GCF_001267315.1_ASM126731v1_genomic.fna'	<i>Pseudomonas xionganensis</i> R-22-3 w-18T	12.9	[10.2 - 16.2]	21.9	[19.6 - 24.3]	13.3	[10.9 - 16.1]	15.78
'GCF_001267175.1_ASM126717v1_genomic.fna'	<i>Pseudomonas xionganensis</i> R-22-3 w-18T	12.9	[10.2 - 16.2]	21.9	[19.7 - 24.4]	13.3	[10.9 - 16.1]	15.62
'GCF_001267195.1_ASM126719v1_genomic.fna'	<i>Pseudomonas pseudoalcaligenes</i> NBRC 14167	12.8	[10.1 - 16.1]	21.9	[19.6 - 24.3]	13.2	[10.8 - 15.9]	14.78
'GCF_001267295.1_ASM126729v1_genomic.fna'	<i>Pseudomonas xionganensis</i> R-22-3 w-18T	12.9	[10.2 - 16.2]	21.9	[19.7 - 24.4]	13.3	[10.9 - 16.1]	15.54
'GCF_001267215.1_ASM126721v1_genomic.fna'	<i>Pseudomonas xionganensis</i> R-22-3 w-18T	12.9	[10.2 - 16.2]	21.9	[19.6 - 24.3]	13.3	[10.9 - 16.1]	15.48
'GCF_001267295.1_ASM126729v1_genomic.fna'	<i>Pseudomonas chaetocerotis</i> LMG 31766	12.8	[10.2 - 16.1]	21.9	[19.6 - 24.3]	13.2	[10.9 - 16.0]	14.97
'GCF_030329025.1_ASM3032902v1_genomic.fna'	<i>Pseudomonas shirazensis</i> SWRI56	12.9	[10.2 - 16.2]	21.9	[19.7 - 24.4]	13.3	[10.9 - 16.0]	14.75

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'GCF_001267215.1_ASM126721v1_genomic.fna'	<i>Pseudomonas yangonensis</i> JCM 33396	12.8	[10.1 - 16.1]	21.9	[19.6 - 24.3]	13.2	[10.9 - 16.0]	15.41
'GCF_001267175.1_ASM126717v1_genomic.fna'	<i>Pseudomonas yangonensis</i> JCM 33396	12.8	[10.1 - 16.1]	21.9	[19.6 - 24.3]	13.2	[10.9 - 16.0]	15.55
'GCF_001267295.1_ASM126729v1_genomic.fna'	<i>Pseudomonas pseudoalcaligenes</i> NBRC 14167	12.9	[10.2 - 16.1]	21.9	[19.6 - 24.3]	13.2	[10.9 - 16.0]	14.8
'GCF_001267195.1_ASM126719v1_genomic.fna'	<i>Pseudomonas xionganensis</i> R-22-3 w-18T	12.8	[10.1 - 16.1]	21.8	[19.6 - 24.3]	13.2	[10.9 - 16.0]	15.52
'GCF_001267315.1_ASM126731v1_genomic.fna'	<i>Pseudomonas abyssi</i> MT5	12.8	[10.1 - 16.0]	21.8	[19.6 - 24.3]	13.1	[10.8 - 15.9]	14.06
'GCF_001267195.1_ASM126719v1_genomic.fna'	<i>Pseudomonas matsuisoli</i> JCM 30078	12.7	[10.0 - 16.0]	21.8	[19.6 - 24.3]	13.1	[10.8 - 15.9]	12.02
'GCF_001267315.1_ASM126731v1_genomic.fna'	<i>Pseudomonas chaetocerotis</i> LMG 31766	12.8	[10.1 - 16.1]	21.8	[19.6 - 24.3]	13.2	[10.9 - 16.0]	15.21
'GCF_030328995.1_ASM3032899v1_genomic.fna'	<i>Pseudomonas tensinigenes</i> ZA 5.3	12.8	[10.1 - 16.1]	21.8	[19.6 - 24.3]	13.2	[10.9 - 16.0]	11.01
'GCF_001267175.1_ASM126717v1_genomic.fna'	<i>Pseudomonas abyssi</i> MT5	12.8	[10.1 - 16.0]	21.8	[19.6 - 24.3]	13.1	[10.8 - 15.9]	13.9
'GCF_001267195.1_ASM126719v1_genomic.fna'	<i>Pseudomonas yangonensis</i> JCM 33396	12.8	[10.1 - 16.0]	21.8	[19.6 - 24.3]	13.1	[10.8 - 15.9]	15.45
'GCF_001267295.1_ASM126729v1_genomic.fna'	<i>Pseudomonas abyssi</i> MT5	12.8	[10.1 - 16.0]	21.8	[19.5 - 24.2]	13.2	[10.8 - 15.9]	13.81
'GCF_001267295.1_ASM126729v1_genomic.fna'	<i>Pseudomonas matsuisoli</i> JCM 30078	12.8	[10.1 - 16.1]	21.7	[19.5 - 24.2]	13.2	[10.8 - 15.9]	12.03
'GCF_001267315.1_ASM126731v1_genomic.fna'	<i>Atopomonas hussainii</i> JCM 19513	12.9	[10.2 - 16.2]	21.7	[19.5 - 24.1]	13.3	[10.9 - 16.0]	11.62
'GCF_001267195.1_ASM126719v1_genomic.fna'	<i>Pseudomonas chaetocerotis</i> LMG 31766	12.8	[10.1 - 16.0]	21.7	[19.4 - 24.1]	13.2	[10.8 - 15.9]	14.96
'GCF_001267215.1_ASM126721v1_genomic.fna'	<i>Pseudomonas chaetocerotis</i> LMG 31766	12.8	[10.1 - 16.1]	21.7	[19.4 - 24.1]	13.2	[10.9 - 16.0]	14.91
'GCF_001267215.1_ASM126721v1_genomic.fna'	<i>Pseudomonas abyssi</i> MT5	12.8	[10.1 - 16.0]	21.7	[19.4 - 24.1]	13.2	[10.8 - 15.9]	13.75
'GCF_001267195.1_ASM126719v1_genomic.fna'	<i>Chryseomonas asuensis</i> JCM 13501	12.7	[10.0 - 16.0]	21.7	[19.4 - 24.1]	13.1	[10.8 - 15.9]	6.12
'GCF_001267275.1_ASM126727v1_genomic.fna'	<i>Pseudomonas abyssi</i> MT5	12.7	[10.0 - 16.0]	21.7	[19.5 - 24.2]	13.1	[10.8 - 15.9]	13.87
'GCF_001267175.1_ASM126717v1_genomic.fna'	<i>Pseudomonas chaetocerotis</i> LMG 31766	12.8	[10.1 - 16.1]	21.7	[19.4 - 24.1]	13.2	[10.9 - 16.0]	15.05
'GCF_001267315.1_ASM126731v1_genomic.fna'	<i>Pseudomonas toyotomiensis</i> JCM 15604	12.8	[10.1 - 16.1]	21.6	[19.3 - 24.0]	13.2	[10.8 - 15.9]	15.41
'GCF_001267195.1_ASM126719v1_genomic.fna'	<i>Pseudomonas toyotomiensis</i> JCM 15604	12.7	[10.0 - 16.0]	21.6	[19.4 - 24.1]	13.1	[10.8 - 15.9]	15.15
'GCF_001267295.1_ASM126729v1_genomic.fna'	<i>Atopomonas hussainii</i> JCM 19513	12.9	[10.2 - 16.2]	21.6	[19.3 - 24.0]	13.3	[10.9 - 16.1]	11.38
'GCF_001267275.1_ASM126727v1_genomic.fna'	<i>Pseudomonas indica</i> NBRC 103045	12.8	[10.1 - 16.0]	21.6	[19.3 - 24.0]	13.1	[10.8 - 15.9]	16.75
'GCF_030328995.1_ASM3032899v1_genomic.fna'	<i>Pseudomonas yangonensis</i> JCM 33396	12.8	[10.1 - 16.1]	21.6	[19.4 - 24.1]	13.2	[10.9 - 16.0]	14.76
'GCF_001267255.1_ASM126725v1_genomic.fna'	<i>Pseudomonas pseudoalcaligenes</i> NBRC 14167	12.8	[10.1 - 16.1]	21.6	[19.3 - 24.0]	13.2	[10.9 - 16.0]	14.82

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'GCF_001267315.1_ASM126731v1_genomic.fna'	<i>Pseudomonas pharmacofabriceae</i> ZYSR67-Z	13.1	[10.4 - 16.4]	21.6	[19.3 - 24.0]	13.4	[11.1 - 16.2]	15.42
'GCF_001267175.1_ASM126717v1_genomic.fna'	<i>Halopseudomonas sabulinigri</i> JCM 14963	12.9	[10.2 - 16.2]	21.6	[19.3 - 24.0]	13.3	[10.9 - 16.0]	12.55
'GCF_001267295.1_ASM126729v1_genomic.fna'	<i>Pseudomonas toyotomiensis</i> JCM 15604	12.8	[10.1 - 16.1]	21.6	[19.4 - 24.1]	13.2	[10.8 - 15.9]	15.16
'GCF_001267295.1_ASM126729v1_genomic.fna'	<i>Pseudomonas indica</i> JCM 21544	12.8	[10.1 - 16.1]	21.6	[19.3 - 24.0]	13.2	[10.8 - 15.9]	16.67
'GCF_001267175.1_ASM126717v1_genomic.fna'	<i>Pseudomonas toyotomiensis</i> JCM 15604	12.8	[10.1 - 16.1]	21.6	[19.3 - 24.0]	13.2	[10.8 - 15.9]	15.25
'GCF_001267275.1_ASM126727v1_genomic.fna'	<i>Pseudomonas sediminis</i> PI11	12.8	[10.1 - 16.1]	21.5	[19.2 - 23.9]	13.2	[10.9 - 16.0]	15.1
'GCF_001267315.1_ASM126731v1_genomic.fna'	<i>Halopseudomonas sabulinigri</i> JCM 14963	12.9	[10.2 - 16.2]	21.5	[19.3 - 24.0]	13.3	[10.9 - 16.0]	12.71
'GCF_001267215.1_ASM126721v1_genomic.fna'	<i>Pseudomonas toyotomiensis</i> JCM 15604	12.8	[10.1 - 16.1]	21.5	[19.3 - 24.0]	13.2	[10.8 - 15.9]	15.1
'GCF_001267215.1_ASM126721v1_genomic.fna'	<i>Pseudomonas indica</i> JCM 21544	12.8	[10.1 - 16.1]	21.5	[19.2 - 23.9]	13.2	[10.8 - 16.0]	16.61
'GCF_001267315.1_ASM126731v1_genomic.fna'	<i>Azomonas agilis</i> DSM 375	12.9	[10.2 - 16.2]	21.5	[19.2 - 23.9]	13.3	[11.0 - 16.1]	4.57
'GCF_001267175.1_ASM126717v1_genomic.fna'	<i>Pseudomonas indica</i> JCM 21544	12.8	[10.1 - 16.1]	21.5	[19.2 - 23.9]	13.2	[10.8 - 15.9]	16.75
'GCF_001267195.1_ASM126719v1_genomic.fna'	<i>Pseudomonas abyssi</i> MT5	12.7	[10.0 - 16.0]	21.5	[19.3 - 23.9]	13.1	[10.8 - 15.8]	13.8
'GCF_001267275.1_ASM126727v1_genomic.fna'	<i>Pseudomonas pseudoalcaligenes</i> NBRC 14167	12.8	[10.1 - 16.1]	21.5	[19.2 - 23.9]	13.2	[10.9 - 16.0]	14.86
'GCF_030328995.1_ASM3032899v1_genomic.fna'	<i>Pseudomonas shirazensis</i> SWRI56	12.9	[10.2 - 16.2]	21.5	[19.2 - 23.9]	13.3	[10.9 - 16.0]	13.7
'GCF_001267255.1_ASM126725v1_genomic.fna'	<i>Pseudomonas sediminis</i> PI11	12.8	[10.2 - 16.1]	21.5	[19.3 - 24.0]	13.2	[10.9 - 16.0]	15.05
'GCF_001267175.1_ASM126717v1_genomic.fna'	<i>Atopomonas hussainii</i> JCM 19513	12.9	[10.2 - 16.2]	21.5	[19.3 - 23.9]	13.3	[10.9 - 16.0]	11.46
'GCF_001267295.1_ASM126729v1_genomic.fna'	<i>Halopseudomonas sabulinigri</i> JCM 14963	12.9	[10.2 - 16.2]	21.5	[19.2 - 23.9]	13.3	[10.9 - 16.0]	12.47
'GCF_030328955.1_ASM3032895v1_genomic.fna'	<i>Chryseomonas asuensis</i> JCM 13501	12.6	[9.9 - 15.9]	21.5	[19.3 - 23.9]	13.0	[10.7 - 15.8]	5.97
'GCF_001267195.1_ASM126719v1_genomic.fna'	<i>Pseudomonas flexibilis</i> ATCC 29606	12.8	[10.1 - 16.1]	21.5	[19.3 - 24.0]	13.2	[10.8 - 15.9]	18.35
'GCF_001267255.1_ASM126725v1_genomic.fna'	<i>Pseudomonas xionganensis</i> R-22-3 w-18T	12.9	[10.2 - 16.2]	21.4	[19.2 - 23.9]	13.3	[10.9 - 16.1]	15.56
'GCF_001267255.1_ASM126725v1_genomic.fna'	<i>Pseudomonas indica</i> NBRC 103045	12.8	[10.1 - 16.0]	21.4	[19.2 - 23.9]	13.1	[10.8 - 15.9]	16.7
'GCF_001267315.1_ASM126731v1_genomic.fna'	<i>Pseudomonas indica</i> JCM 21544	12.8	[10.1 - 16.1]	21.4	[19.1 - 23.8]	13.2	[10.8 - 16.0]	16.91
'GCF_001267275.1_ASM126727v1_genomic.fna'	<i>Atopomonas hussainii</i> JCM 19513	12.9	[10.2 - 16.2]	21.4	[19.2 - 23.8]	13.3	[10.9 - 16.0]	11.44
'GCF_001267255.1_ASM126725v1_genomic.fna'	<i>Pseudomonas yangonensis</i> JCM 33396	12.8	[10.1 - 16.1]	21.4	[19.1 - 23.8]	13.2	[10.9 - 16.0]	15.49

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'GCF_001267275.1_ASM126727v1_genomic.fna'	<i>Pseudomonas xionganensis</i> R-22-3 w-18T	12.9	[10.2 - 16.2]	21.4	[19.2 - 23.9]	13.3	[10.9 - 16.0]	15.6
'GCF_001267315.1_ASM126731v1_genomic.fna'	<i>Pseudomonas alcaligenes</i> NBRC 14159	12.9	[10.2 - 16.2]	21.3	[19.1 - 23.8]	13.2	[10.9 - 16.0]	17.56
'GCF_001267255.1_ASM126725v1_genomic.fna'	<i>Halopseudomonas sabulinigri</i> JCM 14963	12.9	[10.2 - 16.2]	21.3	[19.1 - 23.8]	13.3	[10.9 - 16.0]	12.49
'GCF_001267275.1_ASM126727v1_genomic.fna'	<i>Pseudomonas chaetocerotis</i> LMG 31766	12.8	[10.1 - 16.1]	21.3	[19.1 - 23.7]	13.2	[10.9 - 16.0]	15.03
'GCF_001267195.1_ASM126719v1_genomic.fna'	<i>Pseudomonas indica</i> NBRC 103045	12.7	[10.0 - 16.0]	21.3	[19.1 - 23.8]	13.1	[10.8 - 15.9]	16.67
'GCF_001267315.1_ASM126731v1_genomic.fna'	<i>Thiopseudomonas denitrificans</i> DSM 28679	13.1	[10.3 - 16.4]	21.3	[19.1 - 23.8]	13.4	[11.1 - 16.2]	11.77
'GCF_001267255.1_ASM126725v1_genomic.fna'	<i>Pseudomonas chaetocerotis</i> LMG 31766	12.8	[10.1 - 16.1]	21.3	[19.0 - 23.7]	13.2	[10.9 - 16.0]	14.99
'GCF_001267175.1_ASM126717v1_genomic.fna'	<i>Thiopseudomonas denitrificans</i> DSM 28679	13.0	[10.3 - 16.3]	21.3	[19.0 - 23.7]	13.4	[11.0 - 16.2]	11.61
'GCF_001267295.1_ASM126729v1_genomic.fna'	<i>Thiopseudomonas denitrificans</i> DSM 28679	13.0	[10.3 - 16.3]	21.3	[19.1 - 23.8]	13.4	[11.0 - 16.2]	11.53
'GCF_001267275.1_ASM126727v1_genomic.fna'	<i>Pseudomonas yangonensis</i> JCM 33396	12.8	[10.1 - 16.1]	21.3	[19.1 - 23.8]	13.2	[10.8 - 16.0]	15.53
'GCF_001267215.1_ASM126721v1_genomic.fna'	<i>Azomonas agilis</i> DSM 375	13.0	[10.3 - 16.2]	21.2	[19.0 - 23.7]	13.3	[11.0 - 16.1]	4.27
'GCF_030328955.1_ASM3032895v1_genomic.fna'	<i>Pseudomonas tensinigenes</i> ZA 5.3	12.8	[10.1 - 16.1]	21.2	[19.0 - 23.6]	13.2	[10.8 - 15.9]	11.56
'GCF_001267295.1_ASM126729v1_genomic.fna'	<i>Atopomonas sediminilitoris</i> A3.4T	12.9	[10.2 - 16.2]	21.2	[18.9 - 23.6]	13.3	[10.9 - 16.0]	10.18
'GCF_001267175.1_ASM126717v1_genomic.fna'	<i>Azomonas agilis</i> DSM 375	12.9	[10.2 - 16.2]	21.2	[19.0 - 23.7]	13.3	[11.0 - 16.1]	4.42
'GCF_001267215.1_ASM126721v1_genomic.fna'	<i>Thiopseudomonas denitrificans</i> DSM 28679	13.0	[10.3 - 16.3]	21.2	[19.0 - 23.7]	13.4	[11.0 - 16.2]	11.46
'GCF_001267175.1_ASM126717v1_genomic.fna'	<i>Atopomonas sediminilitoris</i> A3.4T	12.9	[10.2 - 16.1]	21.2	[19.0 - 23.6]	13.2	[10.9 - 16.0]	10.26
'GCF_001267275.1_ASM126727v1_genomic.fna'	<i>Halopseudomonas sabulinigri</i> JCM 14963	12.9	[10.2 - 16.2]	21.2	[19.0 - 23.6]	13.3	[10.9 - 16.0]	12.53
'GCF_001267295.1_ASM126729v1_genomic.fna'	<i>Azomonas agilis</i> DSM 375	13.0	[10.2 - 16.2]	21.2	[19.0 - 23.6]	13.3	[11.0 - 16.1]	4.33
'GCF_001267295.1_ASM126729v1_genomic.fna'	<i>Pseudomonas pharmacofabriceae</i> ZYSR67-Z	13.1	[10.4 - 16.4]	21.2	[18.9 - 23.6]	13.4	[11.1 - 16.2]	15.18
'GCF_001267175.1_ASM126717v1_genomic.fna'	<i>Pseudomonas turukhanskensis</i> VKM B-2935	12.8	[10.1 - 16.1]	21.2	[19.0 - 23.6]	13.2	[10.9 - 16.0]	13.22
'GCF_001267315.1_ASM126731v1_genomic.fna'	<i>Pseudomonas campi</i> DSM 110222	13.0	[10.3 - 16.3]	21.2	[18.9 - 23.6]	13.3	[11.0 - 16.1]	16.25
'GCF_001267175.1_ASM126717v1_genomic.fna'	<i>Pseudomonas alcaligenes</i> NBRC 14159	12.9	[10.2 - 16.2]	21.1	[18.8 - 23.5]	13.3	[10.9 - 16.0]	17.4
'GCF_001267315.1_ASM126731v1_genomic.fna'	<i>Atopomonas sediminilitoris</i> A3.4T	12.9	[10.2 - 16.2]	21.1	[18.8 - 23.5]	13.3	[10.9 - 16.0]	10.42
'GCF_001267295.1_ASM126729v1_genomic.fna'	<i>Pseudomonas campi</i> DSM 110222	13.0	[10.3 - 16.3]	21.1	[18.9 - 23.6]	13.3	[11.0 - 16.1]	16.0
'GCF_001267175.1_ASM126717v1_genomic.fna'	<i>Pseudomonas pharmacofabriceae</i> ZYSR67-Z	13.1	[10.4 - 16.4]	21.1	[18.9 - 23.6]	13.4	[11.1 - 16.2]	15.26

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'GCF_001267275.1_ASM126727v1_genomic.fna'	<i>Pseudomonas toyotomiensis</i> JCM 15604	12.8	[10.1 - 16.0]	21.1	[18.9 - 23.6]	13.2	[10.8 - 15.9]	15.22
'GCF_001267215.1_ASM126721v1_genomic.fna'	<i>Pseudomonas pharmacofabriceae</i> ZYSR67-Z	13.1	[10.4 - 16.4]	21.1	[18.9 - 23.6]	13.4	[11.1 - 16.2]	15.12
'GCF_001267255.1_ASM126725v1_genomic.fna'	<i>Pseudomonas toyotomiensis</i> JCM 15604	12.8	[10.1 - 16.1]	21.1	[18.9 - 23.5]	13.2	[10.8 - 15.9]	15.18
'GCF_001267215.1_ASM126721v1_genomic.fna'	<i>Pseudomonas alcaligenes</i> NBRC 14159	12.9	[10.2 - 16.2]	21.1	[18.8 - 23.5]	13.3	[10.9 - 16.0]	17.26
'GCF_001267175.1_ASM126717v1_genomic.fna'	<i>Pseudomonas campii</i> DSM 110222	13.0	[10.2 - 16.2]	21.1	[18.8 - 23.5]	13.3	[11.0 - 16.1]	16.09
'GCF_001267255.1_ASM126725v1_genomic.fna'	<i>Pseudomonas abyssi</i> MT5	12.8	[10.1 - 16.0]	21.1	[18.8 - 23.5]	13.1	[10.8 - 15.9]	13.83
'GCF_001267295.1_ASM126729v1_genomic.fna'	<i>Pseudomonas alcaligenes</i> NBRC 14159	12.9	[10.2 - 16.2]	21.1	[18.9 - 23.6]	13.3	[10.9 - 16.0]	17.32
'GCF_001267315.1_ASM126731v1_genomic.fna'	<i>Pseudomonas peli</i> DSM 17833	12.9	[10.2 - 16.2]	21.1	[18.9 - 23.5]	13.3	[10.9 - 16.1]	12.52
'GCF_001267315.1_ASM126731v1_genomic.fna'	<i>Pseudomonas turukhanskensis</i> VKM B-2935	12.8	[10.1 - 16.1]	21.1	[18.9 - 23.6]	13.2	[10.9 - 16.0]	13.38
'GCF_030329025.1_ASM3032902v1_genomic.fna'	<i>Pseudomonas tensinigenes</i> ZA 5.3	12.8	[10.1 - 16.1]	21.1	[18.9 - 23.6]	13.2	[10.9 - 16.0]	12.07
'GCF_001267175.1_ASM126717v1_genomic.fna'	<i>Pseudomonas peli</i> DSM 17833	12.9	[10.2 - 16.2]	21.0	[18.8 - 23.4]	13.3	[10.9 - 16.1]	12.36
'GCF_001267195.1_ASM126719v1_genomic.fna'	<i>Thiopseudomonas denitrificans</i> DSM 28679	12.9	[10.2 - 16.2]	21.0	[18.8 - 23.5]	13.3	[10.9 - 16.1]	11.51
'GCF_001267215.1_ASM126721v1_genomic.fna'	<i>Atopomonas sediminilitoris</i> A3.4T	12.9	[10.2 - 16.2]	21.0	[18.8 - 23.5]	13.3	[10.9 - 16.0]	10.12
'GCF_001267315.1_ASM126731v1_genomic.fna'	<i>Pseudomonas taeanensis</i> MS-3	12.8	[10.2 - 16.1]	21.0	[18.8 - 23.4]	13.2	[10.9 - 16.0]	13.7
'GCF_001267255.1_ASM126725v1_genomic.fna'	<i>Atopomonas hussainii</i> JCM 19513	12.9	[10.2 - 16.2]	21.0	[18.8 - 23.5]	13.3	[10.9 - 16.0]	11.39
'GCF_001267195.1_ASM126719v1_genomic.fna'	<i>Pseudomonas pharmacofabriceae</i> ZYSR67-Z	13.0	[10.3 - 16.3]	21.0	[18.8 - 23.4]	13.4	[11.0 - 16.1]	15.16
'GCF_001267255.1_ASM126725v1_genomic.fna'	<i>Azomonas agilis</i> DSM 375	12.9	[10.2 - 16.2]	20.9	[18.7 - 23.4]	13.3	[11.0 - 16.1]	4.35
'GCF_030328955.1_ASM3032895v1_genomic.fna'	<i>Pseudomonas sediminis</i> PI11	12.7	[10.0 - 16.0]	20.9	[18.7 - 23.4]	13.1	[10.8 - 15.8]	14.88
'GCF_001267275.1_ASM126727v1_genomic.fna'	<i>Azomonas agilis</i> DSM 375	12.9	[10.2 - 16.2]	20.9	[18.6 - 23.3]	13.3	[10.9 - 16.1]	4.39
'GCF_001267215.1_ASM126721v1_genomic.fna'	<i>Pseudomonas turukhanskensis</i> VKM B-2935	12.8	[10.1 - 16.1]	20.9	[18.7 - 23.3]	13.2	[10.9 - 16.0]	13.08
'GCF_001267295.1_ASM126729v1_genomic.fna'	<i>Pseudomonas peli</i> DSM 17833	12.9	[10.2 - 16.2]	20.9	[18.7 - 23.3]	13.3	[11.0 - 16.1]	12.28
'GCF_001267275.1_ASM126727v1_genomic.fna'	<i>Pseudomonas indica</i> JCM 21544	12.8	[10.1 - 16.1]	20.9	[18.7 - 23.3]	13.2	[10.8 - 15.9]	16.73
'GCF_001267215.1_ASM126721v1_genomic.fna'	<i>Pseudomonas peli</i> DSM 17833	12.9	[10.2 - 16.2]	20.9	[18.7 - 23.3]	13.3	[11.0 - 16.1]	12.22
'GCF_001267255.1_ASM126725v1_genomic.fna'	<i>Thiopseudomonas denitrificans</i> DSM 28679	13.0	[10.3 - 16.3]	20.9	[18.7 - 23.3]	13.4	[11.0 - 16.2]	11.54
'GCF_001267195.1_ASM126719v1_genomic.fna'	<i>Halopseudomonas sabulinigri</i> JCM 14963	12.8	[10.2 - 16.1]	20.9	[18.7 - 23.3]	13.2	[10.9 - 16.0]	12.46

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'GCF_001267315.1_ASM126731v1_genomic.fna'	<i>Pseudomonas flexibilis</i> ATCC 29606	12.9	[10.2 - 16.2]	20.8	[18.5 - 23.2]	13.3	[10.9 - 16.0]	18.6
'GCF_001267255.1_ASM126725v1_genomic.fna'	<i>Pseudomonas pharmacofabriceae</i> ZYSR67-Z	13.1	[10.4 - 16.4]	20.8	[18.5 - 23.2]	13.4	[11.1 - 16.2]	15.2
'GCF_030328955.1_ASM3032895v1_genomic.fna'	<i>Thiopseudomonas denitrificans</i> DSM 28679	13.0	[10.2 - 16.2]	20.8	[18.6 - 23.2]	13.3	[11.0 - 16.1]	11.37
'GCF_001267295.1_ASM126729v1_genomic.fna'	<i>Pseudomonas flexibilis</i> ATCC 29606	12.9	[10.2 - 16.2]	20.8	[18.6 - 23.2]	13.3	[10.9 - 16.0]	18.36
'GCF_030328955.1_ASM3032895v1_genomic.fna'	<i>Denitrificimonas caeni</i> DSM 24390	14.1	[11.3 - 17.4]	20.8	[18.5 - 23.2]	14.3	[11.9 - 17.2]	0.66
'GCF_001267275.1_ASM126727v1_genomic.fna'	<i>Pseudomonas pharmacofabriceae</i> ZYSR67-Z	13.1	[10.4 - 16.4]	20.8	[18.5 - 23.2]	13.4	[11.1 - 16.2]	15.24
'GCF_001267215.1_ASM126721v1_genomic.fna'	<i>Pseudomonas campii</i> DSM 110222	13.0	[10.3 - 16.3]	20.8	[18.6 - 23.2]	13.4	[11.0 - 16.1]	15.94
'GCF_001267275.1_ASM126727v1_genomic.fna'	<i>Thiopseudomonas denitrificans</i> DSM 28679	13.0	[10.3 - 16.3]	20.8	[18.6 - 23.2]	13.4	[11.0 - 16.2]	11.59
'GCF_001267255.1_ASM126725v1_genomic.fna'	<i>Pseudomonas indica</i> JCM 21544	12.8	[10.1 - 16.1]	20.8	[18.6 - 23.2]	13.2	[10.8 - 15.9]	16.69
'GCF_001267255.1_ASM126725v1_genomic.fna'	<i>Pseudomonas alcaligenes</i> NBRC 14159	12.9	[10.2 - 16.2]	20.7	[18.5 - 23.1]	13.2	[10.9 - 16.0]	17.34
'GCF_030328955.1_ASM3032895v1_genomic.fna'	<i>Azomonas agilis</i> DSM 375	12.8	[10.1 - 16.0]	20.7	[18.4 - 23.1]	13.1	[10.8 - 15.9]	4.17
'GCF_001267195.1_ASM126719v1_genomic.fna'	<i>Azomonas agilis</i> DSM 375	12.9	[10.2 - 16.2]	20.7	[18.4 - 23.1]	13.2	[10.9 - 16.0]	4.32
'GCF_001267215.1_ASM126721v1_genomic.fna'	<i>Pseudomonas flexibilis</i> ATCC 29606	12.9	[10.2 - 16.2]	20.7	[18.5 - 23.1]	13.3	[10.9 - 16.0]	18.3
'GCF_001267275.1_ASM126727v1_genomic.fna'	<i>Pseudomonas campii</i> DSM 110222	12.9	[10.2 - 16.2]	20.7	[18.5 - 23.1]	13.3	[11.0 - 16.1]	16.06
'GCF_001267275.1_ASM126727v1_genomic.fna'	<i>Atopomonas sediminilitoris</i> A3.4T	12.8	[10.2 - 16.1]	20.7	[18.5 - 23.1]	13.2	[10.9 - 16.0]	10.24
'GCF_001267175.1_ASM126717v1_genomic.fna'	<i>Pseudomonas flexibilis</i> ATCC 29606	12.9	[10.2 - 16.2]	20.7	[18.5 - 23.1]	13.3	[10.9 - 16.0]	18.45
'GCF_001267195.1_ASM126719v1_genomic.fna'	<i>Pseudomonas peli</i> DSM 17833	12.9	[10.2 - 16.2]	20.6	[18.3 - 23.0]	13.2	[10.9 - 16.0]	12.26
'GCF_001267195.1_ASM126719v1_genomic.fna'	<i>Atopomonas hussainii</i> JCM 19513	12.9	[10.2 - 16.2]	20.6	[18.4 - 23.1]	13.3	[10.9 - 16.0]	11.36
'GCF_001267315.1_ASM126731v1_genomic.fna'	<i>Pseudomonas fluvialis</i> ASS-1	13.0	[10.3 - 16.3]	20.6	[18.4 - 23.0]	13.4	[11.0 - 16.2]	15.46
'GCF_001267295.1_ASM126729v1_genomic.fna'	<i>Pseudomonas taeanensis</i> MS-3	12.9	[10.2 - 16.2]	20.6	[18.4 - 23.0]	13.3	[10.9 - 16.0]	13.46
'GCF_001267275.1_ASM126727v1_genomic.fna'	<i>Pseudomonas alcaligenes</i> NBRC 14159	12.9	[10.2 - 16.2]	20.6	[18.4 - 23.1]	13.2	[10.9 - 16.0]	17.38
'GCF_001267315.1_ASM126731v1_genomic.fna'	<i>Thiopseudomonas denitrificans</i> DSM 28679	13.0	[10.3 - 16.3]	20.6	[18.3 - 23.0]	13.4	[11.0 - 16.1]	11.77
'GCF_001267255.1_ASM126725v1_genomic.fna'	<i>Pseudomonas campii</i> DSM 110222	13.0	[10.3 - 16.3]	20.6	[18.4 - 23.1]	13.4	[11.0 - 16.1]	16.02
'GCF_001267195.1_ASM126719v1_genomic.fna'	<i>Pseudomonas alcaligenes</i> NBRC 14159	12.8	[10.1 - 16.1]	20.6	[18.4 - 23.0]	13.2	[10.9 - 16.0]	17.31
'GCF_001267275.1_ASM126727v1_genomic.fna'	<i>Pseudomonas peli</i> DSM 17833	12.9	[10.2 - 16.2]	20.6	[18.4 - 23.1]	13.3	[10.9 - 16.0]	12.34
'GCF_001267255.1_ASM126725v1_genomic.fna'	<i>Atopomonas sediminilitoris</i> A3.4T	12.9	[10.2 - 16.2]	20.6	[18.4 - 23.1]	13.2	[10.9 - 16.0]	10.2

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'GCF_001267255.1_ASM126725v1_genomic.fna'	<i>Pseudomonas peli</i> DSM 17833	12.9	[10.2 - 16.2]	20.6	[18.3 - 23.0]	13.3	[10.9 - 16.1]	12.29
'GCF_001267215.1_ASM126721v1_genomic.fna'	<i>Pseudomonas taeanensis</i> MS-3	12.9	[10.2 - 16.2]	20.6	[18.4 - 23.0]	13.2	[10.9 - 16.0]	13.4
'GCF_001267195.1_ASM126719v1_genomic.fna'	<i>Pseudomonas indica</i> JCM 21544	12.8	[10.1 - 16.0]	20.6	[18.4 - 23.0]	13.1	[10.8 - 15.9]	16.65
'GCF_001267255.1_ASM126725v1_genomic.fna'	<i>Pseudomonas turukhanskensis</i> VKM B-2935	12.8	[10.1 - 16.1]	20.5	[18.3 - 22.9]	13.2	[10.9 - 16.0]	13.16
'GCF_030329025.1_ASM3032902v1_genomic.fna'	<i>Pseudomonas straminea</i> JCM 2783	12.7	[10.0 - 16.0]	20.5	[18.3 - 22.9]	13.1	[10.7 - 15.8]	16.12
'GCF_001267295.1_ASM126729v1_genomic.fna'	<i>Pseudomonas fluvialis</i> ASS-1	13.0	[10.3 - 16.3]	20.5	[18.3 - 22.9]	13.4	[11.0 - 16.2]	15.21
'GCF_030329025.1_ASM3032902v1_genomic.fna'	<i>Pseudomonas indoloxydans</i> JCM 14246	12.8	[10.1 - 16.0]	20.5	[18.3 - 22.9]	13.1	[10.8 - 15.9]	15.14
'GCF_001267315.1_ASM126731v1_genomic.fna'	<i>Pseudomonas fluvialis</i> CCM 8778	13.0	[10.3 - 16.3]	20.5	[18.2 - 22.9]	13.4	[11.0 - 16.2]	15.45
'GCF_001267295.1_ASM126729v1_genomic.fna'	<i>Pseudomonas turukhanskensis</i> VKM B-2935	12.8	[10.2 - 16.1]	20.5	[18.3 - 23.0]	13.2	[10.9 - 16.0]	13.14
'GCF_001267195.1_ASM126719v1_genomic.fna'	<i>Atopomonas sediminillitoris</i> A3.4T	12.8	[10.1 - 16.1]	20.5	[18.3 - 22.9]	13.2	[10.9 - 16.0]	10.16
'GCF_030328995.1_ASM3032899v1_genomic.fna'	<i>Thiopseudomonas denitrificans</i> DSM 28679	13.0	[10.3 - 16.3]	20.5	[18.2 - 22.9]	13.3	[11.0 - 16.1]	10.81
'GCF_030328955.1_ASM3032895v1_genomic.fna'	<i>Pseudomonas straminea</i> JCM 2783	12.7	[10.0 - 15.9]	20.5	[18.3 - 22.9]	13.1	[10.7 - 15.8]	15.62
'GCF_001267295.1_ASM126729v1_genomic.fna'	<i>Pseudomonas fluvialis</i> CCM 8778	13.0	[10.3 - 16.3]	20.4	[18.2 - 22.8]	13.4	[11.0 - 16.2]	15.21
'GCF_001267195.1_ASM126719v1_genomic.fna'	<i>Pseudomonas campi</i> DSM 110222	12.9	[10.2 - 16.2]	20.4	[18.1 - 22.8]	13.3	[10.9 - 16.1]	15.99
'GCF_030329025.1_ASM3032902v1_genomic.fna'	<i>Chryseomonas asuensis</i> JCM 13501	12.7	[10.0 - 16.0]	20.4	[18.1 - 22.8]	13.1	[10.7 - 15.8]	6.47
'GCF_001267215.1_ASM126721v1_genomic.fna'	<i>Pseudomonas fluvialis</i> ASS-1	13.1	[10.3 - 16.4]	20.4	[18.2 - 22.9]	13.4	[11.0 - 16.2]	15.15
'GCF_030328955.1_ASM3032895v1_genomic.fna'	<i>Pseudomonas indoloxydans</i> JCM 14246	12.7	[10.1 - 16.0]	20.4	[18.2 - 22.8]	13.1	[10.8 - 15.9]	14.64
'GCF_030328955.1_ASM3032895v1_genomic.fna'	<i>Pseudomonas chaetocerotis</i> LMG 31766	12.7	[10.0 - 16.0]	20.4	[18.2 - 22.8]	13.1	[10.8 - 15.8]	14.81
'GCF_001267295.1_ASM126729v1_genomic.fna'	<i>Pseudomonas oryzae</i> MAHUQ-58	12.8	[10.1 - 16.1]	20.4	[18.2 - 22.8]	13.2	[10.8 - 15.9]	19.98
'GCF_001267175.1_ASM126717v1_genomic.fna'	<i>Pseudomonas fluvialis</i> ASS-1	13.0	[10.3 - 16.3]	20.4	[18.2 - 22.9]	13.4	[11.0 - 16.2]	15.3
'GCF_001267175.1_ASM126717v1_genomic.fna'	<i>Denitrificimonas caeni</i> DSM 24390	14.0	[11.2 - 17.3]	20.4	[18.2 - 22.8]	14.2	[11.8 - 17.0]	0.9
'GCF_001267255.1_ASM126725v1_genomic.fna'	<i>Pseudomonas flexibilis</i> ATCC 29606	12.9	[10.2 - 16.2]	20.3	[18.1 - 22.7]	13.3	[10.9 - 16.0]	18.38
'GCF_001267315.1_ASM126731v1_genomic.fna'	<i>Denitrificimonas caeni</i> DSM 24390	13.9	[11.1 - 17.3]	20.3	[18.1 - 22.8]	14.2	[11.8 - 17.0]	1.06
'GCF_001267275.1_ASM126727v1_genomic.fna'	<i>Pseudomonas flexibilis</i> ATCC 29606	12.9	[10.2 - 16.2]	20.3	[18.1 - 22.7]	13.3	[10.9 - 16.0]	18.42

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'GCF_030328955.1_ASM3032895v1_genomic.fna'	<i>Halopseudomonas sabulinigri</i> JCM 14963	12.8	[10.1 - 16.1]	20.3	[18.1 - 22.8]	13.2	[10.8 - 15.9]	12.31
'GCF_030328995.1_ASM3032899v1_genomic.fna'	<i>Thiopseudomonas denitrificans</i> DSM 28679	13.0	[10.3 - 16.3]	20.3	[18.1 - 22.7]	13.3	[11.0 - 16.1]	10.82
'GCF_001267195.1_ASM126719v1_genomic.fna'	<i>Pseudomonas oryzae</i> MAHUQ-58	12.7	[10.1 - 16.0]	20.3	[18.1 - 22.7]	13.1	[10.8 - 15.9]	19.97
'GCF_001267175.1_ASM126717v1_genomic.fna'	<i>Pseudomonas fluvialis</i> CCM 8778	13.0	[10.3 - 16.3]	20.3	[18.1 - 22.8]	13.4	[11.0 - 16.2]	15.29
'GCF_001267215.1_ASM126721v1_genomic.fna'	<i>Pseudomonas fluvialis</i> CCM 8778	13.1	[10.3 - 16.4]	20.3	[18.1 - 22.8]	13.4	[11.0 - 16.2]	15.15
'GCF_001267315.1_ASM126731v1_genomic.fna'	<i>Pseudomonas oryzae</i> MAHUQ-58	12.8	[10.1 - 16.1]	20.3	[18.1 - 22.8]	13.2	[10.8 - 15.9]	20.22
'GCF_030328995.1_ASM3032899v1_genomic.fna'	<i>Pseudomonas straminea</i> JCM 2783	12.7	[10.0 - 16.0]	20.3	[18.1 - 22.7]	13.1	[10.7 - 15.8]	15.06
'GCF_001267195.1_ASM126719v1_genomic.fna'	<i>Pseudomonas turukhanskensis</i> VKM B-2935	12.8	[10.1 - 16.1]	20.3	[18.1 - 22.7]	13.2	[10.8 - 15.9]	13.13
'GCF_001267175.1_ASM126717v1_genomic.fna'	<i>Pseudomonas taeanensis</i> MS-3	12.9	[10.2 - 16.2]	20.3	[18.1 - 22.7]	13.2	[10.9 - 16.0]	13.54
'GCF_030329025.1_ASM3032902v1_genomic.fna'	<i>Pseudomonas indica</i> NBRC 103045	12.7	[10.0 - 16.0]	20.2	[18.0 - 22.6]	13.1	[10.8 - 15.9]	17.03
'GCF_001267275.1_ASM126727v1_genomic.fna'	<i>Pseudomonas turukhanskensis</i> VKM B-2935	12.8	[10.1 - 16.1]	20.2	[17.9 - 22.6]	13.2	[10.9 - 16.0]	13.2
'GCF_001267255.1_ASM126725v1_genomic.fna'	<i>Denitrificimonas caeni</i> DSM 24390	14.1	[11.3 - 17.4]	20.2	[18.0 - 22.6]	14.3	[11.9 - 17.1]	0.83
'GCF_030328995.1_ASM3032899v1_genomic.fna'	<i>Pseudomonas indoloxdans</i> JCM 14246	12.8	[10.1 - 16.1]	20.2	[18.0 - 22.6]	13.2	[10.8 - 15.9]	14.09
'GCF_001267195.1_ASM126719v1_genomic.fna'	<i>Pseudomonas fluvialis</i> ASS-1	13.0	[10.3 - 16.2]	20.2	[18.0 - 22.6]	13.3	[11.0 - 16.1]	15.2
'GCF_001267175.1_ASM126717v1_genomic.fna'	<i>Pseudomonas oryzae</i> MAHUQ-58	12.8	[10.1 - 16.1]	20.2	[18.0 - 22.6]	13.2	[10.8 - 15.9]	20.06
'GCF_001267215.1_ASM126721v1_genomic.fna'	<i>Pseudomonas oryzae</i> MAHUQ-58	12.8	[10.1 - 16.1]	20.2	[18.0 - 22.6]	13.2	[10.8 - 16.0]	19.92
'GCF_001267295.1_ASM126729v1_genomic.fna'	<i>Thiopseudomonas denitrificans</i> DSM 28679	13.0	[10.3 - 16.3]	20.2	[18.0 - 22.6]	13.3	[11.0 - 16.1]	11.53
'GCF_001267275.1_ASM126727v1_genomic.fna'	<i>Pseudomonas taeanensis</i> MS-3	12.9	[10.2 - 16.1]	20.1	[17.9 - 22.5]	13.2	[10.9 - 16.0]	13.52
'GCF_030328955.1_ASM3032895v1_genomic.fna'	<i>Pseudomonas pseudoalcaligenes</i> NBRC 14167	12.8	[10.1 - 16.1]	20.1	[17.9 - 22.5]	13.2	[10.8 - 15.9]	14.64
'GCF_001267255.1_ASM126725v1_genomic.fna'	<i>Pseudomonas fluvialis</i> ASS-1	13.0	[10.3 - 16.3]	20.1	[17.8 - 22.5]	13.4	[11.0 - 16.2]	15.23
'GCF_001267195.1_ASM126719v1_genomic.fna'	<i>Pseudomonas fluvialis</i> CCM 8778	13.0	[10.3 - 16.3]	20.1	[17.9 - 22.5]	13.3	[11.0 - 16.1]	15.19
'GCF_030328955.1_ASM3032895v1_genomic.fna'	<i>Pseudomonas indica</i> NBRC 103045	12.7	[10.0 - 16.0]	20.1	[17.9 - 22.6]	13.1	[10.8 - 15.9]	16.53
'GCF_001267175.1_ASM126717v1_genomic.fna'	<i>Thiopseudomonas denitrificans</i> DSM 28679	13.0	[10.3 - 16.3]	20.1	[17.9 - 22.5]	13.3	[11.0 - 16.1]	11.61
'GCF_001267255.1_ASM126725v1_genomic.fna'	<i>Pseudomonas taeanensis</i> MS-3	12.9	[10.2 - 16.2]	20.1	[17.9 - 22.5]	13.2	[10.9 - 16.0]	13.47

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'GCF_030329025.1_ASM3032902v1_genomic.fna'	<i>Denitrificimonas caeni</i> DSM 24390	13.9	[11.1 - 17.3]	20.1	[17.9 - 22.5]	14.1	[11.7 - 17.0]	1.16
'GCF_030328995.1_ASM3032899v1_genomic.fna'	<i>Pseudomonas indica</i> NBRC 103045	12.7	[10.0 - 16.0]	20.1	[17.8 - 22.5]	13.1	[10.8 - 15.9]	15.97
'GCF_030329025.1_ASM3032902v1_genomic.fna'	<i>Pseudomonas xionganensis</i> R-22-3 w-18T	12.9	[10.2 - 16.1]	20.1	[17.9 - 22.5]	13.2	[10.9 - 16.0]	15.88
'GCF_030328995.1_ASM3032899v1_genomic.fna'	<i>Halopseudomonas sabulinigri</i> JCM 14963	12.8	[10.1 - 16.1]	20.1	[17.9 - 22.5]	13.2	[10.9 - 16.0]	11.76
'GCF_001267215.1_ASM126721v1_genomic.fna'	<i>Thiopseudomonas denitrificans</i> DSM 28679	13.0	[10.3 - 16.3]	20.1	[17.9 - 22.5]	13.3	[11.0 - 16.1]	11.47
'GCF_001267275.1_ASM126727v1_genomic.fna'	<i>Denitrificimonas caeni</i> DSM 24390	13.9	[11.1 - 17.2]	20.1	[17.9 - 22.5]	14.1	[11.7 - 17.0]	0.88
'GCF_030329025.1_ASM3032902v1_genomic.fna'	<i>Halopseudomonas sabulinigri</i> JCM 14963	12.8	[10.1 - 16.1]	20.1	[17.9 - 22.5]	13.2	[10.9 - 16.0]	12.81
'GCF_001267295.1_ASM126729v1_genomic.fna'	<i>Denitrificimonas caeni</i> DSM 24390	13.9	[11.1 - 17.3]	20.1	[17.9 - 22.5]	14.2	[11.7 - 17.0]	0.82
'GCF_030328995.1_ASM3032899v1_genomic.fna'	<i>Pseudomonas xionganensis</i> R-22-3 w-18T	12.9	[10.2 - 16.1]	20.1	[17.8 - 22.5]	13.2	[10.9 - 16.0]	14.82
'GCF_001267195.1_ASM126719v1_genomic.fna'	<i>Thiopseudomonas denitrificans</i> DSM 28679	12.9	[10.2 - 16.2]	20.1	[17.9 - 22.5]	13.2	[10.9 - 16.0]	11.52
'GCF_001267275.1_ASM126727v1_genomic.fna'	<i>Pseudomonas fluvialis</i> ASS-1	13.0	[10.3 - 16.3]	20.0	[17.8 - 22.4]	13.4	[11.0 - 16.2]	15.27
'GCF_001267275.1_ASM126727v1_genomic.fna'	<i>Pseudomonas oryzae</i> MAHUQ-58	12.8	[10.1 - 16.1]	20.0	[17.8 - 22.4]	13.2	[10.8 - 15.9]	20.04
'GCF_030329025.1_ASM3032902v1_genomic.fna'	<i>Pseudomonas sediminis</i> PI11	12.8	[10.1 - 16.1]	20.0	[17.8 - 22.4]	13.2	[10.8 - 15.9]	15.38
'GCF_030328955.1_ASM3032895v1_genomic.fna'	<i>Thiopseudomonas denitrificans</i> DSM 28679	12.9	[10.2 - 16.2]	20.0	[17.8 - 22.4]	13.3	[10.9 - 16.1]	11.37
'GCF_030328955.1_ASM3032895v1_genomic.fna'	<i>Pseudomonas pharmacofabriceae</i> ZYSR67-Z	13.0	[10.3 - 16.3]	20.0	[17.8 - 22.4]	13.4	[11.0 - 16.1]	15.02
'GCF_001267255.1_ASM126725v1_genomic.fna'	<i>Pseudomonas fluvialis</i> CCM 8778	13.0	[10.3 - 16.3]	20.0	[17.8 - 22.4]	13.4	[11.0 - 16.2]	15.23
'GCF_001267275.1_ASM126727v1_genomic.fna'	<i>Pseudomonas fluvialis</i> CCM 8778	13.0	[10.3 - 16.3]	20.0	[17.8 - 22.4]	13.4	[11.0 - 16.2]	15.27
'GCF_030328955.1_ASM3032895v1_genomic.fna'	<i>Pseudomonas matsuisoli</i> JCM 30078	12.7	[10.0 - 16.0]	20.0	[17.8 - 22.4]	13.1	[10.8 - 15.8]	11.87
'GCF_030329025.1_ASM3032902v1_genomic.fna'	<i>Thiopseudomonas denitrificans</i> DSM 28679	12.9	[10.2 - 16.2]	20.0	[17.8 - 22.5]	13.3	[11.0 - 16.1]	11.87
'GCF_030328995.1_ASM3032899v1_genomic.fna'	<i>Pseudomonas chaetocerotis</i> LMG 31766	12.8	[10.1 - 16.1]	20.0	[17.8 - 22.4]	13.2	[10.8 - 15.9]	14.26
'GCF_030329025.1_ASM3032902v1_genomic.fna'	<i>Pseudomonas matsuisoli</i> JCM 30078	12.7	[10.0 - 16.0]	20.0	[17.8 - 22.4]	13.1	[10.8 - 15.8]	12.37
'GCF_001267255.1_ASM126725v1_genomic.fna'	<i>Thiopseudomonas denitrificans</i> DSM 28679	13.0	[10.3 - 16.3]	20.0	[17.8 - 22.4]	13.3	[11.0 - 16.1]	11.55
'GCF_001267195.1_ASM126719v1_genomic.fna'	<i>Pseudomonas taeanensis</i> MS-3	12.8	[10.1 - 16.1]	20.0	[17.8 - 22.4]	13.2	[10.9 - 16.0]	13.44

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'GCF_030329025.1_ASM3032902v1_genomic.fna'	<i>Pseudomonas chaetocerotis</i> LMG 31766	12.8	[10.1 - 16.1]	20.0	[17.8 - 22.4]	13.2	[10.8 - 15.9]	15.31
'GCF_030329025.1_ASM3032902v1_genomic.fna'	<i>Pseudomonas toyotomiensis</i> JCM 15604	12.7	[10.1 - 16.0]	19.9	[17.7 - 22.3]	13.1	[10.8 - 15.9]	15.5
'GCF_030328995.1_ASM3032899v1_genomic.fna'	<i>Pseudomonas pharmacofabriceae</i> ZYSR67-Z	13.0	[10.3 - 16.3]	19.9	[17.7 - 22.3]	13.4	[11.0 - 16.1]	14.47
'GCF_030329025.1_ASM3032902v1_genomic.fna'	<i>Pseudomonas pseudoalcaligenes</i> NBRC 14167	12.8	[10.1 - 16.1]	19.8	[17.6 - 22.2]	13.2	[10.8 - 15.9]	15.14
'GCF_030328995.1_ASM3032899v1_genomic.fna'	<i>Pseudomonas matsuisoli</i> JCM 30078	12.7	[10.0 - 16.0]	19.8	[17.6 - 22.2]	13.1	[10.8 - 15.9]	11.32
'GCF_030329025.1_ASM3032902v1_genomic.fna'	<i>Pseudomonas pharmacofabriceae</i> ZYSR67-Z	13.0	[10.3 - 16.3]	19.8	[17.6 - 22.2]	13.4	[11.0 - 16.1]	15.52
'GCF_001267275.1_ASM126727v1_genomic.fna'	<i>Thiopseudomonas denitrificans</i> DSM 28679	13.0	[10.3 - 16.3]	19.8	[17.6 - 22.2]	13.3	[11.0 - 16.1]	11.59
'GCF_001267255.1_ASM126725v1_genomic.fna'	<i>Pseudomonas oryzae</i> MAHUQ-58	12.8	[10.1 - 16.1]	19.8	[17.6 - 22.2]	13.2	[10.8 - 15.9]	20.0
'GCF_030329025.1_ASM3032902v1_genomic.fna'	<i>Pseudomonas indica</i> JCM 21544	12.8	[10.1 - 16.0]	19.8	[17.6 - 22.2]	13.1	[10.8 - 15.9]	17.01
'GCF_030328995.1_ASM3032899v1_genomic.fna'	<i>Pseudomonas toyotomiensis</i> JCM 15604	12.8	[10.1 - 16.0]	19.8	[17.6 - 22.2]	13.1	[10.8 - 15.9]	14.45
'GCF_030328955.1_ASM3032895v1_genomic.fna'	<i>Pseudomonas xionganensis</i> R-22-3 w-18T	12.8	[10.2 - 16.1]	19.8	[17.6 - 22.2]	13.2	[10.9 - 16.0]	15.38
'GCF_030328995.1_ASM3032899v1_genomic.fna'	<i>Pseudomonas sediminis</i> PI11	12.8	[10.1 - 16.1]	19.8	[17.6 - 22.2]	13.2	[10.8 - 15.9]	14.32
'GCF_030328995.1_ASM3032899v1_genomic.fna'	<i>Pseudomonas peli</i> DSM 17833	12.9	[10.2 - 16.2]	19.7	[17.5 - 22.1]	13.2	[10.9 - 16.0]	11.56
'GCF_030329025.1_ASM3032902v1_genomic.fna'	<i>Azomonas agilis</i> DSM 375	12.9	[10.2 - 16.2]	19.7	[17.5 - 22.1]	13.3	[10.9 - 16.0]	4.67
'GCF_030329025.1_ASM3032902v1_genomic.fna'	<i>Atopomonas hussainii</i> JCM 19513	12.8	[10.1 - 16.1]	19.7	[17.5 - 22.1]	13.2	[10.9 - 16.0]	11.72
'GCF_030328995.1_ASM3032899v1_genomic.fna'	<i>Pseudomonas pseudoalcaligenes</i> NBRC 14167	12.8	[10.1 - 16.1]	19.7	[17.5 - 22.1]	13.2	[10.8 - 15.9]	14.09
'GCF_030328955.1_ASM3032895v1_genomic.fna'	<i>Atopomonas hussainii</i> JCM 19513	12.8	[10.1 - 16.1]	19.7	[17.5 - 22.1]	13.2	[10.9 - 16.0]	11.22
'GCF_030329025.1_ASM3032902v1_genomic.fna'	<i>Pseudomonas peli</i> DSM 17833	12.9	[10.2 - 16.1]	19.7	[17.5 - 22.1]	13.2	[10.9 - 16.0]	12.62
'GCF_001267215.1_ASM126721v1_genomic.fna'	<i>Denitrificimonas caeni</i> DSM 24390	14.0	[11.2 - 17.3]	19.7	[17.5 - 22.1]	14.2	[11.8 - 17.0]	0.75
'GCF_030328955.1_ASM3032895v1_genomic.fna'	<i>Pseudomonas indica</i> JCM 21544	12.8	[10.1 - 16.0]	19.7	[17.5 - 22.2]	13.1	[10.8 - 15.9]	16.51
'GCF_030329025.1_ASM3032902v1_genomic.fna'	<i>Pseudomonas campi</i> DSM 110222	12.9	[10.2 - 16.2]	19.7	[17.5 - 22.1]	13.3	[10.9 - 16.0]	16.34

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'GCF_030328995.1_ASM3032899v1_genomic.fna'	<i>Pseudomonas indica</i> JCM 21544	12.8	[10.1 - 16.0]	19.6	[17.4 - 22.0]	13.1	[10.8 - 15.9]	15.95
'GCF_030329025.1_ASM3032902v1_genomic.fna'	<i>Thiopseudomonas denitrificans</i> DSM 28679	12.9	[10.2 - 16.2]	19.6	[17.4 - 22.0]	13.3	[10.9 - 16.1]	11.87
'GCF_030328995.1_ASM3032899v1_genomic.fna'	<i>Azomonas agilis</i> DSM 375	12.9	[10.2 - 16.2]	19.6	[17.4 - 22.0]	13.3	[10.9 - 16.0]	3.62
'GCF_030328955.1_ASM3032895v1_genomic.fna'	<i>Pseudomonas campii</i> DSM 110222	12.9	[10.2 - 16.2]	19.6	[17.4 - 22.0]	13.2	[10.9 - 16.0]	15.84
'GCF_030328995.1_ASM3032899v1_genomic.fna'	<i>Denitrificimonas caeni</i> DSM 24390	14.0	[11.2 - 17.3]	19.6	[17.4 - 22.0]	14.2	[11.8 - 17.0]	0.1
'GCF_030329025.1_ASM3032902v1_genomic.fna'	<i>Pseudomonas turukhanskensis</i> VKM B-2935	12.8	[10.1 - 16.0]	19.6	[17.4 - 22.0]	13.1	[10.8 - 15.9]	13.48
'GCF_030328955.1_ASM3032895v1_genomic.fna'	<i>Pseudomonas toyotomiensis</i> JCM 15604	12.7	[10.1 - 16.0]	19.5	[17.3 - 21.9]	13.1	[10.8 - 15.9]	15.0
'GCF_030328955.1_ASM3032895v1_genomic.fna'	<i>Atopomonas sediminilitoris</i> A3.4T	12.8	[10.1 - 16.1]	19.5	[17.3 - 21.9]	13.2	[10.8 - 15.9]	10.02
'GCF_001267195.1_ASM126719v1_genomic.fna'	<i>Denitrificimonas caeni</i> DSM 24390	13.8	[11.0 - 17.2]	19.5	[17.3 - 21.9]	14.1	[11.6 - 16.9]	0.8
'GCF_030328995.1_ASM3032899v1_genomic.fna'	<i>Pseudomonas abyssi</i> MT5	12.7	[10.0 - 16.0]	19.5	[17.3 - 21.9]	13.1	[10.8 - 15.8]	13.1
'GCF_030328995.1_ASM3032899v1_genomic.fna'	<i>Pseudomonas turukhanskensis</i> VKM B-2935	12.8	[10.1 - 16.0]	19.5	[17.3 - 21.9]	13.1	[10.8 - 15.9]	12.43
'GCF_030328955.1_ASM3032895v1_genomic.fna'	<i>Pseudomonas peli</i> DSM 17833	12.9	[10.2 - 16.1]	19.5	[17.3 - 21.9]	13.2	[10.9 - 16.0]	12.12
'GCF_030328995.1_ASM3032899v1_genomic.fna'	<i>Pseudomonas campii</i> DSM 110222	12.9	[10.2 - 16.2]	19.5	[17.3 - 21.9]	13.3	[10.9 - 16.0]	15.29
'GCF_030328955.1_ASM3032895v1_genomic.fna'	<i>Pseudomonas alcaligenes</i> NBRC 14159	12.8	[10.1 - 16.1]	19.5	[17.3 - 21.9]	13.2	[10.8 - 15.9]	17.16
'GCF_030328955.1_ASM3032895v1_genomic.fna'	<i>Pseudomonas taeanensis</i> MS-3	12.8	[10.1 - 16.1]	19.4	[17.3 - 21.8]	13.2	[10.8 - 15.9]	13.3
'GCF_030329025.1_ASM3032902v1_genomic.fna'	<i>Pseudomonas alcaligenes</i> NBRC 14159	12.8	[10.1 - 16.1]	19.4	[17.3 - 21.8]	13.2	[10.9 - 16.0]	17.66
'GCF_030328995.1_ASM3032899v1_genomic.fna'	<i>Pseudomonas alcaligenes</i> NBRC 14159	12.8	[10.1 - 16.1]	19.4	[17.2 - 21.8]	13.2	[10.9 - 16.0]	16.61
'GCF_030328995.1_ASM3032899v1_genomic.fna'	<i>Atopomonas hussainii</i> JCM 19513	12.9	[10.2 - 16.2]	19.4	[17.2 - 21.7]	13.2	[10.9 - 16.0]	10.66
'GCF_030329025.1_ASM3032902v1_genomic.fna'	<i>Pseudomonas abyssi</i> MT5	12.7	[10.0 - 16.0]	19.3	[17.1 - 21.7]	13.1	[10.8 - 15.8]	14.15
'GCF_030328995.1_ASM3032899v1_genomic.fna'	<i>Atopomonas sediminilitoris</i> A3.4T	12.8	[10.1 - 16.1]	19.3	[17.1 - 21.7]	13.2	[10.8 - 15.9]	9.46
'GCF_030328955.1_ASM3032895v1_genomic.fna'	<i>Pseudomonas abyssi</i> MT5	12.7	[10.0 - 16.0]	19.2	[17.0 - 21.6]	13.1	[10.7 - 15.8]	13.65

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'GCF_030329025.1_ASM3032902v1_genomic.fna'	<i>Atopomonas sediminilitoris</i> A3.4T	12.8	[10.1 - 16.1]	19.1	[16.9 - 21.5]	13.2	[10.8 - 15.9]	10.52
'GCF_030328995.1_ASM3032899v1_genomic.fna'	<i>Pseudomonas fluvialis</i> ASS-1	13.0	[10.3 - 16.3]	19.0	[16.8 - 21.3]	13.3	[11.0 - 16.1]	14.5
'GCF_030328995.1_ASM3032899v1_genomic.fna'	<i>Pseudomonas oryzae</i> MAHUQ-58	12.8	[10.1 - 16.1]	19.0	[16.8 - 21.4]	13.1	[10.8 - 15.9]	19.27
'GCF_030328955.1_ASM3032895v1_genomic.fna'	<i>Pseudomonas turukhanskensis</i> VKM B-2935	12.8	[10.1 - 16.1]	19.0	[16.8 - 21.3]	13.2	[10.8 - 15.9]	12.98
'GCF_030329025.1_ASM3032902v1_genomic.fna'	<i>Pseudomonas flexibilis</i> ATCC 29606	12.8	[10.1 - 16.1]	19.0	[16.8 - 21.4]	13.2	[10.9 - 16.0]	18.7
'GCF_030329025.1_ASM3032902v1_genomic.fna'	<i>Pseudomonas fluvialis</i> ASS-1	13.0	[10.3 - 16.3]	18.9	[16.7 - 21.3]	13.3	[11.0 - 16.1]	15.55
'GCF_030328955.1_ASM3032895v1_genomic.fna'	<i>Pseudomonas flexibilis</i> ATCC 29606	12.8	[10.1 - 16.1]	18.9	[16.7 - 21.2]	13.2	[10.9 - 16.0]	18.2
'GCF_030328995.1_ASM3032899v1_genomic.fna'	<i>Pseudomonas flexibilis</i> ATCC 29606	12.8	[10.1 - 16.1]	18.9	[16.8 - 21.3]	13.2	[10.9 - 16.0]	17.65
'GCF_030329025.1_ASM3032902v1_genomic.fna'	<i>Pseudomonas oryzae</i> MAHUQ-58	12.8	[10.1 - 16.0]	18.9	[16.8 - 21.3]	13.1	[10.8 - 15.9]	20.32
'GCF_030328995.1_ASM3032899v1_genomic.fna'	<i>Pseudomonas fluvialis</i> CCM 8778	13.0	[10.3 - 16.3]	18.9	[16.7 - 21.3]	13.3	[11.0 - 16.1]	14.49
'GCF_030328955.1_ASM3032895v1_genomic.fna'	<i>Pseudomonas oryzae</i> MAHUQ-58	12.8	[10.1 - 16.1]	18.8	[16.6 - 21.2]	13.2	[10.8 - 15.9]	19.82
'GCF_030328995.1_ASM3032899v1_genomic.fna'	<i>Pseudomonas taeanensis</i> MS-3	12.8	[10.1 - 16.1]	18.8	[16.7 - 21.2]	13.2	[10.9 - 16.0]	12.74
'GCF_030329025.1_ASM3032902v1_genomic.fna'	<i>Pseudomonas fluvialis</i> CCM 8778	13.0	[10.3 - 16.3]	18.8	[16.7 - 21.2]	13.3	[11.0 - 16.1]	15.55
'GCF_030329025.1_ASM3032902v1_genomic.fna'	<i>Pseudomonas taeanensis</i> MS-3	12.8	[10.1 - 16.1]	18.8	[16.6 - 21.2]	13.2	[10.9 - 16.0]	13.8
'GCF_030328955.1_ASM3032895v1_genomic.fna'	<i>Pseudomonas fluvialis</i> ASS-1	13.0	[10.3 - 16.3]	18.6	[16.5 - 21.0]	13.3	[11.0 - 16.1]	15.05
'GCF_030328955.1_ASM3032895v1_genomic.fna'	<i>Pseudomonas fluvialis</i> CCM 8778	13.0	[10.3 - 16.3]	18.6	[16.4 - 21.0]	13.3	[11.0 - 16.1]	15.05

Table 4: Strains in your dataset

Joint dataset of automatically determined closest type strains (if this mode was chosen), manually selected type strains (if selected accordingly) and the provided user strains, if provided (marked in **yellow**).

Strain	Authority	Other deposits	Synonyms	Base pairs	Percent G+C	No. proteins	Goldstamp	Bioproject accession	Biosample accession	Assembly accession	IMG OID
<i>Thiopseudomonas alkaliphila</i> B4199	(Drobish et al. 2016) Rudra and Gupta 2021	CCUG 67636; DSM 100830	<i>Oblitimonas alkaliphila</i> ; <i>Thiopseudomonas alkaliphila</i>	2494 031	47.4	2365	Gp0132979	PRJNA224116	SAMN03946311	GCF_001267175	
<i>Thiopseudomonas denitrificans</i> DSM 28679	Tan et al. 2015	KCTC 42076; CCTCC M 2013362; X2	<i>Thiopseudomonas denitrificans</i>	2840 727	59.0	2579		PRJNA299732	SAMN04214881	GCA_002866065	
<i>Pseudomonas fluvialis</i> ASS-1	Sudan et al. 2018	ASS-1; KCTC 52437; CCM 8778	<i>Pseudomonas fluvialis</i>	3280 972	62.7	3045	Gp0323573	PRJNA393076	SAMN07314873	GCA_002234375	
<i>Pseudomonas abyssi</i> MT5	Wei et al. 2018	MCCC 1K03351; KCTC 62295	<i>Neopseudomonas abyssi</i> ; <i>Pseudomonas abyssi</i>	4312 941	61.3	3955		PRJNA406957	SAMN07634961	GCA_002307495	
<i>Acinetobacter seohaensis</i> DSM 16313	Yoon et al. 2007	KCTC 12260; SW-100	<i>Acinetobacter seohaensis</i>	2948 101	41.3	2766		PRJDB11573	SAMD00317521	GCA_018403785	
<i>Citrobacter tructae</i> SNU WT2	Jung et al. 2021	KCTC 72517; JCM 33612	<i>Citrobacter tructae</i>	4946 572	52.0	4556		PRJNA224116	SAMN11282944	GCF_004684345	
<i>Pseudomonas xionganensis</i> R-22-3 w-18T	Zhao et al. 2020	CGMCC 1.17250; KCTC 72658	<i>Pseudomonas xionganensis</i>	3951 615	63.0	3621		PRJNA589163	SAMN13268013	GCA_009763245	
<i>Pseudomonas oryzagri</i> MAHUQ-58	Huq et al. 2022	CGMCC 1.18518; KACC 22005	<i>Pseudomonas oryzagri</i>	4533 148	67.4	4064		PRJNA777654	SAMN22870558	GCA_020831405	

Strain	Authority	Other deposits	Synonyms	Base pairs	Percent G+C	No. proteins	Goldstamp	Bioproject accession	Biosample accession	Assembly accession	IMG OID
<i>Pseudomonas straminea</i> JCM 2783	Iizuka and Komagata 1963 emend. Uchino et al. 2000	CIP 106745; ATCC 33636; CCUG 12539; DSM 17727; NRIC 164; IFO 16665; NBRC 16665; IAM 1598	<i>Pseudomonas straminea</i>	4992 003	63.2	4570	Gp0127214	PRJEB17217	SAMN05216372	GCA_900112645	
<i>Pseudomonas toyotomiensis</i> JCM 15604	Hirota et al. 2011	NCIMB 14511; DSM 26169; HT-3	<i>Pseudomonas toyotomiensis</i>	5489 804	62.6	5160	Gp0127184	PRJEB17410	SAMN05216177	GCA_900115695	
<i>Psychrobacter fulvigenes</i> KC40T	Romanenko et al. 2009	NRIC 746; JCM 15525; KMM 3954	<i>Psychrobacter fulvigenes</i>	3465 773	44.1	2982		PRJEB40380	SAMEA7339726	GCF_904846155	
<i>Pseudomonas flexibilis</i> ATCC 29606	(Hespell 1977) Shin et al. 2016	LMG 29034	<i>Pseudomonas flexibilis</i> ; <i>Serpens flexibilis</i>	3757 903	65.8	3448	Gp0127303	PRJNA224116	SAMN05421672	GCF_900155995	2681812811
<i>Pseudomonas tensinigenes</i> ZA 5.3	Girard et al. 2022	CFBP 8882; LMG 32032	<i>Pseudomonas tensinigenes</i>	6621 778	59.2	5788		PRJNA639797	SAMN15248349	GCA_014268445	
<i>Pseudomonas shirazensis</i> SWRI56	Girard et al. 2022	CFBP 8846; LMG 32037	<i>Pseudomonas shirazensis</i>	4747 800	61.9	4198		PRJNA639797	SAMN15248332	GCA_014268785	
<i>Pseudomonas turukhanskensis</i> VKM B-2935	Korshunova et al. 2016	CECT 9091; IB1.1	<i>Pseudomonas turukhanskensis</i>	5863 550	60.6	5326		PRJDB10669	SAMD00253133	GCA_027922365	
<i>Pseudomonas indoloxydans</i> JCM 14246	Manickam et al. 2008	IPL-1; MTCC 8062	<i>Pseudomonas indoloxydans</i>	5198 577	62.2	4666	Gp0323509	PRJNA449191	SAMN08891239	GCA_003052605	
<i>Denitrificimonas caeni</i> DSM 24390	(Xiao et al. 2009) Saati-Santamaria et al. 2021	KCTC 22292; CECT 7778; CCTCC AB 208156; strain HY-14	<i>Denitrificimonas caeni</i> ; <i>Pseudomonas caeni</i> ; <i>Thiopseudomonas caeni</i>	3025 373	48.3	2803	Gp0013191	PRJNA188884	SAMN02440589	GCA_000421765	2524614874

Strain	Authority	Other deposits	Synonyms	Base pairs	Percent G+C	No. proteins	Goldstamp	Bioproject accession	Biosample accession	Assembly accession	IMG OID
<i>Pseudomonas pharmacofabrice</i> ZYSR67-Z	Yu et al. 2019	CGMCC 1.15498; JCM 31306	<i>Pseudomonas pharmacofabrice</i>	3438 518	62.6	3212	Gp0369617	PRJNA421062	SAMN08131258	GCA_002835605	
<i>Pseudomonas yangonensis</i> JCM 33396	Tohya et al. 2020	LMG 31602; MY50	<i>Pseudomonas yangonensis</i>	5040 544	62.9	4626		PRJDB8321	SAMD00171901	GCA_009932725	
<i>Acinetobacter townneri</i> DSM 14962	Carr et al. 2003	AB1110; CIP 107472	<i>Acinetobacter townneri</i>	2854 510	41.2	2749	Gp0013868	PRJNA221010	SAMN02743902	GCA_000688495	2556921621
<i>Thiopseudomonas denitrificans</i> DSM 28679	Tan et al. 2015	KCTC 42076; CCTCC M 2013362; X2	<i>Thiopseudomonas denitrificans</i>	2831 568	59.0	2581	Gp0290550	PRJNA463350	SAMN09074682	GCA_004363035	2770939502
<i>Nitrosomonas stercoris</i> ATCC BAA-2718	Nakagawa and Takahashi 2017	NBRC 110753; KYUHI-S	<i>Nitrosomonas stercoris</i>	2382 370	44.8	2274		PRJDB8366	SAMD00173276	GCA_006742785	
<i>Azomonas agilis</i> DSM 375	(Beijerinck 1901) Winogradsky 1938	NCIMB 11693; ATCC 7494; JCM 21502; NBRC 102607; NCIB 11693	<i>Azomonas agilis</i> ; <i>Azotobacter agilis</i>	3275 197	51.8	3038	Gp0103623	PRJNA262246	SAMN05660238	GCA_007830255	2596583523
<i>Shigella flexneri</i> ATCC 29903	Castellani and Chalmers 1919	CIP 82.48; DSM 4782	<i>Shigella flexneri</i>	4938 295	50.7	5112	Gp0307840	PRJNA218110	SAMN08330274	GCA_002950215	

Strain	Authority	Other deposits	Synonyms	Base pairs	Percent G+C	No. proteins	Goldstamp	Bioproject accession	Biosample accession	Assembly accession	IMG OID
<i>Pseudomonas pseudoalcaligenes</i> NBRC 14167	Stanier 1966	CFBP 2435; VTT E-012029; LMG 1225; CIP 66.14; NCIMB 9946; NCCB 76045; ATCC 17440; CCUG 51525; CECT 318; DSM 50188; JCM 5968; IFO 14167; IFO (now NBRC) 14167; NCTC 10860; NCAIM B.02048; NCIB 9946	<i>Pseudomonas pseudoalcaligenes</i> ; <i>Pseudomonas pseudoalcaligenes</i> subsp. <i>pseudoalcaligenes</i>	4702414	62.2	4507	Gp0023768	PRJDB224	SAMD00046936	GCA_002091775	
<i>Acinetobacter defluvii</i> WCHA30	Hu et al. 2017	KCTC 52503; CCTCC AB 2016203; GDMCC 1.1101	<i>Acinetobacter defluvii</i>	3737173	38.0	3562	Gp0189167	PRJNA224116	SAMN05356262	GCF_001704615	
<i>Acinetobacter baumannii</i> ATCC 19606	Bouvet and Grimont 1986	LMG 1041; CIP 70.34; NCCB 85021; CCUG 19096; DSM 30007; DSM 6974; JCM 6841; NCTC 12156	<i>Acinetobacter baumannii</i>	4025332	39.1	3766	Gp0032321	PRJNA183249	SAMN01828140	GCA_000369385	2534682196

Strain	Authority	Other deposits	Synonyms	Base pairs	Percent G+C	No. proteins	Goldstamp	Bioproject accession	Biosample accession	Assembly accession	IMG OID
<i>Pseudomonas alcaligenes</i> NBRC 14159	Monias 1928 emend. Ling et al. 2023	CFBP 2437; LMG 1224; CIP 101034; NCCB 76044; ATCC 14909; CCUG 1425 A; CCUG 1425; DSM 50342; JCM 5967; NBIMCC 2453; IFO 14159; IFO (now NBRC) 14159; NCTC 10367; VKM B-2171; IAM 12411	<i>Pseudomonas alcaligenes</i>	4823 390	64.8	4531	Gp0024155	PRJDB200	SAMD00041817	GCA_000467105	
<i>Pseudomonas taeanensis</i> MS-3	Lee et al. 2010	KCTC 22612; DSM 25633; JCM 16046; KACC 14032; NBRL 105641	<i>Pseudomonas taeanensis</i>	5460 144	60.9	4594	Gp0049072	PRJNA217843	SAMN02470138	GCA_000498575	
<i>Pseudomonas matsuisoli</i> JCM 30078	Lin et al. 2015	BCRC 80771; CC-MHH0089	<i>Pseudomonas matsuisoli</i>	4603 598	59.5	4102		PRJDB10510	SAMD00245291	GCA_014647635	
<i>Thauera butanivorans</i> NBRC 103042	(ex Takahashi et al. 1980) Dubbels et al. 2009	ATCC 43655; DSM 2080; JCM 20651; Bu-B1211; IAM 12574	<i>Pseudomonas butanovora</i> ; <i>Thauera butanivorans</i>	4806 543	66.1	4511	Gp0023646	PRJDB364	SAMD00046735	GCA_001591165	
<i>Chryseomonas asuensis</i> JCM 13501	(Reddy and Garcia-Pichel 2015) Saati-Santamaría et al. 2021	LMG 28687; KCTC 32484; ATCC BAA-1264; DSM 17866; CP 155-2	<i>Chryseomonas asuensis</i> ; <i>Pseudomonas asuensis</i>	5328 059	53.6	4950		PRJDB10510	SAMD00245237	GCA_014646755	

Strain	Authority	Other deposits	Synonyms	Base pairs	Percent G+C	No. proteins	Goldstamp	Bioproject accession	Biosample accession	Assembly accession	IMG OID
<i>Pseudomonas fluvialis</i> CCM 8778	Sudan et al. 2018	ASS-1; KCTC 52437; CCM 8778	<i>Pseudomonas fluvialis</i>	3304 463	62.7	3092		PRJDB10511	SAMD00244871	GCA_014635625	
<i>Pseudomonas peli</i> DSM 17833	Vanparys et al. 2006	LMG 23201; R-20805	<i>Pseudomonas peli</i>	4486 965	59.7	4256	Gp0127168	PRJEB15912	SAMN05216370	GCA_900099645	
<i>Halopseudomonas sabulinigri</i> JCM 14963	(Kim et al. 2009) Rudra and Gupta 2021	KCTC 22137; DSM 23971; J64	<i>Halopseudomonas sabulinigri</i> ; <i>Neopseudomonas sabulinigri</i> ; <i>Pseudomonas sabulinigri</i>	4030 103	59.9	3624	Gp0127171	PRJEB16439	SAMN05216271	GCA_900105255	
<i>Enterobacter cloacae</i> ATCC 13047	(Jordan 1890) Hormaeche and Edwards 1960	LMG 2783; CIP 60.85; CCUG 28448; CCUG 29301; CCUG 6323; DSM 30054; JCM 1232; NBIMCC 8570; IFO 13535; NBRC 13535; NCTC 10005; HAMBI 1295; HAMBI 96	<i>Bacillus cloacae</i> ; <i>Bacterium cloacae</i> ; <i>Cloaca cloacae</i> ; <i>Enterobacter cloacae</i> ; <i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	5598 795	54.6	5518	Gp0006802	PRJNA45793	SAMN02603901	GCA_000025565	646564529
<i>Ignatzschineria cameli</i> UAE-HKU57	Tsang et al. 2018	NBRC 113042; CCOS 1165	<i>Ignatzschineria cameli</i>	2485 449	41.7	2034	Gp0377909	PRJNA451073	SAMN08954446	GCA_003121895	
<i>Acinetobacter rongchengensis</i> WCHAc060115 T	Qin et al. 2021	JCM 33512; GDMCC 1.1625	<i>Acinetobacter rongchengensis</i>	4067 804	37.6	3752		PRJNA224116	SAMN09842375	GCF_003611475	
<i>Pseudomonas indica</i> JCM 21544	Pandey et al. 2002	DSM 14015; JCM 21544; NBRC 103045; IMT37; MTCC 3713	<i>Pseudomonas indica</i>	5784 665	64.1	5188	Gp0127202	PRJEB16003	SAMN05216186	GCA_900100285	

Strain	Authority	Other deposits	Synonyms	Base pairs	Percent G+C	No. proteins	Goldstamp	Bioproject accession	Biosample accession	Assembly accession	IMG OID
<i>Atopomonas sediminilitoris</i> A3.4T	Li et al. 2023	MCCC 1K07166; LMG 32563	<i>Atopomonas sediminilitoris</i>	3546 461	57.6	3215		PRJNA224116	SAMN26186988	GCF_022601735	
<i>Pseudomonas chaetocerotis</i> LMG 31766	Girard et al. 2023	536; DSM 111343	<i>Pseudomonas chaetocerotis</i>	5372 374	62.4	4980		PRJNA648074	SAMN15618151	GCA_015712105	
<i>Atopomonas hussainii</i> JCM 19513	(Hameed et al. 2014) Rudra and Gupta 2021	BCRC 80696; CC-AMH-11	<i>Atopomonas hussainii</i> ; <i>Parapseudomonas hussainii</i> ; <i>Pseudomonas hussainii</i>	3680 748	58.8	3429	Gp0127201	PRJEB16845	SAMN05216214	GCA_900109735	
<i>Pseudomonas campi</i> DSM 110222	Timsy et al. 2021	31521; LMG 31521; S1-A32-2	<i>Pseudomonas campi</i>	4436 925	63.5	3980		PRJNA631893	SAMN14896266	GCA_013200955	
<i>Pseudomonas indica</i> NBRC 103045	Pandey et al. 2002	DSM 14015; JCM 21544; NBRC 103045; IMT37; MTCC 3713	<i>Pseudomonas indica</i>	5778 617	64.1	5141	Gp0024159	PRJDB211	SAMD00046928	GCA_002091635	
<i>Pseudomonas sediminis</i> PI11	Behera et al. 2018	KCTC 42576; DSM 100245	<i>Pseudomonas sediminis</i>	4878 472	62.5	4443	Gp0365654	PRJNA389586	SAMN07203179	GCA_002741105	
GCF_001267175.1_ASM126717v1_genomic.fna				2494 031	47.4	2366					
GCF_001267195.1_ASM126719v1_genomic.fna				2272 143	47.5	2141					
GCF_001267215.1_ASM126721v1_genomic.fna				2312 033	47.5	2158					
GCF_001267255.1_ASM126725v1_genomic.fna				2294 397	47.4	2139					
GCF_001267275.1_ASM126727v1_genomic.fna				2391 994	47.4	2218					

Strain	Authority	Other deposits	Synonyms	Base pairs	Percent G+C	No. proteins	Goldstamp	Bioproject accession	Biosample accession	Assembly accession	IMG OID
GCF_001267295 .1_ASM126729v 1_genomic.fna				2377 259	47.4	2235					
GCF_001267315 .1_ASM126731v 1_genomic.fna				2397 029	47.2	2269					
GCF_030328955 .1_ASM3032895 v1_genomic.fna				2572 910	47.6	2431					
GCF_030328995 .1_ASM3032899 v1_genomic.fna				2475 608	48.2	2344					
GCF_030329025 .1_ASM3032902 v1_genomic.fna				2440 383	47.1	2368					

Methods, Results and References

The genome sequence data were uploaded to the Type (Strain) Genome Server (TYGS), a free bioinformatics platform available under <https://tygs.dsmz.de>, for a whole genome-based taxonomic analysis [1]. The analysis also made use of recently introduced methodological updates and features [2]. Information on nomenclature, synonymy and associated taxonomic literature was provided by TYGS's sister database, the List of Prokaryotic names with Standing in Nomenclature (LPSN, available at <https://lpsn.dsmz.de>) [2]. The results were provided by the TYGS on 2023-07-10. The TYGS analysis was subdivided into the following steps:

Determination of closely related type strains

Determination of closest type strain genomes was done in two complementary ways: First, all user genomes were compared against all type strain genomes available in the TYGS database via the MASH algorithm, a fast approximation of intergenomic relatedness [3], and, the ten type strains with the smallest MASH distances chosen per user genome. Second, an additional set of ten closely related type strains was determined via the 16S rDNA gene sequences. These were extracted from the user genomes using RNAmmer [4] and each sequence was subsequently BLASTed [5] against the 16S rDNA gene sequence of each of the currently 19201 type strains available in the TYGS database. This was used as a proxy to find the best 50 matching type strains (according to the bitscore) for each user genome and to subsequently calculate precise distances using the Genome BLAST Distance Phylogeny approach (GBDP) under the algorithm 'coverage' and distance formula d_5 [6]. These distances were finally used to determine the 10 closest type strain genomes for each of the user genomes.

Pairwise comparison of genome sequences

For the phylogenomic inference, all pairwise comparisons among the set of genomes were conducted using GBDP and accurate intergenomic distances inferred under the algorithm 'trimming' and distance formula d_5 [6]. 100 distance replicates were calculated each. Digital DDH values and confidence intervals were calculated using the recommended settings of the GGDC 3.0 [2,6].

Phylogenetic inference

The resulting intergenomic distances were used to infer a balanced minimum evolution tree with branch support via FASTME 2.1.6.1 including SPR postprocessing [7]. Branch support was inferred from 100 pseudo-bootstrap replicates each. The trees were rooted at the midpoint [8] and visualized with PhyD3 [9].

Type-based species and subspecies clustering

The type-based species clustering using a 70% dDDH radius around each of the 45 type strains was done as previously described [1]. The resulting groups are shown in Table 1 and 4. Subspecies clustering was done using a 79% dDDH threshold as previously introduced [10].

Results

Type-based species and subspecies clustering

The resulting species and subspecies clusters are listed in Table 4, whereas the taxonomic identification of the query strains is found in Table 1. Briefly, the clustering yielded 41 species clusters and the provided query strains were assigned to 2 of these. Moreover, user strains were located in 3 of 43 subspecies clusters.

Figure caption SSU tree

Figure 1. Tree inferred with FastME 2.1.6.1 [7] from GBDP distances calculated from 16S rDNA gene sequences. The branch lengths are scaled in terms of GBDP distance formula d_5 . The numbers above branches are GBDP pseudo-bootstrap support values > 60 % from 100 replications, with an average branch support of 66.4 %. The tree was rooted at the midpoint [8].

Figure caption genome tree

Figure 2. Tree inferred with FastME 2.1.6.1 [7] from GBDP distances calculated from genome sequences. The branch lengths are scaled in terms of GBDP distance formula d_5 . The numbers above branches are GBDP pseudo-bootstrap support values > 60 % from 100 replications, with an average branch support of 28.0 %. The tree was rooted at the midpoint [8].

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